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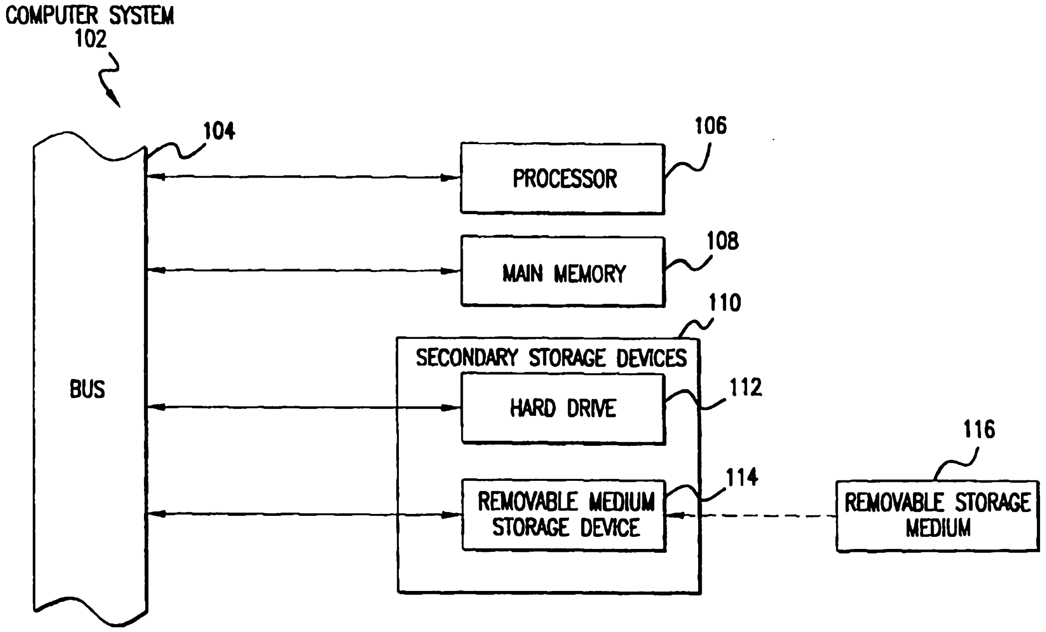

## (57) Abstract

The present invention provides polynucleotide sequences of the genome of *Enterococcus faecalis*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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# *Enterococcus faecalis* Polynucleotides and Polypeptides

## FIELD OF THE INVENTION

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Enterococcus faecalis*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

## BACKGROUND OF THE INVENTION

Enterococci have been recognized as being pathogenic for humans since the turn of the century when they were first described by Thiercelin in 1988 as microscopic organisms. The genus Enterococcus includes the species Enterococcus faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for 80 - 90 percent of all enterococcal infections. *See* Lewis et al. (1990) Eur J. Clin Microbiol Infect Dis. 9:111-117.

The incidence of enterococcal infections has increased in recent years and enterococci are now the second most frequently reported nosocomial pathogens. Enterococcal infection is of particular concern because of its resistance to antibiotics. Recent attention has focused on enterococci not only because of their increasing role in nosocomial infections, but also because of their remarkable and increasing resistance to antimicrobial agents. These factors are mutually reinforcing since resistance allows enterococci to survive in an environment in which antimicrobial agents are heavily used; the hospital setting provides the antibiotics which eliminate or suppress susceptible bacteria, thereby providing a selective advantage for resistant organisms, and the hospital also provides the potential for dissemination of resistant enterococci via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be divided into two general types, inherent or intrinsic property and that which is acquired. The genes for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation in the existing DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the gallbladder, urethra and vagina.

*E. faecalis* has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis (Lewis 1990, *supra*). In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bactermia range from 12% to 68%, with death due to enterococcal sepsis in 4 to 50% of these cases. *See* Emori, T.G. (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, means that these organisms, which usually seem to have relatively low intrinsic virulence, are given an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and control enterococcal infections. Particularly when the various resistance genes come together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by Enterococcus faecalis, involves the programmed expression of *E. faecalis* genes, and that characterizing these genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this organism.

## SUMMARY OF THE INVENTION

The present invention is based on the sequencing of fragments of the *Enterococcus faecalis* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-982.

The present invention provides the nucleotide sequence of hundreds of contigs of the *Enterococcus faecalis* genome, which are listed in tables below and set out in the

Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-982.

The present invention further provides nucleotide sequences which are at least 95%, 96%, 97%, 98%, and 99%, identical to the nucleotide sequences of SEQ ID NOS:1-982.

The nucleotide sequence of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-982 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Enterococcus faecalis* genome.

Another embodiment of the present invention is directed to fragments of the *Enterococcus faecalis* genome having particular structural or functional attributes. Such fragments of the *Enterococcus faecalis* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs, and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORFs in fragments of the *Enterococcus faecalis* genome disclosed in Tables 1-3, and the EMFs found 5' prime of the initiation codon, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Enterococcus faecalis* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Enterococcus faecalis* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Enterococcus faecalis* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Enterococcus faecalis* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a)contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b)determining whether the agent binds to said protein.

The present genomic sequences of *Enterococcus faecalis* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Enterococcus faecalis* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Enterococcus faecalis* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

## DESCRIPTION OF THE FIGURES

**FIGURE 1** is a block diagram of a computer system (102) that can be used to implement computer-based systems of the present invention.

**FIGURE 2** is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Enterococcus faecalis* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Sequis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Enterococcus faecalis* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 1% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research ( TIGR ) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with GeneMark, described in Borodovsky, M. and Mclninch, J.D. (1993) *Comput. Chem.*, 17:123133. The ORFs are searched against *E. faecalis* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol. 215:* 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3.

## DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention is based on the sequencing of fragments of the *Enterococcus faecalis* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS: 1-982. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Enterococcus faecalis* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS: 1-982 , or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-982" refers to any portion of the SEQ ID NOS: 1-982 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Enterococcus faecalis* open reading frames (ORFs ), expression modulating fragment ( EMFs ) and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample (DFs ). A non-limiting identification of preferred representative fragments is provided in Tables 1-3. As discussed in detail below, the information provided in SEQ ID NOS:1-982 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Enterococcus faecalis* proteins.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1-3 and SEQ ID NOS:1-982, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in SEQ ID NOS:1-982 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of SEQ ID NOS:1-982 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of SEQ ID NOS:1-982 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in SEQ ID NOS:1-982. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, of each SEQ ID NO:, are included in the invention.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of SEQ ID NOS:1-982. Any number of fragments of nucleotide sequences in SEQ ID NOS:1-982, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

While the presently disclosed sequences of SEQ ID NOS:1-982 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-982. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS:1-982 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS: 1-982 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotides may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS: 1-982 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-982.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *E. faecalis* strain that provided the DNA of the present Sequence Listing, Strain V586, kindly provided by Dr. Michael Gilmore, University of Oklahoma, has been deposited in the ATCC, as a convenience to those of skill in the art. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, and given accession number 55969. The provision of the deposits is not a waiver of any rights of the inventors or their assignees in the present subject matter.

The nucleotide sequences of the genomes from different strains of *Enterococcus faecalis* differ somewhat. However, the nucleotide sequences of the genomes of all *Enterococcus faecalis* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS: 1-982. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in SEQ ID NOS:

1-982. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis* mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in SEQ ID NOS: 1-982, which do, in fact, encode a polypeptide having *E. faecalis* protein activity By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in SEQ ID NOS: 1-982 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 1 and 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Tables 1 and 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in SEQ ID NOS: 1-982, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the presence invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

## COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-982 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*, a nucleotide sequence provided in SEQ ID NOS:1-982 , a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-982. Such a manufacture provides a large portion of the *Enterococcus faecalis* genome and parts thereof (*e.g.*, a *Enterococcus faecalis* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Enterococcus faecalis* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD- ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially- available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS: 1-982 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol. 215*:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem. 17*:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Enterococcus faecalis* genome which contain homology to ORFs or proteins from both *Enterococcus faecalis* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Enterococcus faecalis* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites, proteins to be used as vaccines or in the generation of immuno-therapeutic reagents, or as drug screening targets.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Enterococcus faecalis* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer- based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBI). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Enterococcus faecalis* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Enterococcus faecalis* genome. In the present examples, implementing software which implement the BLAST algorithm, described in Altschul *et al.* (1990) *J. Mol. Biol. 215:* 403-410, is used to identify open reading frames within the *Enterococcus faecalis* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

## BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Enterococcus faecalis* genome. The fragments of the *Enterococcus faecalis* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Enterococcus faecalis* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Enterococcus faecalis* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-982, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Enterococcus faecalis* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate a *Enterococcus faecalis* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS:1-982. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library or *Enterococcus faecalis* genomic DNA. Thus, given the availability of SEQ ID NOS:1-982, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-982 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA. As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein. Each sequence of SEQ ID NOS:1-982, however, begins and ends with a termination codon. For purposes of numbering and reference to polynucleotide and polypeptide sequences the entire sequence of each sequence of SEQ ID NOS:1-982 is included with the first nucleotide being positon 1. Therefore, for reference purposes the numbering used in the present invention is that provided in the sequence listing for SEQ ID NOS:1-982.

Tables 1, 2, and 3 list ORFs in the *Enterococcus faecalis* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive, or more selective lists.

Table 1 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in March, 1997.

Table 2 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in March, 1997.

Table 3 sets out ORFs in the *Enterococcus faecalis* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in March, 1997.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the coordinate of the first nucleotide of the ORF, counting from the 5' end of the contig strand; the fourth column indicates the coordinate of the final nucleotide of the ORF, counting from the 5' end of the contig strand.

In Tables 1 and 2, column five lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column six in Tables 1 and 2 provides the gene name of the matching sequence.

In Table 1, column seven provides the nucleotide BLAST percent identity score from the comparison of the ORF and the GenBank sequence, column eight indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis, and column nine provides the total length of the ORF in nucleotides.

