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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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PCT Pub. Date: **Nov. 23, 2000**

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(51) **Int. Cl.**  
**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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(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**



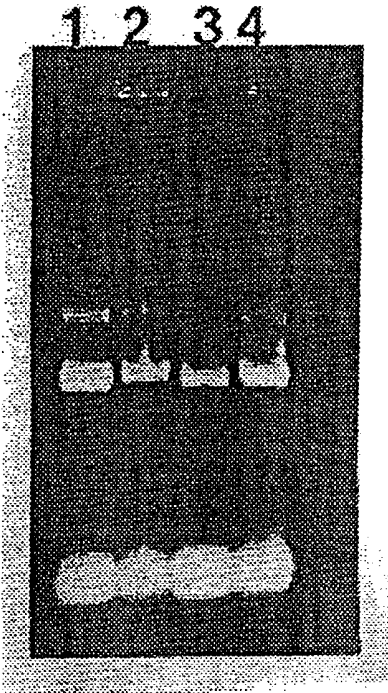


FIG. 2

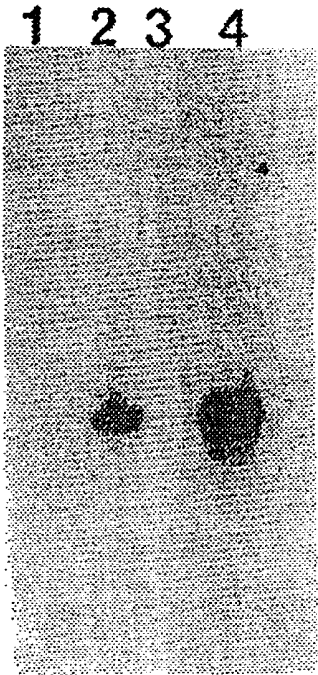


FIG. 3

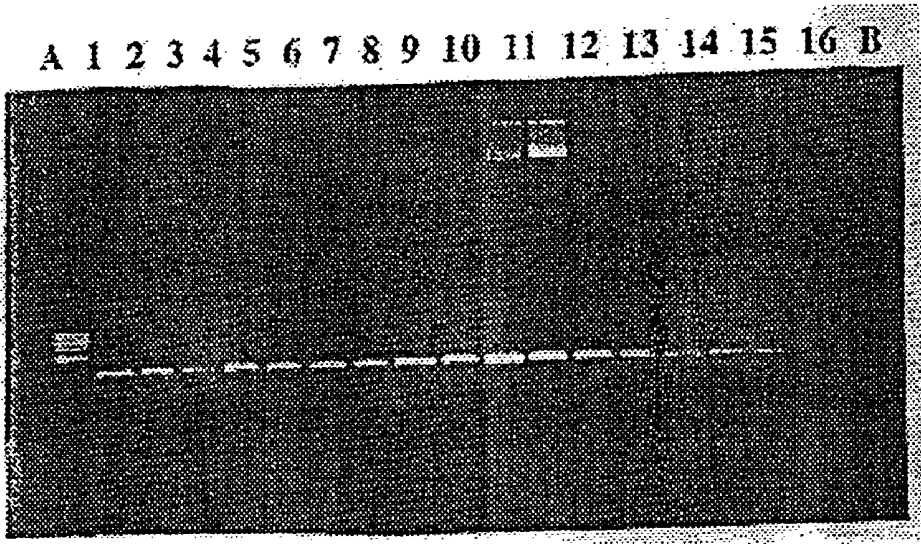


FIG. 4



L8tm  
 L.m. TCTGGGGTAAATAGAGAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT  
 L.i. TCTGAGGTTAAATAGAGAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT  
 L.mu. TCTGAGGTTAAATAGAGAGAGCTTAATGAGACTAGCTGAATGGAAGCCCTGT  
 L.w. TCTGAGGTTAGTTGGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT  
 L.g. TCTGGGGCAACGAGAGAGCAATAATCAGACTAGCTAGATAGAGCCCTGA  
 \* \* \* \* \*

L.m. TACCGGGCCGATGTTTATGCGGAAATGCTAATACGGTGACTACGCTCGTAG  
 L.i. TACCGGGCTGATGTTTATGCGGAAATGCTAATACGGTGACTACGCTCGTAG  
 L.mu. TACCGGGCTGATGTTTATGCGGAAATGCTAATACGGTGACTACGCTCGTAG  
 L.w. TACCGGGCCGATGTTTATGCGGAAATGCTAATACGGTGACTACGCTCGTAG  
 L.g. CGCCGGCAGACATCTATGCGGAAATCCAAATACGGCAACTACGCTCGTAG  
 \* \* \* \* \*

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

FIG. 5B

ACAGGGATGATCGAGCTTGAGCTGCGAGCCGAGAGG--CGATCTCGTAA  
 ACAGGGATAGTTCGAGCTTGAGTTCGAGTCGGGGGATCGTCCTCGTTA  
 \*\*\*\*\* \* \*\*\*\*\* \*\* \* \*\* \* \*\* \* \*\* \* \*\* \* \*\* \*

B. s.  
 L. m.

ACACGCACCTAAATATACTGGCAAACTAACAGTTTAAACCAAAACGTA  
 TCA-ACG-TCAAAGCCAA-TAATA--ACTGGCAAGAAAACAAACCTA  
 \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \*

B. s.  
 L. m.

GCATTAGCTGCCCTAATAAGC-GCAGCGAGACT--CTTCCTGACATTGCC  
 GCTTTCGCTGCCCTAATAAGCAGTAGCATAGCTGATCCTCCGTCATCGCC  
 \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \*

B. s.  
 L. m.

TATGTGT--CTGTGAAGAGCACA-TCCAAGTAGGCTACGCTTGC--GTTC  
 CATGTGCTACGGTAAGGGTCTCACTCTAAGTGGGCTACACTAGTTAATCT  
 \*\*\*\*\* \* \*\* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \*

B. s.  
 L. m.

CCGTC TGAGAACGTA-AGAAGAGATGAA-CAGACTAGCTCTCGGAAGGCC  
 CCGTCTGGGGTTAAATAGAAAGAGCTTAATCAGACTAGCTGAATGGAAGCC  
 \*\*\*\*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \*

B. s.  
 L. m.

CGCCCGCAGGCAAGAAGATGAGTGAACCATAAATATGCAGGCTACGCTC  
 TGTACCGGGCCGATGTTTATGCGAAAT-GCTAATACGGTGACTACGCTC  
 \* \* \* \* \* \* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \* \* \* \* \* \*\* \*

B. s.  
 L. m.

G-AGACGCTTAAGTTAATCGATGTTTCTGG  
 GTAGATATTTAAGT--GCCGATATTTCTGG  
 \* \* \* \* \* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\*

B. s.  
 L. m.

FIG. 6

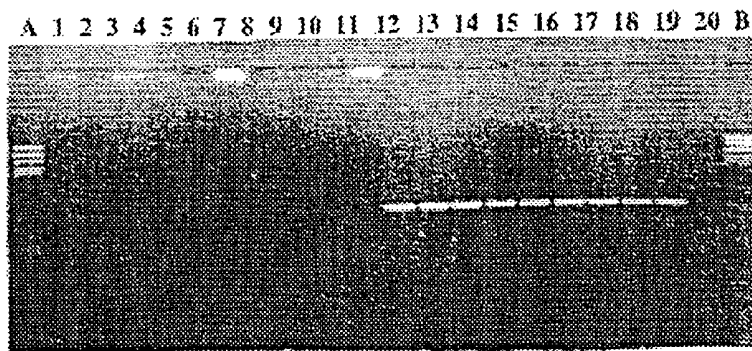


FIG. 7

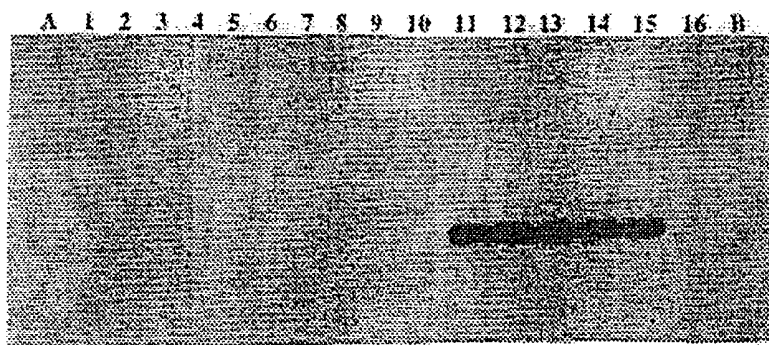


FIG. 8

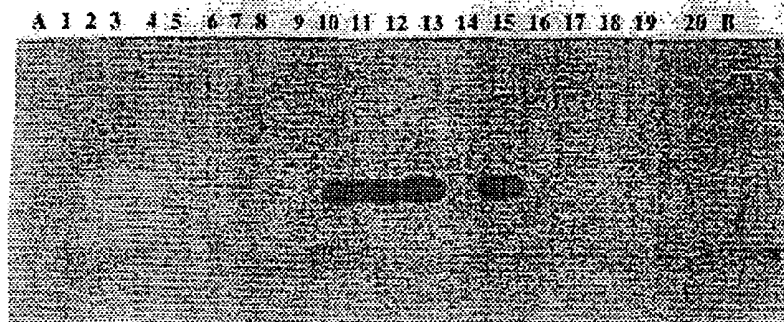


FIG. 9

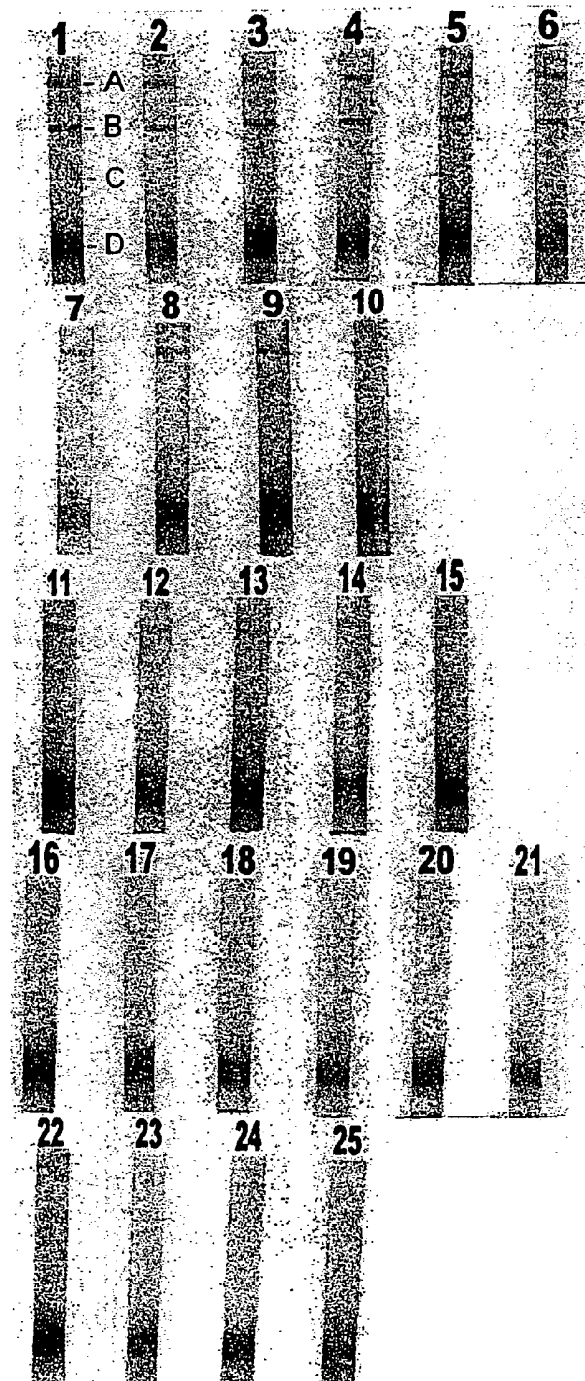


FIG. 10

Ct1 GGGCGTAAAGGTTTCGACTTAGAAATGAAGCGTTAAATTGCATGCCGGAG  
 Ct2 GGGGGTAAAGGTTTCGACTTAGAAATGAAGCGTTAAATTGCATGCCGGAG  
 \*\*\*\*\*

Ct1 GGCGTTGGCTGGCCCTCCATAAAAGCCGACAAACAATAAATGCCGAAACCT  
 Ct2 GGCGTTGGCTGGCCCTCCATAAAAGCCGACAAACAATAAATGCCGAAACCT  
 \*\*\*\*\*

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

Ct1 AGCTGCTTAATTAGCAAAGTTGTTACCTAAATACGGGTGACCCGGTGTTTC  
 Ct2 TGCTGCTTAATTAGCAAAGTTGTTACCTAAAGTACTGGTAACCCGGTGTTTC  
 \*\*\*\*\* \*\* \*\*

Ct1 GCGAGCTCCACCAGAGGTTTTCGAAACACCCGTCATGTATCTGGTTAGAAC  
 Ct2 GCGAGCTCCACCAGAGGTTTTCGAAACGCGCTCATTTATCTGGTTAGAAT  
 \*\*\*\*\* \*\* \*\*

FIG. 11A

```

Ct 1 TTAGGTCCTTTAATTCTCGAGGAAATGAGTTTGAATTTAATGAGAGTCC
Ct 2 TAGGGCCTTTAACTCTCAAGGAACTAATTGAAATTTAATGAGAGTCC
* * * * *
Ct 1 TTAGTCTCTATAGGGGTTTCTAGCTGAGGAGACATAACGTATAGTAC-CT
Ct 2 TTGGTCTCTATAGAGGTTTCTAGCTGAGGAGATATAACGTAAAATATTCT
* * * * *
Ct 1 AGGAACTAAGCATGTAGAGGTTAGCCGGGGAGTTTACTAAGGACGAGAGTT
Ct 2 AGAAACTAAGCATGTAGAGGTTAGCCGGGGAGTTTACTAAGGACGAGAGTT
* * * * *
Ct 1 CGACTCTCTCCACCTCCACCA
Ct 2 CGAATCTCTCCACCTCCACCA
* * * * *

```

FIG. 11B

AGATTTCTTGTGCGCAGATAGCATGCCAAGCGCTGCTTGTAAAACAGCA  
 AGATTTCTTGTGCGCACAGATAGCATGCCAAGCGCTGCTTGTAAAACAGCA  
 \*\*\*\*\*

HP1  
 HP2

ACAAAAATAACTGTAACAACACAGATTACGCTCCAGCTTACGCTAAAGC  
 ACAAAAATAACTGTAACAACACAGATTACGCTCCAGCTTACGCTAAAGC  
 \*\*\*\*\*

HP1  
 HP2

TGCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAAATTTCTAGCGT  
 TGCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAAATTTCTAGCGT  
 \*\*\*\*\*

HP1  
 HP2

TTTAATCGCTCCATAACCTTAAGCTAGACGGCTTTAAAGGTGGTTCGCC  
 TTTAATCGCTCCATAACCTTAAGCTAGACGGCTTTAAAGGTGGTTCGCC  
 \*\*\*\*\*

HP1  
 HP2

TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTTAAGGTTTTAGAAA  
 TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTCAAGGTTTTAGAAA  
 \*\*\*\*\*

HP1  
 HP2

GTTGGACCAGAGCTAGTTTAAAGGCTAAAACCTAACCAATTTTCTAAGC  
 GTTGGACCAGAGCTAGTTTAAAGGCTAAAACCTAACCAATTTTCTAAGC  
 \*\*\*\*\*

HP1  
 HP2

ATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTGGACTGGGG  
 ATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTGGACTGGGG  
 \*\*\*\*\*

HP1  
 HP2

FIG. 12

ACATAATGCTGATAGACAAACAGTAGCATTTGGGGTATGCCCCCTTACAGCG  
 ACATAATGCTGATAGACAAACAGTAGCATTTGGGGTATGCCCCCTTACAGCG  
 \*\*\*\*\*

Mc1  
 Mc2

CTAGGTTCAATAAACCGACAAGAAAAATAACGAAAGTGTGGTAGAACCAAA  
 CTAGGTTCAATAAACCGACAAGAAAAATAACGAAAGTGTGGTAGATCCAAA  
 \*\*\*\*\*

Mc1  
 Mc2

TTTGATCATTAACCAACAAGCAAGTGTAACTTTTGCTTTTGCATAAGTAG  
 TTTGATCATTAACCAACAAGCAAGTGTAACTTTTGCTTTTGCATAAGTAG  
 \*\*\*\*\*

Mc1  
 Mc2

ATACTAAAGCTACAGCTGGTGAATAGTCATAGTTTGGTAGCTGTCAATAGT  
 ATACTAAAGCTACAGCTGGTGAATAGTCATAGTTTGGTAGCTGTCAATAGT  
 \*\*\*\*\*

Mc1  
 Mc2

TTATGACTCGAGGTAAAATCGTTCAATTTAACCTTTAAAAATAGAACTTG  
 TTATGACTCGAGGTAAAATCGTTCAATTTAACCTTTAAAAATAGAACTTG  
 \*\*\*\*\*

Mc1  
 Mc2

TTGTTTCCCATGATTTGTTTGTGATCAATTTGGAACAAGACAAAAATCCAC  
 TTGTTTCCCATGATTTGTTTGTGATCAATTTGGAACAAGACAAAAATCCAC  
 \*\*\*\*\*

Mc1  
 Mc2

AAAACTAAAATGTAGAAGCTGTTTGTGTCTCTTTATGGAAACGGGTTTC  
 AAAACTAAAATGTAGAAGCTGTTTGTGTCTCTTTATGGAAACGGGTTTC  
 \*\*\*\*\*

Mc1  
 Mc2

FIG. 13

GGGGTTGCGAAGCAGATGCGGGCATAACGGGGTCTCAGATTCCCCGTAAA  
GGGGTTGCGAAGCAGATGCGGGCATAACGGGGTCTCAGATTCCCCGTAAA  
\*\*\*\*\*

Ng1  
Ng2

ACACTGAATTCAAATAGTCGCAACGACGAAACTACGCTTTAGCCGCTT  
ACACTGAATTCAAATAGTCGCAACGACGAAACTACGCTTTAGCCGCTT  
\*\*\*\*\*

Ng1  
Ng2

AAGGCTAGCCGTTGCAGCAGTCGGTCAA TGGGCTGTGTGGCGAAAGCCAC  
AAGGCTAGCCGTTGCAGCAGTCGGTCAA TGGGCTGTGTGGCGAAAGCCAC  
\*\*\*\*\*

Ng1  
Ng2

CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGGTACTTGGCAGGA  
CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGGTACTTGGCAGGA  
\*\*\*\*\*

Ng1  
Ng2

AATAAGACTTAAGGTAAC TGGTTTCCAAAAGGCCCTGTTGGTCGGCATGAT  
AATAAGACTTAAGGTAAC TGGTTTCCAAAAGGCCCTGTTGGTCGGCATGAT  
\*\*\*\*\*

Ng1  
Ng2

GGAAATAAGATTTTCAAATAGACACAACTAAGTATGTAGAACGCTTTGTA  
GGAAATAAGATTTTCAAATAGACACAACTAAGTATGTAGAACGCTTTGTA  
\*\*\*\*\*

Ng1  
Ng2

GAGGACTTTCGGACGGGGG  
GAGGACTTTCGGACGGGGG  
\*\*\*\*\*

Ng1  
Ng2

FIG. 14

CAAAGAAAACAACCTAGCTTTCGCTGCCCTAATAAGCAGTAGCATAGC  
 CAAAGAAAACAACCTAGCTTTCGCTGCCCTAATAAGCAGTAGCATAGC  
 \*\*\*\*\*

L.m1  
 L.m2

TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT  
 TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT  
 \*\*\*\*\*

L.m1  
 L.m2

GGGTACACTAGTTAATCTCCGTCGCGGTTAATAAGAGAGCTTAATCA  
 GGGTACACTAGTTAATCTCCGTCGCGGTTAATAAGAGAGCTTAATCA  
 \*\*\*\*\*

L.m1  
 L.m2

GACTAGCTGAATGGAAGCCTGTACC GGCCGATGTTATGCCGAAATGCT  
 GACTAGCTGAATGGAAGCCTGTACC GGCCGATGTTATGCCGAAATGCT  
 \*\*\*\*\*

L.m1  
 L.m2

AATACGGTGACTACGCTCGTAGATATTT  
 AATACGGTGACTACGCTCGTAGATATTT  
 \*\*\*\*\*

L.m1  
 L.m2

FIG. 15

L.m1 CAAAGAAAACA AAAACCTAGCTTTCGGTGCCTAATAAGCAGTAGCATAGC  
 L.m2 CAAAGAAAACA AAAACCTAGCTTTCGGTGCCTAATAAGCAGTAGCATAGC  
 L.i CAAAGAAAACA AAAACCTAGCTTTCGGTGCCTAATAAGCAGTAGCATAGC  
 \*\*\*\*\*

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

L.m1 GGGCTACACTAGTTAATCTCCGTCGCGGTTAAATAGAAGAGCTTAATCA  
 L.m2 GGGCTACACTAGTTAATCTCCGTCGCGGTTAAATAGAAGAGCTTAATCA  
 L.i GGGCTACACTAGTTAATCTCCGTCGCGGTTAAATAGAAGAGCTTAATCA  
 \*\*\*\*\*

L.m1 GACTAGCTGAATGGAAGCCCTGTACC GGGCCGATGTTATGCCGAAATGCT  
 L.m2 GACTAGCTGAATGGAAGCCCTGTACC GGGCCGATGTTATGCCGAAATGCT  
 L.i GACTAGCTGAATGGAAGCCCTGTACC GGGCCGATGTTATGCCGAAATGCT  
 \*\*\*\*\*

L.m1 AATACGGTGACTACGCTCGTAGATATTT  
 L.m2 AATACGGTGACTACGCTCGTAGATATTT  
 L.i AATACGGTGACTACGCTCGTAGATATTT  
 \*\*\*\*\*

FIG. 16

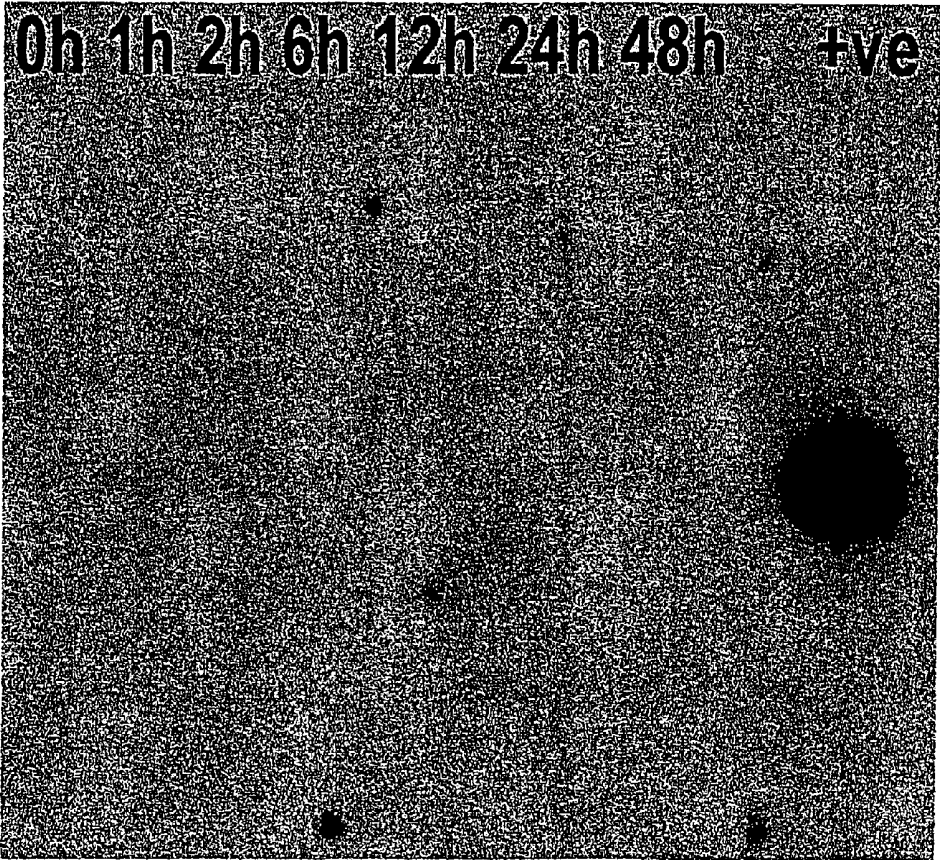


FIG. 17

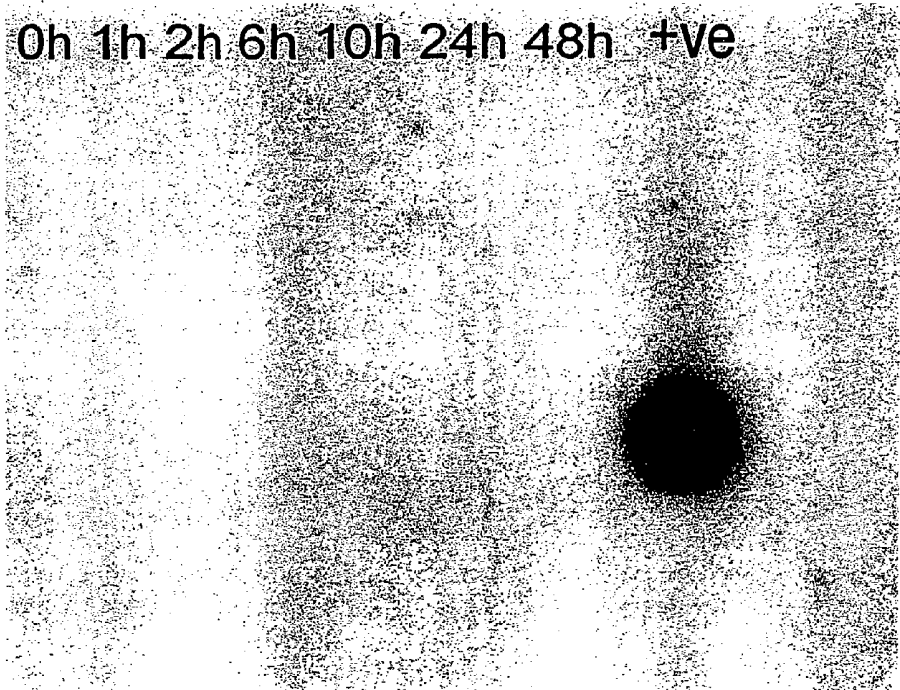


FIG. 18

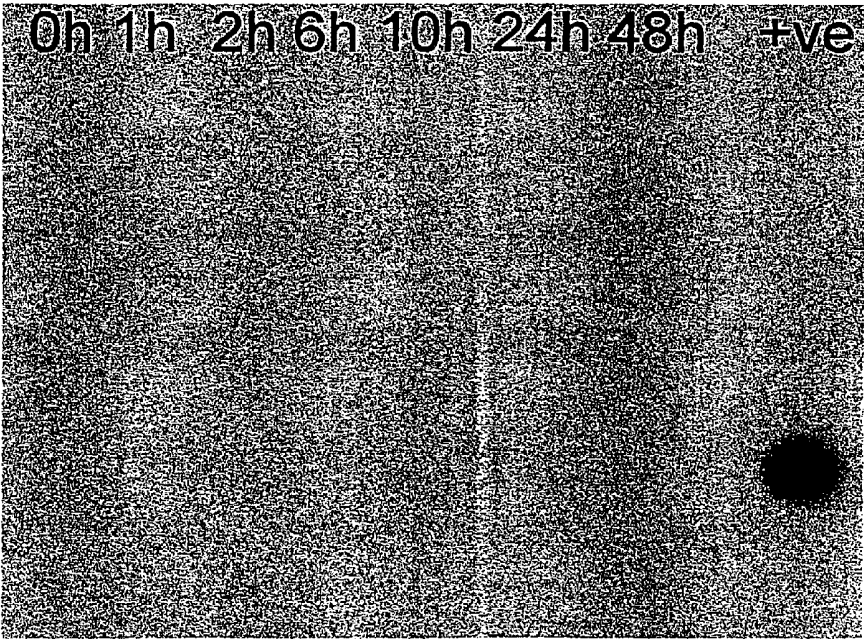


FIG. 19

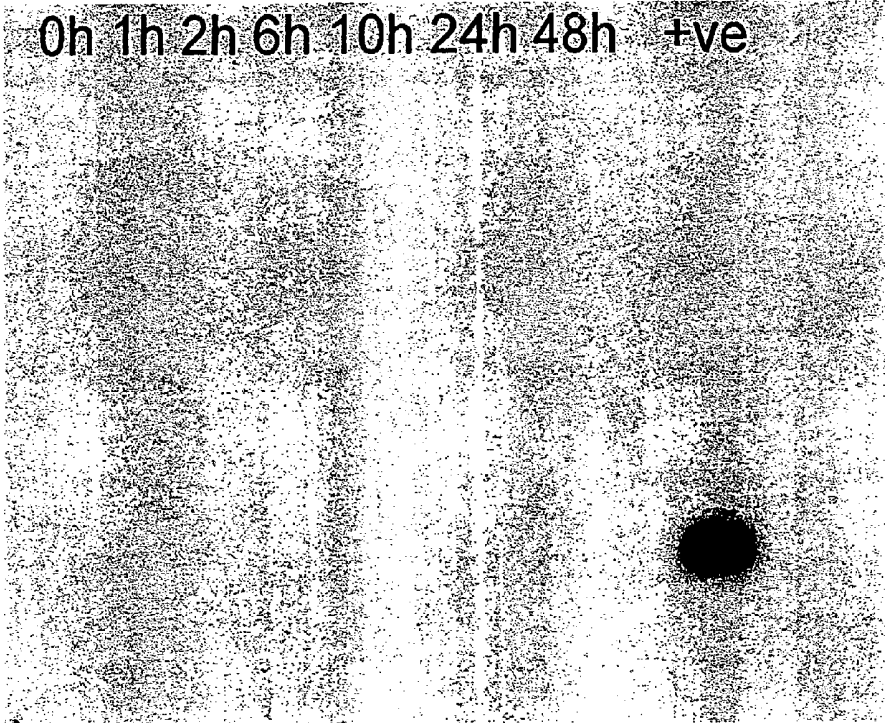


FIG. 20

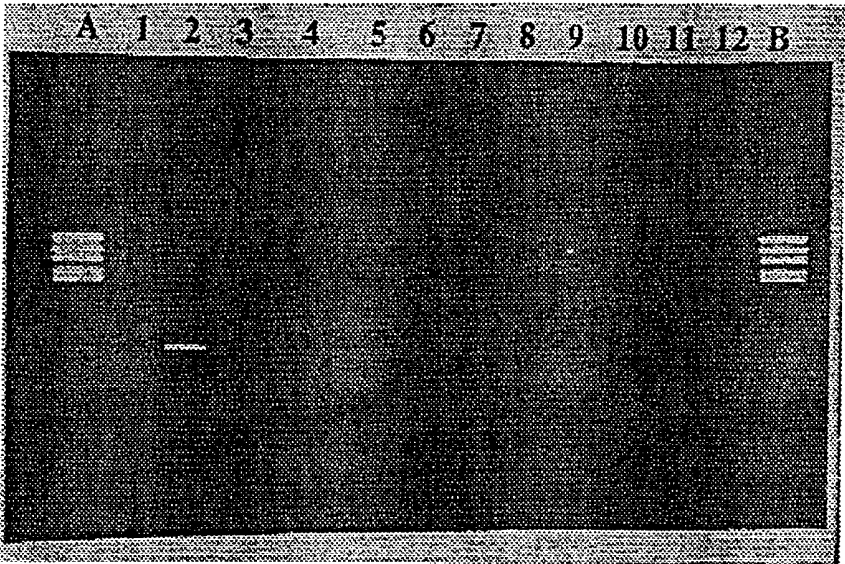


FIG. 21

**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 microorganisms. 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

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sequences or sequences complementary thereto. Representative sequences are as follows:

*Actinobacillus actinomycetemcomitans* ssrA

GGGGCTGATTCTGGATTTCGACGGGATTAGCGAAGCCCGAAGTGC  
 ACGTCGAGGTGCGGTAGGCCCTCGTAAATAAACCGCAAAAAATA  
 GTCGCAAACGACGAACAATACGCTTTAGCAGCTTAATAACCTGC  
 CTTTAGCCTTCGCTCCCCAGCTTCCGCTCGTAAGACGGGGATAAA  
 GCGGAGTCAAACCAAAACGAGATCGTGTGGAAGCCACCGTTTGA  
 GGATCGAAGCATTAAATTAATCAAAGTAGCTTAATGTGCGCT  
 GTCCGTCAGCAGGATTAAGTGAATTTAAAGACCGGACTAAACGT  
 GTAGTGCTAACGGCAGAGGAATTTCCGACGGGGTTCAACTCCC  
 CCCAGCTCCACCA SEQ ID NO: 1

*Actinobacillus actinomycetemcomitans* tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUAGCGAAGCCCGAAGU  
 GCACGUCGAGGUGCGGUAGGCCUCGUAUAUAAACCGCAAAAA  
 AUAGUCGCAAACGACGAACAUAUCGUUUAGCAGCUUAUAAC  
 CUGCCUUUAGCCUUUCGCUCCCGACUUCGUCGUAAGACGGG  
 GAUAAAGCGGAGUCAAAACCAAAACGAGAUUCGUGGAAGCCA  
 CCGUUUAGGGAUCGAAGCAUUAAUUAUAAUCAAAGUAGCUUA  
 AUUGUCGCGUUCGUCAGCAGGAUUAAGUAAUUUAAAGAC  
 CGGACUAAACGUGUAGUCUAACGGGAGAGGAAUUUCGGACG  
 GGGGUUCAACUCCCCCAGCUCCACCA SEQ ID NO: 2

*Aeromonas salmonicida* ssrA, Internal Partial

AAGATTCACGAAACCCAAGGTGCATGCCGAGGTGCGGTAGGCCT  
 CGTTAACAAACCGCAAAAAATAGTCGCAACGACGAAAACTA  
 CGCACTAGCAGCTTAATAACCTGCATAGAGCCCTTCTACCCTAGC  
 TTGCCTGTGTCTTAGGGAATCGAAGGTCATCCTTACAGGATC  
 GTGTGGAAGTCTGTCTCGGGCGGAAGCATTAAACCAATCGAG  
 CTAGTCAATTCGTGGCGTGTCTCTCCGACGGGTTGGCAATGT  
 AAAGAGTGACTAAGCATGTAGTACCAGGATGTAGTAATTTTGG  
 ACGGG SEQ ID NO: 3

*Aeromonas salmonicida* tmRNA, Internal Partial

AAGAUUCACGAAACCCAAGGUGCAUGCCGAGGUGCGGUAGGCC  
 UCGUUAACAAACCGCAAAAAUAGUCGAAACGACGAAACU  
 ACGCACUAGCAGCUUAUAACCUUGCAUAGAGCCUUCUACCCU  
 AGCUUGCCUGUGUCUAGGGAUUCGGAAGGUCAUCCUUCACAG  
 GAUCGUGUGGAAGUCCUGUCGCGGGCGGAAGCAUUAACA  
 AUCGAGCUAGUCAAUUCGUGGCGUGUCUCUCCGACGGGUUG  
 GCGAAUGUAAAGAGUGACUAAGCAUGUAGUACCGAGGAUGUA  
 GUAAUUUUGACGGGG SEQ ID NO: 4

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*Alcaligenes eutrophus* ssrA

TGGGCCGACCTGGTTTCGACGTGGTTACAAAGCAGTGAGGCATA  
 5 CCGAGGACCCGTCACCTCGTTAATCAATGGAATGCAATAACTGC  
 TAACGACGAACGTTACGCACTCGCTTAATTGCGGCCGTCTCGC  
 ACTGGCTCGCTGACGGGCTAGGGTCGCAAGACCACGCGAGGTAT  
 10 TTACGT CAGATAAGCTCCGGAAGGGTCACGAAGCCGGGGACGA  
 AAACCTAGTGACTCGCCGTCTAGAGCGTGTTCGTCGATGCGC  
 CGGTTAAATCAAATGACAGAACTAAGTATGTAGAACTCTCTGTG  
 15 GAGGGCTTACGGACCGGGTTCGATTCGCCCGGCTCCACCA  
 SEQ ID NO: 5

*Alcaligenes eutrophus* tmRNA

UGGGCCGACCUUGGUUUCGACGUGGUUACAAAGCAGUGAGGCA  
 UACCGAGGACCCGUCACCUUGUUAUCAAUGGAAUGCAUAAC  
 25 UGCUAACGACGAACGUUACGCACUCGUUAAUUGCGGCCGUCC  
 UCGCACUGGUCGUCGACGGGCUAGGGUCGCAAGACCACGCGA  
 GGUUUUAACGUCAGAUAAAGCUCCGGAAGGGUCACGAAGCCGG  
 GGACGAAAACCUAGUGACUCGCGGUCGUGAGGCGUGUUCGUCC  
 30 GAUGCGCCGGUAAUCAAUAGACAGAACUAAGUAUGUAGAA  
 CUCUCUGUGGAGGGCUUACGGACCGGGUUCGAUUCGCCCGG  
 CUCCACCA SEQ ID NO: 6

*Aquifex aeolicus* ssrA

GGGGCGGAAAGGATTCGACGGGACAGGCGGTCCCCGAGGAG  
 40 CAGGCCGGGTGGCTCCCGTAACAGCCGCTAAAACAGCTCCCGAA  
 GCTGAACTCGCTCTCGCTGCCTAATTAACGGCAGCGCTCCCC  
 GGTAGGTTTTCGGGTGGCCTACCGAGGGCGTCAGAGACACCCG  
 45 CTCGGGCTACTCGGTCGACGGGGCTGAGTAGCTGACACCTAAC  
 CCGTGCTACCCCTCGGGAGCTTGCCCGTGGGCGACCCGAGGGGA  
 AATCCTGAACACGGGCTAAGCCTGTAGAGCCTCGGATGTGGCCG  
 50 CCGTCTCGGACCGGGTTCGATTCGCCCGCCTCCACCA  
 SEQ ID NO: 7

*Aquifex aeolicus* tmRNA

GGGGCGGAAAGGAUUCGACGGGACAGGCGGUCGCCGAGGA  
 55 GCAGGCCGGGUGGCUCCGUUAACAGCCGCUAAAACAGUCUCCG  
 AAGCUGAACUCGUCUCGUCGCUAAUUAACCGGACGCGGUC  
 60 CCCGUAGGUUUGCGGGGCGCUACCGGAGGGCGUCAGAGACA  
 CCCGCUCCGGGCUACUCGGUCGACGGGGGUCAGUAGCUGACAC  
 CUAACCGGUCUACCCUCCGGGAGCUUCCCGGUGGGGACCCG  
 65 AGGGGAAUUCUGAACACGGGCUAAGCCUGUAGAGCCUCGGAU