In Table 2, column seven provides the protein BLAST percent similarity of the highest scoring segment pair identified, column eight provides the percent identity of the highest scoring segment pair, and column nine provides the total length of the ORF in nucleotides.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the percent identity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Enterococcus faecalis* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Enterococcus faecalis* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Enterococcus faecalis* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Enterococcus faecalis* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Enterococcus faecalis* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 99% and preferably 99.9% identical to SEQ ID NOS:1-982, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Enterococcus faecalis* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Enterococcus faecalis* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5 to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Enterococcus faecalis*. Especially preferred in this regard are ORFs such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Enterococcus faecalis*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Enterococcus faecalis*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251*:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem. 56*:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Enterococcus faecalis* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBS SK (+ or -), pBS KS (+ or -), pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Enterococcus faecalis* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF. The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. Preferred polypeptides and proteins of the present invention are polypeptides and proteins coded for by the polynucleotides of SEQ ID NOS:1-982, wherein the polypeptides and proteins are coded in the same frame as the termination codon at the end of each sequence of SEQ ID NOS:1-982. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group including: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence from the first methionine codon to the termination codon of each sequence listed in SEQ ID NOS:1-982, wherein said termination codon is at the end of each SEQ ID NO: and said first methionine is the first methionine in frame with said termination codon; and (b) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence in (a) excepting the N-terminal methionine.

The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a) and (b) above.

The present invention is further directed to polynucleotide encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences described herein, are at least 5 contiguous amino acid in length, are selected from any two integers, one of which representing a N-terminal position. The initiation codon of the polypeptides of the present inventions position 1. The initiation codon (positon 1) for purposes of the present invention is the first methionine codon of each sequence of SEQ ID NOS:1-982 which is in frame with the termination codon at the end of each said sequence. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given amino acid sequence encoded by a sequence of SEQ ID NOS:1-982 is included in the invention, i.e., from initiation codon up to the termination codon. At least means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in a full length amino acid sequence minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in SEQ ID NOS:1-982 wherein the contiguous fragment is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in a full length sequence minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequences encoded by the sequences of SEQ ID NOS:1-982, as described hererin, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins which are also candidate agonists and antagonists according to the present invention. *See, e.g.,* Fields et al. (1989) Nature 340:245-246.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Enterococcus faecalis* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or "vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual,* 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli, B. subtilis, Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available form Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell 23:*175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5 flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Enterococcus faecalis*, of the fragments of the *Enterococcus faecalis* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Enterococcus faecalis* is defined as a homolog of a fragment of the *Enterococcus faecalis* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Enterococcus faecalis* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-982 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS:1-982 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-982 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS: 1-982, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-982, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-982, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Enterococcus faecalis*.

## ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Enterococcus faecalis* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESES, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

### 1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Enterococcus faecalis* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-982.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*, *Symbiosis 21*:79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series 389*:93 (1989) .

The metabolism of sugars is an important aspect of the primary metabolism of *Enterococcus faecalis*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters 1*:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.,* Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta. 872:*83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, Starch *40*:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, Acid Proteases Structure Function and Biology, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, Industrial Enzymes, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, Report Industrial Enzymes by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London 310*:227 (1985) and Poserke, *Journal of the American Oil Chemist Society 61*:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology 136*:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

### 2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein.

*E. faecalis* protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')2 and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')2 fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, *E. faecalis* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *E. faecalis* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the *E. faecalis* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *E. faecalis* polypeptide-specific antibodies.

Antibodies and fragements thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragements of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragements discussed above., i.e, by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particuarlly discribed fragement of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragements thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragements that do not bind polypeptides of any other species of *Enterococcus* other than *E. faecalis* are included in the present invention. Likewise, antibodies and fragements that bind only species of *Enterococcus*, i.e. antibodies and fragements that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

### 3. Diagnostic and Detection Assays and Kits

The present invention further relates to methods for assaying enterococcal infection in an animal by detecting the expression of genes encoding enterococcal polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. *See, e.g.,* Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Eremeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids *via* PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus* polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in SEQ ID NOS:1-982 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium phosphate buffer. A *E. faecalis* polynucleotide sequence shown in SEQ ID NOS:1-982 labeled according to any appropriate method (such as the $^{32}$P-multiprimed DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (*i.e.*, mRNA encoding *Enterococcus* polypeptides).

Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for *e.g.*, using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm$^2$) and low density chip arrays (<1000 oligonucleotides per $cm^2$). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragements, i.e, by their 5' and 3' positions or length in contigious base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using biosenors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. *See, e.g.,* Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell . Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include radioisotopes, such as iodine ($^{125}$I, $^{121}$I), carbon

($^{14}C$), sulphur ($^{35}S$), tritium ($^{3}H$), indium ($^{112}In$), and technetium ($^{99m}Tc$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include $^{3}H$, $^{111}In$, $^{125}I$, $^{131}I$, $^{32}P$, $^{35}S$, $^{14}C$, $^{51}Cr$, $^{57}To$, $^{58}Co$, $^{59}Fe$, $^{75}Se$, $^{152}Eu$, $^{90}Y$, $^{67}Cu$, $^{217}Ci$, $^{211}At$, $^{212}Pb$, $^{47}Sc$, $^{109}Pd$, etc. $^{111}In$ is a preferred isotope where *in vivo* imaging is used since its avoids the problem of dehalogenation of the $^{125}I$ or $^{131}I$-labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging. *See, e.g.*, Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, $^{111}In$ coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include $^{157}Gd$, $^{55}Mn$, $^{162}Dy$, $^{52}Tr$, and $^{56}Fe$.

Examples of suitable fluorescent labels include an $^{152}Eu$ label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein , typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect

Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragements thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the antibodies or fragements thereof of the present invention, for use in rapid diffenertial pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amio acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragements, i.e, by their N-terminal and C-terminal positions or length in contigious amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

### 4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Enterococcus faecalis* fragment and contigs herein described.

In general, such methods comprise steps of:

(a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Enterococcus faecalis* genome; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in *Synthetic Peptides, A User's Guide*, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry 28:*9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res. 6*:3073 (1979); Cooney *et al.*, *Science 241*:456 (1988); and Dervan *et al.*, *Science 251:*1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem. 56:*560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression,* CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

### 5. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Enterococcus faecalis*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth and/or pathogenicity of *Enterococcus faecalis* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. *See, e.g.*, Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. *See, e.g.*, Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide, immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in SEQ ID NOS:1-982. For example, the *E.*

*faecalis* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing heterologous proteins are known in the art. *See, e.g.*, Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412 . These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*, for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or fragments thereof, with additional non-Enterococcal components (*e.g.*, diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA vaccines are currently being developed for a number of infectious diseases. *See, et al.*, Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct administration of plasmid DNA encoding *B. burgdorgeri* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See,* Luke et al. (1997) J. Infect. Dis. 175:91-97.

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al. (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves. These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and incomplete), mineral salts (for example, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*. Other substances useful as adjuvants are the saponins such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $AlK(SO_4)_2$, $AlNa(SO_4)_2$, and $AlNH_4(SO_4)$.

Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharangeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) Infect. Immun. 63:1195-1200. Similarly, orally administered encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) Infect. Immun. 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 μg/ml per dose, more preferably 0.1-500 μg/ml per dose, and most preferably 10-300 μg/ml per dose.

### 6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large genome can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

## ILLUSTRATIVE EXAMPLES

## LIBRARIES AND SEQUENCING

### 1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics 2:*231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P0, that any given base in a sequence of size L, in nucleotides, is not sequenced after a certain amount, n, in nucleotides, of random sequence has been determined can be calculated by the equation P0 = e-m, where m is L/n, the fold coverage. For instance, for a genome of 2.8 Mb, m=1 when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, P0 = e-1 = 0.37. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L, in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G, is determined by the equation G = Le-m, and the average gap size, g, follows the equation, g = L/n. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

### 2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

*Enterococcus faecalis* DNA is prepared by phenol extraction. A mixture containing 200 μg DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 μl TE buffer.

To create blunt-ends, a 100 μl aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 μl BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 μl TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the DNA. DNA is ethanol precipitated and redissolved in 20 μl of TE buffer for ligation to vector.

A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contains 2 μg of DNA fragments, 2 μg pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr. The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20 μl TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, *etc.* The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20 μl TE. The v+I DNA then is blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 ul) containing the v+I linears, 500 μM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20 μl TE. The final ligation to produce circles is carried out in a 50 μl reaction containing 5 μl of v+I linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E. coli* host cells deficient in all recombination and restriction functions (A. Greener, *Strategies 3 (1)*:5 (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating is carried out as follows. A 100 µl aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 µl aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1 µl aliquot of the final ligation is added to the cells and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and placed back on ice for 2 min. The outgrowth period in liquid culture is eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgC12 (1 M), and 1 ml MgSO4/100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10 µl aliquot of transformation.

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

### 3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science 252*:1651 (1991); Adams *et al.*, *Nature 355*:632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from an *Enterococcus faecalis* lambda genomic library in the vector DASH II (Stratagene). In particular, *Enterococcus faecalis* DNA (> 100 kb) is partially digested in a reaction mixture (200 ul) containing 50 µg DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and fractionated by sucrose density gradient centrifugation. Fractions of the sucrose gradient containing 15 to 25 kb are recovered in a final volume of 6 ul. One µl of fragments is used with 1 µl of lambda DASHII vector (Stratagene) in the recommended ligation reaction. One µl of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage are plated directly without amplification from the packaging mixture (after dilution with 500 µl of recommended SM buffer and chloroform treatment). Yield is about 2.5x103 pfu/ul. An amplified library is prepared by infecting restructure NM539 host E. coli cells eitn approximately 1x104 phage particles and recovering the progeny phages particles. The recovered phage is stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1x109 pfu/ml.

For high throughput sequencing of individual lambda phage clones, liquid lysates (100 µl) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature 368*:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.*, Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

### 4. Protocol for Automated Cycle Sequencing

The sequencing was carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (i.*e.*., one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR- generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

## INFORMATICS

### 1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen is based on a Unix platform, it was necessary to design and implement a variety of multi- user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

### 2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments is employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 104 fragments, the algorithm builds a hash table of 10 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology 164:*765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library).