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GUGGCCGCCGUCCCGGACGCGGGUUCGAUUCGCCGCCUCC

ACCA SEQ ID NO: 8

*Bacillus megaterium* ssrA, Internal Partial

AGGGTAGTTCGAGCTTAGGTMCGAGTCGAGGAGATGGCCTCGT  
 TAAAACATCAACGCCAATAATAACTGGCAAATCTAACAATAACT  
 TCGCTTTAGCTGCATAATAGTAGCTTAGCGTTCTCCCTCCATCG  
 CCCATGTGGTAGGGIAAGGGACTCACTTTAAGTGGCTACGCCG  
 GAGTTCGCCCTCTGAGGACGAAGGAAGAGAATAATCAGACTAG  
 CGACTGGGACGCCCTGTTGGTAGGAGAACAGCTCGCGAATGATC  
 AATATGCCAACTACACTCGTAGACGCTTAAGTGGCCATATTTCTG  
 GACGTGG SEQ ID NO: 9

*Bacillus megaterium* tmRNA, Internal Partial

AGGGUAGUUCGAGCUUAGGUUUCGAGUCGAGGAGAUGGCCUC  
 GUUAAAACAUCACGCCAAUAAUAAACUGGCAAUUAACAUAU  
 AACUUCGUUAGCUGCAUAAUAGUAGCUUAGCGUUCUCCUCCU  
 CCAUCGCCCAUGUGGUAGGGUAAAGGGACUCACUUUAGUGGGC  
 UACGCCGAGUUCGCCGUCUGAGGACGAAGGAAGAGAAUAAU  
 CAGACUAGCGACUGGGACGCCUGUUGUAGGCAGAACAGCUCG  
 CGAAUGAUCAAUAGCCAAUCACACUCGUAGACGCUUAGUGG  
 CCAUAAUUCUGGACGUGG SEQ ID NO: 10

*Bacillus subtilis* ssrA

GGGGACGTTACGGATTTCGACAGGGATGGATCGAGCTTGAGCTGC  
 GAGCCGAGAGCGCATCTCGTAAACACGCACTTAAATATAACTGG  
 CAAAATAACAGTTTTAAACAAAACGTAGCATTAGCTGCCTAAT  
 AAGCGCAGCGAGCTCTTCTGACATGCTTATGTCTGTGAAG  
 AGCACATCCAAGTAGGCTACGCTTGCGTTCCCGTCTGAGAACGT  
 AAGAAGAGATGAACAGACTAGCTCTCGGAAGGCCCGCCCGCAG  
 GCAAGAAGATGAGTGAACCATAAATATGCAGGCTACGCTCGTA  
 GACGCTTAAGTAATCGATGTTTCTGGACGTGGGTTGACTCCAC  
 CGTCTCCACCA SEQ ID NO: 11

*Bacillus subtilis* tmRNA

GGGGACGUUACGGAUUCGACAGGGAUGGAUCGAGCUUAGAGCU  
 GCGAGCCGAGAGGCGAUCUCGUAAAACCGCACUUAAUUAUAC  
 UGGCAAAACUAAACAGUUUAAACAAAACGUAGCAUUAAGCUGCC  
 UAUAUAGCGCAGCGAGCUCUUCUGACAUUGCCUUAUGUGUCUG  
 UGAAGAGCACAUCCAAGUAGGCUACGCUUUGCGUUCGUCUGA  
 GAACGUAAAGAAGAGAUGAACAGACUAGCUCUCGGAAGGCCCGC  
 CCGCAGGCAAGAAGUAGUAGAAACCAUAAUUAUGCAGGCUA

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CGCUCGUAGACGCUUAGUAAUUCGAUGUUUCUGGACGUGGGU

UCGACUCCACCGUCUCCACCA SEQ ID NO: 12

5 *Bordetella pertussis* ssrA

GGGGCCGATCCGGATTTCGACGTGGGTCATGAAACAGCTCAGGGC  
 10 ATGCCGAGCACCAGTAAGTCTGTTAATCCACTGGAACACTACAA  
 ACGCCAACGACGAGCGTCTCGCTCTCGCCGCTTAAGCGGTGAGC  
 CGCTGCACGTATCTGTCTTGGGTCAGGCGGGGAAGGCAACTT  
 15 CACAGGGGGCAACCCCGAACCGCAGCAGCGACATTCAACAAGGA  
 ATCGGCCACCGCTGGGGTCACACGGCGTTGGTTTAAATTACGTG  
 AATCGCCCTGGTCCGGCCCGTTCGATCGGCTAAGTCCAGGGTTAA  
 20 ATCCAAATAGATCGACTAAGCATGTAGAACTGGTTGCGGAGGGC  
 TTGCGGACGGGGTTCAATTCGCCCGGCTCCACCA  
 SEQ ID NO: 13

25 *Bordetella pertussis* tmRNA

GGGGCCGAUCCGGAUUCGACGUGGGUC AUGAAACAGCUCAGGG  
 CAUGCCGAGCACCAGUAAGCUCGUUAAUCCACUGGAACACUAC  
 30 AAACGCCAACGACGAGCGUCUCGUCUCGCGCCUUAAGCGGUG  
 AGCCGUGCACUGAUCUGUCCUUGGGUCAGGCGGGGAAGGCA  
 ACUUCACAGGGGGCAACCCCGAACCGCAGCAGCGACAUUCACA  
 35 AGGAAUCGGCCACCGCUGGGGUCACACGGCGUUGGUUAAAAU  
 ACGUGAAUCGCCUGGUCCGGCCCGUCGAUCGGCUAAGUC CAG  
 GGUUAAUCCAAAAGAUCCGCUAAGCAUGUAGAACUGGUUG  
 40 CCGAGGGCUCGCGGACGGGGUCAAUUCGCCCGGCUCCACC  
 A SEQ ID NO: 14

45 *Borrelia burgdorferi* ssrA

GGGGATGTTTTGGATTGACTGAAAATGTTAATATTGTAAGTTGC  
 AGGCAGAGGGAATCTCTTAAACTTCTAAAATAAATGCAAAAAA  
 TAATAACTTTACAAGCTCAAATCTTGTAATGGCTGCTTAAGTTAG  
 50 CAGAGGGTTTTGTTGAATTTGGCTTTGAGGTTCACTTATACTCTT  
 TTCGACATCAAAGCTTGCTTAAAAATGTTTTCAAGITGATTTTTA  
 GGGACTTTTATACTTGAGAGCAATTTGGTGGTTTCTAGTATTTT  
 55 CAAACCATATTGCTTAATAAATACTAGATAAGCTTTGTAAGC  
 TTATAGTATTATTTTTAGGACGCGGGTTCAATTCGCCCATCTCC  
 ACCA SEQ ID NO: 15

60 *Borrelia burgdorferi* tmRNA

GGGGAUGUUUGGAUUUGACUGAAAUGUUAAUUAUGUAAGU  
 65 UGCAGGCAGAGGGAUUCUUAAAAUCUUAUUUUAAUUGCA

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AAAAAUAUAACUUUACAAGCUCAAAUCUUGUAAUUGCUGCU  
 UAAGUUAGCAGAGGUGUUUUGUUGAAUUUGGCUUUGAGGUUCA  
 CUUAUACUCUUUUCGACAUCAAGCUUGCUUAAAAUGUUUU  
 CAAGUUGAUUUUAGGGACUUUUAUACUUGAGAGCAAUUUGG  
 UGGUUUGCUGAUUUUCCAAACCAUUAUUGCUUAAUAAAAUAC  
 UAGAUAAGCUUGUAGAAGCUUAUAGUAUUUUUUUAGGACGC  
 GGGUUCAAUUCGCCCAUCUCCACCA SEQ ID NO: 16

*Campylobacter jejuni* ssrA

GGGAGCGACTTGGCTTCGACAGGAGTAAGTCTGCTTAGATGGCA  
 TGTCGCTTTGGGCAAAGCGTAAAAGCCAAATAAAATTAACG  
 CAAACAACGTTAAATTCGCTCCTGCTTACGCTAAAGCTGCGTAA  
 GTTCAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCTTAATTT  
 TCGGTCATTTTTGATAGTGTAGCCTTGCCTTGACAAGCGTTGAG  
 GTGAAATAAAGTCTTAGCCTTGCTTTGAGTTTTGGAAGATGAGC  
 GAAGTAGGGTGAAGTAGTCACTTTGCTAAGCATGTAGAGGTCT  
 TTGTGGGATTATTTTTGGACAGGGGTTGATTCCTCGCTTCCA  
 CCA SEQ ID NO: 17

*Campylobacter jejuni* tmRNA

GGGAGCGACUUGGCUUCGACAGGAGUAAGUCUGCUUAGAUGG  
 CAUGUCGCUUUGGGCAAAGCGUAAAAAGCCAAAUAUUUA  
 AACGCAACAACGUAUUUUUUCGCUUCGCUUACGCUAAAGCUG  
 CGUAAGUUCAGUUGAGCCUGAAUUUAAGUCAUACUACUAG  
 CUUAAUUUUCGGUCAUUUUUAGUAGUGUAGCCUUGCGUUUGA  
 CAAGCGUUGAGGGUAAAUAAGUCUUAGCCUUGCUUUUGAGU  
 UUUGGAAGAUGAGCGAAGUAGGGUGAAGUAGUCAUCUUUGCU  
 AAGCAUGUAGAGGUCUUUUGGGUAUUUUUUGGACAGGGGU  
 UCGAUUCCCCCGCUUCCACCA SEQ ID NO: 18

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

GGGGGTGTAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT  
 GCGGAGGGCGTTGGCTGGCTCCATAAAAGCCGACAAAACAATA  
 AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA  
 TCTCGAAGATCTAAGAGTAGCTGCTTAATTAGCAAAGTTGTTACC  
 TAAATACGGGTGACCCGGTGTTCGCGAGCTCCACCAGAGGTTTT  
 CGAAACACCGTCATGTATCTGGTTAGAACTTAGGTCCTTAATTC  
 TCGAGGAAATGAGTTTGAAATTTAATGAGAGTCGTTAGTCTCTAT  
 AGGGGTTTCTAGCTGAGGAGACATAACGTATAGTACCTAGGAAC  
 TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT  
 CGACTCTCCACCTCCACCA SEQ ID NO: 19

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

GGGGGUGUAAAGGUUUCGACUUAAGAAUGAAGCGUUAAUUGC  
 5 AUGCGGAGGGCGUUGGCUUGCCUCCUAAAAAGCCGACAAAACA  
 AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUAUACAGCUUC  
 GCUGAUCUCGAAGAUCUAAGAGUAGCUCUUAUUUAGCAAAG  
 10 UUGUUACCUAAAUAACGGGUGACCCGGUUGUUCGCGAGCUCACC  
 AGAGGUUUUCGAAACACCGUCAUGUAUCUGUUUAGAACUUG  
 GUCCUUAAUUCUCGAGGAAAUGAGUUUGAAAUUUUAUGAGA  
 15 GUCGUUAGUCUCUAUAGGGGUUUCUAGCUGAGGAGACUAUAC  
 GUAUAGUACCUAGGAACUAAGCAUGUAGAGGUUAGCGGGGAG  
 UUUACUAAGGACGAGAGUUCGACUCUCUCCACCUCACCA  
 20 SEQ ID NO: 20

*Chlamydia trachomatis* (Mouse Pneumonitis) ssrA

GGGGGTGTAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT  
 25 GCGGAGGGCGTTGGCTGGCTCCATAAAAGCCGACAAAACAATA  
 AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA  
 TCTTAATGATCTAAGAGTTGCTGCTTAATTAGCAAAGTTGTTACC  
 30 TAAGTACTGGTAACCCGGTGTTCGCGAGCTCCACCAGAGGTTTTC  
 GAAACGCCGTCATTTATCTGGTTAGAAATAGGGCCTTTAACTCT  
 CAAGGGAACATAATTTGAATTTAATGAGAGTCGTTGGTCTCTATA  
 35 GAGGTTTCTAGCTGAGGAGATATAACGTAATAATTTCTAGAAAC  
 TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT  
 CGAATCTCTCCACCTCCACCA SEQ ID NO: 21

*Chlamydia trachomatis* (Mouse Pneumonitis) tmRNA

GGGGGUGUAAAGGUUUCGACUUAAGAAUGAAGCGUUAAUUGC  
 45 AUGCGGAGGGCGUUGGCUUGCCUCCUAAAAAGCCGACAAAACA  
 AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUAUACAGCUUC  
 GCUGAUCUUAUGAUCUAAGAGUUGCUCUUAUUUAGCAAAG  
 50 UUGUUACCUAAGUACUGGUAACCCGGUUGUUCGCGAGCUCACC  
 AGAGGUUUUCGAAACCGUCAUUUAUCUGUUUAGAAUUUAGG  
 GCCUUUUAACUCUCUAGGGAACUAAUUUGAAUUUUAUGAGA  
 55 GUCGUUGGUCUCUAUAGAGGUUUCUAGCUGAGGAGAUUAAC  
 GUAAAUAUUUCUAGAAACUAAGCAUGUAGAGGUUAGCGGGGA  
 GUUUACUAAGGACGAGAGUUCGAAUCUCCACCUCACCA  
 60 SEQ ID NO: 22

*Chlorobium tepidum* ssrA

GGGGATGACAGGCTATCGACAGGATAGTGTGAGATGTCGTTGC  
 65 ACTCCGAGTTTTCAGCATGGACGGACTCGTTAAACAAGTCTATGT

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ACCAATAGATGCAGACGATTATTCGTATGCAATGGCTGCCTGAT  
TAGCACAAAGTTAATTCAGAAAGCCATCGTCTCGCGGTGAATGCGC  
TTACTCTGAAGCCGCCGGATGGCATAACCCGCGCTTGAGCCTAC  
GGGTTTCGCGCAAGTAAGCTCCGTACATTCATGCCCGAGGGGGTG  
TGCGGGTAACCAATCGGATAAGGGGACGAACGCTGCTGGCGGT  
GTAATCGGACCACGAAAAACCAACCACCAGAGATGAGTGTGGT  
AACTGCATCGAGCAGTGTCTGACGCGGGTTCAAGTCCCGCCA  
TCTCCACCA SEQ ID NO: 23

*Chlorobium tepidum* tmRNA

GGGGAUGACAGGCUAUCGACAGGAUAGGUGUGAGAUGUCGUU  
GCACUCCGAGUUUCAGCAUGGACGGACUCGUUAAACAAGUCUA  
UGUACCAUAGAUGCAGACGAUUAUCGUAUGCAAUGGUCUGC  
CUGAUUAGCACAAGUUAUUUAGAAAGCAUCGUCCUGCGGUGA  
AUGCGCUUACUCUGAAGCCGCGGAUAGGCAUAAACCCGCGCUUG  
AGCCUACGGGUUCGCGCAAGUAAGCUCGUAUCAUUGCCCG  
AGGGGUGUGCGGUAACCAUUCGGGAUAGGGGACGAACGC  
UGCUGGCGGUAUUCGAGCACGAACAACCAACCACAGAGA  
UGAGUGUGGUAACUGCAUCGAGCAGUGUCUGGACGCGGGUU  
CAAGUCCCGCAUCUCCACCA SEQ ID NO: 24

*Cyanophora paradoxa* (Alga) Cyanelle ssrA

GGGGCTGTTTAGGTTTCGACGTTTTTTTTCTAATTATGTTTGTAAAG  
CAAGTCGAGGATTTGTTCTATCTCGAAAATCAAGAACTCTCAAA  
ATTTAAACGCAACTAATATTGTACGTTTTAACCGTAAAGCAGCTT  
TCGCTGTTTAATAATTACTTTTTAATTTAAAAACCTAATTTTTTTAG  
GAATTTATTTATTTATGTTTATCTGCTTAATGAATTAAAAAA  
GCTATACTTGTGAATAAACGCATAATTTAAAAAACGGACGTGG  
GTTCAAATCCACCAGCTCCACCA SEQ ID NO: 25

*Cyanophora paradoxa* (Alga) Cyanelle tmRNA

GGGGCUGUUUAGGUUUCGACGCUUUUUUUAUUUAUGUUUGU  
UAAGCAAGUCGAGGAUUUUUCUAUCGAAAAUCAAGAACU  
CUCAAAUUUUAAACGCAACUAUUUAUUGUACGUUUUAACCGUA  
AAGCAGCUUUCGCGUUUAUUUAUUUAUUUUUUUUAAAAAC  
CUAAUUUUUUUAGGAAUUUUUUUUUUUUUUUUUUUUUUUUUU  
UAAUGAAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU  
UU  
SEQ ID NO: 26

*Clostridium acetobutylicum* ssrA, 3' Partial

AATCTGGCGTCGAGAGCGGGGAAACGAGCCTTACAAAGCTTTGA  
GTAAGGAACGGAATTTATGAAGCTACTGAAGTAAAAAGCTTGTT

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TGTAGGCGTTTCATGGAGGGAATGTTAAAAATACAAACTGCCTC  
GGAGATGCTTAATGAAACCATTTTCGGACAGGGGTTTCGATTC  
CTCGCTCCACCA SEQ ID NO: 27

*Clostridium acetobutylicum* tmRNA, 3' Partial

AAUCUGGCGUCGAGAGCGGGGAAACGAGCCUUACAAGCUUU  
GAGUAAGGAACGGAUUUUAUGAAGCUACUGAAGUGAAAAGCU  
UGUUUGUAGGCGUUUCAUGGAGGAAUGUUAAAAUACAACU  
GCACUCGGAGAUUCUUAUGAAACCAUUUUCGGACAGGGUU  
CGAUUCCCCUCGCCUCCACCA SEQ ID NO: 28

*Deinococcus radiodurans* ssrA

GGGGGTGACCCGGTTTCGACAGGGGAACTGAAGGTGATGTTGCC  
TGTCGAGGTGCCGTTGGCTCGTAAACAACCGCAAAGCCATTT  
AACTGGCAACCAGAATACTGCTCTCGCTGCTTAAGTGAATGAC  
GACCGTGCAGCCCGCCTTTGGCGTCGCGGAAGTCACTAAAAA  
GAAGGCTAGCCAGGCGATTCTCCTAGCCGACGGCGAAACTTT  
ATGGAGCTACGGCTGCGAGAACCTGCCACTGGTGAGCGCCGG  
CCGACAATCAACAGTGGGATACACAGTACAGCAGCAGCTGGA  
CGGACCTTTGGACGCGGTTTCGACTCCGCCACCTCCACCA  
SEQ ID NO: 29

*Deinococcus radiodurans* tmRNA

GGGGGUGACCCGGUUUCGACAGGGGAACTGAAGGUGAUGUUUG  
CGUGUCGAGGUGCCGUGGCCUGUAAACAACCGCAAAGCCAA  
UUUUAACUGGCAACCAGAACUACGCUUCGCGUCUUAAGUGAGA  
UGACGACCUGCAGCCCGCCUUUGGCGUCGCGGAAGUCACUA  
AAAAAGAAGGCUAGCCAGGCGAUUUCUUAAGCCGACGGCGA  
AACUUUAUGGAGCUACGGCCUGCGAGAACCUGCCACUGGUGA  
GCGCCGGCCCGACAAUUAACAACAGUGGGAUACACAGUAGACG  
ACGUGGACGGACUUUGGACGGCGGUUCGACUCGCCACCU  
CCACCA SEQ ID NO: 30

*Desulfovibrio desulfuricans* ssrA, Internal Partial

GGGACTGGAACCGTAGCGGCAGGTCGAGGCGCCGCTGGCCTCGT  
AAAAAGCGGCACAAAAGTAATGCCAACAACGATTACGACTAC  
GCTTACGCTGCCTAATAACAGCGAGGCAATGACCGTTTAAACGGT  
CGCGCCGATCAGGGCCATGCCTGATAACCTGATGGCGACACT  
TATCAGGCTGGCGAAAACCGCTCTCGCCGGGTTTTTCGCGAG  
GAGTTTACCGGCGGATTGCTGCGTTGTGCTGGTCAGGGGCCA  
ACAGCGCGGTGAAATACATACTTGACCTAAACCTGTAATGCTTC  
GTGTGGAATGTTCTCGGACGGGG SEQ ID NO: 31

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*Desulfovibrio desulfuricans* tmRNA, Internal Partial

GGGACUGGAACCGUAGCGGCAGGUCGAGGCGCCGUGGCCUCG  
 UAAAAAGCGGCACAAAAGUAAUUGCCAACAACGAUUACGACU  
 ACGCUUACGCGUCUAAUUAACAGCGAGGCAAUGACCGUUUAAC  
 GGUCGCGCCGAUCAGGGCCAUGCCUGAUAAACCUGAUUGGCGA  
 CACUUUACAGGCGGGCAAACCGGCUCUCGCCGGGUUUUUC  
 GCGAGGAGUUUACCGCGGGAAUUGCUGCGUUGGCCUGGUCA  
 GGGGCCAACAGCGCGGUAUUAUACUACUUGACCUAAACCUGU  
 AAUGCUUCGUGGAAUUGUUCUCGACGGGG SEQ ID NO: 32

*Dichelobacter nodosus* ssrA, 3 Partial

CTCGAGGTGCATGTCGAGAATGAGAGAATCTCGTTAAATACTTT  
 CAAAACCTATAGTTGCAACGACGACAACACTACGCTTAGCGGCT  
 TAATTCGCCGTTTCGCTTACCTAGATTGTCTGTGGTTTACCCTA  
 AGCGCATTAACACAGAATCGCTGGTTAACGCGTCCGCTGTAA  
 TCGGTTAAATTAAGCGAATCGCTTGTAAAAATGCCTGAGCGTTG  
 GCTGTTTATGAGTTAAACCTAATTAACCTGCTCTAACATGTTAGTA  
 CCAAAGTTAAGGATTCGCGGACGGGGTTCAAATCCCCCGCC  
 TCCACCA SEQ ID NO: 33

*Dichelobacter nodosus* tmRNA, 3 Partial

CUCGAGGUGCAUGUCGAGAUGAGAGAAUCUCGUUAAAUAUCU  
 UUCAAAAUCUUAUAGUUGCAAACGACGACAAGUACGCUUUAAGCG  
 GCUUAAUUCGCGUUCGCUUACCUAGAUUUGUCUGUGGGUUU  
 ACCGUAAGCGCAUUAACACAGAAUCGCGGUUAACGCGUCG  
 CUGUUAUCGCGUAAAUAAGCGAAUCGCUUGUAAAUGCC  
 UGAGCGUUGGUGUUUAUGAGUUAACCUAAUUAACUGCUCU  
 AAACUAGUAGUACAAAAGUUAAGGAUUCGCGGACGGGGUU  
 CAAUCCCCCGCCUCCACCA SEQ ID NO: 34

*Enterococcus faecalis* ssrA

GGGGCGTTACGGATTTCGACAGGCATAGTTGAGCTTGAATTGCG  
 TTTCTAGGTTACGGCTACGTTAAAACGTTACAGTTAAATATAAC  
 TGCTAAAACGAAAACAATTCTTTCGCTTTAGCTGCCTAAAAAC  
 CAGCTAGCGAAGATCCTCCCGCATCGCCATGTGCTCGGGTCA  
 GGGTCTAATCGAAGTGGGATACGCTAAATTTTCCGTCTGTAA  
 ATTTAGAGGAGCTTACCAGACTAGCAATACAGAATGCCTGTAC  
 TCGGCACGCTGTAAGCGAACCTTTAAATGAGTGTCTATGAACG  
 TAGAGATTTAAGTGGCAATATGTTTGGACGCGGGTTCCGACTCCC  
 GCCGTCTCCACCA SEQ ID NO: 35

14

*Enterococcus faecalis* tmRNA

GGGGCGUUACGGAUUCGACAGGCAUAGUUGAGCUUGAAUUG  
 5 CGUUUCGUAGGUUACGGCUACGUUAAAACGUUACAGUUAAA  
 AUAACUGCUAAAAACGAAAACAUUUUUUCGUUAGCUGCCU  
 AAAAACCGCUAGCGAAGAUCCUCCCGCAUCGCCCAUGUGCU  
 10 CGGGUCAGGGUCCUAAUCGAAGUGGGAUACGCUAAAUUUUUC  
 CGUCUGUAAAUUUAGAGGAGCUUACCAGACUAGCAAUACAG  
 AAUGCCUGUCACUCGGCAGCUGUAAAGCGAACCUUAAAUGA  
 15 GUGUCUAUGAACGUAGAGAUUUAAGUGGCAUUAUGUUUGAC  
 GCGGGUUCGACUCCCGCCGUCUCCACCA SEQ ID NO: 36

*Escherichia coli* ssrA

GGGGCTGATTCTGGATTTCGACGGGATTTCGAAAACCAAGGTGC  
 20 ATGCCGAGGGGCGTTGGCCTCGTAAAAGCCGCAAAAAATAGT  
 CGCAAACGACGAAAACCTACGCTTTAGCAGCTTAATAACCTGCTT  
 25 AGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAAG  
 AGAGGTCAAACCCAAAAGAGATCGCGTGAAGCCCTGCCTGGG  
 GTTGAAGCGTTAAAACCTAATCAGGCTAGTTTGTAGTGGCGTGT  
 30 CCGTCCGCGAGCTGGCAAGCGAATGTAAGACTGACTAAGCATGT  
 AGTACCAGGATGTAGGAATTCGGACGCGGGTTCAACTCCCGC  
 CAGCTCCACCA SEQ ID NO: 37

35 *Escherichia coli* tmRNA

GGGGCUGAUUCUGAUUCGACGGGAUUUGCGAAAACCAAGGU  
 40 GCAUGCCGAGGGGCGUUGGCCUCGUAAAACCGCAAAAAAU  
 AGUCGAAAACGACGAAAACUACGCUUUAAGCAGCUUAAUAAACU  
 GCUUAGAGCCCUUCUCCUAGCCUCCGCUUUAAGGACGGGGA  
 45 UCAAGAGAGGUCAAAACCAAAAGAGAUCCGUGGAAAGCCUUGC  
 CUGGGGUUGAAGCGUAAAACUUAUACAGGCUAGUUUUUAG  
 UGGCGUGUCCGUCGCGAGCUGGCAAGCGAAUGUAAAAGACUGAC  
 50 UAAGCAUGUAGUACCGAGGAUGUAGGAAUUUCGGACGCGGGU  
 UGAACUCCGGCCAG SEQ ID NO: 38

*Haemophilus influenzae* ssrA

GGGGCTGATTCTGGATTTCGACGGGATTTCGAAAGCCCAAGGTGC  
 55 ACGTCGAGGTGCGGTAGGCCTCGTAAATAAACCGCAAAAAATA  
 GTCGCAAACGACGAAACAATACGCTTTAGCAGCTTAATAACCTGC  
 60 ATTTAGCCTTCGCGCTCCAGCTTCCGCTCGTAAGACGGGGATAAC  
 GCGGAGTCAAACCAAAACGAGATCGTGTGGAAGCCACCGTTTGA  
 GGATCGAAGCACTAAATGAAATCAAACCTAGCTTAAGTTTAGCGT  
 65 GTCTGTCCGATGCTTAAGTGAATTAAGACGAGACTAAACGT

15

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GTAGTACTGAAGGTAGAGTAATTCGGACGGGGTTCAACTCCC

CCCAGCTCCACCA SEQ ID NO: 39

*Haemophilus influenzae* tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUAGCGAAGCCCAAGGU

GCACGUCGAGGUGCGGUAGGCCUCGUAUUAAACCGCAAAAA

AUAGUCGCAACGACGAAACAUAUCGUUAGCAGCUUAUAAC

CUGCAUUUAGCCUUCGCGCUCAGCUUCCGUCUGUAAGACGGG

GAUAAACGCGGAGUCAAAACAAAACGAGAUUCGUGGAAAGCCAC

CGUUUGAGGAUCGAAACACUAAAUUGAAUCAAACUAGCUUAA

GUUUAGCGUGUCUGCCGACUUCUAAAGUAAAUAAGACG

AGACUAAACGUGUAGUACUGAAGGUAGAGUAAUUCGGACGG

GGGUUCAACUCCCCCAGCUCCACCA SEQ ID NO: 40

*Helicobacter pylori* (ATCC 43504) *ssrA*, Internal Partial

SEQ ID NO: 41

AGATTTCCTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTAAC

ACAGCAACAAAATAACTGTAAACAACACAGATTACGCTCCAGC

TTACGCTAAAGCTGCGTGAAGTAACTCCTTTTGGAGCTGGACTG

ATTAGAATTTCTAGCGTTTTAATCGCTCCATAACCTTAAGCTAGA

CGCTTTTAAAGGTGGTTCCGCTTTTAAACTAAGAAACAAGAAC

TCTTGAACTATCTTAAGGTTTTAGAAAGTTGGACCAGAGCTAGT

TTTAAAGGCTAAACTAACCATTTTCTAAGCATTGTAGAAGTTT

GTGTTTAGGGCAAGATTTTGGACTGGG

*Helicobacter pylori* (ATCC 43504) tmRNA, Internal Partial

SEQ ID NO: 42

AGAUUUCUUGUCGCGCAGAUAGCAUGCCAAGCGCUGCUUGUAA

AACAGCAACAAAAUAACUGUAAACAACACAGAUUACGCUCCA

GCUUACGCUAAAGCUGCGUGAGUUAUCUCCUUUUGGAGCUG

GACUGAUUAGAAUUUCUAGCGUUUUAUCGCUCCAUAACCUU

AAGCUAGACGCUUUUAAAAGGUGGUUCGCCUUUUAACUAAG

AAACAAGAACUUCUUAACUAUCUUAAGGUUUUAGAAAGUUG

GACCAGAGCUAGUUUUAAGGCUAAAAACUAACCAAUUUUCUA

AGCAUUGUAGAAGUUGUUUUAGGGCAAGAUUUUUGGACUG

GG

*Helicobacter pylori* (strain 26695) *ssrA*

SEQ ID NO: 43

GGGGCTGACTTGGATTCGACAGATTTCTGTGCGCACAGATAGC

ATGCCAAGCGCTGCTTGTAAACAGCAACAAAATAACTGTAAAC

CAACACAGATTACGCTCCAGCTTACGCTAAAGCTGCGTGAGTTA

ATCTCCTTTTGGAGCTGGACTGATTAGAATTTCTAGCGTTTTAAT

16

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CGCTCCATAACCTTAAGCTAGACGCTTTTAAAGGTGGTTTCGCCT

TTTAACTAAGAAACAAGAAGCTCTTGAACTATCTCAAGGTTTT

5 AGAAAGTTGGACCAGAGCTAGTTTTTAAAGGCTAAAAAACCAACCA

ATTTTCTAAGCATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTTG

GACTGGGGTTCGATTCACACAGCTCCACCA

10 *Helicobacter pylori* (Strain 26695) tmRNA

SEQ ID NO: 44

GGGGCUGACUUGGAUUCGACAGAUUUUUGUCGCACAGAUAA

15 GCAUGCCAAGCGCUGCUUGUAAAACAGCAACAAAAUAACUGU

AAACAACACAGAUUACGCUCCAGCUUACGCUAAAGCUGCGUGA

GUUAAUCUCCUUUUGGAGCUGGACUGAUUAGAAUUUCUAGCG

20 UUUUAAUCGCUCCAUAACCUAAGCUAGACGCUUUUAAAAGG

UGGUUCGCCUUUAAAACUAAGAAACAAGAACUCUUGAAACUA

UCUCAAGGUUUUAGAAAGUUGGACCAGAGCUAGUUUUUAAAGG

UAAAAACCAACCAUUUUUCUAGCAUUGUAGAAGUUUGUGU

UUAGGGCAAGAUUUUUGGACUGGGGUUCGAUUCACACAGCUC

CACCA

*Klebsiella aerogenes* (NCTC 9528) *ssrA*, Internal Partial

30

SEQ ID NO: 45

GGGATTCGCGAAACCAAGGTGCATGCCGAGGGGCGTTGGCCT

CGTAAAAAGCCGCAAAAAAATAGTCGCAACAGCAGAAAACTAC

35 GCTTTAGCAGCTTAATAACCTGCTAAGAGCCCTCTCTCCCTAGCT

TCCGCTCCTAAGACGGGAATAAAGAGAGGTCAAACCCAAAAG

AGATCGCGTGGAAGCCCTGCCTGGGGTTGAAGCGTTAAACTAA

40 TCAGGCTAGTTTGTCAAGTGGCGTGTCCGTCGCAGCTGGCCAGC

GAATGTAAGACTGGACTAAGCATGTAGTGCCGAGGATGTAGGA

ATTTT

45 *Klebsiella aerogenes* (NCTC 9528) tmRNA, Internal Partial

SEQ ID NO: 46

GGGAUUCGCGAAACCAAGGUGCAUCCGAGGGGCGUUGGCC

50 UCGUAAAAAGCCGCAAAAAAUAAGUCGCAACAGCAGAAAAACU

ACGCUUAGCAGCUUAAUAACGUCUAAGAGCCUCUCUCUCCU

AGCUUCGCUCCUAAGACGGGAAUAAAGAGAGGUCAAACCCA

55 AAAGAGAUCCGUGGAAGCCUCCUUGGGUUGAAGCGUUA

AACUAAUCAGGCUAGUUUGUCAGUGGCUGUCGCGCAGCU

GGCCAGCGAAUGUAAAGACUGGACUAAGCAUGUAGUGCCGAG

GAUGUAGGAAUUUC

*Lactobacillus lactis* (NCTC 662) *ssrA*, Internal Partial

SEQ ID NO: 47

AAGCACAGTTCGAGCTGAATTGCGTTTCGTAGGTTACGTCTACG

65

TTAAACGTTACAGTTAAATATAACTGCTAAAAACGAAAAAC

17

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TCTTACGCTTTAGCTGCCTAAAAACAGTTAGCGTAGATCCTCTCG  
 GCATCGCCCATGTGCTCGAGTAAGGGTCTCAAATTTAGTGGGAT  
 ACGTTAAACTTTTCGCTGTAAAGTTTAAAAGAGATCATCAGAC  
 TAGCGATACAGAATGCCTGTCTACTCGGCAAGCTGTAAGCGAAA  
 CCTCAAATGAGTTGACTATGAACGTAGATTTTAAAGTGTCTGATG  
 GTTT

*Lactobacillus lactis* (NCTC 662) tmRNA, Internal Partial

SEQ ID NO: 48  
 AAGCACAGUUCGAGCUUGAAUUGCGUUUCGUAGGUUACGUCU  
 ACGUUAAAACGUUACAGUAAAUAUAACUGCUAAAAACGAAA  
 ACAACUCUUACGCUUAGUCGCUAAAACAGUUAAGCGUAGAU  
 CCUCUCGGCAUCGCCAUGUGUCGAGUAAGGGUCUCAAUUU  
 AGUGGGAUACGUUAAAUCUUUCCGUCUGUAAAAGUUAAAAGA  
 GAUCAUCAGACUAGCGAUACAGAAUGCCUGUCACUCGGCAAGC  
 UGUAAAAGCGAAACCUAAAUGAGUUGACUAUGAACGUAGAUU  
 UUUAAAGUGUCGAUGUGUUU

*Legionella pneumophila* ssrA, Internal Partial

SEQ ID NO: 49  
 GTGGGTTGCAAACCGGAAGTGCATGCCGAGAAGGAGATCTCTC  
 GTAAATAAGACTCAATTAATAATAAATGCAAACGATGAAAACCT  
 TGCTGGTGGGGAAGCTATCGCTGCCAATAAGCACTTTAGTTAA  
 ACCATCACTGTGTACTGGCCAATAAACCCAGTATCCCGTTCGACC  
 GAGCCCGCTTATCGGTATCGAATCAACGGTCATAAGAGATAAGC  
 TAGCGTCCTAATCTATCCCGGTATGGCGGAACTCAGGGAA  
 TCGCTGTGTATCATCCTGCCGTCGAGGAGCCACAGTTAAATTC  
 AAAAGACAAGGCTATGCATGTAGAGCTAAAGGCAGAGACTTG  
 CGGACGCGG

*Legionella pneumophila* tmRNA, Internal Partial

SEQ ID NO: 50  
 GUGGGUUGCAAACCGGAAGUGCAUGCCGAGAAGGAGAUUC  
 UCGUAAAUAAGACUCAAUAAAUAUAAAUGCAAACGAUGAAA  
 ACUUUGUCUGGUGGGAAGUCUACGUCGCUAAUUAAGCACUUU  
 AGUUAAAACCAUCACUGUGUACUGGCCAAUAAACCCAGUAUCC  
 GUUCGACCGAGCCCGCUUUAUCGUAUCGAAUACCGGUCAUAA  
 GAGAUAAAGCUAGCGUCCUAAUCUUAUCCCGGUUAUGGCGCGAA  
 ACUCAGGGAAUCGUCUGUUAUCAUCGCGGUCGAGGAGCC  
 ACAGUUAAAUAUCAAAGACAAGGCUAUGCAUGUAGAGCUAAA  
 GCGAGAGGACUUGCGGACGCGG

18

*Listeria grayi* ssrA, Internal Partial

SEQ ID NO: 51  
 5 ACAGGGATAGGTCGAGCTTGTAGTTGCGAGCCGGGGGATCGGCC  
 CGTCATCAACGTCAAAGCCAATAATAACTGGCAAACAAAACAAC  
 AATTTAGCTTTTCGCTGCCTAATAGCAGTCTGAATAGCTGATCCTC  
 10 CGTGCATCACCATGTGCTACGGTAAGGGTCTCACTTTTAAAGTGG  
 GTTACGCTGGCTTATCTCCGTCTGGGGCAAACGAGAAGAGCATA  
 ATCAGACTAGCTAGATAGAGCCCTGACGCCGGGCAGACATCTAT  
 15 GCGAAATCCAAATACGGCAACTACGCTCGTAGATGCTCAAGTGC  
 CGATATTTCTGG

*Listeria grayi* tmRNA, Internal Partial

SEQ ID NO: 52  
 20 ACAGGGAUAGGUCGAGCUUGAGUUGCGAGCCGGGGGAUCGG  
 CCCGUCAUCAACGUCAAAGCCAUAUAACUGGCAAACAAAAC  
 AACAAUUUAGCUUUCGUGCCUAAUAGCAGUCUGAAUAGCUG  
 25 AUCCUCCGUGCAUCACCCAUGUGCUACGGUAAGGGUCACACU  
 UUAAGUGGGUUCGUCGCUUUAUCUCCGUCUGGGCAAACGA  
 GAAGAGCAUAAUCAGACUAGCUAGAUAGAGCCUGACGCCGGG  
 30 CAGACAUCUAUGCGAAAUCCAAUACGGCAACUACGUCUGUAG  
 AUGCUCAAGUGCCGAUUAUUCUGG

*Listeria innocua* ssrA, Internal Partial

SEQ ID NO: 53  
 35 ACAGGGATAGTTCGAGCTTGTAGTTGCGAGTCCGGGGGATCGTCC  
 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAACA  
 40 AAACCTAGCTTTTCGCTGCCAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG  
 GGCTACACTAGTTAATCTCCGTCGAGGTTAAATAGAAGAGCTT  
 45 AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA  
 TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTCAAGTG  
 CCGATATTTCTGG

*Listeria innocua* tmRNA, Internal Partial

SEQ ID NO: 54  
 55 ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGAUCGU  
 CCUCGUUAUCAACGUCAAAGCCAUAUAUACUGGCAAAGAAA  
 ACAAAAACCUAGCUUUCGUCGCUAAUUAAGCAGUAGCAUAGCUG  
 AUCCUCCGUGCAUCGCCAUGUGCUACGGUAAGGGUCACACUC  
 60 UAAGUGGGCUACACUAGUUAUUCUCCGUCUGAGGUUAAAUAG  
 AAGAGCUUAAUCAGACUAGCUGAAUGGAGCCUGUUAACCGGG  
 CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGUCUGUA  
 65 GAUAUUCAGUGCCGAUUAUUCUGG