The process resulted in 982 contigs as represented by SEQ ID NOs:1-982.

### 3. Identifying Genes

The predicted coding regions of the *Enterococcus faecalis* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all *Enterococcus faecali* nucleotide sequences from GenBank (March, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

## ILLUSTRATIVE APPLICATIONS

### 1. Production of an Antibody to a *Enterococcus faecalis* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

### 2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature 256*:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol. 70:*419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al., Basic Methods in Molecular Biology,* Elsevier, New York. Section 21-2 (1989).

### 3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al., J. Clin.* Endocrinol. Metab. 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology,* Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0. 1 to 0. 2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of enterococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.

### 4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Enterococcus faecalis* genome, such as those of Tables 1-3 and SEQ ID NOS:1-982 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

### 5. Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convienent source for obtaining a *E. faecalis* strain although a wide varity of strains *E. faecalis* strains can be used which are known in the art.

*E. faecalis* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, ished two times with TES (3OmM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in

SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with $^{32}$P-$\gamma$-ATP using T4 polynucleotide kinase and purified according to routine methods. (*See, e.g.*, Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. *See, e.g.*, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCALS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of SEQ ID NOS:1-982 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 $\mu$l of reaction mixture with 0.5 ug of the above DNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 $\mu$M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the

DNA product.

Finally, overlapping oligos of the DNA sequences of SEQ ID NOS:1-982 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

### 6(a). Expression and Purification Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragements of the present invention which were used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in SEQ ID NOS:1-982. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in SEQ ID NOS:1-982. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of SEQ ID NOS:1-982, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60 vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*.. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

The purified protein was then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM immidazole. Immidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4° C or frozen at -80° C.

Some of the polypeptide of the present invention were prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was approximately 10-20 O.D./ml. The suspension was then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4° C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant $A_{280}$ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

### 6(b). Alternative Expression and Purification Enterococcal polypeptides in E. coli

Tthe vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example . The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (*i.e.*, a "6 X His tag")) covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of SEQ ID NOS:1-982 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of SEQ ID NOS:1-982 may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragements actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragements therof.

### 6(c). Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4° C or frozen at -80° C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells ware then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x *g* for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x *g* centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x *g*) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 μm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 mm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant $A_{280}$ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

### 6(d). Cloning and Expression of E. faecalis in Other Bacteria

*E. faecalis* polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr.

Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

### 7. Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing $^{35}$S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra* ). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

### 8. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.*, Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human ß-actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLVI. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

### 9. Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. *See,e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5 X $10^8$ cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diliuted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetize briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH20 is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The method can be used to ıdentify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

### 10. Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. *See,e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitonially. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5 X $10^8$ cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diliuted 1:2 in 4% Brewer's yeast in media.
Mice are injected with the bacteria/brewer's yeast challenge intraperitonially. The Brewer's yeast solution alone is used as a control. The mice are then monitered twice daily for the first week following challenge, and once a day for the next week to ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans

and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

### Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 3 | 2 | 423 | 1226 | gb\|U24692\| | "Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds" | 99 | 229 |
| 47 | 14 | 17085 | 16216 | gb\|M81466\| | "Enterococcus faecalis RecA protein (recA) gene, partial cds" | 98 | 308 |
| 52 | 1 | 50 | 1441 | emb\|X62755\|SFNPRG | S.faecalis npr gene for NADH peroxidase | 98 | 1374 |
| 52 | 2 | 2456 | 1494 | emb\|X62755\|SFNPRG | S.faecalis npr gene for NADH peroxidase | 100 | 209 |
| 61 | 1 | 2 | 358 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 99 | 318 |
| 61 | 2 | 467 | 1975 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 98 | 1297 |
| 61 | 3 | 1749 | 1967 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 100 | 136 |
| 61 | 4 | 1990 | 2949 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D- | 100 | 960 |

## Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | | |
| 61 | 5 | 2112 | 2399 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 100 | 288 |
| 61 | 6 | 2922 | 3794 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 100 | 873 |
| 61 | 7 | 3671 | 4762 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 99 | 1092 |
| 61 | 8 | 4312 | 3860 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 100 | 453 |
| 61 | 9 | 4653 | 5783 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), | 100 | 1131 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | | |
| 61 | 10 | 5750 | 6397 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 99 | 648 |
| 61 | 11 | 7158 | 6784 | gb\|U35369\| | "Enterococcus faecalis vancomycin resistance genes, response regulator (vanRB), protein histidine kinase (vanSB), D,D-carboxypeptidase (vanYB), putative D-2-hydroxyacid dehydrogenase (vanHB), D-Ala:D-Lac ligase (vanB), and putative D,D-dipeptidase (vanX>" | 100 | 161 |
| 67 | 1 | 3 | 809 | gb\|U24692\| | "Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds" | 98 | 807 |
| 67 | 2 | 781 | 1512 | gb\|U24692\| | "Enterococcus faecalis pyrimidine biosynthesis D (pyrD) gene, complete cds" | 93 | 92 |
| 69 | 1 | 1 | 228 | gb\|U60038\| | "Enterococcus faecalis major cold-shock protein (cspA) gene, partial cds" | 100 | 136 |
| 72 | 15 | 15814 | 19737 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 92 | 2504 |
| 72 | 16 | 19739 | 20155 | emb\|X62657\|EFORF3 | E.faecalis plasmid pAD1 DNA for orf3 | 96 | 341 |
| 75 | 1 | 3 | 365 | emb\|Z19137\|EFPTSHGN | E.faecalis of ptsH gene encoding HPr | 100 | 267 |
| 83 | 12 | 8766 | 7432 | emb\|X78425\|EFPBP5 | E.faecalis pbp5 gene | 98 | 416 |
| 83 | 13 | 8869 | 9699 | emb\|X78425\|EFPBP5 | E.faecalis pbp5 gene | 99 | 819 |
| 83 | 14 | 9612 | 10913 | emb\|X78425\|EFPBP5 | E.faecalis pbp5 gene | 99 | 1203 |
| 83 | 15 | 10943 | 11746 | emb\|X78425\|EFPBP5 | E.faecalis pbp5 gene | 97 | 286 |

**Table 1: *E. faecalis* - Coding regions containing known sequences**

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 84 | 2 | 1657 | 3558 | emb\|X86176\|EFRPODDNE | E.faecalis dnaE and rpoD gene | 99 | 797 |
| 84 | 3 | 3649 | 4773 | emb\|X86176\|EFRPODDNE | E.faecalis dnaE and rpoD gene | 99 | 1125 |
| 84 | 4 | 4913 | 7000 | emb\|X86176\|EFRPODDNE | E.faecalis dnaE and rpoD gene | 99 | 301 |
| 104 | 2 | 4018 | 2900 | gb\|U36195\| | "Enterococcus faecalis pyrAa gene, partial cds" | 93 | 310 |
| 108 | 7 | 5875 | 5183 | gb\|M58002\| | "Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds" | 98 | 252 |
| 145 | 8 | 8193 | 7234 | gb\|U03756\| | "Enterococcus faecalis endocarditis specific antigen gene, complete cds" | 99 | 960 |
| 145 | 9 | 8836 | 8147 | gb\|U03756\| | "Enterococcus faecalis endocarditis specific antigen gene, complete cds" | 100 | 132 |
| 147 | 3 | 2096 | 3418 | emb\|X68847\|SFNOXAA | S.faecalis nox gene for NADH oxidase | 99 | 1301 |
| 154 | 4 | 2160 | 2492 | emb\|X17092\|PPRRA | Plasmid pAM-beta-1 (from S.faecalis) replication region DNA | 93 | 294 |
| 154 | 10 | 5935 | 6294 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 99 | 355 |
| 154 | 11 | 6279 | 6584 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 98 | 89 |
| 154 | 12 | 7882 | 7097 | gb\|U86375\| | "Enterococcus faecalis ermB regulator and adenine methylase (ermB) genes, complete cds" | 99 | 736 |
| 154 | 13 | 8750 | 8043 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 99 | 498 |
| 159 | 1 | 158 | 1483 | gb\|M58002\| | "Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds" | 98 | 1323 |
| 159 | 2 | 807 | 157 | gb\|M58002\| | "Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds" | 99 | 651 |
| 159 | 3 | 1395 | 2192 | gb\|M58002\| | "Streptococcus faecalis bacterial cell wall hydrolase gene, complete cds" | 93 | 350 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 216 | 2 | 282 | 1841 | gb\|M90060\| | "Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds" | 81 | 1558 |
| 216 | 4 | 2809 | 2967 | gb\|M90060\| | "Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds" | 86 | 132 |
| 216 | 5 | 2940 | 4244 | gb\|M90060\| | "Streptococcus faecalis H+ ATPase a (atpB),b (atpF),c (atpE),alpha (atpA), beta (atpD),gamma (atpG),delta (atpH),and epsilon (atpC) subunits, complete cds" | 83 | 1293 |
| 238 | 3 | 1814 | 2218 | gb\|M38386\| | "Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase" | 96 | 302 |
| 238 | 4 | 2182 | 2670 | gb\|M38386\| | "Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase" | 98 | 480 |
| 238 | 5 | 2634 | 3839 | gb\|M38386\| | "Streptococcus faecalis mtlF enzymeIII, mannitol-mtlD-phosphate- dehydrogenase" | 96 | 459 |
| 261 | 2 | 1397 | 510 | emb\|Z12296\|EFSPREG | E.faecalis sprE gene for serine proteinase homologue | 98 | 888 |
| 261 | 3 | 2474 | 1413 | dbj\|D85393\|ENEGE1E | "Enterococcus faecalis DNA for gelatinase, complete cds" | 98 | 1051 |
| 261 | 4 | 2974 | 2417 | dbj\|D85393\|ENEGE1E | "Enterococcus faecalis DNA for gelatinase, complete cds" | 97 | 516 |
| 275 | 3 | 1472 | 1044 | gb\|L23802\| | "Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region" | 98 | 422 |
| 275 | 4 | 1581 | 2018 | gb\|L23802\| | "Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins | 97 | 438 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region" | | |
| 275 | 5 | 2789 | 2148 | gb\|L23802\| | "Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region" | 98 | 642 |
| 275 | 6 | 3475 | 2660 | gb\|L23802\| | "Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD) genes, complete cds with repeat region" | 98 | 790 |
| 287 | 2 | 1565 | 558 | emb\|X17092\|PPRRA | Plasmid pAM-beta-1 (from S.faecalis) replication region DNA | 97 | 991 |
| 287 | 3 | 2049 | 1582 | emb\|X17092\|PPRRA | Plasmid pAM-beta-1 (from S.faecalis) replication region DNA | 97 | 461 |
| 287 | 6 | 2639 | 3346 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 99 | 498 |
| 294 | 11 | 4519 | 4211 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 100 | 50 |
| 302 | 1 | 1 | 1755 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 sea1 gene and orfy | 83 | 1755 |
| 302 | 2 | 2310 | 2687 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 100 | 378 |
| 302 | 3 | 2865 | 3329 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 99 | 463 |
| 316 | 4 | 2724 | 2110 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 100 | 248 |
| 346 | 5 | 2224 | 2880 | emb\|X62755\|SFNPRG | S.faecalis npr gene for NADH peroxidase | 98 | 351 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 349 | 2 | 686 | 907 | dbj\|D78257\|D78257 | "Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds" | 83 | 200 |
| 355 | 1 | 3 | 1166 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 97 | 1100 |
| 355 | 2 | 1102 | 1548 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 94 | 432 |
| 355 | 3 | 1663 | 2037 | emb\|X62657\|EFORF3 | E.faecalis plasmid pAD1 DNA for orf3 | 99 | 337 |
| 355 | 4 | 2035 | 2445 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 99 | 411 |
| 355 | 5 | 2558 | 2851 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 96 | 280 |
| 355 | 6 | 2838 | 3299 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 97 | 430 |
| 355 | 7 | 3236 | 3739 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 97 | 279 |
| 355 | 8 | 3696 | 4529 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 97 | 537 |
| 355 | 9 | 4587 | 5870 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 98 | 718 |
| 355 | 10 | 5843 | 6490 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 99 | 224 |
| 355 | 11 | 6471 | 6890 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 96 | 361 |
| 355 | 12 | 6881 | 7204 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 98 | 324 |
| 355 | 13 | 7191 | 8231 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 98 | 984 |
| 355 | 14 | 8218 | 8496 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 99 | 279 |
| 355 | 15 | 8412 | 8885 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading | 100 | 474 |