*Listeria monocytogenes* (NCTC 7973) *ssrA*, Internal Partial

SEQ ID NO: 55  
 ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGATCGTCC  
 5  
 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA  
 AAACCTAGCTTTCGCTGCCAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG  
 10  
 GGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTT  
 AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA  
 TCGCAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG  
 CCGATATTTCTGG

*Listeria monocytogenes* (NCTC 7973) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGAUCGU  
 CCUCGUUAUCAACGUCAAAGCCAUAUAUACUGGCAAAGAAAA  
 ACAAAAACCUAGCUUUCGUGCCUAUAUAGCAGUAGCAUAGCUG  
 25  
 AUCCUCCGUGCAUCGCCAUGUGCUACGGUAAGGGUCUCACUC  
 UAAGUGGGCUACACUAGUUAUUCUGUCUGGGGUAAAUAG  
 AAGAGCUUAUCAGACUAGCUGAAUGGAAGCCUGUUAACCGGG  
 CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGUCUGUA  
 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

CAAAGCCAUAUAUACUGGCAAAGAAAAACAAAACCUAGCUU  
 UCGCUGCCUAUAUAGCAGUAGCAUAGCUGAUCCUCCGUGCAUC  
 GCCAUGUGCUACGGUAAGGGUCUCACUCUAAGUGGGCUACAC  
 UAGUUAAUCUCCGUCUGGGUUAAAAGAAGAGCUUAUUCAG  
 ACUAGCUGAAUGGAAGCCUGUUAACCGGGCCGAGUUUAUGCG  
 AAAUGCUAAUACGGUGACUACGUCUGUAGAUUUU  
 SEQ ID NO: 58

*Listeria murrayi* *ssrA*, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGATCGTCC  
 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

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AAACCTAGCTTTCGCTGCCAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG  
 GGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTT  
 AATGAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA  
 TCGCAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG  
 CCGATATTTCTGG SEQ ID NO: 59

*Listeria murrayi* tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGAUCGU  
 CCUCGUUAUCAACGUCAAAGCCAUAUAUACUGGCAAAGAAAA  
 ACAAAAACCUAGCUUUCGUGCCUAUAUAGCAGUAGCAUAGCUG  
 20  
 AUCCUCCGUGCAUCGCCAUGUGCUACGGUAAGGGUCUCACUC  
 UAAGUGGGCUACACUAGUUAUUCUGUCUGAGGUAAAUAG  
 AAGAGCUUAUAGAGACUAGCUGAAUGGAAGCCUGUUAACCGGG  
 25  
 CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGUCUGUA  
 GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 60

*Listeria welshimeri* *ssrA*, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGATCGTCC  
 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA  
 AAACCTAGCTTTCGCTGCCAATAAGCAGTAGCATAGCTGATCCT  
 35  
 CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG  
 GGCTACACTGGCTAATCTCCGTCTGAGGTTAGTTGGAAGAGCTT  
 AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA  
 40  
 TCGCAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG  
 CCGATATTTCTGG SEQ ID NO: 61

*Listeria welshimeri* tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGAUCGU  
 CCUCGUUAUCAACGUCAAAGCCAUAUAUACUGGCAAAGAAAA  
 ACAAAAACCUAGCUUUCGUGCCUAUAUAGCAGUAGCAUAGCUG  
 50  
 AUCCUCCGUGCAUCGCCAUGUGCUACGGUAAGGGUCUCACUC  
 UAAGUGGGCUACACUGGCUAAUUCUGUCUGAGGUUAGUUGG  
 AAGAGCUUAUCAGACUAGCUGAAUGGAAGCCUGUUAACCGGG  
 55  
 CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGUCUGUA  
 GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 62

*Marinobacter hydrocarbonoclasticus* *ssrA*, Internal Partial

GCCGGTGACGAACCCTTGGGTGCATGCCAGATGGCAGCGAATC  
 TCGTAAATCCAAAGCTGCAACGTAATAGTCGCAAACGACGAAAA  
 65  
 CTACGCACCTGGCGGCGTAAGCCGTTCCAGTCGCTCTGGCTGAGG

21

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CGCCTATAACTCAGTAGCAACATCCCAGGACGTCATCGCTTATA  
 GGCTGCTCCGTTACCAGAGCTCACTGGTGTTCGGCTAAGATTAA  
 AGAGCTCGCCTCTTGCAACCTGACCTTCGGGTCGCTTGAGGTTAA 5  
 ATCAATAGAAGGACACTAAGGATGTAGACCTCAAGGCCTAGTGC  
 TGGCGGACGCGG SEQ ID NO: 63

*Marinobacter hydrocarbonoclasticus* tmRNA, Internal Partial 10

GCCGGUGACGAACCCUUGGGUGCAUGCCGAGAUGGCAGCGAAU  
 CUCGUAAAUCCAAAGCUGCAACGUAAUAGUCGCAAAACGACGAA  
 AACUACGCACUGGCGGCGUAAGCCGUUCCAGUCGUCUUGGCUG  
 AGGCGCCUAUAACUAGUAGCAACAUCAGGACGUAUCGCU  
 UAUAGGCGUCUCCGUUACAGAGCUCACUGGUGUUCGGCUAA 20  
 GAUUAAGAGCUCGCCCUCUUGCACCUCGACCUUCGGGUCGCU  
 GAGGUUAAAUCAAUAGAAGGACUAAGCAUGUAGACCUCAA  
 GGCCUAGUGCUGGCGGACGCGG SEQ ID NO: 64

*Mycobacterium avium* ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA  
 CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTACACATC  
 AGCGCGACTTACCTCTCGCTGCCAAGCGACAGCTAGTCCGTCA  
 GCCCGGGAACGCCCTCGACCCGGAGCCTGGCGTCACTAGAGGG  
 ATCCACCGATGAGTTCGGTCGCGGGACTCATCGGACACCAACA 35  
 GCGACTGGGATCGTCATCTGGCTTGTTCGCGTACAGGAGAT  
 CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG  
 GAATGCCGTAGAACCCGGGTTTCGATTCCCAA SEQ ID NO: 65

*Mycobacterium avium* tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG  
 ACCACCGUAAGCGUCGUUUGCAAUAGAUAGCGCCGAUUCACA  
 UCAGCGGACUUAACUUCGUCGCUUAAGCGACAGCUAGUCCG  
 UCAGCCCGGGAACGCCUCGACCCGGAGCCUGGCGUCAGCUAG  
 AGGGAUCCACCGAUGAGUUCGUGCGCGGACUCAUCGGGACAC  
 CAACAGCGACUGGGAUCGUAUCUUGGCUUUGUCGUGACCA  
 GGAGAUCGAGUAGAGGCAUAGCGAACUGCGACGGAGAAGCC  
 UUGAGGGAUUGCCGUAAGCCGGGUUCGAUUCCAA  
 SEQ ID NO: 66

*Mycobacterium bovis* ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGAG  
 ACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTACACAT  
 CAGCGCGACTACCTCTCGCTGCCAAGCGACAGCTAGTCCGTCA

22

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GACCCGGGAACGCCCTCGGCCCGGACCCCTGGCATCAGCTAGAGGG  
 ATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAACCACA  
 GCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCCGGGAGAT  
 CCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG  
 GAATGCCGTAGG SEQ ID NO: 67

*Mycobacterium bovis* tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAGAG  
 ACCACCGUAAGCGUCGUUUGCGACCAAUAAGCGCCGAUUCACA  
 UCAGCGGACUACGUCUCGUCGCUAAGCGACGGCUAGUCUGU  
 CAGACCCGGGAACGCCUCGCGCCGGACCCUGGCAUCAGCUAGA  
 GGGAUCCACCGAUGAGUCCGGUCGCGGGACUUCGCGGACAAAC  
 CACAGCGACUGGGAUCGUAUCUCGGCUAGUUCGCGUGACCCG  
 GAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAGCCU  
 UGAGGGAUUGCCGUAGG SEQ ID NO: 68

*Mycobacterium leprae* ssrA

GGGGCTGAAAGGTTTCGACTTCGCGCATCGAATCAAGGGAAGCG  
 TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCGTTGCAGCAAT  
 ATAAGCGCCGATTATATCAGCGCGACTATGCTCTCGCTGCCTAA  
 GCGATGGCTAGTCTGTGACAGCCGGGAACGCCCTCGTCCGGGAC  
 CTGGCATCAGCTAGAGGATCTACCGATGGGTTTCGGTCCGGGA  
 CTCGTCGGGACACCAACCGCGACTGGGATCGTCATCTGGCTAG  
 TTCGCGTGATCAGGAGATCCGAGTAGAGGCATAGCGAACTACGC  
 ACGGAGAAGCCTTGAGGGAATGCCGTAGGACCCGGGTTTCGATT  
 CCCGGCAGCTCCACCA SEQ ID NO: 69

*Mycobacterium leprae* tmRNA

GGGGCUGAAAGGUUCGACUUCGCGCAUCGAAUCAAGGGAAG  
 CGUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUUUGCAGC  
 AAUAUAAGCGCCGAUUCUAUACAGCGGACUAUGUCUCGUCUG  
 CCUAAGCGAUGGCUAGUCUGUCAGACCCGGGAACGCCUCGUCC  
 CGGAGCCUGGCAUCAGCUAGAGGGAUCUACCGAUGGGUUCGGU  
 CGCGGGACUCGUCGGGACACCAACCGGACUGGGAUCGUAUC  
 CUGGCUAGUUCGCGUGAUCAGGAGAUCGAGUAGAGGCAUAG  
 CGAACUACGCACGGAGAAGCCUUGAGGGAAAUGCCGUAAGGACC  
 CGGGUUCGAUUCGGGACGACUCCACCA SEQ ID NO: 70

60 *Mycobacterium paratuberculosis* ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA  
 CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTACACATC  
 AGCGCGACTTACCTCTCGCTGCCAAGCGACAGCTAGTCCGTCA

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GCCCCGGGAACGCCCTCGACC CGGAGCCTGGCGTCAGCTAGAGGG  
 ATCCACCGATGAGTTCGGTTCGGGACTCATCGGGACACCAACA  
 GCGACTGGGATCGTCATCCTGGCTGTTCGCGTGACCAGGAGAT  
 CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG  
 GAATGCCGTAGAACC CGGGTTCGATTCCCAA SEQ ID NO: 71

*Mycobacterium paratuberculosis* tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG  
 ACCACCGUAAGCGUCGUGCAAUAGAUAAAGCGCCGAUUCACA  
 UCAGCGCGACUUAACUCUCGUCGCCUAAGCGACAGCUAGUCCG  
 UCAGCCCGGGAACGCCUCGACC CGGAGCCUGGCGUCAGCUAG  
 AGGGAUCCACCGAUGAGUUCGGUCGCGGGACUCAUCGGGACAC  
 CAACAGCGACUGGGAUCGUAUCUGGCUUUGUUCGCGUGACCA  
 GGAGAUCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAAGCC  
 UUGAGGGAUUGCCGUAAGAACCGGGUUCGAUUC CCAA  
 SEQ ID NO: 72

*Mycobacterium tuberculosis* ssrA

GGGGCTGAACGGTITCGACITCGCGCATCGAATCAAGGGAAGCG  
 TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCTGTCGACCAA  
 ATAAGCGCCGATTACATCAGCGCGACTACGCTCTCGCTGCCTA  
 AGCGACGGCTAGTCTGTCTAGACC GGGAACGCCCTCGGCCCGGAC  
 CCTGGCATCAGCTAGAGGGATCCACCGATGAGTCCGGTCGCGGG  
 ACTCCTCGGGACAACCACAGCGACTGGGATCGTCATCTCGGCTA  
 GTTCGCGTGACCGGGAGATCCGAGCAGAGGCATAGCGAACTGCG  
 CACGGAGAAGCCTTGAGGGAATGCCGTAGGACCCGGGTTTCGATT  
 CCCGGCAGCTCCACCA SEQ ID NO: 73

*Mycobacterium tuberculosis* tmRNA

GGGGCUGAACGGUUUCGACUUCGCGCAUCGAAUCAAGGGAAGC  
 GUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUGCGACC  
 AAAUAAGCGCCGAUUCACAUACAGCGGACUACGUCUCGCGUC  
 CUAAGCGACGGCUAGUCUGCAGACC GGGAACGCCCCUCGGCCC  
 GGACCCUGGCAUCAGCUAGAGGGAUCCACCGAUGAGUCCGGUC  
 GCGGGACUCCUCGGGACAACCACAGCGACUGGGAUCGUCAUCU  
 CGGCUAGUUCGCGUGACCGGGAGAUCGAGCAGAGGCAUAGCG  
 AACUGCGCACGGAGAAGCCUUGAGGGAUUGCCGUAAGACCCGG  
 GUUCGAUUCGCCGAGCUCACCA SEQ ID NO: 74

*Mycoplasma capricolum* ssrA

GGGGATGTCATGGATTTGACAGGATATCTTTAGTACATATAAGC  
 AGTAGTGTGTAGACTATAAATACTACTAGGITIAAAAAACGC

24

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AAATAAAAACGAAGAACTTTTGAAATGCCAGCATTTATGATGA  
 ATAATGCATCAGCTGGAGCAAACCTTATUTTTGCTTAATAACTAC  
 5 TAGTTTAGTTATAGTATTTTACGAATTATAGATATTTAAGCTTT  
 ATTTATAACCGTATTACCCAAGCTTAATAGAAATATATGATTGCAA  
 TAAATATATTTGAAATCTAATGCAAAATGATATTTAACCTTTAGT  
 10 TAATTTTAGTTAAATATTTTAAATTAGAAAATTAATAAACTGTAG  
 AAAGTATGTATTAATATATCTTGGACGCGAGTTCGATTCTCGCCA  
 TCTCCACCA SEQ ID NO: 75

15 *Mycoplasma capricolum* tmRNA

GGGGAUGUCAUGGAUUUGACAGGAUAUCUUUAGUACAUAUAA  
 GCAGUAGUGUUGUAGACUAUAAAUAUCUAGGUUUAAAAAA  
 20 ACGCAAUAAAAACGAAGAAAUUUUGAAAUGCCAGCAUUUA  
 UGAUGAAUAUGCAUCAGCUGGAGCAAAUUUAUGUUUGCUU  
 AAUAACUAUCUAGUUUAGUUUAGUUAUUUCACGAAUUUAAGAU  
 25 AUUUUAAGCUUUUUUAUAACCGUALTUACCAAGCUUAUAG  
 AAUAUAUGAUUGCAAUAAAUAUUUUGAAAUCUAAUUGCAA  
 UGAUUAUUUAACUUUAGUUAUUUUUAGUUAUUUAUUUUAAU  
 30 AGAAAAUUUAACUAAACUGUAGAAAGUAUGUUAUUAUUAUCU  
 UGGACGCGAGUUCGAUUCUGCCAUCUCCACCA SEQ ID NO: 76

*Mycoplasma genitalium* (ATTC 33530, #1) ssrA

GGGGATGTTTTGGGTTTGACATAATGCTGATAGACAAACAGTAG  
 CATTGGGGTATGCCCTTACAGCGCTAGGTTCAATAACCGACAA  
 40 AGAAAAAACGAAGTGTGGTAGAACCAAAITGATCATTAACC  
 AACAAAGCAAGTGTAAAGCTTTGCTTTTGCATAAGTAGATACTAAA  
 GCTACAGCTGGTGAATAGTCATAGTTTGTCTAGCTGTCATAGTTTA  
 45 TGACTCGAGGTTAAATCGTTCAATTTAACCTTTAAAAATAGAACT  
 TGTGTTTTCCATGATTGTTTTGTGATCAATTGGAACCAAGACAAA  
 AATCCACAAAACATAAATGTAGAAGCTGTTGTTGTCTTTTAT  
 50 GGAAACGGGTTTCGATTCCCGTCATCTCCACCA SEQ ID NO: 77

*Mycoplasma genitalium* (ATTC 33530, #1) tmRNA

GGGGAUGUUUUGGGUUUGACAUAUAGUCGUAUAGACAAAACAGU  
 55 AGCAUUGGGGUAUGCCCUUACAGCGCUAGGUUCAUAACCGA  
 CAAAGAAAUAACGAAGUGUUGGUAAGAACAAAUUUGAUCAU  
 UAACCAACAGCAAGUGUUAACUUUGCUUUUGCAUAAGUAGA  
 60 UACUAAAGCUACAGCUGGUAUAGUCUAVAGUUUGCUAGCUG  
 UCAUAGLTUUAUGACUCGAGGUUAAAUCGUUCAUUUAACCUU  
 UAAAAUAGAACUUGUUGUUUCAUGAUUGUUUUGUGAUCAA  
 65 UUGGAAACAGACAAAAUCCACAAAACUAAAAUGUAGAAGC

25

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UGUUUUGUUGUCCUUUAUGGAAACGGGUUCGAUUCCEGUA

UCUCCACCA SEQ ID NO: 78

*Mycoplasma genitalium* (ATCC 33530, #2) tmRNA, Internal Partial

ACATAATGCTGATAGACAAACAGTAGCATTGGGGTATGCCCTT  
 ACAGCGCTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGT  
 GGTAGATCCAATTTGATCATTAAACCAACAGCAAGTGTAACT  
 TTGCTTTTGCATAAGTAGATACTAAAGCTACAGCTGGTGAATAGT  
 CATAGTTTGTAGCTGTCATAGTTTATGACTCGAGGTTAAATCGT  
 TCAATTTAACCTTTAAAAATAGAAGTGTGTTTCCATGATTGTT  
 TTGTGATCAATTGGAAACAAGACAAAAATCCACAAAATAAAAT  
 GTAGAAGCTGTTTGTGTGTCTTTATGGAAACGGGTTT

SEQ ID NO: 79

*Mycoplasma genitalium* (ATCC 33530, #2) tmRNA, Internal Partial

ACAUAUUGCUGAUAGACAAACAGUAGCAUUGGGUUAUGCCCC  
 UUAACAGCGCUAGGUUCAAUAACCGACAAAGAAAUAACGAAG  
 UGUUGGUAGAUCCAAUUUGAUCAUUAACCAACAGCAAGUG  
 UUAACUUUGCUUUUGCAUAAGUAGAUCAUAAAGCUACAGCUG  
 GUGAAUAGUCAUAGUUUGCUAGCUGUCAUAGUUUAUGACUG  
 AGGUUAAAUCGUUCAUUUAACCUUUAAAAUAAGAUCUUGUU  
 GUUUCCAUGAUUUUGUGAUCAAUUGGAAACAAGACAAAA  
 AUCCACAAAACUAAAUGUAGAAGCUGUUUGUUGUCUUU  
 AUGGAAACGGGUUC SEQ ID NO: 80

*Mycoplasma Pneumophila* ssrA

GGGGATGTAGAGTTTTGACATAATGTTGAAAGGAAAACAGTTG  
 CAGTGGGGTATGCCCTTACAGCTCTAGGTATAATAACCGACAA  
 AAATAACGACGAAGTTTTGGTAGATCCAATGTTGATCGCTAAC  
 AACAGCAAGTATCAACTACGCTTTTCGCTTAGAACATACTAAAG  
 CTACACGAATTGAATCGCCATAGTTTGGTTCGTGTCACAGTTTAT  
 GGCTCGGGTTAACTGGTTCAACTTAATCCTTAAATTATGAACTT  
 ATCGTITACTTGTITGTCTTATGATCTAAAGTAAGCGAGACATTA  
 AAACATAAGACTAACTGTAGAGCTGTTTTACCAATCCTTTATG  
 GAAACGGGITCGATTCCCGTCATCTCCACCA SEQ ID NO: 81

*Mycoplasma pneumophila* tmRNA

GGGGAUGUAGAGGUUUUGACAUAAUGUUAAGGAAAACAGU  
 UGCAGUGGGUUAUGCCCCUACAGCUCUAGGUUAUAUACCGA  
 CAAAAUAACGACGAAGUUUGUAGAUCCAAUGUUAUCG  
 UAACCAACAAGCAAGUAUCAACUACGCUUUCGUUAAGACAU  
 CUAAGCUCACGAAUUGAAUCGCCAUAGUUUGUUCGUGUC

26

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ACAGUUUAUGGCUCGGGUUAACUGGUUACAACUUAAUCCUUA

AAUUAUGAACUUUACGUUUACUUGUUUGUCUUAUGAUCUAAA

GUAAGCGAGACAUUAAAACAUAGACUAAACUGUAGAAGCUG

UUUUACCAAUCCUUUAUGGAAACGGGUUCGAUUCCEGUAUCU

CCACCA SEQ ID NO: 82

*Neisseria gonorrhoeae* (ATCC 19424) ssrA, Internal Partial

GGGGTTCGGAAGCAGATGCGGGCATAACCGGGTCTCAGATTCC  
 CGTAAAACACTGAATTCAAATAGTCGAAACGACGAACTTACG  
 CTTTAGCCGCTTAAGGCTAGCCGTTGACGAGTCGGTCAATGGG  
 CTGTGTGGCGAAAGCCACCGCAACGTCATCTTACATTGACTGGTT  
 TCCAGCCGGTTACTTGGCAGGAAATAAGACTTAAGGTAAGTGG  
 TTTCCAAAAGGCTGTIGGTCGGCATGATGGAAATAAGATTTTC  
 AAATAGACACAACCTAAGTATGTAGAACGCTTTGTAGAGGACTTT

25 CGGACGGGG SEQ ID NO: 83

*Neisseria gonorrhoeae* (ATCC 19424) tmRNA, Internal Partial

GGGGUUGCGAAGCAGAUGCAGGCAUACCGGGUUCUAGAUU  
 CCCGUAAAACUGAAUCAAUAGUCGAAACGACGAAACUU  
 ACGCUUUAAGCCGUUAAGGCUAGCCGUUGCAGCAGUCGGUCA  
 UGGGCUUGUGGCGAAAGCCACCGCAACGCUCAUCUUAUUA  
 CUGGUUUCAGCCGGGUUAUCUUGCAGGAAUUAAGACUUAAG  
 GUAACUGGUUUCAAAAGGCCUGUUGGUCGGCAUGAUGGAAA  
 UAAGAUUUUCAAAUAGACACAACUAAGUUAUGAAGCUCUU  
 GUAGAGGACUUUCGGACGGGG SEQ ID NO: 84

*Neisseria gonorrhoeae* (FA 1090) ssrA

GGGGCGACCTTGGTTTCGACGGGGTTGCGAAGCAGATCGGG  
 CATACCGGGTCTCAGATTCCTGTAACACTGAATTCAAATAG  
 TCGAAACGACGAACTTACGCTTTAGCCGCTTAAGGCTAGCCG  
 TTGCAGCAGTCGGTCAATGGGCTGTGTTGAAAGCCACCGCAA  
 CGTCATCTTACATTGACTGGTTCCAGCCGGTTACTTGGCAGGA  
 AATAAGACTTAAGGTAAGTGGTTTCCAAAAGGCTGTTGGTCGG  
 CATGATGGAAATAAGATTTTCAAATAGACACAACCTAAGTATGTA  
 GAACGCTTTGTAGAGGACTTTCGGACGGGGTTCGATTCCCCC  
 GCCTCCACCA SEQ ID NO: 85

*Neisseria gonorrhoeae* (FA 1090) tmRNA

GGGGCGACCUUGGUUUCGACGGGGUUGCGAAGCAGAUUCG  
 GGCAUACCGGGUUCAGAUUCCCGUAAAACUGAAUCAA

SEQ ID NO: 86

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AUAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGC  
 UAGCCGUUGCAGCAGUCGGUCAUUGGGCUQUGUGGUGAAAGC  
 CACCGCAACGCAUCUUACAUAUGACUGGUUCCAGCCGGGUU  
 ACUUGGCAGGAAUAAGACUUUAAGGUAACUGGUUUCAAAAG  
 GCCUGUUGGUCGGCAUGAUGGAAUAAGAUUUUCAAUAGAC  
 ACAACUAAGUAUGAAGACGCUUUGUAGAGGACUUUCGGACG  
 GGGGUUCGAUUCGCGCCGCCUCCACCA

*Neisseria meningitidis* *ssrA*

SEQ ID NO: 87  
 GGGGCGACCTTGGTTTCGACGGGGTTGCGAAGCAGATGCGGG  
 CATAACGGGTCTCAGATTCCTGTAACACTGAATTCAAATAG  
 TCGCAAACGACGAACTTACGCTTAGCCGCTTAAGGCTAGCCG  
 TTGCAGCAGTCGGTCAATGGCTGTGTGGCGAAAGCCACCGCAA  
 CGTCATCTTACATTGACTGGTTTCTGCCGGTTATTTGGCAGG  
 AAATGAGATTTAAGGTAAGTGGTTTCCAAAAGCCCTGTTGGTCG  
 GCATGATGAAATAAGATTTTCAAATAGACACAATAAGTATGT  
 AGAACGCTTTGTAGAGGACTTTCGGACGGGGTTCGATTCCCCC  
 CGCTCCACCA

*Neisseria meningitidis* *tmRNA*

SEQ ID NO: 88  
 GGGGCGACCUUGGUUUCGACGGGGUUGCGAAGCAGAUGC  
 GGCAUACCGGGGUCUCAGAUUCCGUAAAACACUGAAUCAA  
 AUAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGC  
 UAGCCGUUGCAGCAGUCGGUCAUUGGGCUGUGGGCGAAAGC  
 CACCGCAACGCAUCUUACAUAUGACUGGUUUCGCGGGGUU  
 AUUUGGCAGGAAUAGAUUUUAAGGUAACUGGUUUCAAAAG  
 GCCUGUUGGUCGGCAUGAUGGAAUAAGAUUUUCAAUAGAC  
 ACAACUAAGUAUGAAGACGCUUUGUAGAGGACUUUCGGACG  
 GGGGUUCGAUUCGCGCCGCCUCCACCA

*Nostoc muscorum* PCC7120 *ssrA*

SEQ ID NO: 89  
 GGGTCCGTCGGTTTCGACAGGTTGGCGAACGCTACTCTGTGATT  
 CAGGTCGAGAGTGAGTCTCCTCTGCAATCAAGGCTCAAACAA  
 AAGTAAATGCGAATAACATCGTTAAATTTGCTCGTAAGGACGCT  
 CTAGTAGCTGCCTAAATAGCCTCTTTGAGGTTGAGCGTCTTCTG  
 GTTTGACTCCGTTAAGGACTGAAGACCAACCCCAACGGATGCT  
 CTAGCAATGTTCTCTGGTTGGCTAGCTAAGATTTAATCAG  
 AGCATCCTACGTTCCGGATAATGAACGATTCGCGCTTGAGGGT  
 CAGAAAGGCTAAACCTGTGAATGAGCGGGGGTCAATACCCAAT  
 TTGGACAGCAGTTCGACTCTGCTCGATCCACCA

28

*Nostoc muscorum* PCC7120 *tmRNA*

SEQ ID NO: 90  
 5 GGGUCCGUCGGUUUCGACAGGUUGGGCAACGCUACUCUGUGA  
 UUCAGGUCGAGAGUGAGUCUCUCUGCAAUAAGGCUCAAA  
 ACAAAGUAAAUGCGAAUAACAUUCGUUAAAUUUGCUCGUAAG  
 10 GACGUCUAGUAGCUGCCUAAAUGCCUCUUUCAGGUUCGAGC  
 GUCUUCGGULTUGACUCCGUUAAAGGACUGAAGACCAACCC  
 AACGGAUGCUCUAGCAAUGUUCUCUGGUUGGCUUGCUAGCUA  
 15 AGAUUUAAUCAGAGCAUCUACGUUCGGGAUUAUGAACGAUU  
 CCCGCCUUGAGGGUCAGAAAGGCUAAACCUGUGAAUGAGCGG  
 CGGGUAAUACCCAAUUUGGACAGAGUUCGACUCUGCUCGA  
 UCCACCA

*Odontella sinensis* (diatom) Chloroplast *ssrA*

SEQ ID NO: 91  
 25 GGGGCTGACTTGGTTTCGACATTTAAAAATTGTTACAGTATGA  
 TGCAGGTCGAAGTTTCTAATCTTCGTAATAAAGAGAAATTA  
 TAATAAATGCTAATAATTAATTTCTTCTGTGTTTAAAGTTT  
 ATCAACTAAGCAAAATAGTTTAAATTTAAGTTTGTCTGTTTAA  
 30 GTTTTATGCACATTTAATGATCTAGTAAATAACTTTGTTCTGCT  
 ATAATTTATATTTATAACTAGACTTTTGTCTTTTATAGTTT  
 AGAATAACTTTATCATTTCAAACCTCGTTCCATCTAGTTGAAC  
 35 TAAACCTGTGAACGAATACTATAATAAATTTTAGATGGACGT  
 GGGTTCGACTCCCATCAGCTCCACCA

*Odontella sinensis* (Diatom) Chloroplast *tmRNA*

SEQ ID NO: 92  
 40 GGGGCGACCUUGGUUUCGACALTUUAAAAUUUGUACAGUAUG  
 AUGCAGGUCGAAGUUUCUAUUCUUCGUAATAAAGAGAAUUTU  
 45 UAUAUAAAUGCUAAUAAUUUUUCUTUCUGUGUUTUAAAA  
 GUUUUAUCAACUAAGCAAAUAGUTUAAAUUUAAGUTTTUTGGC  
 UGUUUUAGUUUUUAGCACAUUUAUGAUCUAGUAAAUAACUUU  
 50 GUUCGCUAAUUUUUAUUUAUAACUAGACUUUUGUCUUUUUU  
 AUAGUUUAGAAUAACULTUAUCAUUUCAACCCUCGUTUCCAUC  
 UAGUUGAACUAAACCUGUGAACGAAUACUAUAUAAAAUUUTU  
 55 UAGAUGGACGUGGUUCGACUCCCAUCAGCUCACCA

*Porphyra purpureum* (Red Alga) Chloroplast *ssrA*

SEQ ID NO: 93  
 60 GGGGCTGCAAGGTTTCTAGATTGTGAAAAACAAATATATGAAA  
 GTAAAAAGAGCTCATTATAGAGCTTTTAGTTAAATAAATGCAG  
 AAAATAATATTATTGCTTTTCTCGAAAATTAGCTGTTGCATAA  
 65 ATAGTCTCAATTTTGTAAATTCGAAGTGATAGACTCTTATACAC

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TACGAATATTCTGTAGAGTTGCTCTTAATAAAAAGAAAAGTAAA  
 AAAAAACAATTTCTTATGTTTTTTACCTGAATTGATTCAATTTA  
 AGGTTAGTATTTTTTGATTTTTACAATGGACGTGGGTTCAAGTC  
 CCACCAGCTCCACCA

*Porphyra purpureum* (Red Alga) Chloroplast tmRNA

SEQ ID NO: 94  
 GGGGUCGCAAGGUUCUACAUAUUGGAAAAACAAAUAUAUGA  
 AAGUAAAACGAGCUCAUUAUAGAGCUUUUAGUAAAAUAAU  
 GCAGAAAAUAAUUAUUGCUUUUUUCGAAAAUAGCUGUU  
 GCAUAAUAGUCUCAUUUUUGUAAUUCGAAGUGAUAGACUC  
 UUAUACACUACGAAUUAUCUGUUAAGAGUUGCUCUAAUAAAA  
 GAAAAGUAAAAAAUACAAUUCUUAUUGUUUUUACCUGAAU  
 UGAUUCAAUUUAGGUUAGUUAUUUUUGAUUUUUACAAUGGA  
 CGUGGGUUAAGUCCACCAGCUCACCA

*Porphyromonas gingivalis* ssrA

SEQ ID NO: 95  
 GGGGCTGACCGGCTTTGACAGCGTGATGAAGCGGTATGTAAGCA  
 TGTAGTGCCTGGTGGCTTGCACTATAATCTCAGACATCAAAAAG  
 TTTAATTGGCGAAAATAACTACGCTCTCGCTGCGTAATCGAAGA  
 ATAGTAGATTAGACGCTTCAATCGCCGCCAAAGTGGCAGCGACGA  
 GACATCGCCCAGCAGCTTTTTCCGAAGTAGCTCGATGGTGGC  
 GTGCTGACAAATCGGGAACCGCTACAGGATGCTTCTGCCTGTG  
 GTCAGATCGAACGGAAGATAAGGATCGTGATTGGGTCGTTTCA  
 GCCTCCGCTCGCTCACGAAAATCCAACGAACTAAACATGTA  
 GAAAGCATATTGATTCATGTTTGGACGAGGTTCAATTCCTC  
 CAGCTCCACCA

*Porphyromonas gingivalis* tmRNA

SEQ ID NO: 96  
 GGGGUCGACCGCUUUGACAGCGUGAUGAAGCGGUAUGUAAG  
 CAUGUAGUGCGUGGUGGUCUUGCACUAUAUUCAGACAUC  
 AAAGUUAAUUGGCAAAUAACUACGCUUCGCGUGCGUAU  
 CGAAGAAUAGUAGAUUAGACGCUUCAUCGCCGCCAAAGUGGC  
 AGCGACGAGACAUCGCCGAGCAGCUUUUUCCGAAGUAGCU  
 CGAUGGUGCGGUGCUGACAAUCCGGAAACCGCUACAGGAUGC  
 UUCUGCCUGUGGUCAGAUACGGAAGAUAGGAUCGUGC  
 AUUGGGUCGUUCAGCCUCCGUCGUCACGAAAAUCCAAC  
 UGAAACUAAACUAGUAGAAAGCAUAUUGAUUCCAUUUUGGA  
 CGAGGGUUAUUCUCCAGCUCACCA

*Proteus rettgeri* ssrA (NCTC 10975), Internal Partial

SEQ ID NO: 97  
 5 GGGATTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTGGCC  
 TCGTAAAAAGCCGCAAAAAATAGTCGCAACGACGAAAACTA  
 CGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTA  
 10 GCCTCCGCTCTTGGACGGGATCAAGAGAGGTCAAACCCAAA  
 GAGATCGCGTGGATGCCTTGCCTGGGGTTGAGCGTTAAACTT  
 AATCAGGATAGTTTGTGGTGGCGTGTCTGTCCGAGCTGGCA  
 AAATGATTCAAAGACTAGACTAAGCATGTAGTACCGAGGATGT  
 15 AGAAATTC

*Proteus rettgeri* tmRNA (NCTC 10975), Internal Partial

SEQ ID NO: 98  
 20 GGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGCGGUUGGC  
 CUCGUAAAAAGCCGCAAAAAUAGUCGCAACGACGAAAAAC  
 UACGCUUAGCAGCUUAAUACCUGCUUAGAGCCUCUCUCC  
 25 CUAGCCUCGCUUUGGACGGGGAUCAAGAGAGGUCAAACCC  
 AAAAGAGAUCCGUGGAGUCCUUGCCUGGGUUGAAGCGUUA  
 AACUUAAUCAGGAUAGUUUGUUGGUGGCGUGUCUCCGACG  
 30 CUGGCAAAUGAAUCAAAGACUAGACUAAAGCAUGUAGUACCG  
 AGGAUGUAGAAUUUC

*Pseudoalteromonas haloplanktoni* ssrA, Internal Partial

SEQ ID NO: 99  
 35 GGAATTCAGAAGCCGAGGTGCATGTCGAGGTGCGGTTTGCCT  
 CGTAAAAAGCCGCAATTTAAAGTAATCGCAACGACGATAACT  
 40 ACTCTCTAGCAGCTTAGGCTGGCTAGCGCTCCTTCCATGTATTC  
 TTGTGGACTGGATTTGGAGTGTACCCTAACACCTGATCGGA  
 CGGAAACCTGGCCGGGTTGAGCGTTAAACTAAGCGCCCTC  
 45 GCCTTTATCTACCCTGTTGTCCGGGATTTAAAGGTTAATTA  
 TGACAATACTAAACATGTAGTACCGACGTCGAGGCTTTTCGGA  
 CGGGG

*Pseudoalteromonas haloplanktoni* tmRNA, Internal Partial

SEQ ID NO: 100  
 55 GGAAUUAAGAAGCCGAGGUGCAUGUCGAGGUGCGGUUUGC  
 CUCGUAAAAAGCCGCAUUUAAAGUAAUUCGCAACGACGUAU  
 AACUACUCUAGCAGCUUAGGCGUGGCUAGCGCUUUUCCAU  
 60 GUAUUCUUGGACUGGAUUUUGGAGUGUACCCUAAACACCU  
 GAUCGCGACGGAACCCUGGCCGGGUUGAAGCGUAAAAUCU  
 AAGCGCCUCGCUUUUACUACCGUGUUGUCCGGGAUUUAA  
 AGGUUAAUAAUAGCAAUACUAAACAUGUAGUACCGACGGU  
 65 CGAGGCUUUUCGACGGGG

31

*Pseudomonas aeruginosa* *ssrA*

SEQ ID NO: 101  
 GGGGCGATTAGGATTTCGACGCCGGTAACAAAAGTTGAGGGGCA  
 5 TGCCGAGTTGGTAGCAGAACTCGTAAATTCGCTGCTGCAAACCT  
 ATAGTTGCCAACGACGACAACCTACGCTCTAGCTGCTTAATGCGG  
 CTAGCAGTCGCTAGGGGATGCCTGTAAACCCGAAACGACTGTCA  
 10 GATAGAACAGGATCGCCGCCAAGTTTCGCTGTAGACGTAACGGCT  
 AAAACTCATAACAGTCGCTCCAAGCACCCCTGCCACTCGGGCGGC  
 GCGGAGTTAACTCAGTAGAGCTGGCTAAGCATGTAAAACCGATA  
 15 GCGGAAAGCTGGCGGACGGGGTTCAAATCCCCCGGTTCCACC  
 A

*Pseudomonas aeruginosa* *tmRNA*

SEQ ID NO: 102  
 GGGGCGAUUAGGAUUCGACGCCGGUAAACAAAAGUUGAGGGGCA  
 UGCCGAGUUGUAGCAGAACUCGUAAAUUCGUCGUCGCAAACUU  
 AUAGUUGCCAACGACGACAACUACGCUUAGCUGCUUAAUUGCGG  
 CUAGCAGUCGCUAGGGGUGCCUGUAAAACCCGAAACGACUGUCA  
 GAUAGAAGAGGAUCGCCGCCAAGUUCGUCGUGAGCGUAACGGCU  
 30 AAAACUCUAUCAGCUCGUCCKAGCACCCUGCCACUCGGGCGGC  
 GCGGAGUUAACUCAGUAGAGCUGGCUAAGCAUGUAAAACCGAUA  
 GCGGAAAGCUGGGCGGACGGGGUUA AAAUCCCCCGGUUCCACC  
 A

*Salmonella typhimurium* *ssrA*

SEQ ID NO: 103  
 GGGGCTGATTCTGGATTTCGACGGGATTTGCGAAACCAAGGTGC  
 40 ATGCCGAGGGGCGGTTGGCTTCGTAAAAAGCCGCAAAAAATAG  
 TCGCAAAACGACGAAACCTACGCTTTAGCAGCTTAATAACCTGCT  
 TAGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAA  
 GAGAGGTCAAACCCAAAAGAGATCGCGGGATGCCCTGCCTGGG  
 GTTGAAGCGTTAAACGAATCAGGCTAGTCTGGTAGTGGCGTGT  
 CCGTCCGAGGTGCCAGGCGAATGTAAGACTGACTAAGCATGT  
 50 AGTACCGAGGATGTAGGAATTTCCGACGCGGGTTCAACTCCCGC  
 CAGCTCCACCA

*Salmonella typhimurium* *tmRNA*

SEQ ID NO: 104  
 GGGGCGAUUUCUGGAUUCGACGGGAUUUGCGAAACCAAGGUGC  
 AUGCCGAGGGGCGGUGGCCUCGUAAAAGCCGCAAAAAAUAG  
 UCGCAAAACGACGAAACCUACGCUUAGCAGCUUAAUAAACUAGCU  
 UAGAGCCUCUCUCCUAGCCUCGCUUAGGACGGGGAUCAA  
 GAGAGGUCAAACCCAAAAGAGAUCCGCGGAUGCCUUGCCUGGG  
 60 GUUGAAGCGUUAACGAAUCAGGCUAGUCUGGUAGUGGCGUGU

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CCGUCCGAGGUGCCAGGCGAAUGUAAAGACUGACUAAGCAUGU  
 AGUACCGAGGAUGUAGGAAUUUCGACGCGGGUUAACUCCCGC  
 5 CAGCUCCACCA

*Shewanella putrefaciens* *ssrA*

SEQ ID NO: 105  
 10 GGGGCGGATTCTGGATTTCGACAGGATTACGAAAACCTGGGAGC  
 ATGCCGAGGGGCGGTTGGCTCGTAAAAAGCCGCAAAGTTATAG  
 TTGCAAACGACGATAACTACGCTCTAGCCGCTTAATGCCGCTAG  
 15 CCATCTACCACACGCTTTGCACATGGGCAGTGGATTTGATGGTC  
 ATCTCACATCGTGTAGCGAGGGAACCTGTCTGGGGTGAACC  
 GCGAAACAGTACCGGACTCACCGTGTGGGATCCTGTCTTTCCGA  
 GTTCAAACGGTTAAACAATAGAAAGACTAAGCATGTAGCCCTT  
 20 GGATGTAGTTTTCTGGACGCGGGTTCAAGTCCCGCCCTCCA  
 CCA

*Shewanella putrefaciens* *tmRNA*

SEQ ID NO: 106  
 GGGGCGAUUUCUGGAUUCGACAGGAUUCACGAAAACCTGGGAGC  
 AUGCCGAGGGGCGGUGGCCUCGUAAAAGCCGCAAAGUUUAUG  
 30 UUGCAAACGACGAUAAACUACGCUUAGCCGCUUAAUUGCCGCUAG  
 CCAUCUACACACGCUUUGCACAUGGGCAGUGGAUUUGAUGGUC  
 AUCUCACAUCGUCUAGCGAGGGAACCCUGUCUGGGGUGAACC  
 35 GCGAAACAGUACCGGACUCACCGUUGGGAUCUGUCUUUCGGA  
 GUUCAAAACGGUUTAAACAAGAAAGACUAAGCAUGUAGCCCU  
 UGGAUGUAGGUUUUCUGGACGCGGGUUAAGUCCCGCCGCCUCC  
 40 ACCA

*Staphylococcus aureus* *ssrA*

SEQ ID NO: 107  
 45 GGGGCGTTCATGGATTTCGACAGGGTCCCCGAGCTCATTAAG  
 CGTGTCCGAGGGTTGTCTTCGTCATCAACACACACAGTTTATAA  
 TAACTGGCAAAATCAAACAATAATTTTCGAGTAGCTGCCTAATCG  
 50 CACTCTGCATCGCCTAACAGCATTTCTATGTGCTGTAAACGCG  
 ATTCAAACCTTAATAGGATATGCTAAACACTGCCGTTTGAAGTCT  
 GTTTAGAAGAACTTAATCAAACCTAGCATCATGTTGGTTGTTTA  
 55 TCACTTTTCATGATGCGAAACCTATCGATAAACTACACACGTAG  
 AAAGATGTGATCAGGACCTTTGGACGCGGGTTCAAATCCCGCC  
 GTCTCCACCA

*Staphylococcus aureus* *tmRNA*

SEQ ID NO: 108  
 GGGGCGUUAUGGAUUCGACAGGGGUCGCCGAGCUAUUAAG  
 CGUGUCGGAGGGUUGUCUUCGUCAUCAACACACACAGUUUAUA  
 65 UAACUGGCAAAUCAAAACAUAUUUCGAGUAGCUGCCUAAUCG

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CACUCUGCAUCGCCUAACAGCAUUUCCUAUGUGCUGUUAACGCG  
 AUUCAACCUAAUAGGAUUAUGCUAAACACUGCCGUUUGAAGUCU  
 GUUUAGAAGAAACUUAUCAAACUAGCAUCAUGUUGGUUUGUUA  
 UCACUUUUAUGAUGCGAAACCUAUCGAUAAACUACACACGUAG  
 AAAGAUGUGUAUCAGGACCUUUGGACGCGGGUUCAAAUCCCGCC  
 GUCUCCACCA

*Streptococcus gordonii* ssrA

SEQ ID NO: 109  
 GGGGTCGTTACGGATTTCGACAGGCATTATGAGGCATATTTTGCG  
 ACTCATCTAGCGGATGTAACACGCCAGTTAAATATAACTGCAAA  
 AAATAATACTTCTTACGCTTATAGTGCCTAAAAACCAGCGGGCG  
 TGACCCGATTTCGGATTGCTTGTGTCTGATGACAGGCTTATTAT  
 TAGCAAGCTACGGTAGAATCTTGTCTAGTGATTTTACAAGAGAT  
 TGATAGACTCGCTTATTTGGGCTTGTGTTATGTGTCAAATCA  
 AGTTAAAACAATACATAGCCATGTTGTAGACAAATGTGTTGG  
 CAGATGTTTGGACGTGGGTTGACTCCACCAGCTCCACCA

*Streptococcus gordonii* tmRNA

SEQ ID NO: 110  
 GGGGUCGUUACGGAUUCGACAGGCAUUUAGAGGCAUUAUUUGCG  
 ACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGCAAA  
 AAAUAUAUCUUUACGCUUAGCUGCCUAAAAACCAGCGGGCG  
 UGACCCGAUUCGGAUUGCUUGUGUCUGAUGACAGGUUUUAUUU  
 UAGCAAGCUACGGUAGAAUCUUGUCUAGUGAUUUUAACAAGAGAU  
 UGAUAGACUCGCUUGAUUUGGCUUGAGUUUUGUGUCAAUAUCA  
 AGUUAAAACAUAUAAGCCUUAUGGUUGUAGACAAAUGUGUUGG  
 CAGAUGUUUGGACGUGGUUCGACUCCACCAGCTCCACCA

*Streptococcus mutans* ssrA

SEQ ID NO: 111  
 GGGGTCGTTACGGATTTCGACAGGCATTATGAGACCTATTTTGCG  
 ACTCATCTAGCGGATGTAACACGCCAGTTAAATATAACTGCAAA  
 AAATACAAATCTTACGCGTAGTGCCTAAAAACCAGCCTGTG  
 TGATCAATAACAAATGCTTGTGTTTGTGATTGGTCTTATTGT  
 TAACAAGCTACGTTAGAACTGAGTCAGGCTGTTCTAAAAGAGTT  
 CTACTGACTCGCATCGTTAGAGTTGAGTTATGTATTGTAACGG  
 TGTAAATAAACACATAACCTATAGTTGTAGACAAATGGGTTAG  
 CAGATGTTTGGACGTGGGTTGACTCCACCAGCTCCACCA

*Streptococcus mutans* tmRNA

SEQ ID NO: 112  
 GGGGUCGUUACGGAUUCGACAGGCAUUUAGAGACCUUUUUGCG  
 ACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGCAAA

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AAAUAACAAAUUCUACGCGAGUAGCGCCUAAAAACCAGCCUGUG  
 UGAUCAAAUAAACAAUUGCUUGUUGUUGUUAUUGGUUUUAUUGU  
 5 UAAACAAGCUACGUUAGAACUGAGUCAGGCUGUUCUAAAAGAGUU  
 CUACUGACUCGCAUCGUUAGAGUUUAGUUUAUGUAUUGUAACGG  
 UGUUAAAUAACACAUAAACCUAUGUUGUAGACAAAUGGGUUUG  
 10 CAGAUGUUUGGACGUGGGUUCGACUCCACCAGCTCCACCA

*Streptococcus pneumoniae* ssrA

SEQ ID NO: 113  
 GGGGTCGTTACGGATTTCGACAGGCATTATGAGGCATATTTTGCG  
 ACTCGTGTGGCGACGTAACGCTCAGTTAAATATAACTGCAAAA  
 AATAACACTTCTTACGCTCTAGTGCCTAAAAACCAGCAGCGCT  
 GACCCGATTTCGGATTGCTGCTGTTCATGACAGGCTTATTATT  
 20 AGCGAGATACGATTAAGCCTTGTCTAGCGGTTTGATAAGAGATT  
 GATAGACTCGCAGTTTCTAGACTTGAGTTATGTGTGCGAGGGCT  
 GTTAAATAAATACATAACCTATGGTTGTAGACAAATATGTTGGC  
 25 AGGTGTTTGGACGTGGGTTGACTCCACCAGCTCCACCA

*Streptococcus pneumoniae* tmRNA

SEQ ID NO: 114  
 GGGGUCGUUACGGAUUCGACAGGCAUUUAGAGGCAUUAUUUGCG  
 ACUCGUGUGGCGACGUAAAACGCCAGUUAAAUAUAACUGCAAAA  
 35 AAUAACACUUUUACGCUUAGCUGCCUAAAAACCAGCAGCGCU  
 GACCCGAUUGGAUUGCUCGUGUUCAAUGACAGGUUUUAUUU  
 AGCGAGAUACGAUUUAGCCUUGUCUAGCGGUUUUAUAGAGAUU  
 GAUAGACUCGAGUUUCUAGACUUGAGUUUUGUGUCGAGGGGCU  
 40 GUUAAAUAUAUAACAUAACCUAUGGUUGUAGACAAAUAUGUUGG  
 AGGUGUUUGGACGUGGUUCGACUCCACCAGCTCCACCA

*Streptococcus pyogenes* ssrA

SEQ ID NO: 115  
 GGGGTCGTTACGGATTTCGACAGGCATTATGAGGCATGTTTGCG  
 TCCCATCGGCAGATGTAATTTGCCAGTTAAATATAACTGCAAAA  
 50 AATACAACTCTTACGCTTTAGCTGCCAAAAACCAGCTAGCGT  
 GACTTCTACAAGATTGCTTGTGCTCTGTAGAACTCTCAAATA  
 GCAAGCTACGGTTACGAAATGTCTAGTTTCGTGACAAAGAGATT  
 55 GATAGACTCGCAAACTAATGGCTTGAGTTATGTGCTTTAGTTT  
 GTTAAATGAAGACATAACCTATGGACGTAGACAAATATGTTGGC  
 AGGTGTTTGGACGTGGGTTGACTCCACCAGCTCCACCA

*Streptococcus pyogenes* tmRNA

SEQ ID NO: 116  
 GGGGUCGUUACGGAUUCGACAGGCAUUUAGAGGCAUUAUUUGCG  
 65 GGCAGAUGUAAAUAUCCAGUUAAAUAUAACUGCAAAAAUAACAACUCUUA

35

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CGCUUUAGCUGCCUAAAAACAGCUAGCGUGACUUCUACAAGAUUGCUUGU  
 GUCCUGUUAGAAGUCUAAAAUAGCAAGCUACGGUUACGAAAUUGUCUAGU  
 UUCGUGACAAGAGAUUGAUAGACUCGCAAAUAUUGGCUUGAGUUUAGUGU  
 CUUUAGUUUGUAAAUGAAGACAUAACCUAUGGACGUAGACAAAUAUGUUG  
 GCAGGUGUUUGGACGUGGGUUCGACUCCACCAGCUCACCA

*Synechococcus* sp. PCC6301 ssrA

SEQ ID NO: 117

GGGGCTGTAATGGTTTCGACGTGTTGGTGAATCCTTACCGTATTGAGGC  
 CGAGAGGGAGTCCACTCTCGTAAATCCAGGCTCAACCAAAAGTAACTGCGA  
 ACAACATCGTTCTTTCGCTCGTAAGGCTGCTCCTGTAGTCTGTTAAACGC  
 CACAACTTTCTGGCTCGAGCTTAGTCTGACTCCGTTAATACGCCTA  
 GACTTAAACCCCAACGGATGCTCGAGTGGCGGCTCAGGTCCTCTCTC  
 GCTAAGCAAAAACCTGAGCATCCCGCCACGGGATAATCGTTGGCTCCCGC  
 ACAGTGGGTCAACCGTCTAAGCCTGTGAACGAGCGGAAAGTTACTAGTCA  
 ATGCGGACAGCGGTTTCGATTCCGCTCAGCTCCACCA

*Synechococcus* sp. PCC6301 tmRNA

SEQ ID NO: 118

GGGGCUGUAAUGGUUUCGACGUGUUGGUGAAUCCUACCGUGAUUCAGGC  
 CGAGAGGGAGUCACUCUCGUAUUUCCAGGCUCAACCAAAAGUAAUCUGCGA  
 ACAACAUCGUUCCUUCGUCUGUAAGGUCUCUCUGUAGCUGCUUAAACGC  
 CACAAACUUUCUGGUCGAGCGUCUAGUCGUAAGCUCUCCGUUAAUACGCCUA  
 GACUUAACCCCAACGGAUGUCGAGUUGCGGCCUCAGGUCCGUCCUCUC  
 GCUAAGCAAAAACUGAGCAUCCCGCCAACGGGUAUUCGUUGGCUCCCG  
 CACAGUGGGUCAAACGUGCUAAGCCUGUGAACGAGCGGAAAGUUAUCUAGUC  
 AAUGCGGACAGCGGUUCGAUUCGUCUAGCUCACCA

*Synechocystis* sp. PCC6803 ssrA

SEQ ID NO: 119

GGGGCCGCAATGGTTTCGACAGGTTGGCGAAAGCTTGCCTGATACAGGT  
 CGAGAGTGAAGTCTCTCTCGCAAATCAAAGGCTCAAAAAAAGTAACTGCG  
 AATAACATCGTCAGCTTCAAACGGGTAGCCATAGCAGCCTAGTCTGTAAAA  
 GCTACATTTTCTGTCAAAGACCGTTTACTTCTTTTCTGACTCCGTTAAGG  
 ATTAGAGGTTAACCCCAACGGATGCTTTGTTGGCTCTTCTAGTTAGCT  
 AAACAATCAAGACTCAGACTAGAGCATCCACCATCAGGGATAATCGATGG  
 TCCCCGTCCTAGGGCTAGAAGGACTAAACCTGTGAATGAGCGGAAAGTTAA  
 TACCCAGTTTGGACAGCAGTTCAATTCTGCTCGGCTCCACCA

*Synechocystis* sp. PCC6803 tmRNA

SEQ ID NO: 120

GGGGCCGCAUUGGUUUCGACAGGUGGCGAAAGCUUGCCCGUGAUACAGGU  
 CGAGAGUGAGUCUCUCGCAAAUCAAAGGCUCAAAAAAAGUAAUCUGCG

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AAUAACAUCGUCAGCUUCAAACGGGUAGCCAUAGCAGCCUAGUCUGUAAAA  
 GCUACAUUUUUUUGUCAAAAGACCGUUUACUUCUUUUUCUGACUCGUAAGG  
 5 AUUAGAGGUUAAACCCCAACGGAUUCUUUUUGGUCUUCUCUAGUUAGCU  
 AAACAUAACAAGACUCAGACUAGAGCAUCCACCAUCAGGGUAUUCGAUGG  
 UCCCCGUCUAGGGCUAGAAGGACUAAACCUUGUAAUAGAGCGGAAAGUUA  
 10 UACCCAGUUUGGACAGCAGUUCAAUUCUGCUCGCUCCACCA

*Thermotoga maritima* ssrA

SEQ ID NO: 121

GGGGGCGAACGGGTTTCGACGGGATGGAGTCCCCGGGAAGCGAGCCGAGG  
 TCCCCACCTCTCGTAAAAAAGGTGGGACAAAGAATAAGTGCCAACGAACC  
 TGTGCTGTTGCGCTTAATAGATAAGCGGCGCTCTCTCCGAAGTTGGCT  
 20 GGGCTTCGGAAGGGCGTGAGAGATCCAGCTACCGATTAGCTTCGCTT  
 TCCGGCTGAATCGGGAAAACCTCAGGAAGGCTGTGGGAGAGGACACCTGC  
 CCGTGGGAGGTCCCTCCGAGAGCGAAAACACGGGCTGCGCTCGGAGAAGC  
 25 CCAGGGGCTCCATCTTCGGACGGGGTTTGAATCCCCCGCTCCACCA

*Thermotoga maritima* tmRNA

SEQ ID NO: 122

GGGGGCGAACGGGUUCGACGGGAUGGAGUCCCCUGGGAAGCGAGCCGAGG  
 UCCCCACCUCUCUGUAAAAAAGGUGGACAAAGAUAUAGUCCAACGAACC  
 UGUUGCUGLUGCGCUUAAUAGAUUAGCGGCGGUCUCUCGGAAGUUGGC  
 35 UGGGCUUCGGAAGGGGCGUGAGAGAUCCAGCCUACCGAUUCAGCUUCGCC  
 UUCGGCCUGAAUCGGGAAAACUCAGGAAGGCGUGGGGAGAGGACACCCUG  
 CCCGUGGGAGGUCUCCCGAGAGCGAAAACACGGGCGGCGUCGAGAGAAG  
 CCCAGGGGCCUCCAUUCUGGACGGGGUUCGAAUCCCCCGCUCACCA  
 40

*Thermus thermophilus* ssrA

SEQ ID NO: 123

GGGGGTGAAACGGTCTCGACGGGGTTCGCCGAGGGCTGGCTGCGCGCCGA  
 GGTGCGGGTGGCTCGTAAAAACCGCAACGGCATAACTGCCAACACCAAC  
 TACGCTCTCGCGCTTAATGACCGGACCTCGCCCGGTAGCCCTGCGGGG  
 GCTCACCGGAAGCGGGGACACAAACCGGCTAGCCCGGGGCCACGCCCTCT  
 50 AACCCCGGGCGAAGCTTGAAGGGGCTCGCTCCTGGCCGCCCTCGCGGG  
 CCAAGCCAGGAGGACACGCGAAAACCGGACTACGCGCGTAGAGGCCCGCGG  
 TAGAGACCTTCGGACGGGGTTCGACTCCCCCACCTCCACCA  
 55

*Thermus thermophilus* tmRNA

SEQ ID NO: 124

GGGGGUGAAACGGUUCGACGGGGUUCGCCGAGGGGUGGUGCGCGCCGA  
 GGUGCGGGUGGCCUCGUAAAAACCGCAACGGCAUAAUCGCAACACCAAC  
 UACGCUUCGCGGCUUAAUGACCGGACCUCCGCCGUAAGCCUGCCGGGG  
 GCUCACCGGAAGCGGGGACACAAACCGGCUAGCCCGGGGCCACGCCUCU  
 65 AACCCCGGGCGAAGCUUAAAGGGGUCGCUUCUGGCGGCCCGGUCGCGGG

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CCAAGCCAGGAGACACGCCAAACGCGGACUACGCGGUAGAGGCCCGCCG  
UAGAGACCUUCGACGGGGUUCGACUCCCCCACCUCACCA

*Treponema pallidum* ssrA

SEQ ID NO: 125  
GGGGATGACTAGGTTTCGACTAGGGATGTGGGTGTTGCGCTGCAGGTGGA  
GTGTCGATCTCCTGATTGCGGCCTTTATAACTGCCAATTCTGACAGTTTC  
GACTACGCGCTCGCGCTAATCGCGGGCCTGTGTTTGCCTGCTCTGAGC  
GAACATATCGGCCCGACGCCAAACGGAGCTTGTCTTACGTTGTGCACGGC  
GGACGTAGGGGACTTTTGTCTGTGTAAGACTCTGGCGCTGCGGTGCAG  
GCCTAGCAGAGTCCGACAAACGCAGTACGCACCGCTAAACCTGTAGGCGCG  
CAGCACTCGCGCTTTAGGACGGGGTTCGATTCCCCCATCTCCACCA

*Treponema pallidum* tmRNA

SEQ ID NO: 126  
GGGGAUGACUAGGUUUCGACUAGGGAUGUGGGUGUUGCGCUGCAGGUGGA  
GUGUCGAUCUCCGAUUCGCGCCUUUUUAUAACUGCCAAUUCUGACAGUUU  
CGACUACGCGCUCGCCGUAUUCGCGGGCCUGUUGUUGCGCUGCUGAG  
CGAACAUUACGGCCCGACGCCAAACGGAGCUUGCUUUACGUUGUGCACGG  
CGGACGUAGGGGACUUUUGUCUGUGCUAAGACUCUGGCGGUGCGGUGCA  
GGCCUAGCAGAGUCGACAAACGCAGUACGCACCGCUAAACUGUAGGCGC  
GCAGCACUCGCUUUUAGGACGGGGUUCGAUUCCCCCAUCUCCACCA

*Vibrio cholerae* ssrA

SEQ ID NO: 127  
GGGGCTGATTGAGGATTCGACGGGAATTTGCACTCTGAGGTGCATGCCGA  
GGTGCAGTGGCCTCGTTAAACAAACCGCAAAAAAATAGTCGAAACGACGA  
AAACTACGCACTAGCAGCTTAATACCCTGCTCAGAGCCCTTCCCTCCTAGC  
TTCCGCTTGTAAAGACGGGAAATCAGGAAGGTCAAACCAAATCAAGCTGGC  
GTGATTCCCCCCTGAGGATGAAGCGGAGATCTAATTCAGGTTAGCCA  
TTAGCGTGTGCGTTTCGACGGTGTGTAATTAAGATCGACTAAGCATG  
TAGTACCAAAGATGAATGGTTTTTCGGACGGGGTTCAACTCCCCCAGCTC  
CACCA

*Vibrio cholerae* tmRNA

SEQ ID NO: 128  
GGGGCUGAUUCAGGAUUCGACGGGAAUUUGCAGUCUGAGGUGCAUCCGA  
GGUGCGGUAGGCCUCGUUAAACAAACCGCAAAAAAUAUGUCGAAACGACGA  
AAACUACGCACUAGCAGCUUAAUACCCUGCUCAGAGCCUUCUCCUAGC  
UUCGCUUGUAAGACGGGAAUUCAGGAAGGUCAAACCAAUCAAGCUGGC  
GUGGAUUCUCCACUGAGGGAUGAAGCGGAGAUCAAUUCAGGUUAGCC  
AUUCGUUAGCGUGUCGGUUCGACGGCGGUGGAAUUAAGAUCGACUAA  
GCAUGUAGUACCAAAGAUGAAUGGUUUUCGACGGGGUUCAAUCUCCCCC  
AGCUCCACCA

*Yersinia pestis* ssrA

SEQ ID NO: 129  
5 GGGGCTGATTCTGGATTGACGGGATTCGCGAAACCCAAAGGTGCATGCCGA  
GGTGCAGTGGCCTCGTAAAAAACCGCAAAAAAATAGTTGCAAACGACGAA  
AACTACGCACTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTGCCTAGCC  
10 TCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCTAAAAGAGCTCGTGT  
GGAAACCTTGCTGGGTGGAAGCATTAATACTAATAGGATAGTTTGTCA  
GTAGCGTGTCCATCCGACAGCTGGCCGCGAATGTAATGATTGGACTAAGCA  
15 TGTAGTGCAGCGGTGTAGTAATTTCCGACGGGGTTCAAATCCCCCAGC  
TCCACCA

*Yersinia pestis* tmRNA

20  
SEQ ID NO: 130  
GGGGCUGAUUCUGGAUUCGACGGGAUUCGCGAAACCCAAAGGUGCAUCCGA  
GGUGCGGUGGCCUCGUAAAAAACCGCAAAAAAUAUUGCAAACGACGAA  
25 AACUACGCACUAGCAGCUAAUAACCGCUUAGAGCCUCUCUGCCUAGCC  
UCCGCUUAGGACGGGGAUCAAGAGAGGUCAAACCUAAAAGAGCUCGUGU  
GGAAACCUUGCCUGGGUGGAAGCAUUAACCUAAUCAGGAUAGUUUGUCA  
30 GUAGCGUGUCAUCCGACGUGCCGCGGAAUGUAUUGGACUAGCA  
UGUAGUGCCGACGGUGUAUUAUUCGACGGGGUUCAAUCCCCCAGC  
UCCACCA

35 *Campylobacter fetus* ssrA, Internal Partial

SEQ ID NO: 131  
40 AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGCGTAAAAAGC  
CCAAATAAAATTAACGCAACAACGTTAAATTCGCTCCTGCTTACGCTAA  
AGCTGCGTAAGTTAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCTTA  
ATTTTCGGTCATCTTTGATAGTGTAGCCTTGCCTTGGACAAGCGTTAGGT  
45 GAAATAAAGTCTTAGCCTTGCTTTGAGTTTGGAAAGATGAGCGAAGTAGG  
GTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCTTTGTGGATTATTTT  
TGG

50 *Campylobacter fetus* tmRNA, Internal Partial

SEQ ID NO: 132  
55 AGGAGUAAGUCUGCUUAGAUUGGCAUGUCGUUUGGGCAAAGCGUAAAAAGC  
CCAAUAAAAUAAACGCAACAACGUUAAUUCGCUCCUGCUUACGCUAA  
AGCUGCGUAAGUUCAGUUGAGCCUGAAUUUAAGUCAUACUAGCUUA  
60 AUUUUCGGUCAUCUUTUGAUAGUGAGCCUUGCGUUUGACAAGCGUUUGAG  
GUGAAAUAAGUCUUGCCUUGCUUUUGAGUUUGGAAGAUGAGCGAAGUA  
GGGUGAAGUAGUCAUCUUUGCUAAGCAUGUAGAGGUUUUGGGAAUUAU  
UUUGG

39

*Campylobacter coli* (BM2509) *ssrA*, Internal Partial

SEQ ID NO: 133  
 AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGACAAAGCGTAAAAAGT  
 CCAAATAAAAATAAACGCAATAACGTTAAATTTGCTCCTGCTTACGCTA  
 AAGCTGCGTAAGTTAGTTGAGCCGAACTCAAGTGATGCTATCTAGCTT  
 GAATTTGGTCATCTTTGATAGTGTAGATTGAAAATTGACAACTTTAATC  
 GAAGTTAAAGTCTTAGTCTAGCTTGAATTTTGGAGGTGAGTTTAGCCAG  
 ATGAAGTTTTACCTTTGCTAAACATGTAGAAGTCTTTGTGGGTTATTTT  
 TGG

*Campylobacter coli* (BM2509) tmRNA, Internal Partial

SEQ ID NO: 134  
 AGGAGUAAAGUCUGCUUAGAUGGCAUGUCGUUUGGACAAAGCGUAAAAAG  
 UCCAAAUAUUUUAAACGCAAAUAACGUUUUUUUGCUCUUCGCUUACGCU  
 AAAGCUGCGUAAGUUCAGUUGAGCCGAAACUCAAGUGAUGCUAUCUAGCU  
 UGAAUUUUGGUCUUCUUUGAUAGUGUAGAUUGAAAUAUGACAACUUUUAAU  
 CGAAGUUAAGUCUUAAGUCUAGCUUGAAAUUUUGAAGGUGAGUUUAGCCA  
 GAUGAAGUUUACCUUUGCUAAACAUGUAGAAGUCUUUUGGGGUUAUUU  
 UUGG

*Campylobacter* Chicken Isolate *ssrA*, Internal Partial

SEQ ID NO: 135  
 ACAGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGCGTAAAAA  
 GCCCAAATAAAATTAACGCAAAACAAGTAAATTCGCTCCTGCTTACGCT  
 AAAGCTGCGTAAGTTAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCT  
 TAATTTTCGGTCATTTTTGATAGTGTAGCCTTGCGTTTGACAAGCGTTGAG  
 GTGAAATAAGTCTTAGCCTTGCTTTGAGTTTGGAAAGATGAGCGAAGTA  
 GGGTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCTTTGTGGGATTATT  
 TTTGG

*Campylobacter* Chicken Isolate tmRNA, Internal Partial

SEQ ID NO: 136  
 ACAGGAGUAAAGUCUGCUUAGAUGGCAUGUCGUUUGGCAAAGCGUAAAAA  
 GCCCAAUAUUUUAAACGCAAAACAAGUUAUUUUGCUCUUCGCUUACGCU  
 AAAGCUGCGUAAGUUCAGUUGAGCCGAAAUUUUAGUCAUACUUCUAGCU  
 UAAUUUTUCGGUCAUUUUUGAUAGUGUAGCCUUGCGUUUGACAAGCGUUGA  
 GGUUAAAUAAGGUCUAGCCUUGCUUUUGAGUUUUUGAAGAUAGCGAAG  
 UAGGGUGAAGUAGUCAUUCUUUGCUAAGCAUGUAGAGGUUUUUGGGGAUUA  
 UUUUUGG

*Clostridium perfringens* *ssrA*, Internal Partial

SEQ ID NO: 137  
 ACGGGGTAGGATGGGTTTGATAAGCGAGTCGAGGGAAGCATGGTGCCTCG  
 ATAATAAGATGATGATTAAGATAAACGACGAGATAATTTGCATTAGCA

40

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GCTTAAGTTAGCGCTGCTCATCTTCTCCTCAATTGCCACGGTTGAGAGTAA  
 GGGTGTCAATTTAAAGTGGGGAAACCGAGCCTAGCAAAGCTTTGAGCTAGGA  
 5 ACGGAATTTATGAAGCTTACCAAAGAGGAAGTTGTCTGTGGAGCTTCTCT  
 GAGGGAAATTTAAACACAAGACTACACTCGTAGAAAGTCTTACTGGTCTG  
 CTTTCGG

10 *Clostridium perfringens* tmRNA, Internal Partial

SEQ ID NO: 138  
 ACGGGGUAGGAUGGUUUUGAUAAAGCAGUCGAGGGAAGCAUGGUGCCUCG  
 15 AUAUAAGUAUGCAUUAAGAUAAACGCACGAGAUAAUUUUGCAUUAGCA  
 GCUUAAGUUAGCGCUGCUCAUCCUUCUCAAUUUGCCACGGUUGAGAGUAA  
 GGGUGUCAUUUUAAAGUGGGGAAACCGAGCCUAGCAAAGCUUUGAGCUAGGA  
 20 ACGGAAUUUAUGAAGCUUACCAAAGAGGAUUUUGUCUGUGGACGUUCUCU  
 GAGGGAAUUUUAAACACAAGACUACACUCUGAAGUUCUUCUGGUCUG  
 CUUUCGG

25 *Haemophilus ducreyi* (NCTC 10945) *ssrA*, Internal Partial

SEQ ID NO: 139  
 ACGGGATTAGCGAAGTCCAAGGTGCACGTCGAGGTGCGGTAGGCTCGTAA  
 30 CAAACCGCAAAAAATAGTCGCAACGACGAACAATACGCTTTAGCAGCTT  
 AATAACCTGCATTTAGCCTTCGCGCCCTAGCTTTCTGCTCGTAAGACGGGGA  
 GCACGCGGAGTCAAACCAAACGAGATCGTGTGGACGCTTCCGCTTGTA  
 35 TGAAACTAATTAATCAAGCTAGTTTATTTCTTGGTGTCTGTCCGCT  
 GGAGATAAGCGAAATTAAGACCAGACTAAACGTGTAGTACTGAAGATAGA  
 GTAATTTTCGGACCCGGGTTCCGACTC

40 *Haemophilus ducreyi* (NCTC 10945) tmRNA, Internal Partial

SEQ ID NO: 140  
 ACGGGAUUAGCGAAGUCCAAAGGUGCAGUCGAGGUGCGGUAAGCCUCGUAA  
 45 CAAACCGCAAAAAAUAGUCGCAACGACGAACAUAACGUUUUAGCAGCUU  
 AAUAACCGCAUUUAGCCUUCGCGCCUAGCUUUCGUCUUAAGACGGGG  
 AGCACGCGGAGUCAAACCAAACGAGAUUCGUGGACGCUUCCGCUUUGUAG  
 50 AUGAAACACUAAAUAAGCAAGCUAGUUUUUUUUGCGUGUCUGUCCG  
 CUGGAGUAAGCGAAAUAAGACCAGACUAAACGUGUAGUACUGAAGAUUA  
 UAGUAAUUUCGACCCGGGUUCGACUC

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

SEQ ID NO: 141  
 GGCAAAGAAAAACAAAACCTAGCTTTTCGCTGCCTAATAACAGTAGCATAG  
 60 CTGATCCTCCGTGCATCGCCATGTGCTACGGTAAGGCTCTCACTCTAAGT  
 GGGCTACACTAGTTAATCTCCGCTGAGGTAATAGAAAGCTTAATCAGA  
 CTAGCTGAATGGAAGCCTGTACCGGCTGATGTTTATGCGAAATGCTAAT  
 65 ACGGTGACTACGCTCGTAGATATTCAA

41

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

SEQ ID NO: 142  
 GGCAAAGAAAAACAAAACCUAGCUUUCGUGCCUAAUAACAGUAGCAUAG  
 5 CUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAAGGGUCUCACUCUAAGU  
 GGGCUACACUAGUUAAUCUCCGUCUGAGGUAAAUAAGAAGAGCUUAAUCAG  
 ACUAGCUGAAUGAAGCCUGUUAACGGGCGUAGUUUAUGCGAAAUGCUAA  
 10 UACGGUGACUACGCUCGUAUAUCAA

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

SEQ ID NO: 143  
 GGCAAAGAAAAACAAAACCTAGCTTTTCGCTGCCTAATAAGCAGTAGCATAG  
 CTGATCCTCCGTGCATCGCCATGTGCTACGGTAAGGGTCTCACTCTAAGT  
 GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCAG  
 20 ACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA  
 TACGGTGACTACGCTCGTAGATATTTAA

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

SEQ ID NO: 144  
 GGCAAAGAAAAACAAAACCUAGCUUUCGUGCCUAAUAAGCAGUAGCAUAG  
 CUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAAGGGUCUCACUCUAAGU  
 GGGCUACACUAGUUAAUCUCCGUCUGAGGUAAAUAAGAAGAGCUUAAUCAG  
 30 ACUAGCUGAAUGAAGCC

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

SEQ ID NO: 145  
 GGCAAAGAAAAACAAAACCTAGCTTTTCGCTGCCTAATAAGCAGTAGAATAG  
 CTGATCCTCCGTGCATCGCCATGTGCTACGGTAAGGGTCTCACTCTAAGT  
 40 GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCCG  
 ACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA  
 TACGGTGACTACGCTCGTAGATATTTAA

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

GGCAAAGAAAAACAAAACCUAGCUUUCGUGCCUAAUAAGCAG  
 UAGAAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA  
 GGGUCUCACUCUAAGUGGGUACACUAGUUAAUCUCCGUCUGA  
 GGUAAAUAAGAAGAGCUUAAUCGGACUAGCUGAAUGGAAGCC  
 UGUUAACGGGCGAUGUUUAUGCGAAAUGCUAAUACGGUGAG  
 UACGCUCGUAUAUCAA SEQ ID NO: 146

*Listeria innocua* (ATCC 12210) ssrA, Internal Partial

GGCAAAGAAAAACAAAACCTAGCCGCTGCCTAATAAGCAGT  
 AGCATAGCTGATCCTCCGTGCATCGCCATGTGCTACGGTAAGG  
 GTCTCACTCTAAGTGGCTACACTAGTTAATCTCCGTCTGGGGTT  
 AAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGTTAC

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TGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG  
 5 TAGATATTTA SEQ ID NO: 147

*Listeria innocua* (ATCC 12210) tmRNA, Internal Partial

GGCAAAGAAAAACAAAACCUAGCUUUCGUGCCUAAUAAGCAG  
 UAGCAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA  
 GGGUCUCACUCUAAGUGGGUACACUAGUUAAUCUCCGUCUGG  
 GGUAAAUAAGAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCC  
 15 UGUUAACUGGGCCGUAUUUAUGCGAAAUGCUAAUACGGUGAG  
 UACGCUCGUAUAUCAA SEQ ID NO: 148

*Listeria ivanovii* (NCTC 11846) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC  
 TCGTTATTAACGTCAAAGCCAATAAATACTGGCAAAGAAAAACA  
 25 AACCTAGCTTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG  
 GCTACACTAAATAATCTCCGTCTGGGTTAGTTAGAAGAGCTTA  
 30 ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT  
 GCGAAATGCTAATAACGGTGACTACGCTCGTAGATATTTAAGTGC  
 CGATATTTCTGG SEQ ID NO: 149

*Listeria ivanovii* (NCTC 11846) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUUCGAGUCGGGGGAUCGU  
 CCUCGUUAUUAACGUCAAAAGCCAAUUAUACUGGCAAAGAAA  
 AACAAAACCUAGCUUUCGUGCCUAAUAAGCAGUAGCAUAGCU  
 GAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAAGGGUCUCACU  
 45 UUAAGUGGGCUACACUAAAUAUUCUCCGUCUGGGUUAGUUA  
 GAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGG  
 GCUGAUGUUUAUGCGAAAUGCUAAUACGGUAGCUCGUCUGUA  
 GAUAAUUAAGUGCCGAUUAUUCUG SEQ ID NO: 150

*Listeria seeligeri* (NCTC 11856) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC  
 55 TCGTTATCAACGTCAAAGCCAATAAATACTGGCAAAGAAAAACA  
 AACCTAGCTTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCATGTGCTACGGAAAGGGTCTCACTTTAAGTGG  
 60 GGCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTT  
 AATCAGACTAGCTGAATGGAAGCCTUTTACCGGGCTGATGTTTA  
 TCGAAATACTAATAACGGTGACTACGCTCGTAGATATTTAAGTGG  
 65 CCCATATTTCTGG SEQ ID NO: 151



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ACGCCAACGACGAGCGUUUCGUCUCGCGCCGUUAGCGGUGAGC

CGCUGCACUGAUCUGUCCUUGGGUCACGCGGGGGAA

SEQ ID NO: 160

*Chlamydia pneumoniae* (CWL029), *ssrA*

GGGGGTGTATAGTTCGACTTGAAAAATGAAGTGTAAATTGCAT  
 GCGGAGGGCGTTGGCTGGCCCTCCTAAAAAGCCAACAAAACAATA  
 AATGCCGAACCTAAGGCTGAATGCGAAATTATTAGCTTGTTTGA  
 CTCAGTAGAGGAAAGACTAGCTGCTTAATTAGCAAAAGTTGTTA  
 GCTAGATAATCTCTAGGTAACCCGGTATCTGCGAGCTCCACCAG  
 AGGCTTGCAAATACCGTCAATTTATCTGGTTGGAACCTACTTTCT  
 CTAATTCCTCAAGGAAGTTCGTTCCGAGATTTTGGAGTCAATTGGC  
 TGCTATAGAGGCTTCTAGCTAAGGGAGTCCAATGTAACAATTC  
 TAGAAGATAAGCATGTAGAGGTTAGCAGGGAGTTTGTCAAGGAC  
 GAGAGTTCGAGTCTCTCCACCTCCACCA SEQ ID NO: 161