**Table 1:** ***E. faecalis* - Coding regions containing known sequences**

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | frames" | | |
| 355 | 17 | 9479 | 9952 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 98 | 417 |
| 365 | 1 | 3 | 380 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 100 | 248 |
| 370 | 1 | 1 | 1299 | dbj\|D78016\|ENEPPD1A | "Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds" | 73 | 1267 |
| 407 | 3 | 963 | 2162 | gb\|U38590\| | "Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds" | 98 | 257 |
| 407 | 5 | 3811 | 4131 | gb\|U38590\| | "Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds" | 86 | 317 |
| 417 | 1 | 42 | 419 | gb\|U00681\| | "Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds" | 98 | 304 |
| 417 | 2 | 313 | 41 | gb\|U00681\| | "Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds" | 97 | 198 |
| 417 | 3 | 440 | 754 | gb\|U00681\| | "Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds" | 100 | 219 |
| 426 | 1 | 112 | 462 | emb\|Z49243\|EF4110SOD | E.faecalis partial sod gene for superoxide dismutase (strain=BM4110) | 98 | 291 |
| 426 | 2 | 628 | 419 | emb\|Z49243\|EF4110SOD | E.faecalis partial sod gene for superoxide dismutase (strain=BM4110) | 100 | 148 |
| 426 | 3 | 456 | 725 | emb\|Z49243\|EF4110SOD | E.faecalis partial sod gene for superoxide dismutase (strain=BM4110) | 100 | 148 |
| 429 | 1 | 840 | 79 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 98 | 737 |
| 429 | 2 | 1087 | 767 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 99 | 321 |
| 429 | 4 | 2765 | 2460 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 | 98 | 89 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | tetracycline resistant (tetL) gene, complete cds" | | |
| 429 | 5 | 3166 | 2750 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 99 | 413 |
| 435 | 5 | 2731 | 2324 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 97 | 97 |
| 459 | 2 | 1330 | 1067 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 248 |
| 506 | 1 | 1242 | 4 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 99 | 1144 |
| 514 | 3 | 1496 | 1113 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 100 | 248 |
| 527 | 2 | 1733 | 1371 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 98 | 153 |
| 544 | 1 | 309 | 4 | gb\|U38590\| | "Enterococcus faecalis plasmid pCF10 PrgN, PrgO, and PrgP genes, complete cds" | 95 | 306 |
| 561 | 1 | 3 | 761 | dbj\|D78016\|ENEPPD1A | "Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds" | 77 | 528 |
| 561 | 2 | 772 | 1566 | gb\|U00681\| | "Enterococcus faecalis plasmid pAD1 TraB (traB) gene, complete cds (traC) and (repA) genes, partial cds" | 99 | 795 |
| 566 | 3 | 874 | 2037 | dbj\|D78016\|ENEPPD1A | "Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds" | 90 | 1160 |
| 581 | 1 | 398 | 3 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading | 100 | 393 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | frames" | | |
| 581 | 2 | 908 | 540 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 100 | 369 |
| 597 | 1 | 573 | 7 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 99 | 566 |
| 597 | 2 | 1247 | 516 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 97 | 701 |
| 604 | 7 | 3265 | 2903 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 100 | 143 |
| 618 | 1 | 1 | 534 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 470 |
| 622 | 1 | 864 | 16 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 849 |
| 622 | 2 | 1317 | 862 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 256 |
| 622 | 3 | 1586 | 1311 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 248 |
| 624 | 6 | 5641 | 8001 | gb\|U66286\| | "Enterococcus faecalis gyrase A (gyrA) gene, partial cds" | 98 | 219 |
| 635 | 1 | 516 | 953 | dbj\|D78257\|D78257 | "Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds" | 94 | 404 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 635 | 2 | 920 | 1222 | dbj\|D78257\|D78257 | "Enterococcus faecalis plasmid pYI17 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds" | 83 | 299 |
| 637 | 1 | 3 | 545 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 92 | 506 |
| 658 | 2 | 1198 | 365 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 100 | 819 |
| 658 | 3 | 1446 | 1189 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 98 | 258 |
| 664 | 1 | 490 | 65 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 sea1 gene and orfy | 88 | 423 |
| 664 | 2 | 737 | 417 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 sea1 gene and orfy | 94 | 321 |
| 743 | 1 | 561 | 4 | dbj\|D78016\|ENEPPD1A | "Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, iPD1, TRAE, TRAF, complete cds and partial cds" | 87 | 305 |
| 747 | 2 | 1139 | 324 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 99 | 691 |
| 747 | 3 | 577 | 783 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 100 | 207 |
| 747 | 4 | 1474 | 1133 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 99 | 248 |
| 777 | 1 | 401 | 3 | gb\|M38052\| | "Enterococcus faecalis cytolysin B transport protein gene, complete cds" | 100 | 335 |
| 816 | 1 | 793 | 512 | gb\|M13771\| | "Streptococcus faecalis 6'-aminoglycoside acetyltransferase phosphotransferase (AAC(6')-APH(2')) bifunctional resistance protein, complete cds" | 100 | 243 |
| 842 | 1 | 418 | 89 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 91 | 303 |
| 842 | 2 | 856 | 605 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 sea1 gene and orfy | 92 | 246 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| 847 | 1 | 1481 | 3 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 92 | 1479 |
| 864 | 1 | 36 | 1106 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 93 | 945 |
| 864 | 2 | 1571 | 3550 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 96 | 1979 |
| 872 | 1 | 263 | 3 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 98 | 261 |
| 874 | 1 | 833 | 693 | dbj\|D31675\|ENE16RNA8 | "Enterococcus faecalis 16S ribosomal RNA, partial sequence" | 100 | 98 |
| 878 | 1 | 302 | 30 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 94 | 94 |
| 878 | 2 | 263 | 445 | gb\|U17153\| | "Enterococcus faecalis plasmid pjh1 tetracycline resistant (tetL) gene, complete cds" | 99 | 181 |
| 921 | 1 | 748 | 26 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 95 | 612 |
| 929 | 1 | 484 | 2 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 99 | 409 |
| 946 | 1 | 3 | 422 | emb\|X62657\|EFORF3 | E.faecalis plasmid pAD1 DNA for orf3 | 99 | 341 |
| 946 | 2 | 420 | 830 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 98 | 411 |
| 946 | 3 | 866 | 1123 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 96 | 230 |
| 947 | 1 | 112 | 498 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 96 | 378 |
| 951 | 1 | 484 | 26 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 seal gene and orfy | 95 | 353 |
| 956 | 1 | 3 | 545 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 96 | 543 |
| 956 | 2 | 524 | 721 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 94 | 161 |
| 957 | 1 | 616 | 2 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading frames" | 99 | 615 |
| 957 | 2 | 42 | 686 | emb\|X96977\|EFPAD1ORF | "E.faecalis plasmid pAD1, open reading | 99 | 595 |