*Chlamydia pneumoniae* (CWL029) tmRNA

GGGGGUGUUAUAGGUUUCGACUUGAAAAUGAAGUUAUUUUGC  
 AUGCGGAGGGCGUUUGGCGGCCUCCUAAAAAGCCAACAAAACA  
 AUAUUUGCCGAACCUAAGGCGUAAUGCGAAAAUUUUAGCUUG  
 UUUAGCUCAGUAGAGGAAAGACUAGCUGCUUAAUUAGCAAAA  
 GUUGUUAGCUAGAUAAUCUCUAGGUAACCCGGUAUCUGCGAG  
 CUCCACCAGAGGCUUGCAAAAUACCGUCAUUUAUCUGGUUGGA  
 ACUUACUUUCUCUAAUUCUCAAGGAAGUUCGUUCGAGAUUUU  
 UGAGAGUCAUUGGCGUCAUAGAGGCUUUCUAGCUAAGGGAGU  
 CCAAUGUAAACAUAUUCUAGAAGUAAGCAUGUAGAGGUUAGC  
 AGGGAGUUUGUCAAGGACGAGAGUUCGAGUCUCUCCACCUCCA  
 CCA SEQ ID NO: 162

*Francisella tularensis* *ssrA*

GGGGCGAATATGTTTCGACATGAATGTCAAAATCTAAGGTGC  
 ATGCCGAGGAAGTACCGTAACCTCGTTAATAACAGTACAAATGC  
 CAATAATAACTGGCAACAAAAAGCAAACCCGCTAGCGGCTAA  
 CGACAGCAACTTTGCTGCTGTTGCTAAAGCTGCCTAGTCTAGCTT  
 AATAATCTAGATGCGCACGGATATGATAGTCTTTCTTATGACACT  
 ATCTATACATCCGTTTATATCCGCATAAGACGGTCTTTGCTTTTT  
 GTCTGGGAGTTAAGGCTGTATTTAACAGACTCGCTAACTATTACC  
 CTGGCTAATTGGGAATAGTCAAGCTAAACTCAAATAGATTAGC  
 CTAAGCATGTAGATCCAAGATCTAGAGTTTGTGGACGCGGGTT  
 CAAATCCCGCCCTCCACCA SEQ ID NO: 163

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*Francisella tularensis* tmRNA

GGGGCGAAUAUGGUUUCGACUAGAAUGUCAAAAUCUAAGGU  
 5 GCAUGCCGAGGAAGUACCGUAACCUCGUUAAUAAACAGUACAAA  
 UGCCAAUAAUAAACUGGCAACAAAAAGCAAACCGCGUAGCGGC  
 UAACGACAGCAACUUUGCUGCUGUUGCUAAAGCUGCCUAGUCU  
 10 AGCUAAUAAUUCUAGAUGCGCACGGAUUAGUAGUCUUUCUU  
 AUGACACUAUCUAUACAUCCGUUCUAUUAUCCGCAUAAGACGGU  
 CUUUGCUUUUUGUCUGGGAGUUAAGGCUGUAUUUACAGACU  
 15 CGCUAACUAUUACCCUGGCUAAUUGGGAAUAGUCAAGCUAA  
 ACUCAAAUAGAUUAGCCUAAGCAUGUAGAUCCAAAGAUCUAG  
 AGUUUGGACGCGGGUCAAUCCCGCCGCCUCCACCA  
 20 SEQ ID NO: 164

*Guillardia theta* (Plastid) *ssrA*

GGGGCTGATTTGGATTCGACATATAAATTTGCGTGTTCATTATG  
 25 AAGCAAGTCAAGTTTAAATGATCTTGTA AAAAACATTAAAGTACA  
 AATAAATGCAAGCAATATAGTTTCAATTTAGTTCAAAACGTTTGT  
 CTCTTTTGATAAGCAAAATGTGTTAATAACTTTCTTAGTAGAAA  
 30 TTGGAGAAGTTTACTAAGATTATATTTACTCCATAATTATTTTA  
 AAGATGGTAAAAGGTGATTCATCATTTGTATGTTTCTAAACTTT  
 GTGAAAGAATAGTGGGCTCCATTTATAATGAACGTGGGTTCAA  
 35 TCCCACCAGCTCCACCA SEQ ID NO: 165

*Guillardia theta* (Plastid) tmRNA

GGGGCUGAUUUGGAUUCGACAUUAAAUUUGCGUUUCAUU  
 40 AUGAAGCAAGUCAAGUUUAAUGAUUCUUGUAAAAACAUAUAAA  
 GUACAAAUAUUAAGCAAGCAUUAUAGUUUCAUUUAGUUCAAAA  
 45 CGUUUAGUCUUUUUGCAUAGCAAAAUGUGUUUAAUAAACUUU  
 CUUAGUAGAAAUUGGAGAAGUUUACUAAGAUUUUUAUUUUAU  
 CCAUAAUUUUUUAAAAGUUGUAAAAAGGUGAUUCAUUAUUU  
 50 GUAUGUUUCUAAAACUUUGUAGAAAGAAUAGUGGGCUCAUUUA  
 UAAUGAACGUGGUUCAAAUCCACCAGCUCACCA  
 SEQ ID NO: 166

*Thalassiosira weissflogii* (Plastid) *ssrA*

GGGGCTGATTTGGTTCGACATTTAAACTTCTTCTATGTGTCA  
 55 GGTCAAAGTTTGTATTCTTTGTA AAAAATACTAAAATACTAATA  
 60 AATGCTAATAATATAATACCGTTTATTTTAAAGCAGTAAAAAC  
 AAAAAAGAAGCAATGGCTTTAAATTTTGTGCTATAGTTCATTA  
 ACTTAGGTTATTAATATTTTTTCAATATAACTGGACTTTTCTCTA  
 65 GTTTATAGTTTAGAATAAATTTAAATTTTGCAAAACTCGTTTCGAA

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AATTTTCGGGCTAAACCTGTAAACGCAAACTACTAAGAAATTTTA  
 GATGGACATGGGTTC AATTC CCAATCAGTTCACCA  
 SEQ ID NO: 167

*Thalassiosira Weissflogii* (Plastid) tmRNA

GGGGCUGAUUUGGUUUCGACAUUUAACUUCUUUCUAUGUG  
 UCAGGUCAAAGUUUGUAUUCUUUGUAAAAAAUACUAAAAUA  
 CUAUAAAUGCUAAUUAUUAUACCGUUUAUUUUAAAGCA  
 GUAAAAACA AAAAAGAAGCAAUGGCUUUAUUUUGCUGUA  
 UAGUUCAUUAACUUAGGUUAUUAAAUAUUUUUCAUUAUAA  
 UGGACUUUUCUCUAGUUUAUAGUUUAGAAUAAAUAUUUU  
 UGCAAAACUCGUUCGAAAUUUUCGGGCUAAACUGUAAACGC  
 AAAUACUAAGAAUUUUAUGAUGGACAUGGGUUCAAUUCUCA  
 CAGUCCACCA SEQ ID NO: 168

*Helicobacter pylori* srrA, (Clinical Isolate 1), Internal Partial

TGGGGATGTTACGGTTTCGACAGGGTAGTTCGAGCTTAGGTGG  
 CGAGTCGAGGGGATCGGCCTCGTTAAAACGTC AAGCCTATAAC  
 TGGCAACAACA AAAAACA AACTTCGCTTAGCAGCTTAATAAGCTC  
 TTAGCGGTTCCCTCCATCGCCATGTGGTAGGGTAAGGGACT  
 CAAATTAAGTGGGTACGCTGGATTCCACCGCTCAGGATGAAA  
 GAAGAGAACAACCACTAGCTACCCGGACGCCCGTCGATAGG  
 CAGATGGAGTAGCGAATCGCAATATATCGACTACTCGTAGA  
 AGCTTAAGTCCGATATCTTGGACGTGGGTTGACTCCC  
 SEQ ID NO: 176

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

UGGGGAUGUUACGGUUUCGACAGGGUAGUUCGAGCUUAGGU  
 GGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUC AAGCCUAU  
 AACUGGCAACAACA AAAACAACUUCGUUUAAGCAGCUAAUUA  
 GCUCUUAAGCGGUUC CUCCUCCAUCGCCAUGUGGUAGGGUAA  
 GGGACUCAAAUUAAGUGGGUACGCUUGAUUCCACCGUCUGAG  
 GAUGAAAAGAGAACAACCAAGACUAGCUACCCGGACGCCCGU  
 CGAUAGGCAGAUUGGAGUAGCGAAUCGCGAAUUAUUCGACUAC  
 ACUCGUAGAAGCUUAAGUGCCGAUUAUUUGGACGUGGGUUC  
 GACUCC SEQ ID NO: 177

*Helicobacter pylori* srrA, (Clinical Isolate 2), Internal Partial

TGGGGACGTTACGGTTTCGACAGGGATAGTTCGAGCTTAGGTTG  
 CGAGTCGAGGGGATCGGCCTCGTTAAAACGTC AAGCCTATAAT  
 TGGCAACAACA AACTCTTCTTAGCTGCTAATTGCACTAAAG

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GTTCTCCCTCCATCGTCCATGTGGTAGGGTAAGGGACTCAA  
 AAGTGGACTACGCCGAGTTCGCCGTCTGAGGACAAAGGAAGA  
 GAACAACCAGACTAGCAACTTGGAGCCTGTGATAGGCCGAAG  
 AGTTCGCGAAATGCTAATATATCGACTACTCGTAGAAGCTTA  
 AGTGCCGATATTTTGGACGTGGGTTTCGATTCCT SEQ ID  
 NO: 178

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

UGGGGACGUUACGGUUUCGACAGGGUAGUUCGAGCUUAGGU  
 UGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUC AAGCCUAU  
 AAUUGGCAACA AAAACAACUUCUUUAGCUGCUUAAUUGCA  
 CUAAGGUUCCUCCUCCAUCGUCCAUGUGGUAGGGUAAGGGA  
 CUCAAAUUAAGUGGACUACGCCGGAGUUCGCCGUCUGAGGACA  
 AAGGAAGAGAACAACCAAGACUAGCAACUUGAAGCCUGUCGA  
 UAGGCCGAAGAGUUCGCGAAAUGCUAAUUAUUCGACUACACUC  
 GUAGAAGCUUAAGUGCCGAUUAUUUUGGACGUGGGUUCGAUU  
 CCCU SEQ ID NO: 179

*Listeria seeligeri* (NCTC 11856) srrA, Internal Partial

ACAGGGATAGTTCGAGCTTGTAGTTCCGAGTCGGGGGATCGTCC  
 TCGTTATCAACGTCAAAGCCAATAAATACTGGCAAGAAAAACA  
 AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCATGTGCTACGAAAGGGTCTCCTTTAAGTG  
 GGCTACACTAAATAATCTCCGTCTGGGTTAGTTAGAAAGGCTT  
 AATCAGACTAGCTGAATGGAAGCCTGTACCGGGCTGATGTTTA  
 TCGCAATACTAATAACGGTGACTACGCTCGTAGATATTTAAGTG  
 CCCATATTTCTGG SEQ ID NO: 180

*Listeria seeligeri* (NCTC 11856) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUAGUUCGAGUCGAGGGGAUCGU  
 CCUCGUUAUCAACGUC AAGCCAAUUAUAUCUGGCAAGAAAA  
 ACAAAAACUAGCUUUCGUGCUAAUUAAGCAGUAGCAUAGCUG  
 AUCCUCGUGCAUCGCCAUGUGCUACGGAAAGGGUUCACUUC  
 UAAGUGGGCUACACUAAUUAUUCUGGUCUGGGUUAGUUAG  
 AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUUCACCGGG  
 CUGAUGUUUAUGCGAAAUAUUAUACGGUGACUACGUCUGUA  
 GAUUAUUUAGUGCCAUUAUUUCUG SEQ ID NO: 181

*Listeria ivanovii* (NCTC 11846) srrA, Internal Partial

ACAGGGATAGTTCGAGCTTGTAGTTCCGAGTCGGGGGATCGTCC  
 TCGTTATTAACGTCAAAGCCAATAAATACTGGCAAGAAAAACA

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AAACCTAGCTTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT  
 CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG  
 GCTACACTAAATAATCTCCGCTGGGGTTAGTTAGAAGAGCTTA  
 ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT  
 GCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTGC  
 CGATATTTCTGG SEQ ID NO: 182

*Listeria ivanovii* (NCTC 11846) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGAUCGU  
 CCUCGUUAUUAAACGUCAAAGCCAAUAAUACUGGCAAAGAAA  
 AACAAAACCUAGCUUUCGUCGCCUAAUAAGCAGUAGCAUAGCU  
 GAUCCUCGUGCAUCGCCCAUGUGCUACGGUAAGGGUUCACU  
 UUAAGUGGGCUACACUAAUAAUUCUGGUCUGGGUUAGUUA  
 GAAGAGCUAAUACAGACUAGCUGAAUGGAAGCCUGUUAACCGG  
 GCUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUCGUCUGUA  
 GAUUAUUAAAGUCCGAUUAUUUCUGG SEQ ID NO: 183

*Mycobacterium africanum* (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCA  
 TCAGCGGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGT  
 AGACCGGGAACGCCCTCGGCCGACCTGGCATCAGCTAGAGG  
 GATCCACCGATGAGTCCGGTGCGGGACTCCTCGGGACAACCAC  
 AGCGACTGGGATCGTCATCTCGGCTAGTTGCGGTGACCGGGAGA  
 TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG  
 GGAATGCCGTA SEQ ID NO: 184

*Mycobacterium africanum* (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCGACCAAUAAGCGCCGAUUA  
 CAUCAGCGGACUACGCUUCGUCGCCUAAAGCGACGGCUAGUC  
 UGUCAGACCGGGAACGCCUUCGCGCCGGACCCUGGC AUCAGCU  
 AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUGGGAC  
 AACCACAGCGACUGGGAUCGUCAUUCGGCUAGUUCGCGUGAC  
 CGGGAGAUCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG  
 CCUUGAGGGAUUGCCGUA SEQ ID NO: 185

*Mycobacterium gordonae* (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCAACCAATAAGCGCCGATTCA

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TCAGCGGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC  
 GGACCGGGAACGCCCTCGCCCGGACCCGGCATCAGCTAGAGG  
 GATCAACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAAC  
 AGCGACTGGGATCGTCATCCTGGCTAGTCCGTGTGACCAGGAGA  
 TCCGAGCAGAGACATAGCGGACTGCGCACGGAGAAGCCTTGAG  
 GGAATGCCGTA SEQ ID NO: 186

*Mycobacterium gordonae* (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCAACCAUUAAGCGCCGAUUA  
 CAUCAGCGGACUACGCUUCGUCGCCUAAAGCGACGGCUAGUC  
 UGUCGAGACCGGGAACGCCUUCGCCCGGACCCGGCAUCAGCU  
 AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUACUCCGGAC  
 ACCAACAGCGACUGGGAUCGUCAUCUGGCUAGUCCGUGUGAC  
 CAGGAGAUCCGAGCAGAGACAUAGCGGACUGCGCACGGAGAAG  
 CCUUGAGGGAUUGCCGUA SEQ ID NO: 187

*Mycobacterium kansasii* (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCAACCAAATAAGCGCCGATTCA  
 TCAGCGGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGT  
 AGACCGGGAACGCCCTCGGCCGACCTGGCATCAGCTAGAGG  
 GATCAACCGATGAGTTCGGTCGCGGGACTCGTCGGACACCAAC  
 AGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGCACAGGAGA  
 TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG  
 GGAATGCCGTA SEQ ID NO: 188

*Mycobacterium kansasii* (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCAACCAAUAAGCGCCGAUUA  
 CAUCAGCGGACUACGCUUCGUCGCCUAAAGCGACGGCUAGUC  
 UGUCAGACCGGGAACGCCUUCGCGCCGGACCCUGGC AUCAGCU  
 AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUGGGAC  
 AACCACAGCGACUGGGAUCGUCAUUCGGCUAGUUCGCGUGAC  
 CGGGAGAUCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG  
 CCUUGAGGGAUUGCCGUA SEQ ID NO: 189

*Mycobacterium chelonae* ssrA, Internal Partial

ACAGCGAGTCTCGACTTAAGGGAAGCGTGCCGGTGCAGGCAAG  
 AGACCACCGTAAGCGTCATTGCAACCAATTAAGCGCCGATTCTC

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ATCAGCGCGACTACGCACTCGCTGCCTAAGCGACTGCGTGTCTG  
 TCAGACCGGGAGCGCCCTCAGCCCGGACCCCTGGCATCAGCTAGA  
 GGGACAAACTACGGGTTTCGGTTCGCGGGACCCGTAGGGACATCAA  
 ACAGCGACTGGGATCGTCATCTCGGCTTGTTTCGCGGACCCGAGA  
 GATCCAAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTA  
 ATGAACGGCCGTTG SEQ ID NO: 190

*Mycobacterium chelonae* tmRNA, Internal Partial

ACAGCGAGUCUCGACUUAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGAUUCU  
 CAUCAGCGCGACUACGCACUCGCGGCCUAAGCGACUGCGUGUC  
 UGUCAGACCGGGAGCGCCUCAGCCCGGACCCUGGCAUCAGCU  
 AGAGGGACAAACUACGGGUUCGUGCGCGGACCCGUAAGGGACA  
 UCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGGGAC  
 CGAGAGAUCCAAGUAGAGGCAUAGCGAACUGCGCACGGAGAA  
 GCCUUAUGAACGGCCGUUG SEQ ID NO: 191

*Mycobacterium szulgai* (ATCC 35799) *ssrA*, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCTGTGCAACCAATTAAGCGCCGAGAACAC  
 TCAGCGCGACTTCGCTCTCGTGCCTAAGCGACAGCAAGTCCGT  
 CAGACCGGAAAGCCCTCGACCCGGACCCCTGGCGTCATCTAGAG  
 GGATCCACCGTGAGTTCGGTTCGCGGGACTCATCGGGACACCAA  
 CAGCGACTGGGATCGTCATCTGGCTAGTTCGCGTGACCAGGAG  
 ATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTTGA  
 GGGAAATGCCGTAG SEQ ID NO: 192

*Mycobacterium szulgai* (ATCC 35799) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGAGAAC  
 ACUCAGCGCGACUUCGUCUCGCGGCCUAAGCGACAGCAAGUC  
 CGUCAGACCGGAAAGCCUCGACCCGGACCCUGGCUCAUCU  
 AGAGGGAUCCACCGGUGAGUUCGUGCGCGGACUCAUCGGGAC  
 ACCAACAGCGACUGGGAUCGUCAUCUCGGCUAGUUCGCGUGAC  
 CAGGAGAUCGAGUAGAGACAAGCGAACUGCGCACGGAGAA  
 GCCUUGAGGGAUAGCCGUAG SEQ ID NO: 193

*Mycobacterium malmoense* (Clinical Isolate) *ssrA*, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCTGTGCAACCATATAAGCGCCGTTTCAAC

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ACAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT  
 CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTGGAG  
 5 GGATCCACCGGTGAGTCCGGTTCGCGGGACTCATCGGGACATACA  
 CAGCGACTGGGATCGTCATCTCGGCTGGTTCGCGTGACCCGGAG  
 ATCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGA  
 10 GGGAAATGCCGTAG SEQ ID NO: 194

*Mycobacterium malmoense* (Clinical Isolate) tmRNA, Internal Partial

15 ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGUUUA  
 ACACAGCGCGACUACGCUCUCGCGGCCUAAGCGACAGCUAGUC  
 20 CGUCAGACCGGAAACGCCUCGACCCGGAGCCUGGCGUCAGCU  
 GGAGGGAUCCACCGGUGAGUCCGGUCGCGGACUCAUCGGGAC  
 AUACACAGCGACUGGGAUCGUCAUCUUGGCUUGUUCGCGUGAC  
 25 CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG  
 CCUUGAGGGAUAGCCGUAG SEQ ID NO: 195

*Mycobacterium flavescens* *ssrA*, Internal Partial

30 ACTTCGAGCGTCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG  
 AGACCACCGTAAGCGTCTGTGCAACCAATTAAGCGCCGATTCCA  
 ATCAGCGCGACTACGCACTCGTGCCTAAGCGACTGCGTGTCTG  
 35 TCAGCCCGGGAGAGCCCTCGACCCGGTCTGGCATCAGCTAGA  
 GGGATAAACCGGTGGTCCGGTTCGCGGACTCATCGGGACATCA  
 AACAGCGACTGGGATCGTCATCTGACTTGTTCGCGTGATCAGG  
 40 AGATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTT  
 GAGGGAACGCCGTAG SEQ ID NO: 196

*Mycobacterium flavescens* tmRNA, Internal Partial

45 ACUUCGAGCGUCAUUAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGAUUC  
 50 AAUCAGCGCGACUACGCACUCGUGCCUAAGCGACUGCGUGUC  
 UGUCAGCCCGGAGAGCCUCGACCCGGUGUCUGGCAUCAGCU  
 AGAGGGAUAAACCGGUGGGUCCGGUCGCGGGACUCAUCGGGAC  
 55 AUCAAACAGCGACUGGGAUCGUCAUCUAGUUCGCGUGA  
 UCAGGAGAUCGAGUAGAGACAAGCGAACUGCGCACGGAGA  
 AGCCUUGAGGGAACGCCGUAG SEQ ID NO: 197

*Mycobacterium marinum* *ssrA*, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCTGTGCAACCATATAAGCGCCGATTCAAC  
 65 TCAGCGCGACTACGCTCTCGTGCCTAAGCGACGGCTAGTCTGTG

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GGACCGGGAACGCCCTCGCCCGGACCCCGGCATCAGCTAGAGG  
 GATCAACCGATGAGTTCGGTCGCGGGGCTCATCGGGACATCAAC  
 AGCGACTGGGATCGTCATCTGGCTAGTTCCGCTGACCGAGAGA  
 TCCGAGCAGAGACCTAGCGGACTGCGCACGGAGAAGCCTTGAG  
 GGAATGCCGTAG SEQ ID NO: 198

*Mycobacterium marinum* tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGAUGCAACUAGAUAGCGCCGAUUA  
 CAUCAGCGCGACUACGUCUCGUCGCCUAAGCGACGGCUAGUC  
 UGUCGGACCGGGAACGCCUCGCCCCGGACCCCGGCAUCAGCU  
 AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGGCUAUCGGGAC  
 AUCAACAGCGACUGGGAUUCGUCAUCCUGGCUAGUUCGCGUGAC  
 CAGGAGAUCCGAGCAGAGACCUAGCGGACUGCGCACGGAGAAG  
 CCUUGAGGGAUUGCCGUAG SEQ ID NO: 199

*Mycobacterium microti* (Environmental Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTACA  
 TCAGCGCGACTACGCTCTCGTGCCTAAGCGACGGCTAGTCTGTG  
 AGACCGGGAACGCCCTCGGCCGGACCTGGCATCAGCTAGAGG  
 GATCCACCGATGAGTTCGGTTCGCGGGACTCCTCGGGACAGCCAC  
 AGCGACTGGGATCGTCATCTCGGCTAGTTCCGCTGACCGGGAGA  
 TCCGAGCAGAGGACATAGCGAACTGCGCACGGAGAAGCCTTGAG  
 GGAATGCCGTA SEQ ID NO: 200

*Mycobacterium microti* (Environmental Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCGACCAAUAAGCGCCGAUUA  
 CAUCAGCGCGACUACGUCUCGUCGCCUAAGCGACGGCUAGUC  
 UGUCAGACCGGGAACGCCUCGCCCCGGACCCUGGCAUCAGCU  
 AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUGGGAC  
 AGCCACAGCGACUGGGAUUCGUCAUUCUGGCUAGUUCGCGUGAC  
 CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG  
 CCUUGAGGGAUUGCCGUA SEQ ID NO: 201

*Mycobacterium smegmatis* (ATCC 10143) ssrA, Internal Partial

ACTTCGAGCATCGAATCCAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCAA

54

-continued

TCAGCGCGACTACGCCCTCGCTGCCTAAGCGACGGCTGGTCTGT  
 CAGACCGGAGTGCCTCGGCCGGATCCTGGCATCAGCTAGAG  
 5 GGACCCACCCACGGGTTTCGGTTCGCGGGACCTGTGGGACATCAA  
 ACAGCGACTGGGATCGTCATCTCGGCTTGTTCGTGTGACCGGGA  
 GATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTCG  
 10 AGGACATGCCGTAG SEQ ID NO: 202

*Mycobacterium smegmatis* (ATCC 10143) ssrA, Internal Partial

15 ACUUCGAGCAUCGAAUCCAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUA  
 AAUCAGCGCGACUACGCCUCGCGUCCUAAGCGACGGCUGGUC  
 20 UGUCAGACCGGAGUGCCUCGCGCCGGAUCCUGGCAUCAGCU  
 AGAGGGACCCACCCACGGGUUCGGUCGCGGGACCUUGGGGAC  
 AUCAAACAGCGACUGGGAUUCGUCAUCUCGCGCUUGUUCGUGUGA  
 25 CCGGGAGAUCCGAGUAGAGACAUAGCGAACUCGCGCACGGAGAA  
 GCCUCGAGGACAUGCCGUAG SEQ ID NO: 203

*Mycobacterium xenopi* (Clinical Isolate) ssrA, Internal Partial

30 ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA  
 GACCACCGTAAGCGTCGTTGCAACTAAATAAGCGCCGATTACA  
 TCAGCGCGACTACGCTCTCGTGCCTAAGCGACAGCTAGTCCGT  
 35 CAGGCCGGGAGTTCCTCGACCCGGATCCTGGCTCAGCTAGAG  
 GGATCCACCGATGGGTTTCGGTTCGCGGGACCCATCGGGACACCAC  
 ACAGCGACTGGGATCGCCGTCGCGGCTAGTTGCGGAGACCGGGA  
 40 GATCCGAGTAAGGGCAAAGCGAACTGCGCACGGAGAAGCCTTG  
 AGGGTATGCCGTA SEQ ID NO: 204

*Mycobacterium xenopi* (Clinical Isolate) tmRNA, Internal Partial

45 ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUA  
 50 CAUCAGCGCGACUACGUCUCGUCGCCUAAGCGACAGCUAGUC  
 CGUCAGGCCGGGAGUUCUCCGACCCGGAUCCUGGCGUCAGCU  
 AGAGGGAUCCACCGAUGGUAUCGGUCGCGGGACCCAUCCGGGAC  
 55 ACCACACAGCGACUGGGAUUCGCGGUCCCGGCUAGUUCGCGAGA  
 CCGGGAGAUCCGAGUAGGGCAAAGCGAACUCGCGCACGGAGAA  
 GCCUUGAGGGAUUGCCGUA SEQ ID NO: 205

*Mycobacterium intracellulare* (NCTC 10425) ssrA, Internal Partial

60 ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACC  
 65 GACCACCGTAAGCGTCGTTGCAACAGATAAGCGCCGATTCAA

55

-continued

TCAGCGCGACTACGCTCTCGCTGCTAAGCGACAGTAGTCCGT  
 CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAG  
 GGATCCACCGATGAGTCCGGTCGCGGGACTTATCGGGACACCAA  
 CAGCGACTGGGATCGTCATCTCGGCTTGTTCGCGTGACCCGGGAG  
 ATCCGAGTAGAGGCATAGCGAAGTGCACGCGAGAGAAGTCTTGAG  
 GGAATGCCGTAG SEQ ID NO: 206

*Mycobacterium intracellulare* (NCTC 10425) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAC  
 CGACCACCGUAAGCGUCGUUGCAAACAGAUAGCGCCGAUUCA  
 CAUCAGCGCGACUACGUCUCGCGUGCCUAAGCGACAGCUAGUC  
 CGUCAGACCGGGAACGCCUUCGACCCGGAGCCUGGCGUCAGCU  
 AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUUAUCGGGAC  
 ACCAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGUGAC  
 CGGGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAA  
 GUCUUGAGGGAUAGCCGUAG SEQ ID NO: 207

*Mycobacterium scrofulaceum* (NCTC 10803) ssrA, Internal Partial

ACATCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG  
 AGACCACCGTAAGCGTCTGTTGCAACCAATTAAGCGCCGATTCCAC  
 ATCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCG  
 TCAGACCGGGAAGCCCTCGACCCGGAGCCTGGCGTCAGCTAGA  
 GGGATCAACCGATGAGTTCGGTTCGCGGGACTCATCGGGACACCA  
 ACAGCGACTGGGATCGTCATCTGGTAGTCCGCGTGACCAGGA  
 GATCCGAGCAGAGGCATAGCGGACTGCGCACGGAGAAGTCTTG  
 AGGGAAATGCCGTTG SEQ ID NO: 208

*Mycobacterium scrofulaceum* (NCTC 10803) tmRNA, Internal Partial

ACAUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG  
 AGACCACCGUAAGCGUCGUUGCAAACAAUUAAGCGCCGAUUCA  
 CAUCAGCGCGACUACGUCUCGCGUGCCUAAGCGACAGCUAGUC  
 CGUCAGACCGGGAAGCCUUCGACCCGGAGCCUGGCGUCAGCU  
 AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCAUCGGGAC  
 ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUCCGCGUGAC  
 CAGGAGAUCCGAGCAGAGGCAUAGCGGACUGCGCACGGAGAAG  
 UCUUGAGGGAUAGCCGUUG SEQ ID NO: 209

*Nocardia asteroides* ssrA, Internal Partial

ACTGTGTGCGCCGAGGTAGGGGAAGCGTGTGCGTGCAGGCTGGA  
 GACCACCGTTAAGCGTTCGCGCAACCAATTAAGCGCCGATTCCA

56

-continued

ATCAGCGCGACTACGCCCTCGCTGCCTGATCAGCGACGGCTAGC  
 TGTCGGCCCGGGTTGTGTTCCCGAACCCGGATGCCGGCATCATCT  
 CAGGGAACTCACCGTGTTCGCGGTCGCGGACGGACACGGGACA  
 GCAAACAGCGACTGGGATCGTCATCTCGGCTTGTTCGCGTGACC  
 GGGAGATCCAAGTAGAGACATAGCGGACTGCACACGGAGAAGC  
 CCTACTGACTCGACACAG SEQ ID NO: 210

*Nocardia asteroides* tmRNA, Internal Partial

ACUGUGUGCGCCGAGGUAGGGGAAGCGUGUCGGUGCAGGCUUG  
 GAGACCACCGUUAAGCGUCGCGGCAACCAAUUAAGCGCCGAUU  
 CCAAUCAGCGCGACUACGCCUUCGCGUGCCUGAUCAGCGACGGC  
 UAGCUGUCGGCCCGGGUUGUUCGAAACCCGGAUGCCGGCA  
 UCAUCUCAGGGAACUCACCGUGUUCGCGGUCGCGGACGGACA  
 CGGGACAGCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUC  
 GCGUGACCGGGAGAUCCAAGUAGAGACAUAGCGGCGUCACACG  
 GAGAAGCCUACUGACUCGACACAG SEQ ID NO: 211

*Salmonella enteritidis* ssrA, Internal Partial

ACGGGATTTGCGAAACCCAAGTGCATGCCGAGGGGCGGTTGGC  
 CTCGTAAAAGCCGCAAAAAATAGTTCGCAAAACGACGAAACCT  
 ACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAG  
 CCTCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCCAAAAG  
 AGATCGCGTGGATGCCCTGCCCTGGGGTTGAAGCGTTAAAACGAA  
 TCAGGCTAGTCTGGTAGTGGCGTGTCCGTCGCGAGGTGCCAGGC  
 GAATGTAAAGACTGACTAAGCATGTAGTACCAGGATGTAGGAA  
 TTTCGG SEQ ID NO: 212

*Salmonella enteritidis* tmRNA, Internal Partial

ACGGGAUUUGCGAAACCCAAGGUGCAUAGCCGAGGGGCGGUUG  
 GCCUCGUAAAAAGCCGCAAAAAAUAGUCGCAAAACGACGAAAC  
 CUACGCUUAGCAGCUUAAUAAACCGUCUAGAGCCUCUCUCC  
 CUAGCCUCCGCUUAGGACGGGAUCAAGAGAGGUCAAACCC  
 AAAAGAGAUCCGUGGAUGCCUGCCUGGGGUUGAAGCGUUA  
 AAACGAAUCAGGCUAGUCUGGUAGUGGCGUCCGUCGCGCAGG  
 UGCCAGGCGAAUGUAAAGACUGACUAAGCAUGUAGUACCGAG  
 GAUGUAGGAAUUUCGG SEQ ID NO: 213

*Staphylococcus epidermidis* (NCTC 11047) ssrA, Internal Partial

ACAGGGTCCCCGAGCTTATTAAGCGTGTGCGAGGGTTGGCTC  
 CGTCATCAACACATTTCCGTTAAATATAACTGACAAATCAAACA

57

-continued

ATAATTTTCGCAGTAGCTGCGTAATAGCCACTGCATCGCCTAACA  
GCATCTCCTACGTGCTGTTAACGCGATTCAACCCCTAGTAGGATAT  
GCTAAACACTGCCGCTTGAAGTCTGTTTAGATGAAATATAATCA  
AGCTAGTATCATGTTGGTTGTTTATTGCTTAGCATGATGCGAAAA  
TTATCAATAAACTACACACGTAGAAAGATTGTATCAGGACCTC  
TGG SEQ ID NO: 214

*Staphylococcus epidermidis* (NCTC 11047) tmRNA, Internal Partial

ACAGGGGUCCCCGAGCUUUAUUAAGCGUGUCGGAGGUUGGCU  
CCGUCAUCAACACAUUUUCGUAUAAUUAACUGACAAUCAA  
CAAUAAUUUCGAGUAGCUGCGUAAUAGCCACUGCAUCGCCUA  
ACAGCAUCUCCUACGUGCUGUUAACGCGAUUCAACCCUAGUAG  
GAUAUGCUAACACUGCCGCUUAGUUGUUAUAGUAGAAU  
AUAAUCAAGCUAGUAUCAUGUUGUUGUUAUUGCUUAGCAU  
GAUGCGAAAAUUAUCAAUAAACUACACACGUAAGAAUUAU  
UAUCAGGACCUCUGG SEQ ID NO: 215

*Streptococcus agalactiae* (NCTC 8181) ssrA, Internal Partial

ACAGGCATTATGAGGTATATTTTGCAGCTCATCGGCAGATGTAA  
AATGCCAGTTAAATATAACTGCAAAAAATACAAATTCTTACGCA  
TTAGTGCCTAAAAACAGCCTGCGTGATCTTACAAAGATTGTTT  
GCGTTTTGCTAGAAGGCTTATTATTCAGCAAACCTAGTTGGCT  
ACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGA  
GGGCTTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACC  
TATAGITGTAGACAAATATATTAGCAGATGTTTGG SEQ ID  
NO: 216

*Streptococcus agalactiae* (NCTC 8181) tmRNA, Internal Partial

ACAGGCAUUAUGAGGUUAUUAUUUGCGACUCAUCGGCAGAUGU  
AAAAUGCCAGUUAUUAUUAUCUGCAAAAAUACAAUUCUUA  
CGCAUUAAGCUGCCUAAAAACAGCCUGCGUGAUUCUACAAGA  
LTUGUUUGCGUUUUGCUAGAAGGUCUUAUUUAUCAGCAAACUA  
CGUUUGGCUACUGUCUAGUUAUUAAAAAGAGAUUUUAUAGAC  
UCGCUAUGUGAGGGCUUGAGUUAUGUGUCAUCACCUAGUUAA  
AUCAAUAUAUAAACUUAUAGUUGUAGCAAAUUAUUAGCAGA  
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.

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

*Salmonella*:

1) Genus 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'-AGTTTTCGTCGTTTGGCA-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. subtilis* *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.		
	<i>Escherichia coli</i> vs. <i>Vibrio cholerae</i>	<i>Bacillus subtilis</i> vs. <i>Mycobacterium tuberculosis</i>
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 asterisk 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  $\gamma$ P<sup>32</sup>. 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'- GGG(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: *Staphylococcus aureus*
- Lane 8: *Enterococcus faecalis*
- Lane 9: *Lactobacillus lactis*
- Lane 10: *Bacillus subtilis*
- 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	<i>Escherichia coli</i>	+
Negative	<i>Salmonella poona</i>	+
Bacteria	<i>Klebsiella aerogenes</i>	+
	<i>Proteus mirabilis</i>	+
	<i>Proteus rettgeri</i>	+
	<i>Aeromonas hydrophilia</i>	+

TABLE 2-continued

Bacterial species tested with universal amplification primers.		PCR Product
Gram	<i>Staphylococcus aureus</i>	+
Positive	<i>Enterococcus faecalis</i>	+
Bacteria	<i>Lactobacillus lactis</i>	+
	<i>Bacillus subtilis</i>	+
	<i>Listeria monocytogenes</i>	+
	<i>Listeria innocua</i>	+
	<i>Listeria murrayi</i>	+
	<i>Listeria welshimeri</i>	+
	<i>Listeria grayi</i>	+
	<i>Mycobacterium bovis</i>	+

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 demon-

strated 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' <i>Listeria</i> genus specific amplification primer 5'-AAAGCCAATAATAACTGG-3' SEQ ID NO: 172
(b)	Ltm2:	3' <i>Listeria</i> genus specific amplification primer 5'-CCAGAAATATCGGCACTT-3' SEQ ID NO: 173
(c)	LGtm:	<i>Listeria</i> genus specific hybridisation probe 5'-GTGAGACCCTTACCGTAG-3' SEQ ID NO: 174
(d)	LStm:	<i>L. monocytogenes</i> species specific hybridisation probe 5'-TCTATTTAACCCAGACG-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. subtilis*
- 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 <i>Listeria</i> specific amplification primers.		PCR Product
Gram	<i>Escherichia coli</i>	-
Negative	<i>Salmonella poona</i>	-
Bacteria	<i>Klebsiella aerogenes</i>	-
	<i>Proteus mirabilis</i>	-
	<i>Proteus rettgeri</i>	-
	<i>Aeromonas hydrophilia</i>	-

TABLE 3-continued

Bacterial species tested with <i>Listeria</i> specific amplification primers.		PCR Product	
5	Gram	<i>Staphylococcus aureus</i>	-
	positive	<i>Enterococcus faecalis</i>	-
	bacteria	<i>Lactobacillus lacus</i>	-
		<i>Bacillus subtilis</i>	-
		<i>Listeria monocytogenes</i> strain 1	+
10		<i>Listeria monocytogenes</i> strain 2	+
		<i>Listeria monocytogenes</i> strain 3	+
		<i>Listeria monocytogenes</i> strain 4	+
		<i>Listeria monocytogenes</i> clinical isolate	+
		<i>Listeria innocua</i>	+
15		<i>Listeria murrayi</i>	+
		<i>Listeria welshimeri</i>	+
		<i>Listeria grayi</i>	+
		<i>Mycobacterium bovis</i>	-

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: *Staphylococcus aureus*
- Lane 8: *Enterococcus faecalis*
- Lane 9: *Lactobacillus lactis*
- Lane 10: *Bacillus subtilis*
- 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. subtilis*
- 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	<i>Escherichia coli</i>	-	-
	<i>Salmonella poona</i>	-	-
	<i>Klebsiella aerogenes</i>	-	-
	<i>Proteus mirabilis</i>	-	-
	<i>Proteus rettgeri</i>	-	-
	<i>Aeromonas hydrophila</i>	-	-
Gram positive bacteria	<i>Staphylococcus aureus</i>	-	-
	<i>Enterococcus aecalis</i>	-	-
	<i>Lactobacillus lactis</i>	-	-
	<i>Bacillus subtilis</i>	-	-
	<i>Listeria monocytogenes</i> strain 1	+	+
	<i>Listeria monocytogenes</i> strain 2	+	+
	<i>Listeria monocytogenes</i> strain 3	+	+
	<i>Listeria monocytogenes</i> strain 4	+	-
	<i>Listeria monocytogenes</i> clinical isolate	+	+
	<i>Listeria innocua</i>	+	-
	<i>Listeria murrayi</i>	+	-
	<i>Listeria welshimeri</i>	+	-
	<i>Listeria grayi</i>	+	-
	<i>Mycobacterium bovis</i>	-	-

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' CATTAACTTTAGCAAG-GAAGTG 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. welshimeri* (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. subtilis*, *L. lactis*, *S. aureus*, *S. epidermis*, *E. faecalis*, *C. perfringens* (16-21) and the Gram-negative bacteria *E. coli*, *S. enteritidis*, *P. Rettgeri*, *K. aerogenes* (22-25). As shown in FIG. 10 after hybridisa-

tion, 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);	20

-continued

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;	5
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;	10
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;	15
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;	20
Lane B:	Molecular weight marker V.	

## SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 239

<210> SEQ ID NO 1

<211> LENGTH: 366

<212> TYPE: DNA

<213> ORGANISM: *Actinobacillus actinomycetemcomitans*

<400> SEQUENCE: 1

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ggggctgatt ctggattcga cgggattagc gaagcccga gtcacgctcg aggtgccgta      60
ggcctcgtaa ataaaccgca aaaaaatagt cgcaaacgac gaacaatacg ctttagcagc      120
ttaataacct gcctttagcc ttcgctcccc agcttccgct cgtaagacgg ggataaagcg      180
gagtcaaacc aaaacgagat cgtgtggaag ccaccgtttg aggatcgaag cattaaatta      240
aatcaaagta gcttaattgt cgcgtgtccg tcagcaggat taagtgaatt taaagaccgg      300
actaaacgtg tagtgctaac ggcagaggaa ttccggacgg gggttcaact cccccagct      360
ccacca                                           366

```

<210> SEQ ID NO 2

<211> LENGTH: 366

<212> TYPE: RNA

<213> ORGANISM: *Actinobacillus actinomycetemcomitans*

<400> SEQUENCE: 2

```

ggggcugauu cuggauucga cgggauuagc gaagcccga gugcacgucg aggugccgua      60
ggccucguua auaaacccgca aaaaaauagu cgcaaacgac gaacaauacg cuuuagcagc      120
uuauuaaccu gccuuuagcc uucgcucccc agcuuccgcu cguaagacgg ggauaaagcg      180
gagucaaacc aaaacgagau cguguggaag ccaccguuug aggaucaag cauuuuuuuu      240
aaucuaagua gcuuuuuuu cgcguguccg ucagcaggau uaagugaauu uaaagaccgg      300
acuaaacgug uagugcuaac ggcagaggaa uuucggacgg ggguucaacu cccccagcu      360
ccacca                                           366

```

<210> SEQ ID NO 3

<211> LENGTH: 315

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<212> TYPE: DNA  
 <213> ORGANISM: *Aeromonas salmonicida*

<400> SEQUENCE: 3

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 aaaaatagtc gcaaacgacg aaaactacgc actagcagct taataacctg catagagccc 120  
 ttctacccta gcttgctgt gtcctagggg atcggaaggt catccttcac aggatcgtgt 180  
 ggaagtcctg ctccggggcg aagcattaaa accaatcgag ctagtcaatt cgtggcgtgt 240  
 ctctccgag cgggttgccg aatgtaaaga gtgactaagc atgtagtacc gaggatgtag 300  
 taattttggg cgggg 315

<210> SEQ ID NO 4  
 <211> LENGTH: 315  
 <212> TYPE: RNA  
 <213> ORGANISM: *Aeromonas salmonicida*

<400> SEQUENCE: 4

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 aaaaauaguc gcaaacgacg aaaacuacgc acuagcagcu uaauaaccug cauagagccc 120  
 uucuaccua gcuugccugu guccuagggg aucggaaggu cauccuucac aggaucgugu 180  
 ggaaguccug cucggggcgg aagcauuaaa accaacgag cuagucaauu cguggcgugu 240  
 cucuccgag cggguugccg aauguaaaga gugacuaagc auguaguacc gaggauguag 300  
 uaaaauugga cgggg 315

<210> SEQ ID NO 5  
 <211> LENGTH: 349  
 <212> TYPE: DNA  
 <213> ORGANISM: *Alcaligenes eutrophus*

<400> SEQUENCE: 5

tgggcccacc tggtttcgac gtggttaca agcagtgagg cataccgagg acccgccacc 60  
 tcgttaatca atggaatgca ataactgcta acgacgaacg ttacgcaact gcttaattgc 120  
 ggccgctctc gcaactggctc gctgacgggc tagggtcgca agaccacgag aggtatttac 180  
 gtcagataag ctccggaagg gtcacgaagc cggggacgaa aacctagtga ctgcccgtcg 240  
 tagagcgtgt tcgtccgatg cgccgggttaa atcaaatgac agaactaagt atgtagaact 300  
 ctctgtggag ggcttacgga cgccgggttcg attcccgcgc gctccacca 349

<210> SEQ ID NO 6  
 <211> LENGTH: 349  
 <212> TYPE: RNA  
 <213> ORGANISM: *Alcaligenes eutrophus*

<400> SEQUENCE: 6

ugggcccacc ugguuucgac gugguuacaa agcagugagg cauaccgagg acccgucacc 60  
 ucguuaauca auggaauagc auaacugcua acgacgaacg uuacgcauc gcuuuuuugc 120  
 ggccgucuc gcacuggcuc gcugacgggc uagggucgca agaccacgag agguuuuuac 180  
 gucagauaag cuccggaagg gucacgaagc cggggacgaa aaccuaguga cucgccgucg 240  
 uagagcgugu ucguccgaug cgccgguuua aucaaaugac agaacuaagu auguagaacu 300  
 cucugggag ggcuuacgga cgccgguuuc auucccgccg gcuccacca 349

<210> SEQ ID NO 7  
 <211> LENGTH: 347

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<212> TYPE: DNA
<213> ORGANISM: Aquifex aeolicus

<400> SEQUENCE: 7

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gtaacagccg ctaaaacagc tccgaagct gaactcgctc tcgctgccta attaaacggc   120
agcgcgtccc cggtaggttt gcgggtggcc taccggaggg cgtcagagac acccgctcgg   180
gctactcggc gcacacgggc tgagtagctg acacctaacc cgtgctaccc tcggggagct   240
tgcccgtggg cgacccgagg ggaatcctg aacacgggct aagcctgtag agcctcggat   300
gtggccgccc tcctcggacg cgggttcgat tcccgcgcc tccacca                   347

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<210> SEQ ID NO 8
<211> LENGTH: 347
<212> TYPE: RNA
<213> ORGANISM: Aquifex aeolicus

<400> SEQUENCE: 8

gggggcgaa aggauucgac ggggacaggc gguccccgag gagcaggccg gguggcuccc   60
guaacagccg cuaaaaacag ucccgaagcu gaacucguc ugcugccua auuaaacggc   120
agcgcguccc cgguaaguuu gcggguggcc uaccggaggg cgucagagac acccgucgag   180
gcuacucggu cgcacggggc ugaguagcug acaccuaacc cgucuaacc ucggggagcu   240
ugcccugggg cgacccgagg ggaauucug aacacgggcu aagccuguag agccucggau   300
guggccgccc uccucggacg cggguucgau ucccgcgcc uccacca                   347

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<210> SEQ ID NO 9
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Bacillus megaterium

<400> SEQUENCE: 9

aggtagttc gagcttaggt tgcgagtcga ggagatggcc tcgttaaac atcaacgcca   60
ataataactg gcaaatctaa caataacttc gctttagctg cataatagta gcttagcgtt   120
cctccctcca tcgccatgt ggtagggtaa gggactcact ttaagtgggc tacgccggag   180
ttcgcgtctc gaggacgaag gaagagaata atcagactag cgactgggac gcctgttggc   240
aggcagaaca gctcgcgaat gatcaatatg ccaactacac tcgtagacgc ttaagtggcc   300
atatttctgg acgtgg                                           316

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```

<210> SEQ ID NO 10
<211> LENGTH: 316
<212> TYPE: RNA
<213> ORGANISM: Bacillus megaterium

<400> SEQUENCE: 10

aggguaguuc gagcuuaggu ugcgagucga ggagauggcc ucguuaaac aucaacgcca   60
auaauaacug gcaaaucuaa caauaacuuc gcuuagcug cauaauagua gcuuagcguu   120
ccuccucca ucgcccaugu gguaggguaa gggacucacu uuaagugggc uaccgccggag   180
uucgccgucu gaggacgaag gaagagaaua aucagacuag cgacugggac gccuguuggu   240
aggcagaaca gcucgcgaau gaucaauaug ccaacuacac ucguagacgc uuaaguggcc   300
auuuucugg acgugg                                           316

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<210> SEQ ID NO 11
<211> LENGTH: 363

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<212> TYPE: DNA
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 11

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tcgtaaacac gcacttaaat ataactggca aaactaacag ttttaaccaa aacgtagcat   120
tagctgccta ataagcgcag cgagctcttc ctgacattgc ctatgtgtct gtgaagagca   180
catccaagta ggctacgctt ccgttcccgt ctgagaacgt aagaagagat gaacagacta   240
gctctcggaa ggcccccccg caggcaagaa gatgagttaa accataaata tgcaggctac   300
gctcgtagac gcttaagtaa tcgatgtttc tggacgtggg ttcgactccc accgtctcca   360
cca                                                                                   363

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<210> SEQ ID NO 12
<211> LENGTH: 363
<212> TYPE: RNA
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 12

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ucguaaacac gcacuuaaa uaaacuggca aaacuaacag uuuuaaccaa aacguagcau   120
uagcugccua auaagcgcag cgagcucuuc cugacauugc cuaugugucu gugaagagca   180
cauccaagua ggcuacgcuu gcguuuccgu cugagaacgu aagaagagau gaacagacua   240
gcucucggaa ggcccccccg caggcaagaa gaugagugaa accauaaaau ugcaggcuac   300
gcucguagac gcuaaagua ucgauguuuc uggacguggg uucgacuccc accgucucca   360
cca                                                                                   363

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<210> SEQ ID NO 13
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 13

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agctcgtaa tccactggaa cactacaaac gccaacgacg agcgtctcgc tctcgcgct   120
taagcgtgta gccgctgcac tgatctgtcc ttgggtcagg cgggggaagg caacttcaca   180
gggggcaacc ccgaaccgca gcagcgacat tcacaaggaa tcggccaccg ctggggtcac   240
acggcgttgg ttaaaattc gtgaatcgcc ctggtccggc ccgtcgatcg gctaagtcca   300
gggttaaate caaatagatc gactaagcat gtagaactgg ttgaggaggg cttgaggacg   360
ggggttcaat tccccccg cccacca                                                                                   387

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<211> LENGTH: 387
<212> TYPE: RNA
<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 14

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agcucguuaa uccacuggaa cacuacaaac gccaacgacg agcguucgcg ucucgcccgu   120
uaagcgguga gccgcugcag ugauucgucc uugggucagg cgggggaagg caacuucaca   180
gggggcaacc ccgaaccgca gcagcgacau ucacaaggaa ucggccaccg cuggggucac   240
acggcguugg uuuuuuuac gugaaucgcc cugguuccgc ccgucgaucg gcuaagucca   300

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ggguuaaauc caaaugauc gacuaagcau guagaacugg uugcggaggg cuugcggagc 360

gggguucaau ucccccggc uccacca 387

<210> SEQ ID NO 15

<211> LENGTH: 362

<212> TYPE: DNA

<213> ORGANISM: *Borrelia burgdorferi*

<400> SEQUENCE: 15

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cttaaaactt ctaaaataaa tgcaaaaaat aataacttta caagctcaaa tcttgaatg 120

gctgcttaag ttagcagagg gttttgtga atttgcttt gaggttact tatactctt 180

tcgacatcaa agcttgctta aaaatgtttt caagttgatt tttaggact tttatacttg 240

agagcaatth ggtggtttgc tagtatttcc aaacatatt gcttaataaa atactagata 300

agcttgtaga agcttatagt attattttta ggacgagggt 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 gagggaauuc 60

cuuaaaacu cuaaaauaaa ugcaaaaaa auaacuuaa caagcucaaa ucuuguaaug 120

gcugcuuaag uuagcagagg guuuuguuga auuuggcuuu gagguucacu uauacucuuu 180

ucgacaucaa agcuugcuua aaaauguuuu caaguugauu uuuagggacu uuuauacuug 240

agagcauuu gguguuuugc uaguauuuuc aaaccuuuu gcuuaaaaa auacuagaua 300

agcuuguaga agcuuuauug auuuuuuua ggacgagggu ucaauucccg ccaucccac 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 ggcagtgcgc tttgggcaaa 60

gcgtaaaaag cccaaataaa attaaacgca aacaacgta aattcgctcc tgcttacgct 120

aaagctcgcg aagttcagtt gagcctgaaa ttaagtcat actatctagc ttaattttcg 180

gtcatttttg atagtgtagc cttgcgtttg acaagcgttg aggtgaaata aagtcttagc 240

cttgcttttg agttttggaa gatgagcgaa gtaggtgaa gtagtcatct ttgctaagca 300

tgtagaggtc tttgtgggat tatttttggg 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 ggcaugcgc uuugggcaaa 60

gcuuaaaaag cccaaauaaa auuaaacgca aacaacguua aaucgcucc ugcuuacgcu 120

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```

aaagcugcgu aaguucaguu gagccugaaa uuaaagucou acuaucuagc uuaauuuucg 180
gucauuuuug auaguguagc cuugcguuug acaagcguug aggugaaaau aagucuuagc 240
cuugcuuuug aguuuuggaa gaugagcgaa guaggugaa guagucaucu uugcuaagca 300
uguagagguc uuuguggau uauuuugga cagggguucg auccccucg cuuccacca 359

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

```

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<400> SEQUENCE: 19

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```

gggggtgtaa aggtttcgac ttagaatga agcgtaatt gcctgaggag ggcgttgct 60
ggcctcctaa aaagccgaca aaacaataaa tgccgaacct aaggctgaat gcgaaattat 120
cagcttcgct gatctcgaag atctaagagt agctgcttaa ttagcaaagt tgttacctaa 180
atacgggtga cccgggtgtc gcgagctcca ccagaggttt tcgaaacacc gtcatttatc 240
tggttagaac ttaggctcct 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

```

```

ggggguguaa agguuucgac uuagaaauga agcguuaauu gcaugcggag ggcguuggcu 60
ggccuccuaa aaagccgaca aaacaauaaa ugccgaaccu aaggcugaau gcgaaauuuu 120
cagcuucgcu gaucucgaag aucuaagagu agcugcuuaa uuagcaaagu uguuaccuaa 180
auacggguga cccggguuuc gcgagcucca ccagagguuu ucgaaacacc gucauguauc 240
ugguuagaac uuagguccuu uauuucucga ggaaaugagu uugaaauuuu 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 ttagaatga agcgtaatt gcctgaggag ggcgttgct 60
ggcctcctaa aaagccgaca aaacaataaa tgccgaacct aaggctgaat gcgaaattat 120
cagcttcgct gatcttaatg atctaagagt tgctgcttaa ttagcaaagt tgttacctaa 180
gtactgtaa cccgggtgtc gcgagctcca ccagaggttt tcgaaacgcc gtcatttatc 240
tggttagaat tagggccttt taactctcaa gggaactaat ttgaaattta atgagagtcg 300
ttgtctcta tagaggtttc tagctgagga gatataacgt aaaatattct agaaactaag 360
catgtagagg ttagcgggga gtttactaag gacgagagtt cgaatctctc cacctccacc 420
a 421

```

```

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

```

-continued

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```

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

<400> SEQUENCE: 22

ggggguguaa agguuucgac uuagaaauga agcguaaaau 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 uaacucucuaa gggaacuaau uugaauuuaa augagagucg   300
uuggucucua uagagguuuc uagcugagga gauauaacgu aaaaauuucu 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 cgtaaacaat gtctatgtac caatagatgc agacgattat tcgtatgcaa   120
tggctgcctg attagcacia gttaattcag aagccatcgt cctgcggtga atgcgcttac   180
tctgaagccg ccggatggca taaccgcgac ttgagcctac gggttcgcgc aagtaagctc   240
cgtacattca tgcccagagg ggtgtgcggg taaccaatcg ggataagggg acgaacgctg   300
ctggcggtgt aatcggacca cgaaaaacca accaccagag atgagtgtgg taactgcac   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 cguuaaaca gucuauguac caauagaugc agacgauuau ucguaugcaa   120
uggcugccug auuagcacia guuaauucag aagccaucgu ccugcgguga augcgcuuac   180
ucugaagccg ccggauggca uaaccgcgac uugagccuac ggguucgcgc aaguaagcuc   240
cguacauuca ugcccagagg ggugugcggg uaaccaaucg ggauaagggg acgaacgcug   300
cuggcggugu aaucggacca cgaaaaacca accaccagag augagugugg uaucugcauc   360
gagcaguguc cuggacgcgg guucaaguuc 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 gtttaagcaag tcgaggattt   60
gttctatctc gaaaatcaag aactctcaaa atttaaacgc aactaatatt gtacgtttta   120
accgtaaagc agctttcgct gtttaataat tacttttaat ttaaaaacct aattttttta   180
ggaatttatt tattttattg ttatcctgct taatgaatta aaaaaagcta tacttgtgaa   240

```

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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 guuuuuuuu aauuauguuu guuaagcaag ucgaggauuu 60  
 guucuaucuc gaaaaucaag aacucucaaa auuuuaacgc aacuaauuu guacguuuua 120  
 accguaaagc agcuuucgcu guuuuaauau uacuuuuauu uuaaaaaaccu aauuuuuuuu 180  
 ggaauuuuuu uauuuuuuuu uuauccugcu uaaugaauua aaaaaagcua uacuugugaa 240  
 uaaacgcaua auuuuuuuuu 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 agcttggttg taggcgttcc atggaggga tgttaaata 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 auggaggga uguuuuuuuu 120  
 caaacugcac ucggagaugc uuaaugaaac cauuuucgga cagggguucg auccccucg 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 ggaagtcaact aaaaaagaag 180  
 gctagcccag gcgattctcc atagccgacg gcgaaacttt atggagctac ggctgcgag 240  
 aacctgccc a ctggtgagcg ccggcccgc aatcaaacag tgggatacac acgtagacgc 300  
 acgctggacg gacctttgga cggcgggttc 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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```

gggggugacc cgguuucgac aggggaacug aaggugaugu ugcgugucga ggugccguug    60
gccucguaaa caaacggcaa agccauuuua cuggcaacca gaacuacgcu cucgcugcuu    120
aagugagaug acgaccgugc agcccggccu uuggcgucgc ggaagucacu aaaaaagaag    180
gcuagcccag gcgauucucc auagccgacg gcgaaacuuu auggagcuac ggccugcgag    240
aaccugccca cuggugagcg ccggcccgcg 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 aggtcgaggg gccgctggcc tcgtaaaaag cggcacaaaa    60
gtaattgcc acaacgatta cgactacgct tacgctgctt aataacagcg aggcaatgac    120
cgtttaacgg tcgcgccgat cagggccatg cctgataacc ctgattggcg acacttatca    180
ggctggcgaa aaccggtctt cgccgggggtt tttcgcgagg agtttaccgg cgggattgct    240
gcgttgtgcc tggtcagggg ccaacagcgc ggtgaaatac atacttgacc taaacctgta    300
atgcttcgtg tggaatgttc tcggacgggg

```

```

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

```

```

<400> SEQUENCE: 32

```

```

gggacuggaa ccguagcggc aggucgaggg gccgcuggcc ucguaaaaag cggcacaaaa    60
guaaaugcca acaacgauua cgacuacgcu uacgcugccu aauaacagcg aggcaaugac    120
cguuuacgg ucgcgccgau cagggccaug ccugauaacc cugauuggcg acacuuauca    180
ggcuggcgaa aaccggcucu cgccgggguu uuucgcgagg aguuuaccgg cgggauugcu    240
gcuuugucc uggucagggg ccaacagcgc ggugaaaauac auacuugacc uaaaccugua    300
augcuucgug uggaanguuc ucggacgggg

```

```

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

```

```

<400> SEQUENCE: 33

```

```

ctcaggtgac atgtcgagaa tgagagaatc tcgttaaata ctttcaaac ttatagttgc    60
aaacgacgac aactacgctt tagcggctta attcccgtt tcgcttacct agatttgtct    120
gtgggtttac cgtaagcgcg attaacacag aatcgctggt taacgcgtcc gctgttaatc    180
ggttaaatta agcggaatcg cttgtaaaat gcctgagcgt tggctgttta tgagttaaac    240
ctaattaact gctctaaaca tgtagtacca aaagttaagg attcgcggac gggggttcaa    300
atccccccgc ctccacca

```

```

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

```

```

<400> SEQUENCE: 34

```

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---

```

cucgaggugc augucgagaa ugagagaauc ucguaaaaua cuuucaaac uuauaguugc 60
aaacgacgac aacuacgcuu uagcggcuua auucccgcuu ucgcuuaccu agauuugucu 120
guggguuuac cguaaagcag auuaacacag aaucgcuggu uaacgcgucc gcuguuauac 180
gguuuuuuu agcggaaucg cuuguaaaau gccugagcgu uggcuguuuu ugaguuaaac 240
cuuuuuacu gcucuaaaca uguaguacca aaaguuaagg auucgcggac ggggguucaa 300
auccccccgc cuccacca 318

```

```

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

```

```

<400> SEQUENCE: 35

```

```

gggggcggtta cggattcagc aggcatagtt gagcttgaat tgcgtttcgt aggttacggc 60
tacgttaaaa cgttacagtt aaatataact gctaaaaacg aaaacaattc tttcgcttta 120
gctgcctaaa aaccagctag cgaagatcct ccggcactcg cccatgtgct cgggtcaggg 180
tcctaatacga agtgggatac gctaaatatt tccgtctgta aaatttagag gagcttacca 240
gactagcaat acagaatgcc tgtcactcgg cacgctgtaa agcgaacctt taatgagtg 300
tctatgaacg tagagattta agtggcaata tgtttggacg cgggttcgac tcccgcgctc 360
tccacca 367

```

```

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

```

```

<400> SEQUENCE: 36

```

```

gggggcgguua cggauucgac aggcgauagu gagcuugaau ugcguuuuugc agguuacggc 60
uacguuuuuu cguuacaguu aaauuuuuu gcuuuuuuacg aaacaauuc uuucgcuuuu 120
gcugccuuuu aaccagcuag cgaagaaucc ccggcgaucg cccaugugcu cgggucaggg 180
uccuuuucga agugggauac gcuaauuuuu uccgucugua aaauuuagag gagcuuacca 240
gacuagcaau acagaauccg ugucacucgg cacgucugua agcgaaccuu uaaugagug 300
ucuauaagc uagaguuuuu aguggcaaua uguuuggacg cggguucgac ucccgcguc 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 gtgcatgccc aggggcggtt 60
ggcctcgtaa aaagccgcaa aaaatagtcg caaacgacga aaactacgct ttagcagctt 120
aataacctgc ttagagccct ctctccctag cctccgctct taggacgggg atcaagagag 180
gtcaaaccga aaagagatcg cgtggaagcc ctgcctgggg ttgaagcgtt aaaacttaat 240
caggctagtt tgttagtggc gtgtccgtcc gcagctggca agcgaatgta aagactgact 300
aagcatgtag taccgagat gtaggaattt cggacgctgg ttcaactccc gccagctcca 360
cca 363

```

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```

<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 aaaaauagucg caaacgacga aaacuacgcu uuagcagcuu    120
aauaacccugc uuagagcccu cucuccuag ccuccgcucu uaggacgggg aucaagagag    180
gucaaaccga aaagagaucg cguggaagcc cugccugggg uugaagcguu aaaacuuaau    240
caggcuaguu uguuaguggc guguccgucc gcagcuggca agcgaugua aagacugacu    300
aagcauguag uaccgaggau guaggaauuu cggacgcggg uucaacuccc gccagcuca    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 gaacaatcgc ctttagcagc    120
ttaataacct gcatttagcc ttcgcgctcc agcttcgctc cgtaagacgg ggataacgcg    180
gagtcaaacc aaaacgagat cgtgtggaag ccaccgtttg aggatcgaag cactaaattg    240
aatcaaaacta gcttaagttt agcgtgtctg tccgcatgct taagtgaat taaagacgag    300
actaaacgtg tagtactgaa ggtagagtaa tttcggacgg gggttcaact cccccagct    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 gugcagucg aggugcggua    60
ggccucguaa auaaacccga aaaaaauagu cgcaaacgac gaacaauacg cuuuagcagc    120
uuaauaacccu gcauuuagcc uucgcguccc agcuuccgcu cguaagacgg ggauaacgcg    180
gagucaaaacc aaaacgagau cguguggaag ccaccguuug aggaucgaag cacuaaaauug    240
aaucaaaacua gcuuaaguuu agcgugucug uccgcaugcu uaagugaaa uaaagacgag    300
acuaaacgug uaguacugaa gguagaguaa uuucggacgg ggguucaacu cccccagcu    360
ccacca                                                                    366

```

```

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

<400> SEQUENCE: 41
agatttcttg tcgcgagat agcatgccaa gcgctgcttg taaaacagca acaaaaataa    60
ctgtaaacia cacagattac gctccagctt acgctaaagc tgcgtgagtt aatctccttt    120
tggagctgga ctgattagaa tttctagcgt tttaatcgct ccataacctt aagctagacg    180
cttttaaaag gtggttcgcc ttttaacta agaacaaga actcttgaaa ctatcttaag    240

```

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```

gttttagaaa gttggaccag agctagtttt aaggctaaaa actaaccaat tttctaagca 300
ttgtagaagt ttgtgttttag ggcaagattt ttggactggg 340

```

```

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

```

```

<400> SEQUENCE: 42

```

```

agauuuuug ucgcgagau agcaugccaa gcgugcuug uaaaaagca acaaaaaaa 60
cuguaaaaa cacagauuac gcuccagcuu acgcuaaagc ugcgugaguu aaucuccuu 120
uggagcugga cugauuagaa uuucuaagcu uuuaaucgu ccuaaacuu aagcuagacg 180
uuuuuuuag gugguucgcc uuuuuuuacua agaaacaaga acucuugaaa cuaucuuuag 240
guuuuagaaa guuggaccag agcuaguuuu aaggcuuuuu acuaaccaau uuucuaagca 300
uuguagaagu uuguguuuuag ggcaagauuu uuggacuggg 340

```

```

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

```

```

<400> SEQUENCE: 43

```

```

ggggctgact tggatttcca cagatttctt gtcgcacaga tagcatgcca agegctgctt 60
gtaaaacagc acaaaaaata actgtaaaac acacagatta cgctocagct tacgctaaag 120
ctgctgtgagt taatctcctt ttggagctgg actgattaga atttctagcg ttttaatcgc 180
tccataacct taagctagac gcttttaaaa ggtggttcgc cttttaact aagaaacaag 240
aactcttgaa actatctcaa ggttttagaa agttggacca gagctagttt taaggctaaa 300
aaaccaacca attttctaag cattgtagaa gtttgtgtt agggcaagat ttttgactg 360
gggttegatt cccacagct ccacca 386

```

```

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

```

```

<400> SEQUENCE: 44

```

```

ggggcugacu uggauuucga cagauuuuuu gucgcacaga uagcaugcca agegcuugcu 60
guaaaacagc acaaaaaaua acuguaaaca acacagauua cgcuccagcu uacgcuaaag 120
cugcgugagu uaaucuccuu uuggagcugg acugauuaga auuucuaagc uuuuuauucg 180
uccauaacuu uaagcuagac gcuuuuuuuu ggugguucgc cuuuuuuacu aagaacaag 240
aacucuugaa acuaucuaaa gguuuuagaa aguuggacca gagcuaguuu uaaggcuaaa 300
aaaccaacca auuuucuaag cauuguagaa guuuguuuu agggcaagau uuuggacug 360
ggguucgauu cccacagcu ccacca 386

```

```

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

```

```

<400> SEQUENCE: 45

```

```

gggattcgcg aaaccaagg tgcatgccga gggcggttg gcctcgtaaa aagccgcaaa 60
aaaatagtcg caaacgacga aaactacgct ttagcagctt aataacctgc taagagcct 120

```

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```

ctctccctag cttccgctcc taagacgggg aataaagaga ggtcaaacc aaagagatc 180
gcggtggaagc cctgcctggg gttgaagcgt taaaactaat caggctagtt tgtcagtggc 240
gtgtccgtcc gcagctggcc agcgaatgta aagactggac taagcatgta gtgccgagga 300
ttaggaatt 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 ggggcggguug gccucguaaa aagccgcaaa 60
aaaauagucg caaacgacga aaacuacgcu uuagcagcuu aauaaccugc uaagagcccu 120
cucuccuag cuuccgcucc uaagacgggg aauaaagaga ggucaaaacc 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 ttgcttttcg taggttacgt ctacgttaaa acgttacagt 60
taaatataac tgctaaaaac gaaaacaact cttacgcttt agctgcctaa aaacagttag 120
cgtagatcct ctggccatcg cccatgtgct cgagtaaggg tctcaaatTT agtgggatac 180
gttaacttt tccgtctgta aagtttaaaa gagatcatca gactagcgat acagaatgcc 240
tgtaactcgg 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
uaaaauaac ugcuaaaaac gaaaacaacu cuuacgcuuu agcugccuaa aaacaguuag 120
cguagaucuu cucggcaucg cccaugugcu cgaguaaggg ucuaaaauuu agugggauac 180
guaaaacuuu uccgucugua aaguuaaaaa gagaucauca gacuagcgau acagaaugcc 240
ugucacucgg caagcuguaa agcgaaacuu 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 tgcctgccga gaaggagatc tctcgtaaat aagactcaat 60
taaatataaa tgcaaacgat gaaaactttg ctggtgggga agctatcgct gcttaataag 120

```

-continued

---

```

cacttttagtt aaaccatcac tgtgtactgg ccaataaacc cagtatcccg ttcgaccgag 180
cccgcattatc ggtatcgaat caacggatcat aagagataag ctagcgtcct aatctatccc 240
gggttatggc gcgaaactca gggaaatcgt 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

```

```

guggguugca aaaccggaag ugcaugccga gaaggagauc ucucguaaa aagacucaau 60
uaaaauuaaa ugcaaacgaa gaaaacuuug cuggugggga agcuauvcgu gccuaauaag 120
cacuuuaguu aaaccaucac uguguacugg ccaauaaacc caguaucccg uucgaccgag 180
cccgcuaauc gguauvcgaa caacggucac aagagauaag cuagcgvucc aaucuaucce 240
ggguuauggc gcgaaacuca gggaaucvcu guguaucauc cugcccvcug gaggagccac 300
aguuaaauc aaaagacaag gcuauvcag 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 cggggggatc ggcccgtcat caacgtcaaa 60
gccaaataata actggcaaac aaaacaacia tttagcttcc gctgcctaata agcagctcga 120
atagctgata ctccgtgcat cacccatgtg ctacggaag ggtctcactt ttaagtgggt 180
tacgctggct tatctccgct 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 gucagcuug aguugcagc cggggggauc ggcccgucac caacgucaaa 60
gccaaauaau acuggcaaac aaaacaacia uuuagcuuc gcugccuaau agcagucuga 120
auagcugauc cuccgvcac cacccaugug cuacgvuaag ggucucacuu uuaagugggu 180
uacgvuggcu uaucucvcg ugvggcaaac gagaagagca uauvcagacu agcuagauag 240
agccvcgacg ccgggcagac aucuaugcga aaucuaaa cggcaacvac gcvcguagau 300
gcucaagugc cgauuuuuu gg 322

```

```

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

```

```

<400> SEQUENCE: 53

```

-continued

---

```

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgta tcaacgtcaa 60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120
catagctgat cctccgtgca tcgcccattg gctacggtaa gggctcact ctaagtgggc 180
tacctagtt aatctccgct tgagggttaa tagaagagct taatcagact agctgaatgg 240
aagcctgtta ccgggctgat gtttatgca aatgctaata cggtgactac gctcgtatag 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 cggggggau cguccugua ucaacgucaa 60
agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120
cauagcugau ccuccgugca ucgcccangu gcuacgguaa gggucucacu cuaagugggc 180
uacacuaguu aaucuccguc ugagguuaaa uagaagagcu aaucagacu agcugaauagg 240
aagccuguaa ccgggugcug guuuauugca aaugcuaa cggugacuac gcucguagau 300
auucaagugc cgauuuuucu 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 gtcctcgta tcaacgtcaa 60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120
catagctgat cctccgtgca tcgcccattg gctacggtaa gggctcact ctaagtgggc 180
tacctagtt aatctccgct tgggggttaa tagaagagct taatcagact agctgaatgg 240
aagcctgtta ccgggcccgat gtttatgca aatgctaata cggtgactac gctcgtatag 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 cggggggau cguccugua ucaacgucaa 60
agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120
cauagcugau ccuccgugca ucgcccangu gcuacgguaa gggucucacu cuaagugggc 180
uacacuaguu aaucuccguc ugggguuuaa uagaagagcu aaucagacu agcugaauagg 240
aagccuguaa ccgggcccga guuuauugca aaugcuaa cggugacuac gcucguagau 300
auuuuagugc cgauuuuucu gg 322

```

```

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

```

```

<400> SEQUENCE: 57

```

-continued

---

```

caaagccaat aataactggc aaagaaaaac aaaacctagc ttctgctgcc taataagcag    60
tagcatagct gatcctccgt gcatcgccca tgtgctacgg taagggtctc actctaagtg    120
ggctacacta gttaatctcc gtctgggggtt aaatagaaga gcttaatcag actagctgaa    180
tggagcctg ttaccggggc gatgtttatg cgaatgcta 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 uuucgugcc uauaagcag    60
uagcauagcu gaucuccgcu gcaucgcccc ugugcuacgg uaagggucc acucuaagug    120
ggcuacacua guuaucucc gucugggguu aaauagaaga gcuuaucag acuagcugaa    180
uggaagccug uuaccggggc gauguuuuug cgaauugcua auaccggugac uacgcucgua    240
gauuuuu                                         247

```

```

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

```

```

<400> SEQUENCE: 59

```

```

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgta tcaacgtcaa    60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag    120
catagctgat cctccgtgca tcgcccattg gctacggtaa ggggtcact ctaagtgggc    180
tacactagtt aatctccgtc tgagggttaa tagaagagct taatgagact agctgaatgg    240
aagcctgtta ccgggctgat gtttatgca 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 cggggggauc guccuguaa ucaacgucaa    60
agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag    120
cauagcugau ccuccgugca ucgcccangu gcuacgguaa gggucucacu cuaagugggc    180
uacacuaguu aaucuccguc ugagguuaaa uagaagagcu uaaugagacu agcugaaugg    240
aagccuguaa ccgggcugau guuuuugcga aaugcuaaua cggugacuac gcucguagau    300
auucaagugc cgauuuuucu gg                                         322

```

```

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

```

```

<400> SEQUENCE: 61

```

```

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgta tcaacgtcaa    60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag    120

```

-continued

---

```

catagctgat cctccgtgca tcgcccattgt gctacggtaa gggctcact ctaagtgggc 180
tacactggct aatctccgtc tgaggtagt tggaagagct taatcagact agctgaatgg 240
aagcctgtta cggggccgat gtttatgcca 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
agccaaauau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120
cauagcugau ccuccugca ucgcccangu gcuacgguaa gggucucacu cuaagugggc 180
uacacuggcu aaucuccgcu ugagguuagu uggaagagcu uaaucagacu agcugaauagg 240
aagccuguaa cggggccgau guuuauagca aaugcuaaua cggugacuac gcucguagau 300
auuuuagugc cgauuuuuu gg 322

```

```

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

```

```

<400> SEQUENCE: 63

```

```

gccggtgacg aacccttggg tgcattgccg gatggcagcg aatctcgtaa atccaaagct 60
gcaacgtaat agtcgcaaac gacgaaaact acgcactggc ggcgtaagcc gttccagtcg 120
tcctggctga ggcgcctata actcagtagc aacatcccag gacgtcatcg cttataggct 180
gctccgttca ccagagctca ctggtgttcg gctaagatta aagagctcgc ctcttgacc 240
ctgaccttcg ggtcgttga ggttaaata 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 aaccuuggg ugcaugccga gauggcagcg aaucucguua auccaaagcu 60
gcaacguauu agucgcaaac gacgaaaacu acgcacuggc ggcguaagcc guuccagucg 120
uccuggcuga ggcgccuaau acucaguagc aacaucccag gacgucaucg cuuauaggcu 180
gcuccguuca ccagagcuca cugguguuucg gcuagaaua aagagcucgc cucuugcacc 240
cugaccuucg gguucguuga gguuauaaua auagaaggac acuaagcaug uagaccucaa 300
ggccuagugc ugccggacgc 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 taagcgcca ttcacatcag cgcgacttac ctctcgtcgc ctaagcgaca 120

```

-continued

---

```

gctagtccgt cagcccggga acgcccctga cccggagcct ggcgtcagct agagggatcc 180
accgatgagt tcggtcgagg gactcatcgg gacaccaaca gcgactggga tcgtcatcct 240
ggcttggttcg cgtgaccagg agatccgagt agaggcatag cgaactgcgc acggagaagc 300
cttgagggaa tgcgtagaa cccgggttcg attcccaa 338

```

```

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

```

```

<400> SEQUENCE: 66

```

```

uucgcgauc gaaucaaggg aagcgugccg gugcaggcaa cugaccaccg uaagcgucgu 60
ugcaaauga uaagcgccga uucacaucag cgcgacuac cucucgcugc cuaagcgaca 120
gcuaguccgu cagcccggga acgcccucga cccggagccu ggcgucagcu agagggaucc 180
accgaugagu ucggucgagg gacucaucgg gacaccaaca gcgacuggga ucucauccu 240
ggcuuguucg cugaccagg 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
tgcgacaaa taagcgccga ttcacatcag cgcgactacg tctcgtgcc taagcgacgg 120
ctagtctgtc agaccgggaa cgccctcggc cgggacctg gcatacagta gagggatcca 180
ccgatgagtc cggtcgaggg actcctcggg acaaccacag cgactgggat cgtcatctcg 240
gctagtctgc 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

```

```

uucgcgauc gaaucaaggg aagcgugccg gugcaggcaa gagaccaccg uaagcgucgu 60
ugcgacaaa uaagcgccga uucacaucag cgcgacuac ucucgcugcc uaagcgacgg 120
cuagucuguc agaccgggaa cgccucggc cgggaccug gcaucagcua gagggaucca 180
ccgaugaguc cggucgaggg acucccggg acaaccacag cgacugggau cgucaucucg 240
gcuaguucgc gugaccggga gauccgagca gaggcgauagc gaacugcgcga cggagaagcc 300
uugagggaaug gccguagg 318