Table 1: *E. faecalis* - Coding regions containing known sequences

| Contig ID | Orf ID | Start (nt) | Stop (nt) | Match Accession | Match Gene Name | Percent Indent | HSP nt length |
|---|---|---|---|---|---|---|---|
| | | | | | frames" | | |
| 968 | 1 | 1 | 456 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 96 | 366 |
| 968 | 2 | 339 | 641 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 95 | 158 |
| 968 | 3 | 395 | 658 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 94 | 126 |
| 977 | 1 | 5 | 943 | emb\|X17214\|SFPASA1 | S. faecalis plasmid pAD1 asa1 gene for aggregation substance and ORF 1 | 99 | 847 |
| 982 | 1 | 376 | 2 | emb\|X62658\|EFSEA1 | E.faecalis plasmid pAD1 sea1 gene and orfy | 95 | 365 |
| 985 | 1 | 85 | 471 | emb\|X62656\|EFASP1 | "E.faecalis plasmid pPD1 asp1 and URFs pd57, pd125 and pd113 genes" | 91 | 362 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 137 | 3 | 3208 | 2003 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 154 | 14 | 9166 | 9750 | gi\|141861 | traA gene product [Plasmid pAD1] | 100 | 100 |
| 276 | 16 | 11268 | 11047 | gnl\|PID\|e284733 | C34B7.2 [Caenorhabditis elegans] | 100 | 71 |
| 287 | 1 | 485 | 234 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 287 | 7 | 3454 | 3765 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 292 | 6 | 3001 | 4185 | gi\|488330 | alpha-amylase [unidentified cloning vector] | 100 | 100 |
| 429 | 3 | 2013 | 1654 | gi\|141863 | regulatory protein [Plasmid pAD1] | 100 | 100 |
| 604 | 3 | 1243 | 1043 | gi\|559860 | clyLs [Plasmid pAD1] | 100 | 98 |
| 604 | 4 | 1492 | 1268 | gi\|559859 | clyLl [Plasmid pAD1] | 100 | 100 |
| 656 | 7 | 7592 | 6834 | gi\|488339 | alpha-amylase [unidentified cloning vector] | 100 | 100 |
| 658 | 1 | 312 | 4 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 674 | 3 | 1236 | 1589 | gi\|1196996 | unknown protein [Transposon Tn10] | 100 | 98 |
| 700 | 1 | 375 | 4 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 961 | 1 | 1 | 450 | gi\|152947 | transposase [Staphylococcus aureus] | 100 | 100 |
| 72 | 17 | 20153 | 21040 | gi\|150556 | surface protein [Plasmid pCF10] | 99 | 99 |
| 99 | 5 | 3117 | 1933 | gi\|1006839 | malic enzyme [Streptococcus bovis] | 99 | 99 |
| 154 | 3 | 1955 | 1491 | gi\|149482 | transposase [Lactococcus lactis] | 99 | 99 |
| 326 | 3 | 3030 | 1774 | pir\|S16989\|S16989 | dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Enterococcus faecalis | 99 | 98 |
| 407 | 6 | 4636 | 4235 | gi\|141859 | replication-associated protein [Plasmid pAD1] | 99 | 99 |
| 692 | 1 | 3 | 485 | gi\|559861 | clyM [Plasmid pAD1] | 99 | 99 |
| 99 | 6 | 3904 | 3134 | gi\|1146122 | L-malate permease [Streptococcus bovis] | 98 | 98 |
| 326 | 4 | 3358 | 3002 | pir\|S16989\|S16989 | dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Enterococcus faecalis | 98 | 97 |
| 346 | 1 | 606 | 4 | gi\|1146122 | L-malate permease [Streptococcus bovis] | 98 | 98 |
| 367 | 31 | 14415 | 13999 | gi\|1644226 | ribosomal protein S10 [Bacillus subtilis] | 98 | 88 |
| 367 | 6 | 2797 | 2495 | gi\|142459 | initiation factor 1 [Bacillus subtilis] | 97 | 88 |
| 407 | 9 | 5454 | 4894 | gi\|141858 | replication-associated protein [Plasmid | 97 | 97 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | pAD1] | | |
| 497 | 6 | 3514 | 3762 | gi\|532552 | ORF19 [Enterococcus faecalis] | 97 | 87 |
| 558 | 1 | 1 | 399 | gi\|46638 | ORF 2 (AA 1 - 236) [Staphylococcus aureus] | 97 | 97 |
| 829 | 1 | 169 | 2 | gnl\|PID\|e283110 | femD [Staphylococcus aureus] | 97 | 86 |
| 407 | 8 | 4970 | 4599 | gi\|141858 | replication-associated protein [Plasmid pAD1] | 96 | 96 |
| 777 | 2 | 1102 | 380 | gi\|559861 | clyM [Plasmid pAD1] | 96 | 96 |
| 23 | 33 | 20797 | 21126 | gnl\|PID\|e223402 | DNA topoisomerase IV C subunit [Streptococcus pneumoniae] | 95 | 80 |
| 32 | 5 | 3454 | 3071 | gi\|147194 | phnA protein [Escherichia coli] | 95 | 87 |
| 95 | 8 | 5493 | 6875 | gi\|391682 | Na+ -ATPase beta subunit [Enterococcus hirae] | 95 | 89 |
| 138 | 25 | 16587 | 16745 | gi\|143136 | L-lactate dehydrogenase [Bacillus megaterium] | 95 | 70 |
| 367 | 20 | 9198 | 8797 | gi\|40150 | L14 protein (AA 1-122) [Bacillus subtilis] | 95 | 90 |
| 367 | 21 | 9519 | 9223 | gi\|1044973 | ribosomal protein L17 [Bacillus subtilis] | 95 | 89 |
| 439 | 2 | 846 | 1241 | gi\|488334 | alpha-amylase [unidentified cloning vector] | 95 | 94 |
| 604 | 1 | 792 | 4 | gi\|559861 | clyM [Plasmid pAD1] | 95 | 93 |
| 722 | 1 | 1 | 504 | gi\|47453 | ribosomal protein S12 [Streptococcus pneumoniae] | 95 | 94 |
| 17 | 8 | 7317 | 7676 | gi\|532554 | ORF21 [Enterococcus faecalis] | 94 | 86 |
| 95 | 2 | 1288 | 1791 | gi\|416405 | Na+-ATPase K subunit [Enterococcus hirae] | 94 | 88 |
| 97 | 3 | 2481 | 1432 | gi\|1750264 | heat shock protein 70 [Streptococcus pneumoniae] | 94 | 90 |
| 117 | 5 | 2700 | 3842 | gi\|467376 | unknown [Bacillus subtilis] | 94 | 89 |
| 327 | 3 | 3283 | 3762 | gi\|153566 | ORF (19K protein) [Enterococcus faecalis] | 94 | 87 |
| 327 | 5 | 4782 | 5054 | gi\|153568 | H+ ATPase [Enterococcus faecalis] | 94 | 82 |
| 387 | 4 | 3608 | 1728 | gi\|153661 | translational initiation factor IF2 [Enterococcus faecium] sp\|P18311\|IF2_ENTFC INITIATION FACTOR IF-2. | 94 | 88 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 455 | 1 | 2 | 259 | gi\|532549 | ORF16 [Enterococcus faecalis] | 94 | 82 |
| 97 | 2 | 1444 | 677 | gi\|450684 | dnaK gene product [Lactococcus lactis] | 93 | 83 |
| 188 | 2 | 1690 | 1911 | gi\|43865 | nifJ gene product [Klebsiella pneumoniae] | 93 | 78 |
| 216 | 6 | 4234 | 4680 | gi\|153574 | H+ ATPase [Enterococcus faecalis] | 93 | 86 |
| 298 | 2 | 2798 | 1221 | gi\|143012 | GMP synthetase [Bacillus subtilis] | 93 | 86 |
| 329 | 2 | 1538 | 771 | gi\|153826 | adhesin B [Streptococcus sanguis] | 93 | 83 |
| 367 | 15 | 7675 | 7247 | gi\|1044978 | ribosomal protein S8 [Bacillus subtilis] | 93 | 82 |
| 722 | 2 | 527 | 1030 | gi\|1644222 | ribosomal protein S7 [Bacillus subtilis] | 93 | 83 |
| 803 | 1 | 657 | 151 | gi\|1196998 | unknown protein [Transposon Tn10] | 93 | 93 |
| 962 | 1 | 130 | 636 | gi\|152947 | transposase [Staphylococcus aureus] | 93 | 92 |
| 237 | 12 | 6056 | 6385 | gi\|963038 | ArpU [Enterococcus hirae] | 92 | 76 |
| 309 | 4 | 8218 | 4541 | gi\|402363 | RNA polymerase beta-subunit [Bacillus subtilis] sp\|P37870\|RPOB_BACSU DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC .7.7.6) (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT). | 92 | 82 |
| 329 | 4 | 2529 | 1717 | gi\|310632 | hydrophobic membrane protein [Streptococcus gordonii] sp\|P42361\|P29K_STRGC 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1). | 92 | 78 |
| 367 | 4 | 1942 | 1544 | gi\|142462 | ribosomal protein S11 [Bacillus subtilis] | 92 | 82 |
| 367 | 8 | 3648 | 3457 | pir\|C44859\|C44859 | adenylate kinase - Bacillus sp. (fragment) | 92 | 88 |
| 367 | 12 | 6183 | 5641 | gi\|1044981 | ribosomal protein S5 [Bacillus subtilis] | 92 | 81 |
| 367 | 17 | 8427 | 7885 | pir\|A29102\|R5BS5F | ribosomal protein L5 - Bacillus stearothermophilus | 92 | 83 |
| 527 | 1 | 1404 | 373 | gi\|153092 | replication protein [Staphylococcus aureus] | 92 | 81 |
| 701 | 1 | 2 | 352 | gi\|143793 | tyrosyl-tRNA synthetase [Bacillus caldotenax] | 92 | 74 |