```

```

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

```

```

<400> SEQUENCE: 69

```

```

ggggctgaaa ggtttcagct tcgctcatcg aatcaaggga agcgtgccgg tgcaggcaag 60
agaccaccgt aagcgtcgtt gcagcaatat aagcgccgat tcatatcagc ggcactatgc 120

```

-continued

---

```

tctcgtgcc taagegatgg ctagtctgtc agaccgggaa cgccctegtc ceggagcctg 180
gcatcagcta gagggateta ccgatgggtt cggtcgctgg actcgtcggg acaccaaccg 240
cgactgggat cgtcatcctg gctagtctgc 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 aaucaggga agcgugccgg ugcaggcaag 60
agaccaccgu aagcgcuguu gcagcaauau aagcgccgau ucauauacgc ggcacuauagc 120
ucucgcugcc uaagcgaugg cuagucuguc agaccgggaa cgcccucguc ceggagccug 180
gcaucagcua gagggauca ccauggguu cggucgctgg acucgucggg acaccaaccg 240
cgacugggau cgucauccgg gcuaguucgc gugaucagga gaudccagua gaggcgauagc 300
gaacuacgca cggagaagcc uugagggaaa ugccguagga cccggguucg auucccgga 360
gcuccacca 369

```

```

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

```

```

<400> SEQUENCE: 71

```

```

ttcgcgcacg gaatcaaggg aagcgtgccg gtgcaggcaa ctgaccaccg taagcgtcgt 60
tgcaaataga taagcgccga ttcacatcag cgcgacttac ctctcgtctc ctaagcgaca 120
gctagtccgt cagcccggga acgcccctga cccggagcct ggcgtcagct agagggatcc 180
accgatgagt tcggtcggcg gactcatcgg gacaccaaca gcgactggga tcgtcaccct 240
ggcttgctcg cgtgaccagg agatccgagt agaggcatag cgaactgcgc acggagaagc 300
cttgagggaa tgccgtagaa cccgggttcg attcccga 338

```

```

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

```

```

<400> SEQUENCE: 72

```

```

uucgcgcauc gaaucaggga aagcgcugcc gugcaggcaa cugaccaccg uaagcgcugc 60
ugcaaauga uaagcgccga uucacaucag cgcgacuac cucucgcugc cuaagcgaca 120
gcuaguuccg cagcccggga acgcccucga cccggagccu ggcgucagcu agagggaucc 180
accgaugagu ucggucgctg 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

```

-continued

---

```

ggggctgaac ggtttcgact tcgcgcatcg aatcaagga agcgtgccgg tgcaggcaag    60
agaccaccgt aagcgtcgtt gcgaccaa at aagcgcgat tcacatcagc gcgactacgc    120
tctcgtgcc taagcgacgg ctagtctgtc agaccgggaa cgccctcggc cgggacctg    180
gcatcagcta gagggatcca ccgatgagtc cggtcgctgg actcctcggg acaaccacag    240
cgactgggat cgtcatctcg gctagtctgc 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 aaucaggga agcguccgg ugcaggcaag    60
agaccaccgu aagcgcguu gcgaccaa at aagcgcgau ucacaucagc gcgacuacgc    120
ucucgcugcc uaagcgacgg cuagucuguc agaccgggaa cgccucggc cgggaccug    180
gcaucagcua gagggaucca ccgaugaguc cggucgctgg acuccucggg acaaccacag    240
cgacugggau cgcaucucgc gcuaguucgc gugaccggga gaucgagca gaggcauagc    300
gaacugcgca cggagaagcc uugagggau gccguaggac ccggguucga ucccggcag    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 ttattataa 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 uggaauugac aggauaucuu uaguacauau aagcaguagu guuguagacu    60
auaaaucua cuagguuuua aaaaacgcaa auaaaaacga agaaacuuuu gaaaugccag    120
cauuuugau gaauaaugca ucagcuggag caaacuuuuu guuugcuuaa uaacuacuag    180
uuuaguuaa guuuucacg aauuuuagau auuuuagcu uuuuuuuaa ccguuuuacc    240
caagcuuaa agaauuuuug auugcaauaa auuuuuuga aaucuaauug caaauugauu    300
uuuaccuuua guuuuuuuu guuuuuuuu uuuuuuagaa auuuuacuaa acuguagaaa    360
guauguaua auuuuucug gacgcgaguu cgauucucgc caucuccacc a          411

```

-continued

---

```

<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 agtgttgga gaaccaaatt    120
tgatcattaa ccaacaagca agtgtaact ttgcttttgc ataagtagat actaaagcta    180
cagctggtga atagtcatag tttgctagct gtcatagttt atgactcgag gttaaatcgt    240
tcaatttaac cttaaaaaa agaacttggt gtttccatga ttgttttggt atcaattgga    300
aacaagacaa aaatccacaa aactaaaatg tagaagctgt ttgttggtgc ctttatggaa    360
acgggttcga ttcccgatct 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 agguucauaa accgacaaag aaaauaacga aguguuggua gaaccaaauu    120
ugaucuuuaa ccaacaagca aguguaacu uugcuuuugc auaaguagau acuaaagcua    180
cagcugguga auagucuaug uuugcuagcu gucauaguuu augacucgag guuaaaucgu    240
ucauuuuuac cuuuuuuuu agaacuuguu guuuccauga uuguuuugug aucaauugga    300
aacaagacaa aaauccacaa aacuaaaug uagaagcugu uuguuguguc cuuuuaggaa    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 gagaccaaaag acaaaccaac aagcaaggaa cgcgcaaaga gaacaaagca    120
cagcgggaaa gcaagggcagc gcaagagacc gaggaaacgc aaaaccaaaa aagaacggcc    180
agagggacaa ggaacaaga 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 agaaaaaac gaaguguugg uagauccaaa uuugaucuu aaccaacaag    120
caaguguuaa cuuugcuuuu gcauaaguag auacuaaagc uacagcuggu gaauagucau    180
aguuuugcuag cugucauagu uuaugacucg agguuaaauc guucauuua accuuuuuuu    240
auagaacuug uuguuuuccau gauuguuuug ugaucaauug gaaacaagac aaaaauccac    300

```

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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 ataatgtga aaggaaaaca gttgcagtgg ggtatgcccc 60  
 ttacagctct aggtataata accgacaaaa ataacgacga agtttttgta gatccaatgt 120  
 tgatcgctaa ccaacaagca agtatcaact acgctttcgc ttagaacata ctaaagctac 180  
 acgaattgaa tcgccatagt ttggttcgtg tcacagttta tggctcgggg ttaactggtt 240  
 caacttaatc cttaaattat gaacttatcg tttacttgtt tgtettatga tctaaagtaa 300  
 gcgagacatt aaaacataag actaaactgt agaagctggt ttaccaatcc tttatggaaa 360  
 cgggttegat tcccgtcac tccacca 387

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

<400> SEQUENCE: 82

ggggauuguag agguuuugac auaauguuga aaggaaaaca guugcagugg gguaugcccc 60  
 uuacagcucu agguuaaaua accgacaaaa auaacgacga aguuuuggua gauccaaugu 120  
 ugaucgcuaa ccaacaagca aguaucaacu acgcuuucgc uuagaacaua cuaaagcuac 180  
 acgaaauugaa ucgccauagu uugguucgug ucacaguuuu uggcucgggg uuaacugguu 240  
 caacuuaauc cuuaaaauuau gaacuuauucg uuuacuuguu ugucuuauga ucuaaaguaa 300  
 gcgagacauu aaaacauaag acuaaacugu agaagcuguu uuaccaaucc uuuauaggaaa 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 ggtctcaga ttcccgtaaa aactgaatt 60  
 caaatagtcg caaacgacga aacttacgct ttagccgctt aaggctagcc gttgcagcag 120  
 tcggtcaatg gctgtgtgg cgaaagccac cgcaacgtca tcttacattg actggtttcc 180  
 agccgggtta cttggcagga aataagactt aaggtaactg gtttccaaaa ggcctgttgg 240  
 tcggcatgat gaaataaga ttttcaata 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  
 caaaauugcg caaacgacga aacuuacgcu uuagccgcuu aaggcuagcc guugcagcag 120  
 ucggucaaug ggcugugugg cgaaagccac cgcaacguca ucuuacauug acugguuucc 180

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```

agccggguua cuuggcagga aauaagacuu aagguaacug guuuccaaaa ggccguugg 240
ucggcaugau ggaaaaaaga uuuucaaaua gacacaacua aguanguaga acgcuuugua 300
gaggacuuc 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 aacctgaaat tcaaatagtc gcaaacgacg aaacttacgc ttagccgct 120
taaggctagc cgttcagca gtcggtcaat gggctgtgtg gtgaaagcca ccgcaacgtc 180
atcttacatt gactggtttc cagccgggtt acttggcagg aaataagact taaggtaact 240
ggtttccaaa aggcctgttg gtcggcatga tggaaataag attttcaaat agacacaact 300
aagtatgtag aacgctttgt agaggacttt cggacggggg ttcgattccc cccgctcca 360
cca 363

```

```

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

```

```

<400> SEQUENCE: 86

```

```

gggggcgacc uuguuucga cggggguugc gaagcagaug cgggcuaacc ggggucucag 60
auucccguaa aacacugaau ucaaaauaguc gcaaacgacg aaacuucgc uuuagccgcu 120
uaaggcuagc cguugcagca gucguucaau gggcugugug gugaaagcca ccgcaacguc 180
aucuuacauu gacugguuuc cagccggguu acuuggcagg aaauaagacu uaagguaacu 240
gguuuccaaa aggcctgttg gtcggcauga uggaaauaag auuuucaaau agacacaacu 300
aaguaugua gacgcuuugu agaggacuuu cggacggggg uucgauuccc cccgcuuca 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 aacctgaaat tcaaatagtc gcaaacgacg aaacttacgc ttagccgct 120
taaggctagc cgttcagca gtcggtcaat gggctgtgtg gcgaaagcca ccgcaacgtc 180
atcttacatt gactggtttc ctgcccgggtt atttggcagg aaatgagatt taaggtaact 240
ggtttccaaa aggcctgttg gtcggcatga tggaaataag attttcaaat agacacaact 300
aagtatgtag aacgctttgt agaggacttt cggacggggg ttcgattccc cccgctcca 360
cca 363

```

```

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

```

```

<400> SEQUENCE: 88

```



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<210> SEQ ID NO 92  
 <211> LENGTH: 371  
 <212> TYPE: RNA  
 <213> ORGANISM: *Odontella sinensis* (diatom) chloroplast  
 <400> SEQUENCE: 92

```

ggggcugacu ugguuucgac auuuuuuuuu uguuacagua ugaugcaggu cgaaguuuucu   60
aaucucgua  aaaaaagaga auuuuuuuuu aaauugcuaau auuuuuuuuu cuucuguguu   120
uaaaauuuuu ucaacuaagc aaaaauuuuu aaaaauuagu uuugcuguuu aaguuuuuuag   180
cacauuuuuu gaucuaguua auuacuuugu ucgcuuuuuu uuauuuuuuu aacuagacuu   240
uugucuuuuu uauaguuuuag auuacuuuuu ucauuuuaaa ccucguucca ucuaguugaa   300
cuuaccugu  gaacgaauac uuuuuuuuuu uuuuuuagaug gacgugguuu 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
gctgttgcac aaatagtctc aatttttcta attcgaagtg atagactctt atacactacg   180
aatattctgt tagagtgtct cttaataaaa gaaaagtaaa aaaatacaaa ttcttatggt   240
ttttacctga attgattcaa tttaaggtta gtattttttg 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 gguuuuucua uugugaaaaa acauuuuuuu gaaaguuaaa cgagcucuuu   60
auuagagcuu uuaguuuuuu aaauugcagaa auuuuuuuuu uugcuuuuuu ucgaaaauuu   120
gcuguugcau aaauagucuc auuuuuuuuu auucgaagug auagacucuu auacacuacg   180
aaauuucugu uagaguugcu cuuuuuuuuu gaaaaguuaa auuuuuuuuu uuuuuuuuuu   240
uuuuaccuga auugauucaa uuuuagguua guuuuuuuuu auuuuuuuuu 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
cttgactat  aatctcagac atcaaaagt  taattggcga aaataactac gctctcgtg   120
cgtaatcgaa gaatagtaga ttagacgctt catcgccgcc aaagtggcag cgacgagaca   180
tcgcccagac agctttttcc cgaagttagct cgatggtgcg gtgctgacaa atcggaacc   240
gctacaggat gcttctgccc tgtggtcaga tcgaacggaa gataaggatc gtgcattggg   300

```

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tcgtttcagc ctccgctcgc tcacgaaaaat tccaactgaa actaacaatg tagaaaagcat 360

attgattcca tgtttggacg agggttcaat tcctccagc 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 uaaauggcga aaauaacuac gcucucgcug 120

cguaaucgaa gaauaguaga uuagacgcuu caucgccgcc aaaguggcag cgacgagaca 180

ucgcccagc agcuuuuucc cgaaguagcu cgauggugcg gugcugacaa aucgggaacc 240

gcuacaggau gcuuccugcg uguggucaga ucgaacggaa gauaaggauc gugcauuggg 300

ucguuucagc cuccgcucgc ucacgaaaa 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 aaaccaagg tgcatgccga ggggcggttg gcctcgtaaa aagccgcaaa 60

aaaatagtcg caaacgacga aaactacgct ttagcagctt aataacctgc ttagagccct 120

ctctcctag cctccgctct tggacgggga tcaagagagg tcaaacccaa aagagatcgc 180

gtggatgcct tgectggggt tgaagcgta 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 aaaccaagg ugcaugccga ggggcgguug gccucguaaa aagccgcaaa 60

aaaauagucg caaacgacga aaacuacgcu uuagcagcuu aaauaccugc uuagagcccu 120

cucuccuag ccuccgcucu uggacgggga ucaagagagg ucaaacccaa aagagaucgc 180

guggaugccu ugccuggggu ugaagcguaa aacuuauca ggauaguuuug uugguggcgu 240

gucuguccgc agcuggcaaa ugaauucaa gacuagacua agcauguagu accgaggau 300

uagaaauuuc 310

<210> SEQ ID NO 99

<211> LENGTH: 241

<212> TYPE: DNA

<213> ORGANISM: Pseudoalteromonas haloplanktis

<400> SEQUENCE: 99

gggagcgaaa cccaagggc gcccaggggc ggggcccgaa aaagccgcaa aaaaaagcgc 60

aaacgacgaa aacacgcagc agcaaaaccg cagagcccc cccagcccc cggacgggg 120

acaagagagg caaacccaaa agagacgcgg gagccgccgg gggaagcgaa acaacaggaa 180

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```

ggggggcgcc 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
ggaaaucaag aagcccagg ugcaugucga ggugcgguuu gccucguaaa aaagccgcaa 60
uuuaaaguaa ucgcaaacga cgauaacuac ucucuagcag cuuaggcugg cuagcgcucc 120
uuccauguau ucuuguggag uggauuuugg agugucaccc uaacaccuga ucgcgacgga 180
aaccucggcc gggguugaag cguuaaaacu aagcggccuc gccuuuauu accguguuug 240
uccgggauuu aaagguuuuu 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 aggattcga cccggtaaca aaagttgagg ggcattgccga gttgtagca 60
gaactcgtaa attcgtctg ccaaacttat agttgccaac gacgacaact acgctctagc 120
tgcttaatgc ggctagcagt cgctagggga tgctgtataa cccgaaacga ctgtcagata 180
gaacaggatc gccccaagt tcgctgtaga cgtaacggct aaaactcata cagctcgtc 240
caagcaccct gccactcggg cggcgcggag ttaactcagt agagctggct aagcatgtaa 300
aaccgatagc gaaaagctgg cggacggggg ttcaaatccc cccgatcca 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 ggcuaagcgu cgcuaagggga ugccuguaaa cccgaaacga cugucagaua 180
gaacaggau cccccaagu ucgcuguaga cguaacggcu aaaacucaua cagcucgcuc 240
caagcaccu gccacucggg cggcgcggag uuaacucagu agagcuggcu aagcauguaa 300
aaccgauagc gaaaagcugg cggacggggg uucaaaucce cccggcuca 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
ggtaaacccc aaaagagatc gcgcggatgc cctgcctggg gttgaagcgt taaacgaat 240

```

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```

caggctagtc tggtagtggc gtgtccgtcc gcaggtgccca ggccaatgta aagactgact 300
aagcatgtag taccgaggat gtaggaatth 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
ggccucguua aaagccgcaa aaaaauaguc gcaaacgacg aaaccuacgc uuuagcagcu 120
uaauaacccug cuuagagccc ucucuccua gccuccgcuc uuaggacggg gaucaagaga 180
ggucaaaacc aaaagagauc gcgcggauuc ccugccuggg guugaagcgu uaaaacgaau 240
caggcuaguc ugguaguggc guguccgucc gcaggugcca ggccaugua aagacugacu 300
aagcauguag uaccgaggau guaggaaauu cggacgcggg uucaacucc gccagcucca 360
cca 363

```

```

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

```

```

<400> SEQUENCE: 105

```

```

gggggcgatt ctgattcga caggattcac gaaacctgg gagcatgccg aggggcggtt 60
ggcctcgtaa aaagccgcaa agttatagtt gcaaacgacg ataactacgc tctagccgct 120
taatgccgct agccatctac cacacgcttt gcacatgggc agtggatttg atggctatct 180
cacatcgtgc tagcgaggga accctgtctg ggggtgaacc gcgaaacagt accggactca 240
ccgtgtggga tctgtcttt cggagttcaa acggttaaac aatagaaaga ctaagcatgt 300
agcgccttgg atgtaggttt tctggacgcg ggttcaagtc ccgcccctc cacca 355

```

```

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

```

```

<400> SEQUENCE: 106

```

```

gggggcgauu cuggauucga caggauucac gaaaccucgg gagcaugccg aggggcgguu 60
ggccucguua aaagccgcaa aguuauaguu gcaaacgacg auaacuacgc ucuagccgcu 120
uaaugccgcu agccaucac cacacgcuuu gcacaugggc aguggauuug auggucaucu 180
cacaucgugc uagcgaggga acccugucug ggggugaacc gcgaaacagu accggacuca 240
ccguguggga uccugucuuu cggaguucua acgguuuaac aauagaaaga cuaagcaugu 300
agcgcuuugg auguagguuu ucuggacgcg gguucaaguc ccgcccucuc cacca 355

```

```

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

```

```

<400> SEQUENCE: 107

```

```

ggggacgttc atggattcga cagggttccc ccgagctcat taagcgtgtc ggagggttgt 60
cttcgtcatc aacacacaca gtttataata actggcaaat caaacaataa tttcgcagta 120

```

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```

gctgcctaataat cgcactctgc atcgccaaac agcatttcct atgtgctggt aacgcgattc 180
aaccttaata ggatatgcta aacactgccc tttgaagtct gtttagaaga aacttaataca 240
aactagcattc atgttggttg tttatcactt ttcattgatgc gaaacctatc gataaactac 300
acacgtagaa agatgtgtat caggaccttt ggacgcgggt tcaaatcccc cgtctccac 360
ca 362

```

```

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

```

```

<400> SEQUENCE: 108

```

```

ggggacguuc auggauucga cagggguccc ccgagcucuu uaagcguguc ggaggguuuu 60
cuucgucauc aacacacaca guuuuaaaua acuggcauuu caaacaauua uuucgcagua 120
gcugccuuuu cgcacucugc aucgccuaac agcauuuccu augugcuguu aacgcgauuc 180
aacuuuaaua ggauaugcua aacacugccc uuugaagucu guuuagaaga aacuuuaaua 240
aacuagcauc auguuguuug uuuaucacuu uucaugauc gaaaccuauc gauaaacuac 300
acacguagaa agauguguuu caggaccuuu ggacgcgggu ucaaaucucc cgcucuccac 360
ca 362

```

```

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

```

```

<400> SEQUENCE: 109

```

```

ggggctgcta cggattcgac aggcattatg aggcattatg tgcgactcat ctacgggatg 60
taaaacgcca gttaaatata actgcaaaaa ataatacttc ttacgcttta gctgcctaaa 120
aacacgccc cgtgacccga ttcggattgc ttgtgtctga tgacaggtct tattattagc 180
aagctacggt agaattctgt ctatgtatgt tacaagagat tgatagactc gcttgatttg 240
ggcttgagtt atgtgtcaaa atcaagttaa aacaatacat agcctatggt ttagacaaa 300
tgtgttgcca 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 aggcuuuauu aggcuuuuuu ugcgacucuu cuagcggauu 60
uaaaacgcca guuuuuuuuu acugcaaaaa auuuuuuuuu uuacgcuuuu gcugccuuuu 120
aacacgccc cugacccgca uucggauucg uuugucugua ugacaggucu uuuuuuuuag 180
aagcuacggu agaauuuuuu cuaguuuuuu uacaagagau ugauagacuc gcuuuuuuuu 240
ggcuuaguuu auguguuuuu aucauuuuuu acauuuuuuu agccuuuuuu uguuuuuuuu 300
uguuuuuuuu gauguuuuuu cguuuuuuuu acuuuuuuuu guuuuuuuuu 349

```

```

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

```

```

<400> SEQUENCE: 111

```

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```

ggggtcgta cggattcgac aggcattatg agacctatgt tgcgactcat ctageggatg    60
taaaacgcc a gttaaatata actgcaaaaa atacaaatc ttacgcagta gctgcctaaa    120
aaccagcctg tgtgatcaat aacaaattgc ttgtgtttgt tgattggtct tattgttaac    180
aagctacgtt agaactgagt caggctgttc taaaagagtt ctactgactc gcatcgtag    240
agtttgagtt atgtattgta acggtgttaa ataacacat aacctatagt tgtagacaaa    300
tgggttagca gatgtttgga cgtgggttcg actccccaccg gctccacca                349

```

```

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

```

```

<400> SEQUENCE: 112

```

```

ggggucguua cggauucgac aggcuuuauug agaccuuuuu ugcgacucau cuagcggauug    60
uaaaaaccca guuuuuuuua acugcaaaaa auacaaaauu uuacgcagua gcugccuaaa    120
aaccagccug ugugaucaau aacaaaauugc uuguguuuugu ugauuggucu uauuguuaac    180
aagcuacguu agaacugagu caggcuguuc uaaaagaguu cuacugacuc gcaucguuag    240
aguuugaguu auguauugua acgguguuua auaaacacau aaccuuuagu 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

```

```

ggggtcgta cggattcgac aggcattatg aggcattatgt tgcgactcgt gtggcgacgt    60
aaacgctcag ttaaatataa ctgcaaaaaa taacacttct tacgctctag ctgcctaaaa    120
accagcagc gtgaccgat ttggattgct cgtgttcaat gacaggtctt attattagcg    180
agatacgatt aagccttctc tagcggtttg ataagagatt gatagactcg cagtttctag    240
acttgagtta tgtgtcgagg ggctgttaaa ataatacata acctatggtt gtagacaaat    300
atgttgccag gtgtttgac gtgggttcga ctcccaccg ctccacca                348

```

```

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

```

```

<400> SEQUENCE: 114

```

```

ggggucguua cggauucgac aggcuuuauug aggcuuuuu ugcgacucgu guggcgacgu    60
aaacgcucag uuuuuuuuaa cugcaaaaaa uaacacuucu uacgcucuag cugccuaaaa    120
accagcagc gugaccgag uuggauugcu cguguucaau gacaggucuu auuuuuagcg    180
agauacgauu aagccuugc uagcgguuug auuagagauu gauagacucg caguuuuag    240
acuugaguuu ugugucgagg ggcuguuuuu auuuuacauu accuauuguu guagacaaau    300
auguugcag guguuugac guggguucga cucccaccg cuccacca                348

```

```

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

```

```

<400> SEQUENCE: 115

```

-continued

---

```

ggggttgta cggattcgac aggcattatg aggcattggt tgcgtcccat cggcagatgt    60
aaattgccag ttaaatataa ctgcaaaaaa tacaaactct tacgctttag ctgcctaaaa    120
accagctagc gtgacttcta caagattgct tgtgtcctgt tagaagtctc aaaatagcaa    180
gctacgggta cgaattgtc tagtttcgtg acaagagatt gatagactcg caaactaatg    240
gcttgagtta tgtgtcttta gtttggttaa tgaagacata acctatggac gtagacaaat    300
atgttgccag gtgtttggac gtgggttcga ctcccaccag ctcccacca                348

```

```

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

```

```

<400> SEQUENCE: 116

```

```

gggguuuuua cggauucgac aggcuuuauug aggcuuuuu ugcgucccau cggcagaugu    60
aaaauuccag uuaaaauuaa cugcaaaaaa uacaaacucu uacgcuuuag cugccuaaaa    120
accagcuagc gugacuucua caagauugcu uguguccugu uagaagucuc aaaaauagcaa    180
gcuacggguu cgaauuugc uaguuuucgug acaagagauu gauagacucg caaacuaaug    240
gcuugaguua ugugucuuua guuuguuaaa ugaagacaua accuauaggac guagacaaau    300
auguuggcag guguuuggac guggguucga cucccaccag cucccacca                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 cggagagggga    60
gtccactctc gtaaatccag gctcaaccaa aagtaactgc gaacaacatc gttcctttcg    120
ctcgtaaggc tgcctctgta gctgcttaaa cgccacaaac tttctggctc gagcgtctag    180
tcgtagactc cgtaataacg cctagactta aacccccaac ggatgctcga gtggcggcct    240
caggctccgc ctctcgctaa gcaaaaacct gagcatcccg ccaacgggga taatcgttgg    300
ctccgcaca gtgggtcaac cgtgctaagc ctgtgaacga gcggaagtt actagtcaat    360
gcgacagcgc 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 guguuuggua auccuucacc gugauucagg cggagagggga    60
guccacucuc guaaaaccag gcucaaccaa aaguaacugc gaacaacauc guuccuuucg    120
cucguaaggc ugcuccugua gcugcuuaaa cgccacaaac uuucuggcuc gagcgcucag    180
ucguagacuc cguuaauacg ccuagacuua aacccccaac ggaugcucga guggcggccu    240
cagguccguc cucucgcuaa gcaaaaaccu gagcaucccg ccaacgggga uauucguugg    300
cucccgcaca gugggucaac cgugcuuagc cugugaacga gcggaaguu acuagucaau    360
gcgacagcgc guucgauucc gcucagcucc acca                                394

```

```

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

```

-continued

&lt;212&gt; TYPE: DNA

<213> ORGANISM: *Synechocystis* PCC6803

&lt;400&gt; SEQUENCE: 119

```

ggggccgcaa tggtttcgac aggttggcga aagcttgccc gtgatacagg tcgagagtga    60
gtctcctctc gcaaatcaaa ggctcaaaaa aaagtaactg cgaataacat cgtcagcttc    120
aaacgggtag ccatagcagc ctagtctgta aaagctacat tttcttgta aagaccgttt    180
acttcttttc tgactccgtt aaggattaga ggtaacccc aacggatgct ttgtttggct    240
cttctctagt tagctaaaca atcaagactc agactagagc atcccaccat cagggataat    300
cgatggcccc cgtcctaggg ctagaaggac taaacctgtg aatgagcgga aagttaatac    360
ccagtttga cagcagttca attctgctcg gctccacca                               399

```

&lt;210&gt; SEQ ID NO 120

&lt;211&gt; LENGTH: 399

&lt;212&gt; TYPE: RNA

<213> ORGANISM: *Synechocystis* PCC6803

&lt;400&gt; SEQUENCE: 120

```

ggggccgcaa ugguuucgac agguuggcga aagcuugccc gugauacagg ucgagaguga    60
gucuccucuc gcaaucaaaa ggcucaaaaa aaaguaacug cgaauacau cgucagcuuc    120
aaacggguag ccauagcagc cuagucugua aaagcuacau uuucuugua aagaccguuu    180
acuucuuuuc ugacuccguu aaggauuaga gguuaacccc aacggaugcu uuguuuggcu    240
cuucucuagu uagcuaaaa aucaagacuc agacuagagc aucccaccu cagggaauuu    300
cgaugguucc cguccuaggg cuagaaggac uaaaccugug aaugagcgga aaguuaauac    360
ccaguuugga cagcaguuca auucugcucg gcuccacca                               399

```

&lt;210&gt; SEQ ID NO 121

&lt;211&gt; LENGTH: 356

&lt;212&gt; TYPE: DNA

<213> ORGANISM: *Thermotoga* *maritima*

&lt;400&gt; SEQUENCE: 121

```

gggggcgaac gggttcgacg gggatggagt ccctgggaa gcgagccgag gtccccacct    60
cctcgtaaaa aaggtgggac aaagaataag tgccaacgaa cctgtgctg ttgccgctta    120
atagataagc ggccgtcctc tccgaagtgt gctgggcttc ggaagagggc gtgagagatc    180
cagcctaccg attcagcttc gccttccggc ctgaatcggg aaaactcagg aaggctgtgg    240
gagaggacac cctgcccgtg ggaggtccct cccgagagcg aaaacacggg ctgcgctcgg    300
agaagcccag gggcctccat ctctggacgg gggttcgaat cccccgcct ccacca       356

```

&lt;210&gt; SEQ ID NO 122

&lt;211&gt; LENGTH: 356

&lt;212&gt; TYPE: RNA

<213> ORGANISM: *Thermotoga* *maritima*

&lt;400&gt; SEQUENCE: 122

```

gggggcgaac gguuucgacg ggauggagu cccuugggaa gcgagccgag guccccaccu    60
ccucguaaaa aaggugggac aaagaauaag ugccaacgaa ccuguugcug uugccgeuuu    120
auagauaagc ggccguccuc uccgaaguug gcugggcuuc ggaagagggc gugagagauc    180
cagccuaccg auucagcuuc gccuuccggc cugaaucggg aaaacucagg aaggcugugg    240
gagaggacac ccugcccugug ggagguccuc cccgagagcg aaaacacggg cugcgcucgg    300
agaagcccag gggccuccau cuucggacgg gguucgaa cccccgccu ccacca       356

```

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

<400> SEQUENCE: 123

```

gggggtgaaa cggctcgcac gggggtcgcc gagggcgtgg ctgcgcgccg aggtgcgggt    60
ggcctcgtaa aaaccgcgaa cggcataact gccaacacca actacgctct cgcggcttaa    120
tgaccgcgac ctgcgccggt agccctgccg ggggctcacc ggaagcgggg acacaaacct    180
ggctagcccg gggccacgcc ctctaaccce gggcgaaget tgaagggggc tcgctcctgg    240
ccgcccgtcc gcgggccaag ccaggaggac acgcgaaacg cggactacgc gcgtagaggg    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
ggccucguua aaaccgcgaa cggcauaacu gccaacacca acuaacgcucu cgcggcuuaa    120
ugaccgcgac cugcggcggu agccucgccg ggggucaccc ggaagcgggg acacaaacct    180
ggcuagcccg gggccacgcc cucuaaccce gggcgaagcu ugaagggggc ucgcuccugg    240
ccgcccgucc gcgggccaag ccaggaggac acgcgaaacg cggacuacgc gcguagaggg    300
ccgccguaga gaccuucgga cggggguucg acuccccccca ccuccacca                349

```

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

<400> SEQUENCE: 125

```

ggggatgact aggtttcgac tagggatgtg ggggtgttgc ctgcaggtgg agtgtcgatc    60
tcctgattcg gcgcctttat aactgccaat tctgacagtt tcgactacgc gctcgcgccg    120
taatcgcggg cctgtgtttg cgctgctctg agcgaacata tcggccccgac gccaaacgga    180
gcttgcctct acgttgtgca cggcggacgt agggggactt ttgtctgtgc taagactctg    240
gcgcgtgctg tgcaggccta gcagagtccg acaaacgcag tacgcaccgc taaacctgta    300
ggcgcgcgag actcgtcttt 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 gcgcuuuuau aacugccaau ucugacaguu ucgacuacgc gcucgcgccg    120
uaaucgcggg ccuguguuug gcgucgucug agcgaacaua ucggccccgac gccaaacgga    180
gcuugcucuu acguugugca cggcggacgu agggggacuu uugucugugc uaagacucug    240
gcgcgugcgg ugcaggccua gcagaguccg acaaacgcag uacgcaccgc uaaaccugua    300
ggcgcgcgag acucgcucuu uaggacgggg guucgauucc ccccaucucc acca                354

```

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```

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

<400> SEQUENCE: 127

ggggctgatt caggattcga cgggaatddd gcagtctgag gtgcatgccg aggtgctgta    60
ggcctcgtaa acaaacccga aaaaaatagt cgcaaacgac gaaaactacg cactagcagc    120
ttaataccct gctcagagcc cttcctccct agcttccgct tgtaagacgg ggaaatcagg    180
aaggtcaaac caaatcaagc tggcgtggat tccccacacg gagggatgaa gcgagagatc    240
taattcaggt tagccattcg ttagcgtgtc ggttcgcagg cgggtgtgaa attaaagatc    300
gactaagcat gtagtaccaa agatgaatgg ttttcggacg ggggttcaac 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 acaaacccga aaaaaauagu cgcaaacgac gaaaacuacg cacuagcagc    120
uuaauaccuu gcucagagcc cuuccucuccu agcuuccgcu uguaagacgg ggaaucagg    180
aaggucaaac caaaucagc uggcugggau uccccaccu gagggaugaa gcgagagauc    240
uaauucaggu uagccauucg uuagcuguc gguucgcagg cgguggugaa auuaaagauc    300
gacuaagcau guaguaccaa agaugaauug uuuucggacg gggguucaac uccccccagc    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 aggtgctggtg    60
gcctcgtaaa aaaccgcaaa aaaaatagtt gcaaacgacg aaaactacg actagcagct    120
taataacctg cttagagccc tctctgccta gcctcgcctc ttaggacggg gatcaagaga    180
ggtcaaacct aaaagagctc gtgtggaac cttgcctggg gtggaagcat taaaactaat    240
caggatagtt tgtcagtagc gtgtccatcc gcagctggcc ggcgatgta atgattggac    300
taagcatgta gtgccgacgg tgtagtaatt tcggacgggg gttcaaatcc cccagctcc    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 aaaaauagu gcaaacgacg aaaacuacg acuagcagcu    120
uuaauaccug cuuagagccc ucucugccua gccuccgcuc uuaggacggg gaucaagaga    180

```

-continued

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```

ggucaaaaccu aaaagagcuc guguggaaac cuugccuggg guggaagcau uaaaacuaau 240
caggauaguu ugucaguagc guguccaucc gcagcuggcc ggcgaaugua augauuggac 300
uaagcaugua gugccgacgg uguaguauuu ucggacgggg guucaaaacc ccccagcucc 360
acca 364

```

```

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

```

```

<400> SEQUENCE: 131
aggagtaagt ctgcttagat ggcattgctc tttgggcaaa gcgtaaaaag cccaaataaa 60
attaaacgca aacaacgta aattcgtccc tgcttacgct aaagctcgt aagttcagtt 120
gagcctgaaa ttaagtcat actatctagc ttaattttcg gtcattcttg atagtgtagc 180
cttgctttg acaagcgttg aggtgaaata aagtcttagc cttgctttg agttttggaa 240
gatgagcgaa gtagggtaga gtagtcatct ttgctaagca ttagtagggtc 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 aaauugcucc ugcuuacgcu aaagcugcgu aaguucaguu 120
gagccugaaa uuuaagucac acuauaucgc uuaauuuucg gucaucuuug auaguguagc 180
cuugcguuug acaagcguug aggugaaaau aagucuuagc cuugcuuuug aguuuuggaa 240
gagagcgaa guagggugaa guagucaucu uugcuaagca uguagagguc uuugugggaa 300
uuuuuuugg 309

```

```

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

```

```

<400> SEQUENCE: 133
aggagtaagt ctgcttagat ggcattgctc tttggacaaa gcgtaaaaag tccaaattaa 60
aattaaacgc aaataacgta aaatttgctc ctgcttacgc taaagctgcg taagttcagt 120
tgagcccga aactcaagtga tgctatctag cttgaatttt ggtcattctt gatagtgtag 180
attgaaaatt gacaactttt aatcgaagtt aaagtcttag tctagcttga aattttggaa 240
ggtgagttta gccagatgaa gttttcacct ttgctaaaca ttagagaagtc 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 uccaaauaaa 60
aauuuaacgc aaauaacguu aaauuugcuc cugcuuacgc uaaagcugcg uaaguucagu 120

```

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---

```

ugagcccga acucaaguga ugcuaucuag cuugaauuuu ggucaucuuu gauaguguag 180
auugaaaaau gacaacuuuu aaucgaaguu aaagucuuag ucuagcuuga aauuuuggaa 240
ggugaguuua gccagaugaa guuuucaccu uugcuaaaca uguagaaguc uuuguggggg 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 agcccaata 60
aaattaaacg caaacaacgt taaattcgct cctgcttacg ctaaagctgc gtaagttcag 120
ttgagcctga aatttaagtc atactatccta gcttaatfff cggtcatttt tgatagtgt 180
gccttgcggt tgacaagcgt tgaggtgaaa taaggtctta gccttgcttt tgagttttgg 240
aagatgagcg aagtgggtg aagtagtcat ctttgctaag catgtagagg tctttgtggg 300
attatfffft 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 agcccaaua 60
aaauuaaacg caaacaacgu uaaauucgcu ccugcuuacg cuaaagcugc gaaaguucag 120
uugagccuga aauuuuaguc auacuauca gcuuaauuuu cggucauuuu ugauagugua 180
gccuugcguu ugacaagcgu ugaggugaaa uaaggucuaa gccuugcuuu ugaguuuugg 240
aagaugagcg aaguagggug aaguagucuu cuuugcuaag cauguagagg ucuuuguggg 300
auuauuuuug 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 tagcctgct 120
cctcctcct caattgccca cggttgagag taagggtgct atttaaaagt ggggaaccga 180
gcctagcaaa gctttgagct aggaacggaa tttatgaagc ttaccaaaaga ggaagtttgt 240
ctgtgacgt 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

&lt;400&gt; SEQUENCE: 138

```

acggggguag gauggguuug auaagcgagu cgaggggaagc auggugccuc gauaauaaag    60
uauagcauuua agauaaacgc acgagauaa uugcauuag cagcuuaagu uagcgugcu    120
cauccuuccu caauugccca cgguugagag uaaggguguc auuuuuuagu ggggaaccga    180
gccuagcaaa gcuuugagcu aggaacggaa uuuaugaagc uuaccaaaga ggaaguuuu    240
cuguggacgu ucucugaggg auuuuuuaaa cacaagacua cacucguaga aagucuuacu    300
ggucugcuuu cgg                                         313

```

&lt;210&gt; SEQ ID NO 139

&lt;211&gt; LENGTH: 331

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Haemophilus ducreyi (NCTC 10945)

&lt;400&gt; SEQUENCE: 139

```

acgggattag cgaagtccaa ggtgcacgtc gaggtgcggt aggcctcgta acaaacgca    60
aaaaaatagt cgcaaacgac gaacaatagc ctttagcagc ttaataacct gcatttagcc    120
ttcgcgccct agctttcgct cgtaagacgg ggagcacgcg gagtcaaacc aaaacgagat    180
cgtgtggacg cttccgcttg tagatgaaac actaaattga atcaagctag tttatttctt    240
gcgtgtctgt ccgctggaga taagcgaaat taaagaccag actaaactgt tagtactgaa    300
gatagagtaa ttccggaccc gggttcgact c                                         331