| 23 | 28 | 17420 | 17566 | sp\|P45692\|EUTX_SALTY | ETHANOLAMINE UTILIZATION PROTEIN EUTX (FRAGMENT). | 91 | 73 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 57 | 5 | 4129 | 4701 | gi\|1595810 | type-I signal peptidase SpsB [Staphylococcus aureus] | 91 | 67 |
| 57 | 12 | 13281 | 13970 | gnl\|PID\|e254999 | phenylalany-tRNA synthetase beta subunit [Bacillus subtilis] | 91 | 75 |
| 156 | 5 | 4609 | 6474 | gi\|1303804 | YqeQ [Bacillus subtilis] | 91 | 79 |
| 216 | 3 | 1848 | 2765 | gi\|153572 | H+ ATPase [Enterococcus faecalis] | 91 | 81 |
| 367 | 24 | 10802 | 10128 | gi\|1165309 | S3 [Bacillus subtilis] | 91 | 78 |
| 415 | 1 | 452 | 883 | pir\|B56272\|B56272 | probable pheromone-responsive regulatory protein R - Enterococcus faecalis plasmid pCF10 | 91 | 90 |
| 466 | 2 | 1313 | 2065 | gi\|142443 | adenylosuccinate synthetase [Bacillus subtilis] sp\|P29726\|PURA_BACSU ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) IMP--ASPARTATE LIGASE). | 91 | 79 |
| 545 | 1 | 1 | 345 | gi\|532549 | ORF16 [Enterococcus faecalis] | 91 | 80 |
| 572 | 1 | 8 | 652 | gi\|347998 | uracil phosphoribosyltransferase [Streptococcus salivarius] sp\|P36399\|UPP_STRSL PROBABLE URACIL PHOSPHORIBOSYLTRANSFERASE (EC .4.2.9) (UMP PYROPHOSPHORYLASE) (UPRTASE). | 91 | 78 |
| 599 | 1 | 8 | 343 | gi\|42029 | ORF1 gene product [Escherichia coli] | 91 | 75 |
| 600 | 2 | 585 | 779 | pir\|B48396\|B48396 | ribosomal protein L33 - Bacillus stearothermophilus | 91 | 81 |
| 652 | 1 | 394 | 2 | gi\|535662 | transposase [Insertion sequence IS1251] | 91 | 81 |
| 1 | 4 | 3465 | 2557 | gi\|1644224 | elongation factor Tu [Bacillus subtilis] | 90 | 83 |
| 17 | 19 | 14844 | 17297 | gi\|532549 | ORF16 [Enterococcus faecalis] | 90 | 77 |
| 52 | 3 | 2650 | 2811 | gi\|473902 | alpha-acetolactate synthase [Lactococcus lactis] | 90 | 68 |
| 74 | 9 | 5870 | 5469 | gi\|1653508 | hypothetical protein [Synechocystis sp.] | 90 | 52 |
| 75 | 3 | 1177 | 2091 | gi\|153615 | phosphoenolpyruvate:sugar phosphotransferase system enzyme I Streptococcus salivarius] | 90 | 83 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 117 | 10 | 6591 | 8126 | gi\|924848 | inosine monophosphate dehydrogenase [Streptococcus pyogenes] pir\|JC4372\|JC4372 IMP dehydrogenase (EC 1.1.1.205) - Streptococcus yogenes | 90 | 80 |
| 276 | 1 | 577 | 95 | gi\|530798 | LysB [Bacteriophage phi-LC3] | 90 | 72 |
| 287 | 5 | 2611 | 2441 | gi\|1333835 | copS gene product [Streptococcus pyogenes] | 90 | 78 |
| 290 | 1 | 1 | 708 | gi\|897795 | 30S ribosomal protein [Pediococcus acidilactici] sp\|P49668\|RS2_PEDAC 30S RIBOSOMAL PROTEIN S2. | 90 | 75 |
| 309 | 3 | 4401 | 1093 | gnl\|PID\|e187579 | DNA-directed RNA polymerase [Listeria innocua] | 90 | 81 |
| 367 | 22 | 9731 | 9513 | pir\|A02825\|R5BS29 | ribosomal protein L29 - Bacillus stearothermophilus | 90 | 76 |
| 452 | 4 | 2224 | 2508 | gi\|434759 | ORF [Homo sapiens] | 90 | 54 |
| 455 | 2 | 2776 | 323 | gi\|532549 | ORF16 [Enterococcus faecalis] | 90 | 77 |
| 623 | 1 | 3 | 221 | gi\|460259 | enolase [Bacillus subtilis] | 90 | 80 |
| 624 | 5 | 3612 | 5615 | gnl\|PID\|e208213 | DNA gyrase [Streptococcus pneumoniae] | 90 | 81 |
| 853 | 2 | 752 | 282 | gnl\|PID\|e13389 | translation initiation factor IF3 (AA 1-172) [Bacillus stearothermophilus] | 90 | 82 |
| 966 | 1 | 1 | 462 | gi\|532549 | ORF16 [Enterococcus faecalis] | 90 | 83 |
| 1 | 3 | 2596 | 2219 | gi\|1661195 | elongation factor-Tu [Streptococcus mutans] | 89 | 78 |
| 1 | 5 | 4314 | 3556 | gi\|1644223 | elongation factor G [Bacillus subtilis] | 89 | 79 |
| 23 | 21 | 13990 | 14295 | gi\|466518 | pduA [Salmonella typhimurium] | 89 | 75 |
| 23 | 32 | 19927 | 20799 | gnl\|PID\|e208211 | DNA topoisomerase IV [Streptococcus pneumoniae] | 89 | 83 |
| 42 | 2 | 349 | 1989 | gi\|287871 | groEL gene product [Lactococcus lactis] | 89 | 79 |
| 45 | 15 | 11835 | 12167 | gi\|150554 | surface exclusion protein [Plasmid pCF10] | 89 | 68 |
| 53 | 2 | 685 | 1797 | gnl\|PID\|e221213 | ClpX protein [Bacillus subtilis] | 89 | 81 |
| 86 | 4 | 3374 | 4024 | gi\|537286 | triosephosphate isomerase [Lactococcus lactis] | 89 | 78 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 95 | 7 | 3677 | 5506 | gi\|912449 | Na+ -ATPase alpha subunit [Enterococcus hirae] | 89 | 80 |
| 128 | 18 | 11348 | 11013 | gi\|466473 | cellobiose phosphotransferase enzyme II' [Bacillus tearothermophilus] | 89 | 60 |
| 132 | 1 | 180 | 2180 | gi\|153854 | uvs402 protein [Streptococcus pneumoniae] | 89 | 78 |
| 342 | 1 | 783 | 4 | gi\|1041115 | TRAC [Plasmid pPD1] | 89 | 79 |
| 367 | 23 | 10146 | 9691 | sp\|P14577\|RL16_BACSU | 50S RIBOSOMAL PROTEIN L16. | 89 | 80 |
| 367 | 27 | 12377 | 11541 | gi\|1165306 | L2 [Bacillus subtilis] | 89 | 79 |
| 435 | 4 | 2424 | 2215 | gi\|559863 | clyA [Plasmid pAD1] | 89 | 89 |
| 466 | 3 | 1972 | 2736 | gi\|467328 | adenylosuccinate synthetase [Bacillus subtilis] | 89 | 75 |
| 512 | 3 | 999 | 1607 | gi\|1477776 | ClpP [Bacillus subtilis] | 89 | 73 |
| 518 | 1 | 1 | 174 | gi\|786163 | Ribosomal Protein L10 [Bacillus subtilis] | 89 | 76 |
| 604 | 2 | 1000 | 713 | gi\|559861 | clyM [Plasmid pAD1] | 89 | 89 |
| 615 | 2 | 888 | 691 | gi\|467469 | unknown [Bacillus subtilis] | 89 | 75 |
| 677 | 2 | 992 | 429 | gi\|1389732 | S-adenosylmethionine synthetase [Bacillus subtilis] | 89 | 76 |
| 677 | 3 | 1315 | 950 | gi\|1020317 | S-adenosylmethionine synthetase [Staphylococcus aureus] | 89 | 73 |
| 722 | 3 | 1102 | 1278 | pir\|PW0010\|PW0010 | translation elongation factor G - Bacillus stearothermophilus (fragment) | 89 | 72 |
| 850 | 1 | 464 | 3 | gi\|142521 | deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl\|PID\|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis] | 89 | 72 |
| 17 | 5 | 3711 | 4751 | gi\|532554 | ORF21 [Enterococcus faecalis] | 88 | 72 |
| 37 | 5 | 3322 | 3717 | gi\|1216488 | uncharacterized open reading frame; hypothetical protein displaying similarity to a Bacillus subtilis hypothetical protein (Ylm [Streptococcus mutans] | 88 | 75 |
| 39 | 6 | 2454 | 2630 | sp\|P49865\|NTPR_ENT | NTPR PROTEIN (FRAGMENT). | 88 | 77 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | HR | | | |
| 48 | 3 | 1740 | 2666 | gi\|557492 | dihydroxynapthoic acid (DHNA) synthetase [Bacillus subtilis] gi\|143186 dihydroxynapthoic acid (DHNA) synthetase [Bacillus ubtilis] | 88 | 75 |
| 63 | 5 | 2753 | 3607 | gi\|1064814 | homologous to sp:PHOP_BACSUB [Bacillus subtilis] | 88 | 77 |
| 86 | 2 | 1004 | 2047 | gi\|153763 | plasmin receptor [Streptococcus pyogenes] | 88 | 79 |
| 104 | 6 | 6431 | 6213 | gi\|431231 | uracil permease [Bacillus caldolyticus] | 88 | 60 |
| 110 | 19 | 18174 | 16891 | gi\|217040 | acid glycoprotein [Streptococcus pyogenes] | 88 | 72 |
| 145 | 10 | 9040 | 8834 | gi\|393268 | 29-kiloDalton protein [Streptococcus pneumoniae] sp\|P42362\|P29K_STRPN 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1). | 88 | 71 |
| 151 | 1 | 1620 | 316 | gi\|143366 | adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir\|C29326\|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis | 88 | 78 |
| 171 | 10 | 9676 | 10119 | gi\|1591672 | phosphate transport system ATP-binding protein [Methanococcus jannaschii] | 88 | 63 |