```

&lt;210&gt; SEQ ID NO 140

&lt;211&gt; LENGTH: 331

&lt;212&gt; TYPE: RNA

&lt;213&gt; ORGANISM: Haemophilus ducreyi (NCTC 10945)

&lt;400&gt; SEQUENCE: 140

```

acgggauuag cgaaguccaa ggugcacguc gaggugcggu aggccucgua acaaacgca    60
aaaaauagu cgcaaacgac gaacaauacg cuuugcagc uuaauaacu gcauuuagcc    120
uucgcgcccu agcuuucgcu cguuagacgg ggagcacgcg gagucaaacc aaaacgagau    180
cguguggacg cuuccgcuug uagaugaaac acuaaaauuga aucaagcuag uuuuuuuuu    240
gcgugucugu ccgucggaga uaagcgaaau uaaagaccag acuaaacgug uaguacugaa    300
gauagaguaa uuucggaccc ggguuacgac c                                         331

```

&lt;210&gt; SEQ ID NO 141

&lt;211&gt; LENGTH: 232

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Listeria innocua (food isolate #1)

&lt;400&gt; SEQUENCE: 141

```

ggcaaagaaa aacaaaacct agctttcgct gcctaataac cagtagcata gctgacctc    60
cgtgcatcgc coatgtgcta cggtaagggc ctcactctaa gtgggctaca ctagttaatc    120
tccgtctgag gttaaataga agagcttaat cagactagct gaatggaagc ctgttaccgg    180
gctgatgttt atgcgaaatg ctaatacggc gactacgctc gtagatattc aa          232

```

&lt;210&gt; SEQ ID NO 142

&lt;211&gt; LENGTH: 232

&lt;212&gt; TYPE: RNA

&lt;213&gt; ORGANISM: Listeria innocua (food isolate #1)

&lt;400&gt; SEQUENCE: 142

```

ggcaaagaaa aacaaaaccu agcuuucgcu gccuaauaac caguagcaua gcugaaccuc    60

```

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```

cgugcaucgc ccaugugcua cgguaaaggu cucacucuaa gugggcuaca cuaguuaaau 120
uccgucugag guuaaaauaga 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 cggtaaaggt ctcactctaa gtgggttaca ctagttaatc 120
tccgtctgag gttaaataga agagcttaat cagactagct gaatggaagc ctgttaccgg 180
gccgatgttt atgcgaaatg ctaatacggg 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 gccuaaauag caguagcaua gcugauccuc 60
cgugcaucgc ccaugugcua cgguaaaggu cucacucuaa gugggcuaca cuaguuaaau 120
uccgucugag guuaaaauaga agagcuuaau cagacuagcu gaauggaagc cuguuaccgg 180
gccgauguuu augcgaaaug cuaauacggu gacuacgcuc guagauuuu 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 cggtaaaggt ctcactctaa gtgggttaca ctagttaatc 120
tccgtctgag gttaaataga agagcttaat cggactagct gaatggaagc ctgttaccgg 180
gccgatgttt atgcgaaatg ctaatacggg 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 gccuaaauag caguagaaua gcugauccuc 60
cgugcaucgc ccaugugcua cgguaaaggu cucacucuaa gugggcuaca cuaguuaaau 120
uccgucugag guuaaaauaga agagcuuaau cggacuagcu gaauggaagc cuguuaccgg 180
gccgauguuu augcgaaaug cuaauacggu gacuacgcuc guagauuuu 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

```

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---

```

cgtgcatcgc ccatgtgcta cggtaaaggt ctcaactctaa gtgggctaca ctagttaatc 120
tccgtctggg gttaaataga agagcttaat cagactagct gaatggaagc ctgttactgg 180
gccgatgttt atgcgaaatg ctaatacggg 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 cgguaagggg cucacucuaa gugggcuaca cuaguuaaau 120
uccgucuggg guuaaaauaga agagcuuaau cagacuagcu gaauggaagc cuguuacugg 180
gccgauguuu augcgaaaug cuaauacggg gacuacgcuc guagauuuu aa 232

```

```

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

```

```

<400> SEQUENCE: 149

```

```

acagggatag ttcagcttg agttgcgagt cggggggatc gtcctcgta ttaacgtcaa 60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120
catagctgat cctccgtgca tcgccatgt gctacggtaa gggctcact ttaagtgggc 180
tacctaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg 240
aagcctgtta ccgggctgat gtttatgcca aatgctaata cggtgactac gctcgtagat 300
athtaagtgc 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 ccucggugca ucgcccaugu gcuaacgguaa gggucucacu uuaagugggc 180
uacacuaaa uaucuccguc ugggguuagu uagaagagcu uauacagacu agcugauggg 240
aagccuguaa ccgggcugau guuuauagcca aaugcuaaua cggugacucg cucguagaua 300
uuuaagugcc gauuuucug g 321

```

```

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

```

```

<400> SEQUENCE: 151

```

```

acagggatag ttcagcttg agttgcgagt cggggggatc gtcctcgta tcaacgtcaa 60
agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120
catagctgat cctccgtgca tcgccatgt gctacggaaa gggctcact ttaagtgggc 180
tacctaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg 240
aagcctgtta ccgggctgat gtttatgcca aataactaata cggtgactac gctcgtagat 300

```

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---

atттаagtgc 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  
 agccaauau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120  
 cauagcugau ccuccgugca ucgcccangu gcuacggaaa gggucucacu uuaagugggc 180  
 uacacuaaa auucuccguc ugggguuagu uagaagagcu uaucagacu agcugaaugg 240  
 aagccuguaa cggggcugau guuuaugcga aaucuaaau cggugacuac gcucguagau 300  
 auuaagugc ccauuuuuuc gg 322

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

<400> SEQUENCE: 153

acgggatttg cgaaaccaa ggtgcatgcc gaggggcggt tggcctcgta aaaagccgca 60  
 aaaaaatagt cgcaaacgac gaaacctacg ctttagcagc ttaataacct gcttagagcc 120  
 ctctctcct agcctccgct cttaggacgg ggatcaagag aggtcaaacc caaaagagat 180  
 cgcgtggatg cctgctctgg ggttgaagcg ttaaacgaa tcaggctagt ctggtagtgg 240  
 cgtgtccgtc cgcagggtcc aggcgaatgt aaagactgac taagcatgta gtaccgagga 300  
 ttaggaatt tcgg 314

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

<400> SEQUENCE: 154

acgggauuug cgaaaccaa ggugcaugcc gaggggcggu uggccucgua aaaagccgca 60  
 aaaaauagu cgcaaacgac gaaaccuacg cuuagcagc uuaauaaccu gcuuagagcc 120  
 cucucuccu agccuccgcu cuuaggacgg ggaucaagag aggucaaacc caaaagagau 180  
 cgcgugaug ccucgucgug gguugaagcg uuaaacgaa ucaggcuagu cugguagugg 240  
 cguguccguc cgcaggugcc aggcgaangu aaagacugac uaagcaugua guaccgagga 300  
 uguaggaau ucgg 314

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

<400> SEQUENCE: 155

acagggttcc cccagctta ttaagcgtgt cggagggttg gtcogtcat caacacattt 60  
 cggttaata taactgaaa atcaacaat aatttcgag tagctgctga atagccactg 120  
 catcgcctaa cagcatctcc tacgtgctgt taacgcgatt caaccctagt aggatatgct 180  
 aaactgccc 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 cggagggguug gcuccgucan caacacauuu 60  
 cgguaaaaua uaacugacaa aucaacaau aauuucgag uagcugcgua auagccacug 120  
 caucgccuaa cagcaucucc uacgugcugu uaacgcgau caaccuagu aggauaugcu 180  
 aaacacugcc gcuugaagug uguuuagaug aaauuaauc aagcuaguau cauguugguu 240  
 guuuuugcu uagcaugaug cgaaaauuu caauaacua 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 tgaggatat tttcgactc atcggcagat gtaaatgcc agttaatat 60  
 aactgcaaaa aatacaaat cttacgcatt agctgcctaa aaaacagcct gcgtgatctt 120  
 cacaagattg tttcgctttt gctagaaggt cttattatc agcaactac gtttgctac 180  
 tgtctagtta gttaaaaaga gatttataga ctcgctatgt gagggcttga gttatgtgc 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

acaggcaua ugagguauu uuugcgacuc aucggcagau guaaaugcc aguuauuuu 60  
 aacugcaaaa auuacaaau cuuacgcauu agcugccuaa aaaacagccu gcgugaucuu 120  
 cacaagaug uuugcguuuu gcuagaaggu cuuauuuuac agcaaacuac guuuggcuac 180  
 ugucuaguua guuuuuuaga gauuuuaga cucgcuauu gagggcuuga guuuuguguc 240  
 aucaccuagu uaaaacaaua cauaaccuau aguuguagac aaauuuuuu 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 aggcattgcc agcaccagta 60  
 agctcgtaa tccactgaa cactacaaac gccaacgacg agcgtttcgc tctcgcgct 120  
 taagcgtga gccgctgcac tgatctgtcc ttgggtcagc 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 ucucgcccgu 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

gggggtgat aggtttcgac ttgaaaatga agtgtaatt gcatgcccag ggcgttgct 60  
 ggctctctaa aaagccaaca aaacaataaa tgcccgaacct aaggctgaat gcgaaattat 120  
 tagcttgttt gactcagtag aggaaagact agctgcttaa ttagcaaaag ttgttagcta 180  
 gataatctct aggtaaccog gtatctgcga gctccaccag aggettgcaa aataccgtca 240  
 tttatctggt tggaacttac tttctctaat tctcaaggaa gttcgttcga gatttttgag 300  
 agtcattggc tgctatagag gcttctagct aaggaggtcc 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

ggggguguau agguuucgac uugaaaauga aguguuuuu gcaugccggag ggcguuggcu 60  
 ggccuccuaa aaagccaaca aaacaauaaa ugcccgaaccu aaggcugaau gcgaaauuu 120  
 uagcuuuuuu gacucaguag aggaaagacu agcugcuuaa uuagcaaaag uuguuagcua 180  
 gauaaucucu agguaaccog guaucugcga gcuccaccag aggcuuugcaa aauaccguca 240  
 uuuauucggg uggaacuuac uuucucuauu ucucaaggaa guucguucga gauuuuugag 300  
 agucauuggc ugcuauagag gcuucuagcu aaggagucc aauguaaaca auucuagaag 360  
 auaagcaugu agagguuagc agggaguuuu 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 acaaatgcc aataaactg gcaacaaaaa agcaaaccgc 120  
 gtacgggcta acgacagcaa ctttctgct gttgctaaag ctgctagtc tagcttaata 180  
 atctagatgc gcacggatat gatagtcttt cttatgacac tatctatata tccgttcata 240  
 ttccgcataa gacggtcttt gctttttgct tgggagtaa ggctgtattt aacagactcg 300  
 ctaactatta ccttgctaa ttggggaata gtcaagctaa actcaaatag attagcctaa 360  
 gcatgtagat ccaaagatct agagtttggt gacgcggggt caaatcccgc cgctccacc 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 uauaacagau acaaaugcca auauaacug gcaacaaaaa agcaaaccgc 120  
 guagcggcua acgacagcaa cuuugcugcu guugcuaaag cugccuaguc uagcuuaaua 180  
 aucuagaugc gcacggauau gauagucuuu cuuauagacac uaucuauaca uccguucaua 240  
 uuccgcauaa gacggucuuu gcuuuuuguc ugggaguuaa ggcuguauuu aacagacucg 300  
 cuaacuauua cccuggcuaa uuggggaaua gucaagcuaa acucaaaauag auuagccuaa 360  
 gcauguagau ccaaagaucu agaguuuugug gacgcggguu caaaucccgc cgcuccacc 420

a 421

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

<400> SEQUENCE: 165

ggggctgatt tggattcgac atataaat tgcgtgtttca ttatgaagca agtcaagttt 60  
 aatgatcttg taaaaaacat taaagtacaa ataaatgcaa gcaatatagt ttcatttagt 120  
 tcaaaacggt tagtctcttt tgcataagca aaatgtgtta ataactttct tagtagaaat 180  
 tggagaagtt tactaagatt tatatttact ccataattat tttaaagatg gtaaaaaggt 240  
 gattcatcat ttgtatgttt ctaaactttg tgaagaata gtgggctcca tttataatga 300  
 acgtgggttc aaatcccacc agtcccacca 330

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

<400> SEQUENCE: 166

ggggcugauu uggauucgac auauaaaauuu gcguguuua uuaugaagca agucaaguuu 60  
 aaugaucuuu uaaaaaacau uaaaguacaa auaaaugcaa gcaauauagu uucauuuagu 120  
 ucaaaacguu uagucucuuu ugcauaagca aaauguguua auaacuuucu uaguagaaau 180  
 uggagaaguu uacuaagauu uauuuuuacu ccuaauuuu uuuuaaagau guaaaaaggu 240  
 gauucaucau uuguauuuu cuaaacuuug ugaagaaua gugggcucca uuuaaauga 300  
 acguggguuc 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 tgcaggtca aagtttgtat 60  
 tctttgtaaa aaaatactaa aatactaata aatgctaata atataatacc gtttattttt 120  
 aaagcagtaa aacaaaaaaa agaagcaatg gctttaaatt ttgctgtata gttcattaac 180

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```

ttaggttatt aaatattttt tcattataac tggacttttc tctagtttat agtttagaat 240
aaatttaaat tttgcaaaac tcgttcgaaa attttcgggc taaacctgta aacgcaata 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 auuuuuuuuu ucuuuuuaug ugucagguca aaguuuguau 60
ucuuuuuuuuu aaaaauacuaa aaauacuaaa aaugcuaaua auuaauuacc guuuuuuuuu 120
aaagcaguaa aaacaaaaaa agaagcaaug gcuuuuuuuu uugcuguaua guucauuuac 180
uuagguuuuu aaaauuuuuu ucauuuuuac uggacuuuuc ucuaguuuuu aguuuagaau 240
aaauuuuuuu uuugcaaaaac ucguucgaaa auuuucgggc uaaaccugua aacgcaaua 300
cuaagaaauu uuagauggac augguuucaa 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  
  
 tggggatggt acggtttcga caggggtagt tcgagcttag gtggcgagtc gaggggatcg 60  
 gcctcgtaa aacgtcaaag cctataactg gcaacaaca aaacaacttc gcttttagcag 120  
 ctaataaagc tcttagcgtt tcctccctcc atcgcccatg tggtaggta agggactcaa 180  
 attaagtggg ctacgtgga ttccaccgtc tgaggatgaa agaagagaac aaccagacta 240  
 gctaccgga 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 aacgcucaa ccuuaaacug gcaacaaca aaacaacuuc gcuuagcag 120  
 cuuaaauaagc ucuuagcggg uccuccucc aucgcccgaug ugguaaggua agggacucaa 180  
 auuaaguggg cuacgcugga uuccaccguc ugaggauaaga agaagagaac aaccagacua 240  
 gcuaaccgga cgcccugcga uaggcagaug gaguagcgaa ucgcgaauau aucgacuaca 300  
 cucguagaag cuuaagugcc gauauucug gacguggguu cgacuccc 348  
  
 <210> SEQ ID NO 178

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

<400> SEQUENCE: 178

tggggacgtt acggtttcga cagggatagt tcgagcttag gttgagatc gaggggatcg 60  
 gcctcgtaa aacgtcaaag cctataattg gcaaacaaaa caatctttct ttagctgctt 120  
 aattgcacta aaggttcctc cctccatcgt ccatgtggtg gggttaagga ctcaactaa 180  
 gtggactacg ccggagttcg ccgtctgagg acaaaggaag agaacaacca gactagcaac 240  
 ttggaagcct gtcgatagcg cgaagagttc gcgaaatgct aatatatcga ctacactcgt 300  
 agaagcttaa gtgccgatat ttttgacgt gggttcgatt cact 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 ccuauuuug gcaaacaaaa caaucuuuc uagcugcuu 120  
 aaugcacua aagguuccc ccuccaucgu ccauguggua gguuaagga cucaaacuaa 180  
 guggacuacg ccggaguucg ccgucgagg acaaaggaag agaacaacca gacuagcaac 240  
 uuggaagccu gucgauagcg cgaagaguuc gcgaaaugcu aauauaucga cuacacucgu 300  
 agaagcuuaa gugccgauau uuuggacgu gguucgauu cccu 344

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

<400> SEQUENCE: 180

acagggatag ttcgagcttg agttgagatc cgggggagtc gtcctcgta tcaacgtcaa 60  
 agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120  
 catagctgat cctccgtgca tcgcccattg gctacggaaa gggctcact ttaagtggc 180  
 tacactaat aatctcctgc tggggtagt tagaagagct taatcagact agctgaatgg 240  
 aagcctgta ccggctgat gtttatgca aataactaata cgggtactac gctcgtatg 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 ucgcccgaug gcuacggaaa gggucucacu uuaaguggc 180  
 uacacuaaa uaucuccguc ugggguuagu uagaagagcu uauacagacu agcugaauug 240  
 aagccuguaa ccgggcugau guuuuagcga aaucuaaau cggugacuac gcucguagau 300  
 auuuagugc ccuuuuuc 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 gtcctcgta ttaacgtcaa 60  
 agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120  
 catagctgat cctccgtgca tgcgccatgt gctacggtaa gggctcact ttaagtgggc 180  
 tacactaaat aatctccgtc tgggggttagt tagaagagct taatcagact agctgaatgg 240  
 aagcctgtta ccgggtgat 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 cggggggau cguccugua uuaacgucaa 60  
 agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120  
 cauagcugau ccuccgugca ugcgccaugu gcuacgguaa gggucucacu uuaagugggc 180  
 uacacuaaa uaucuccguc ugggguuagu uagaagagcu uaucagacu agcugaauagg 240  
 aagccuguaa ccgggcugau guuuaugcga aaugcuaaua cggugacucg cucguagaua 300  
 uuaaagugcc gauuuucug g 321

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

<400> SEQUENCE: 184

acttcgcga tcgaatcaag ggaagcgtgc cggcgcagc aagagaccac cgtaagcgtc 60  
 gttgcgacca aataagcgc gattcacatc agcgcgacta cgctctcgt gcctaagcga 120  
 cggctagtct gtcagaccgg gaacgcctc ggcccggacc ctggcatcag cttagaggat 180  
 ccaccgatga gtcggctgc gggactcctc gggacaacca cagcgactgg gatcgtcatc 240  
 tcgctagtt 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 cggugcagc aagagaccac cguaagcgc 60  
 guugcgacca auaagcgc gaaucacauc agcgcgacua cgcucucgu gccuaagcga 120  
 cggcuagucu gucagaccgg gaacgcccuc ggcccggacc cuggcaucag cuagagggau 180  
 ccaccgauga guccggucgc gggacuccuc gggacaacca cagcgacugg gaucgucauc 240  
 ucggcuaguu cgcgugaccg ggagauccga gcagaggcau agcgaacucg gcacggagaa 300  
 gccuugaggg aaugccgua 319

<210> SEQ ID NO 186

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

<400> SEQUENCE: 186
acttcgcgca tcgaatcaag ggaagcgtgc cggcgcagc aagagaccac cgtaagcgtc    60
gttgcaacca tataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga    120
cggctagtct gtcggaccgg gaacgcctc gccccggacc cggcatcag ctagagggat    180
caaccgatga gttcggcgc gggactcctc gggacaccaa cagcgactgg gatcgtcctc    240
ctggctagtc cgtgtgacca ggagatccga gcagagacat agcggactgc gcacggagaa    300
gccttgaggg aatgccgta                                     319

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

<400> SEQUENCE: 187
acuucgcgca ucgaaucaag ggaagcgucc cggugcagc aagagaccac cguaagcgcg    60
guugcaacca uauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga    120
cggcuagucu gucggaccgg gaacgcctc gccccggacc cggcaucag cuagagggau    180
caaccgauga guucggucgc gggacucauc gggacaccaa cagcgacugg gaucgucauc    240
cuggcuaguc cguugacca ggagauccga gcagagacau agcggacugc gcacggagaa    300
gccuugaggg aaugccgua                                     319

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

<400> SEQUENCE: 188
acttcgcgca tcgaatcaag ggaagcgtgc cggcgcagc aagagaccac cgtaagcgtc    60
gttgcaacca aataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga    120
cggctagtct gtcagaccgg gaccgcctc gaccggactc ctggcatcag ctagagggat    180
caaccgatga gttcggcgc gggactcctc gggacaccaa cagcgactgg gatcgtcctc    240
ctggctagtt cgcgtgacca ggagatccga gcagaggcat agcgaactgc gcacggagaa    300
gccttgaggg aatgccgta                                     319

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

<400> SEQUENCE: 189
acuucgcgca ucgaaucaag ggaagcgucc cggugcagc aagagaccac cguaagcgcg    60
guugcaacca aauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga    120
cggcuagucu gucagaccgg gaccgcctc gaccggacu cuggcaucag cuagagggau    180
caaccgauga guucggucgc gggacucguc gggacaccaa cagcgacugg gaucgucauc    240
cuggcuaguu cgcgugacca ggagauccga gcagaggcau agcgaacugc gcacggagaa    300
gccuugaggg aaugccgua                                     319

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<210> SEQ ID NO 190

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

<400> SEQUENCE: 190
acagcgagtc tgcacttaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc   60
attgcaacca attaagcgcc gattctcadc agcgcgacta cgcactcgct gcctaagcga   120
ctgcgtgtct gtcagaccgg gagcgccttc agcccggacc ctggcatcag ctagagggac   180
aaactacggg ttcggtcgcg ggacccgtag ggacatcaaa cagcgactgg gatcgtcadc   240
tcggcttgtt cgcgggaccg agagatccaa gtagagggat agcgaactgc gcacggagaa   300
gccttaatga acggccgttg                                     320

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

<400> SEQUENCE: 191
acagcgaguc ucgacuuaag ggaagcguvc cggugcaggc aagagaccac cguaagcgvv   60
auugcaacca auuaagcgvv gauucucavc agcgcgacua cgcacucgvv gccuaagcga   120
cugcgvvuvv gvcagaccgv gagcgvvctc agcccgvvacc cuggcavcag cuagagggac   180
aaacucaggg uucgvvvcgv ggacccgvag ggacavcaaa cagcgvvcvg gvavcgvavc   240
ucgvvuvvuv cgcgggaccg agagavccaa gvagaggvav agcgvavcvc gcacggagaa   300
gcvvuaavag acggccgvvg                                     320

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

<400> SEQUENCE: 192
acttcgcgca tcgaatcaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc   60
gttgcaacca attaagcgvv gagaacactc agcgcgactt cgtctcgvv gcctaagcga   120
cagcaagtcc gtcagaccgv gaaagcctc gaccgvvacc ctggcgvvcat ctagagggat   180
ccaccgvvga gttcgvvvcgv gggactcadc gggacaccaa cagcgvvactgv gatcgvvadc   240
ctgvvtagtt cgcgvvaccg ggagatccga gtagagacat agcgvvactgv gcacggagaa   300
gccttgaggg aatgvvvcgvv                                     320

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

<400> SEQUENCE: 193
acuvcgvvca ucgaaucavv ggaagcgvvc cggugcaggvv aagagaccac cguaagcgvv   60
gvvvcavvca auuaagcgvv gagaacavc agcgcgacuu cgvvucgvv gccuaagcga   120
cagcaagvvc gvcagaccgv gaaagcctc gaccgvvacc cuggcgvvav cuagagggav   180
ccaccgvvga gvvcgvvvcgv gggavcavc gggacaccaa cagcgvvcvg gvavcgvavc   240
cvggvavvuv cgcgvvaccg ggagavccga gvagagavav agcgvvavcvc gcacggagaa   300
gcvvuvaggg avvgccgvvav                                     320

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<210> SEQ ID NO 194

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

<400> SEQUENCE: 194
acttcgcgca tcgaatcaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc   60
gttgcaacca tataagcgcc gtttcaacac agcgcgacta cgctctcgct gcctaagcga   120
cagctagtcc gtcagaccgg gaacgcctc gaccgggagc ctggcgtcag ctggagggat   180
ccaccggtga gtcgggtcgc gggactcacc gggacataca cagcgactgg gatcgtcacc   240
ctggctggtt cgcgtgaccg ggagatccga gcagaggcat agcgaactgc gcacggagaa   300
gccttgaggg aatgccgtag                                     320

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

<400> SEQUENCE: 195
acuucgcgca ucgaaucaag ggaagcgucc cggugcaggc aagagaccac cguaagcgucc   60
guugcaacca uauaagcgcc guuucacac agcgcgacua cgcucucgcu gccuaagcga   120
cagcuagucc gucagaccgg gaacgcctc gaccgggagc cuggcgucag cuggagggau   180
ccaccgguga guccggucgc gggacucauc gggacauaca cagcgacugg gaucgucauc   240
cuggcugguu cgcgugaccg ggagauccga gcagaggcau agcgaacugc gcacggagaa   300
gccuugaggg aaugccguag                                     320

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

<400> SEQUENCE: 196
acttcgagcg tcgaatcaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc   60
gttgcaacca attaagcgcc gattccaatc agcgcgacta cgcactcgct gcctaagcga   120
ctgcgtgtct gtcagcccg gtagccctc gaccgggtgt ctggcatcag cttagaggat   180
aaaccggtgg gtcgggtcgc gggactcacc gggacatcaa acagcgactg ggatcgtcac   240
cctgacttgt tcgctgatc aggagatccg agtagagaca tagcgaactg cgcacggaga   300
agccttgagg gaacgccgta g                                     321

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

<400> SEQUENCE: 197
acuucgagcg ucgaaucaag ggaagcgucc cggugcaggc aagagaccac cguaagcgucc   60
guugcaacca auuaagcgcc gauuccaac agcgcgacua cgcacucgcu gccuaagcga   120
cugcgugucu gucagcccg gtagccctc gaccgggugu cuggcaucag cuagagggau   180
aaaccggugg guccggucgc gggacucauc gggacaucaa acagcgacug ggauucgucau   240
ccugacuugu ucgcgugauc aggagauccg aguagagaca uagcgaacug cgcacggaga   300
agccuugagg gaacgccgua g                                     321

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<210> SEQ ID NO 198

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

<400> SEQUENCE: 198

acttcgcgca tcgaatcaag ggaagcgtgc cggcgcagc aagagaccac cgtaagcgtc 60  
 gatgcaacta gataagcgcc gattcacatc agcgcgacta cgctctcgtc gcctaagcga 120  
 cggctagtct gtcggaccgg gaacgcctc gccccggacc cggcatcag ctagagggat 180  
 caaccgatga gttcggtcgc ggggtcctc 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 ggaagcgtgc cggcgcagc aagagaccac cguaagcgtc 60  
 gaugcaacua gaaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120  
 cggcuagucu gucggaccgg gaacgcctc gccccggacc cggcaucag 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 cggcgcagc aagagaccac cgtaagcgtc 60  
 gttgcgacca aataagcgcc gattcacatc agcgcgacta cgctctcgtc gcctaagcga 120  
 cggctagtct gtcagaccgg gaacgcctc gccccggacc ctggcatcag ctagagggat 180  
 ccaccgatga gtcggtcgc 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 ggaagcgtgc cggcgcagc aagagaccac cguaagcgtc 60  
 guugcgacca auaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120  
 cggcuagucu gucagaccgg gaacgcctc gccccggacc cuggcaucag cuagagggau 180  
 ccaccgauga guccggucgc gggacuccc gggacagcca cagcgacugg gaucgucauc 240  
 ucggcuaguu cgcgugaccg ggagauccga gcagaggcau agcgaacugc gcacggagaa 300  
 gccuugaggg aaugccgua 319

<210> SEQ ID NO 202

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

<400> SEQUENCE: 202

acttcgagca tcgaatccag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc 60  
 gttgcaacca attaagcgcc gattccaatc agcgcgacta cgccctcgct gcctaagcga 120  
 cggctggtct gtcagaccgg gagtgccttc 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 ggaagcguvc cggugcaggc aagagaccac cguaagcgvv 60  
 guugcaacca auuaagcgvv gauuccaavc agcgcgacua cgccucvcu gccuaagcga 120  
 cggcgvvuvu gvcagaccgvv gagvccccvc ggcccgvvac cuggcavcag cvagagggac 180  
 ccacccacgvv guucgvvvcvc gggaccvvgv gggacavcava acagcgvvacv ggavcgvvacv 240  
 cvcgvvcvuvu ucgvvgvacc gggagavccv agvavagava uagcgvvacv cgcacgvvaga 300  
 agccvcgvv gvacvccvva g 321

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

<400> SEQUENCE: 204

acttcgcgca tcgaatcaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc 60  
 gttgcaacta aataagcgvv gattcacatc agcgcgacta cgctctcgct gcctaagcga 120  
 cagctagtcc gtcaggccgvv gaggccctc gaccvcgvc ctagcgtcag ctagagggat 180  
 ccacccgatgvv gttcggtcvc gggaccatc gggacaccac acagcgvvacv ggatcgvvcv 240  
 cccgvvctagt tcgvvgvacc gggagatccv agtaagggca aagcgvvacv cgcacgvvaga 300  
 agccttgagg gtatgccgta 320

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

<400> SEQUENCE: 205

acuucgcgca ucgaaucaag ggaagcgvvc cggugcaggc aagagaccac cguaagcgvv 60  
 guugcaacua auvaagcgvv gauvcacavc agcgcgacua cgvcucvcu gccvaagcga 120  
 cagcvagvcc gvcagvcgvv gagvccccvc gaccvcgvvac cuggcgvvacv cvagagggav 180  
 ccacccgavv gvucgvvvcvc gggaccavc gggacaccac acagcgvvacv ggavcgvvcv 240  
 cccgvvcvavv ucgvvgvacc gggagavccv agvaagggca aagcgvvacv cgcacgvvaga 300  
 agccvvgagg gvavcvcvva 320

<210> SEQ ID NO 206

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

<400> SEQUENCE: 206
acttcgcgca tcgaatcaag ggaagcgtgc cggcgcaggc aaccgaccac cgtaagcgtc   60
gttgcaaaaca gataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga   120
cagctagtcc gtcagaccgg gaagcgcctc gaccgggagc ctggcgtcag ctagagggat   180
ccaccgatga gtcgggtcgc gggacttacc gggacaccaa cagcgactgg gatcgtcatc   240
tcggcttggt cgcgtgaccg ggagatccga gtagaggcat agcgaactgc gcacggagaa   300
gtcttgaggg aatgccgtag                                     320

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

<400> SEQUENCE: 207
acuucgcgca ucgaaaucaag ggaagcguvc cggugcaggc aaccgaccac cguaagcgvca   60
guugcaaaaca gaaagcgvcc gauucacauc agcgcgacua cgcucucvcu gccuaagcga   120
cagcuagucc gucagaccgv gaagcgvccvc gaccgggagc cuggcgvucag cuagagggvau   180
ccaccgauga guccgvvcvc gggacuuauvc gggacaccaa cagcgvacvgg gaucgvcauc   240
ucgvcuuguu cgcgvagaccg ggagauccga guagaggvcau agcgvacvcg gcacggagaa   300
gucuuagaggv aavgcgvuag                                     320

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```

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

<400> SEQUENCE: 208
acatcgcgca tcgaatcaag ggaagcgtgc cggcgcaggc aagagaccac cgtaagcgtc   60
gttgcaacca attaagcgvcc gattcacatc agcgcgacta cgctctcgct gcctaagcga   120
cagctagtcc gtcagaccgv gaaagcgvcc gaccgggagc ctggcgtcag ctagaggvat   180
caaccgatga gttcgvvcvc gggactcacc gggacaccaa cagcgvactgg gatcgtcatc   240
ctgvctagtc cgcgvtagca ggagatccga gcagaggvat agcgvactvc gcacggagaa   300
gtcttgaggg aatgvccgttgc                                     320

```

```

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

<400> SEQUENCE: 209
acaucgcgca ucgaaaucaag ggaagcgvvc cggugcaggc aagagaccac cguaagcgvca   60
guugcaacca auuaagcgvcc gauucacauc agcgcgacua cgcucucvcu gccuaagcga   120
cagcuagucc gucagaccgv gaaagcgvcc gaccgggagc cuggcgvucag cuagagggvau   180
caaccgauga guccgvvcvc gggacuuauvc gggacaccaa cagcgvacvgg gaucgvcauc   240
cuggcuagvc cgcgvagaccg ggagauccga gcagaggvcau agcgvacvcg gcacggagaa   300
gucuuagaggv aavgcgvuug                                     320

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<210> SEQ ID NO 210

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

<400> SEQUENCE: 210

actgtgtgcg ccgaggtagg ggaagcgtgt cggcgcaggc tggagaccac cgtaagcgt    60
cgcggaacc aattaagcgc cgattccaat cagcgcgact acgcctcgc tgctgatca    120
cgcacggcta gctgtcggcc cgggttgtgt tcccgaacc ggatgccggc atcatctcag    180
ggaactcacc gtgttcgccg gtcgcggacg gacacgggac agcaaacagc gactgggatc    240
gtcatctcgg ctgttcgcg tgaccgggag atccaagtag agacatagcg gactgcacac    300
ggagaagccc tactgactcg acacag                                     326

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```

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

<400> SEQUENCE: 211

acugugugcg ccgagguagg ggaagcugug cggugcaggc uggagaccac cguaaagcgu    60
cgcggaacc aauaaagcgc cgauccaau cagcgcgacu acgcccucgc ugccugauca    120
cgcacggcua gcugucggcc cggguugugu ucccgaacc ggaugccggc aucaucucag    180
ggaacucacc guguuccgcg gucgcggacg gacacgggac agcaaacagc gacugggaur    240
gucaucucgg cuuguuccgc ugaccgggag auccaaguag agacauagcg gcugcacacg    300
gagaagcccu acugacucga cacag                                     325

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```

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

<400> SEQUENCE: 212

acgggatttg cgaaaccaa ggtgcatgcc gagggcggtt tggcctcgtt aaaagccgca    60
aaaaaatagt cgaaacgac gaaacctacg ctttagcagc ttaataacct gcttagagcc    120
ctctctccct agcctccgct cttaggacgg ggatcaagag aggtcaaacc caaaagagat    180
cgcgtggatg cctgctcgtt ggttgaagcg ttaaacgaa tcaggctagt ctggtagtgg    240
cgtgtccgtc cgcaggtgcc aggcgaatgt aaagactgac taagcatgta gtaccgagga    300
ttaggaatt tcgg                                             314

```

```

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

<400> SEQUENCE: 213

acgggaauug cgaaaccaa ggugcaugcc gagggcgguu uggccucgua aaaagccgca    60
aaaaauagu cgaaacgac gaaaccuacg cuuagcagc uuaauaaccu gcuuagagcc    120
cucucucccu agccuccgcu cuuaggacgg ggaucaagag aggucaaacc caaaagagau    180
cgcgugaug cccugccugg gguugaagcg uuaaacgaa ucaggcuagu cugguagugg    240
cguguccguc cgcagguacc aggcgaauu aaagacugac uaagcaugua guaccgagga    300
uguaggaauu ucgg                                             314

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<210> SEQ ID NO 214

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

<400> SEQUENCE: 214
acaggggtcc cccgagctta ttaagcgtgt cggaggggtg gctccgcat caacacattt    60
cggttaaata taactgacaa atcaacaat aatttcgcag tagctgcgta atagccactg    120
catcgcctaa cagcatctcc tacgtgctgt taacgcgatt caaccctagt aggatatgct    180
aaacactgcc gcttgaagtc tgtttagatg aatatataatc aagctagtat catggttggt    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 cggagggguug gcuccgucan caacacauuu    60
cgguuuuuuu uaacugacaa aucaaacuuu aauuucgcag uagcugcgua auagccacug    120
caucgccuaa cagcaucucc uacgugcugu uaacgcgauu caaccuagu aggauaugcu    180
aaacacugcc gcuugaaguc uguuuagaug aaauuuuauc aagcuaguau cauguugguu    240
guuuuuugcu uagcaugaug cgaaaauuuu 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 tgaggatat tttgcgactc atcggcagat gtaaaatgcc agttaaatat    60
aactgcaaaa aatacaaat cttacgcatt agctgcctaa aaaacagcct gcgtgatctt    120
cacaagattg tttgcgtttt gctagaaggt cttatttata agcaaacctac gtttgctac    180
tgtctagtta gttaaaaaga gatttataga ctgcgtatgt gagggcttga gttatgtgtc    240
atcacctagt taatcaata 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
acaggcauuu ugagguuuuu uuugcgacuc aucggcgagu guaaaaugcc aguuuuuuuu    60
aacugcaaaa auuacaaauu cuuacgcauu agcugccuaa aaaacagccu gcgugaucuu    120
cacaagaauu uuugcguuuu gcuagaaggu cuuuuuuuu agcaaacuac guuuggcuac    180
ugucuaguua guuuuuuuuu gauuuuuuaga cucgcuauuu gagggcuuga guuuuguguc    240
aucaccuagu uuuuuuuuuu cauuuuuuuu aguuuuuuuu aaauuuuuuu gcagauguuu    300
gg                                                    302

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<210> SEQ ID NO 218

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<211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Salmonella  
 genus specific 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  
  
 tttgttttt 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 gtttgcca 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  
 mycobacterial sequences

<400> SEQUENCE: 225

ggatctccyg rtcwrcrga 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:  
 Oligonucleotide primer for amplification of M.  
 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:  
 Oligonucleotide primer for amplification of M.  
 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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caaagaaaa caaacctag ctttcgctgc ctaataagca gtagcatagc tgatcctccg      60
tgcacgccc atgtgctacg gtaagggtct cactctaagt gggtacact agttaatctc      120
cgtctgaggt taaatagaag agcttaatca gactagctga atggaagcct gttaccgggc      180
cgatgtttat gcgaaatgct aatcgggtga ctacgctcgt agatattt                    228

```

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<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:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n is c or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: n is a or t

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<400> SEQUENCE: 230

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gggnntacgg nttcgac                                                    17

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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
oligonucleotide primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n is a or g
<220> FEATURE:
<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

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<400> SEQUENCE: 231

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gggantcgaa ccnngtcc                                                    18

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<210> SEQ ID NO 232
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide primer

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<400> SEQUENCE: 232

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ggggctgatt ctggattcga c                                              21

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

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<400> SEQUENCE: 233  
ggagttgaac ccccgtcgc 19

<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  
oligonucleotide primer

<400> SEQUENCE: 234  
tgggtggagcc 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  
oligonucleotide primer

<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  
oligonucleotide primer

<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  
oligonucleotide primer  
<220> FEATURE:  
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<222> LOCATION: (9)..(9)  
<223> OTHER INFORMATION: n is c or g  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (16)..(16)  
<223> OTHER INFORMATION: n is c or t

<400> SEQUENCE: 237  
ggagatggng ggaatnga 18

<210> SEQ ID NO 238  
<211> LENGTH: 17  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
oligonucleotide primer

<400> SEQUENCE: 238  
tgggtggagat gacggga 17

<210> SEQ ID NO 239

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<211> LENGTH: 18  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 oligonucleotide primer

<400> SEQUENCE: 239

ggggatgtag aggttttg

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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

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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  
 5 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, 10 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, 15 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 20 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 data- 25 base of *ssrA* gene sequences is used to identify a prokaryotic or eukaryotic organism.

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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	<a href="#">US7972777</a>	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		
当前申请(专利权)人(译)	爱尔兰企业局 爱尔兰国立高威大学		
[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	<a href="#">Espacenet</a> <a href="#">USPTO</a>		

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。