| 190 | 3 | 1997 | 975 | gi\|532554 | ORF21 [Enterococcus faecalis] | 88 | 76 |
| 229 | 6 | 5712 | 5954 | gi\|143648 | ribosomal protein L28 [Bacillus subtilis] | 88 | 70 |
| 270 | 2 | 895 | 1869 | gi\|1303828 | YqfJ [Bacillus subtilis] | 88 | 75 |
| 275 | 7 | 3761 | 3552 | gi\|425474 | SMDR1 [Schistosoma mansoni] | 88 | 72 |
| 293 | 1 | 614 | 3 | gi\|1783246 | highly homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis] | 88 | 80 |
| 367 | 1 | 485 | 72 | gi\|142464 | ribosomal protein L17 [Bacillus subtilis] | 88 | 76 |
| 367 | 5 | 2335 | 1961 | gi\|1044989 | ribosomal protein S13 [Bacillus subtilis] | 88 | 80 |
| 367 | 16 | 7887 | 7681 | pir\|S48688\|S48688 | ribosomal protein S14 - Bacillus stearothermophilus | 88 | 83 |
| 598 | 1 | 1006 | 23 | gi\|565287 | transposase-like protein of PS3IS [thermophilic bacterium PS3] | 88 | 66 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | pir\|JC4292\|JC4292 insertion sequence element 1341 - *thermophilic acterium PS-3* | | |
| 600 | 3 | 1640 | 882 | gi\|763052 | integrase [Bacteriophage T270] | 88 | 68 |
| 669 | 1 | 2 | 514 | gi\|153801 | enzyme scr-II [Streptococcus mutans] | 88 | 75 |
| 808 | 2 | 624 | 394 | gi\|1574781 | exodeoxyribonuclease V (recB) [Haemophilus influenzae] | 88 | 77 |
| 871 | 1 | 714 | 229 | gi\|1574120 | branched-chain-amino-acid transaminase [Haemophilus influenzae] | 88 | 79 |
| 979 | 1 | 1 | 384 | gnl\|PID\|e187579 | DNA-directed RNA polymerase [Listeria innocua] | 88 | 78 |
| 983 | 1 | 34 | 282 | gi\|40026 | homologous to E.coli gidA [Bacillus subtilis] | 88 | 78 |
| 47 | 5 | 6799 | 5810 | gi\|532204 | prs [Listeria monocytogenes] | 87 | 79 |
| 69 | 3 | 2033 | 750 | gi\|1377831 | unknown [Bacillus subtilis] | 87 | 74 |
| 73 | 2 | 1432 | 167 | gi\|143434 | Rho Factor [Bacillus subtilis] | 87 | 76 |
| 76 | 5 | 2412 | 3740 | gi\|496283 | lysin [Bacteriophage Tuc2009] | 87 | 75 |
| 88 | 3 | 1600 | 2016 | gnl\|PID\|e137596 | heat shock induced protein HtpO [Lactobacillus leichmannii] | 87 | 75 |
| 89 | 7 | 6003 | 5608 | gi\|1695686 | pyruvate carboxylase [Bacillus stearothermophilus] | 87 | 77 |
| 93 | 1 | 283 | 119 | gi\|1124825 | unknown protein [Chlamydia trachomatis] | 87 | 56 |
| 104 | 1 | 2945 | 3 | gnl\|PID\|e199387 | carbamoyl-phosphate synthase [Lactobacillus plantarum] | 87 | 75 |
| 124 | 4 | 3191 | 2274 | gi\|995767 | UDP-glucose pyrophosphorylase [Streptococcus pyogenes] | 87 | 76 |
| 273 | 2 | 608 | 1108 | gi\|1184680 | polynucleotide phosphorylase [Bacillus subtilis] | 87 | 76 |
| 293 | 2 | 1020 | 532 | gi\|153741 | ATP-binding protein [Streptococcus mutans] | 87 | 74 |
| 326 | 5 | 4534 | 3533 | gi\|143378 | pyruvate decarboxylase (E-1) beta subunit [Bacillus subtilis] gi\|1377836 pyruvate decarboxylase E-1 beta subunit [Bacillus ubtilis] | 87 | 74 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 334 | 3 | 3182 | 3340 | pir\|A36324\|A36324 | growth arrest-specific protein - mouse | 87 | 50 |
| 337 | 1 | 1382 | 186 | gi\|308861 | GTG start codon [Lactococcus lactis] | 87 | 75 |
| 338 | 8 | 6925 | 5723 | gi\|149575 | L(+)-lactate dehydrogenase [Lactobacillus casei] sp\|P00343\|LDH_LACCA L-LACTATE DEHYDROGENASE (EC 1.1.1.27). {SUB -326} | 87 | 73 |
| 367 | 18 | 8782 | 8450 | pir\|A02819\|R5BS24 | ribosomal protein L24 - Bacillus stearothermophilus | 87 | 70 |
| 388 | 2 | 410 | 183 | gnl\|PID\|e225674 | unknown [Schizosaccharomyces pombe] | 87 | 75 |
| 440 | 1 | 466 | 1797 | gi\|520754 | putative [Bacillus subtilis] | 87 | 75 |
| 508 | 1 | 694 | 137 | gi\|496558 | orfX [Bacillus subtilis] | 87 | 73 |
| 654 | 3 | 530 | 802 | pir\|A47079\|A47079 | heat shock protein DnaJ - Lactococcus lactis | 87 | 70 |
| 18 | 1 | 3 | 413 | gi\|46912 | ribosomal protein L13 [Staphylococcus carnosus] | 86 | 70 |
| 18 | 2 | 406 | 819 | pir\|S08564\|R3BS9 | ribosomal protein S9 - Bacillus stearothermophilus | 86 | 73 |
| 50 | 1 | 84 | 1148 | gi\|452398 | threonine synthase [Bacillus sp.] | 86 | 74 |
| 74 | 14 | 10547 | 10080 | gi\|1314299 | ORF6; putative glutamyl-tRNA-transferase; similar to glutamyl-tRNA-transferase from Bacillus subtilis [Listeria monocytogenes] | 86 | 74 |
| 95 | 5 | 3176 | 3406 | gi\|487276 | Na+ -ATPase subunit C [Enterococcus hirae] | 86 | 62 |
| 114 | 8 | 9216 | 10313 | gi\|853776 | peptide chain release factor 1 [Bacillus subtilis] pir\|S55437\|S55437 peptide chain release factor 1 - Bacillus ubtilis | 86 | 69 |
| 115 | 2 | 501 | 899 | gi\|551879 | ORF 1 [Lactococcus lactis] | 86 | 70 |
| 164 | 26 | 25639 | 25842 | pir\|S34762\|S34762 | L-serine dehydratase beta chain - Clostridium sp. | 86 | 81 |
| 243 | 2 | 2143 | 1082 | gi\|143607 | sporulation protein [Bacillus subtilis] | 86 | 70 |
| 255 | 1 | 2 | 196 | gi\|755604 | unknown [Bacillus subtilis] | 86 | 64 |
| 257 | 3 | 3565 | 983 | gi\|928832 | ORF259; putative [Lactococcus lactis phage BK5-T] | 86 | 66 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| **Contig ID** | **ORF ID** | **Start (nt)** | **Stop (nt)** | **Match accession** | **Match gene name** | **% Sim** | **% Ident** |
|---|---|---|---|---|---|---|---|
| 273 | 3 | 943 | 1314 | gi\|1184680 | polynucleotide phosphorylase [Bacillus subtilis] | 86 | 65 |
| 288 | 2 | 554 | 1087 | gi\|153033 | tagatose 6-phosphate isomerase [Staphylococcus aureus] pir\|B38158\|B38158 galactose-6-phosphate isomerase 19K chain - taphylococcus aureus | 86 | 74 |
| 327 | 7 | 5183 | 5722 | gi\|153569 | H+ ATPase [Enterococcus faecalis] | 86 | 71 |
| 345 | 7 | 5111 | 5620 | gi\|1314294 | ORF1; putative 17 kDa protein [Listeria monocytogenes] | 86 | 63 |
| 350 | 3 | 1900 | 2781 | gi\|511015 | dihydroorotate dehydrogenase A [Lactococcus lactis] sp\|P54321\|PYDA_LACLC DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1) DIHYDROOROTATE OXIDASE A) (DHODEHASE A). | 86 | 73 |
| 363 | 3 | 3328 | 4233 | gi\|1657517 | hypothetical protein [Escherichia coli] | 86 | 59 |
| 367 | 25 | 11216 | 10851 | gi\|1165308 | L22 [Bacillus subtilis] | 86 | 68 |
| 367 | 26 | 11534 | 11220 | gi\|1165307 | S19 [Bacillus subtilis] | 86 | 77 |
| 367 | 30 | 13995 | 13453 | gi\|1165303 | L3 [Bacillus subtilis] | 86 | 75 |
| 393 | 1 | 1 | 660 | sp\|P33898\|G3P3_ECOLI | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE C (EC 1.2.1.12) (GAPDH-C). | 86 | 77 |
| 396 | 1 | 1 | 192 | gi\|944942 | RipX [Bacillus subtilis] | 86 | 77 |
| 438 | 3 | 1279 | 1560 | gi\|1001878 | CspL protein [Listeria monocytogenes] | 86 | 75 |
| 510 | 1 | 1008 | 199 | gi\|473795 | 'ORF' [Escherichia coli] | 86 | 71 |
| 510 | 2 | 1912 | 962 | gi\|473794 | 'ORF' [Escherichia coli] | 86 | 76 |
| 539 | 1 | 705 | 4 | gi\|467477 | unknown [Bacillus subtilis] | 86 | 79 |
| 570 | 2 | 2069 | 1023 | gi\|881511 | Ccpa protein [Lactobacillus casei] | 86 | 72 |
| 654 | 2 | 240 | 575 | pir\|A47079\|A47079 | heat shock protein DnaJ - Lactococcus lactis | 86 | 77 |
| 677 | 1 | 431 | 102 | gi\|1389732 | S-adenosylmethionine synthetase [Bacillus subtilis] | 86 | 80 |
| 984 | 1 | 1 | 147 | pir\|A56922\|A56922 | transcription factor shn - fruit fly (Drosophila melanogaster) | 86 | 73 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 5 | 11 | 7720 | 8487 | gi\|41015 | aspartate-tRNA ligase [Escherichia coli] | 85 | 71 |
| 34 | 2 | 2133 | 1711 | gi\|47828 | pyruvate kinase [Bacillus stearothermophilus] | 85 | 75 |
| 97 | 4 | 2666 | 2517 | pir\|S39341\|S39341 | grpE protein - Lactococcus lactis | 85 | 66 |
| 103 | 2 | 1263 | 946 | gi\|143364 | phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus ubtilis] | 85 | 68 |
| 103 | 3 | 1465 | 1169 | gi\|143364 | phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus ubtilis] | 85 | 67 |
| 129 | 3 | 2395 | 3258 | gi\|143766 | (thrSv) (EC 6.1.1.3) [Bacillus subtilis] | 85 | 67 |
| 129 | 4 | 3240 | 4445 | gi\|143766 | (thrSv) (EC 6.1.1.3) [Bacillus subtilis] | 85 | 78 |
| 188 | 1 | 86 | 1447 | gnl\|PID\|e214721 | glutamine synthetase [Staphylococcus aureus] | 85 | 71 |
| 217 | 3 | 673 | 1086 | gi\|520540 | unknown [Bacillus subtilis] | 85 | 72 |
| 241 | 2 | 1715 | 1086 | gi\|495089 | recombinase [Staphylococcus aureus] | 85 | 68 |
| 285 | 2 | 712 | 993 | gi\|40014 | pot. ORF 446 (aa 1-446) [Bacillus subtilis] | 85 | 77 |
| 293 | 3 | 1149 | 1595 | gi\|755604 | unknown [Bacillus subtilis] | 85 | 66 |
| 300 | 2 | 2738 | 2220 | gi\|289261 | comE ORF2 [Bacillus subtilis] | 85 | 72 |
| 305 | 2 | 1853 | 2695 | pir\|S09411\|S09411 | spoIIIE protein - Bacillus subtilis | 85 | 70 |
| 322 | 1 | 1 | 171 | gi\|153562 | aspartate beta-semialdehyde dehydrogenase (EC 1.2.1.11) Streptococcus mutans] | 85 | 67 |
| 327 | 4 | 4056 | 4784 | gi\|153567 | H+ ATPase [Enterococcus faecalis] | 85 | 66 |
| 367 | 10 | 5417 | 4959 | pir\|A02795\|R5BS15 | ribosomal protein L15 - Bacillus stearothermophilus | 85 | 76 |
| 383 | 3 | 3168 | 2953 | gnl\|PID\|e274577 | csp [Lactobacillus plantarum] | 85 | 79 |
| 404 | 3 | 3069 | 2101 | gi\|143402 | recombination protein (ttg start codon) [Bacillus subtilis] gi\|1303923 RecN [Bacillus subtilis] | 85 | 72 |
| 469 | 1 | 2 | 724 | gi\|508979 | GTP-binding protein [Bacillus subtilis] | 85 | 78 |
| 488 | 1 | 1 | 996 | gi\|532548 | ORF15 [Enterococcus faecalis] | 85 | 67 |
| 535 | 5 | 6468 | 4849 | gi\|634107 | kdpB [Escherichia coli] | 85 | 68 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 584 | 3 | 732 | 562 | gi\|467374 | single strand DNA binding protein [Bacillus subtilis] sp\|P37455\|SSB_BACSU SINGLE-STRAND BINDING PROTEIN (SSB) HELIX-DESTABILIZING PROTEIN). | 85 | 75 |
| 695 | 1 | 78 | 500 | gi\|499384 | orf189 [Bacillus subtilis] | 85 | 75 |
| 836 | 1 | 1 | 357 | gi\|153801 | enzyme scr-II [Streptococcus mutans] | 85 | 69 |
| 17 | 20 | 17212 | 18813 | gi\|532548 | ORF15 [Enterococcus faecalis] | 84 | 68 |
| 23 | 31 | 18728 | 19987 | gnl\|PID\|e208211 | DNA topoisomerase IV [Streptococcus pneumoniae] | 84 | 68 |
| 34 | 3 | 3112 | 2144 | gi\|143312 | 6-phospho-1-fructokinase (gtg start codon; EC 2.7.1.11) [Bacillus tearothermophilus] | 84 | 69 |
| 36 | 1 | 1 | 1152 | gi\|1644223 | elongation factor G [Bacillus subtilis] | 84 | 73 |
| 49 | 12 | 6730 | 8190 | gi\|456319 | 74kDa protein [Bacteriophage FC1] | 84 | 65 |
| 51 | 2 | 1379 | 1663 | gi\|468207 | Submitter comments: A Mg2+ transporting P-type ATPase highly omologous with mgtB ATPase at 80 min on Salmonella chromosome. ediates the influx of Mg2+ only. Transcription regulated by xtracellular Mg2+ [Salmonella typhimurium] | 84 | 71 |
| 95 | 6 | 3330 | 3707 | gi\|487277 | Na+ -ATPase subunit G [Enterococcus hirae] | 84 | 64 |
| 104 | 5 | 6250 | 5459 | gnl\|PID\|e199440 | aspartate carbamoyltransferase, aspartate transcarbamylase, carbamylaspartotranskinase [Lactobacillus plantarum] | 84 | 65 |
| 105 | 6 | 4605 | 5273 | gi\|467411 | recombination protein [Bacillus subtilis] | 84 | 65 |
| 114 | 11 | 12278 | 12997 | gi\|556886 | serine hydroxymethyltransferase [Bacillus subtilis] pir\|S49363\|S49363 serine hydroxymethyltransferase - Bacillus ubtilis | 84 | 74 |
| 117 | 2 | 705 | 1484 | gi\|580906 | B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] gi\|467381 regulation of Spo0J and Orf283 (probable) | 84 | 70 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
|  |  |  |  |  | [Bacillus ubtilis] |  |  |
| 121 | 2 | 1274 | 2119 | gi\|290643 | ATPase [Enterococcus hirae] | 84 | 67 |
| 121 | 6 | 5016 | 5219 | gi\|153765 | DNA polymerase I [Streptococcus pneumoniae] | 84 | 66 |
| 128 | 27 | 22456 | 20453 | gi\|437916 | isoleucyl-tRNA synthetase [Staphylococcus aureus] | 84 | 71 |
| 130 | 1 | 2 | 133 | gi\|1237013 | ORF2 [Bacillus subtilis] | 84 | 74 |
| 138 | 35 | 26712 | 25777 | gi\|143795 | transfer RNA-Tyr synthetase [Bacillus subtilis] | 84 | 69 |
| 164 | 28 | 26378 | 27277 | gnl\|PID\|e247026 | orf6 [Lactobacillus sake] | 84 | 72 |
| 171 | 1 | 158 | 2719 | gi\|499335 | secA protein [Staphylococcus carnosus] | 84 | 68 |
| 210 | 5 | 4870 | 3884 | gi\|950062 | hypothetical yeast protein 1 [Mycoplasma capricolum] pir\|S48578\|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment) | 84 | 75 |
| 217 | 7 | 5222 | 3546 | gi\|143597 | CTP synthetase [Bacillus subtilis] | 84 | 68 |
| 243 | 1 | 1088 | 126 | gi\|143608 | sporulation protein [Bacillus subtilis] | 84 | 70 |
| 275 | 1 | 578 | 48 | gi\|1103865 | formyl-tetrahydrofolate synthetase [Streptococcus mutans] | 84 | 72 |
| 281 | 1 | 333 | 698 | gi\|1303962 | YqjK [Bacillus subtilis] | 84 | 68 |
| 292 | 23 | 18340 | 18038 | gi\|142988 | membrane transport protein [Bacillus stearothermophilus] pir\|A42478\|A42478 glutamine transport protein glnQ - Bacillus tearothermophilus | 84 | 61 |
| 309 | 2 | 1114 | 722 | gi\|1644219 | RNA polymerase beta' subunit [Bacillus subtilis] | 84 | 72 |
| 315 | 1 | 668 | 3 | gi\|149601 | thymidylate synthase (EC 2.1.1.45) [Lactobacillus casei] | 84 | 72 |
| 334 | 6 | 5375 | 6862 | gi\|1354211 | PET112-like protein [Bacillus subtilis] | 84 | 71 |
| 338 | 10 | 7585 | 10479 | gi\|467444 | transcription-repair coupling factor [Bacillus subtilis] sp\|P37474\|MFD_BACSU TRANSCRIPTION-REPAIR COUPLING FACTOR | 84 | 68 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | (TRCF). | | |
| 338 | 14 | 12713 | 13018 | gi\|467448 | unknown [Bacillus subtilis] | 84 | 64 |
| 340 | 3 | 1068 | 2273 | gi\|40046 | phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir\|S15936\|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus | 84 | 69 |
| 375 | 2 | 1430 | 1780 | gi\|1402531 | ORF10 [Enterococcus faecalis] | 84 | 64 |
| 381 | 1 | 2 | 1279 | gnl\|PID\|e208212 | DNA topoisomerase IV [Streptococcus pneumoniae] | 84 | 67 |
| 421 | 1 | 5 | 151 | gi\|710632 | beta-glucosidase [Bacillus subtilis] | 84 | 73 |
| 421 | 3 | 1229 | 1465 | gi\|710632 | beta-glucosidase [Bacillus subtilis] | 84 | 65 |
| 445 | 1 | 1080 | 190 | gi\|46985 | glucose-1-phosphate thymidylyltransferase [Salmonella enterica] ir\|S23342\|S23342 hypothetical protein 6.1 - Salmonella choleraesuis p\|P55254\|RFBA_SALAN GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 7.7.24) (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHO | 84 | 71 |
| 466 | 9 | 10467 | 11006 | gi\|147403 | mannose permease subunit II-P-Man [Escherichia coli] | 84 | 61 |
| 497 | 2 | 469 | 1680 | gi\|1220529 | methyl transferase [Streptococcus pneumoniae] | 84 | 72 |
| 545 | 2 | 309 | 2171 | gi\|532548 | ORF15 [Enterococcus faecalis] | 84 | 68 |
| 550 | 5 | 2744 | 2265 | gi\|455528 | ORF2 [Streptococcus thermophilus bacteriophage] | 84 | 54 |
| 637 | 5 | 2679 | 3545 | gnl\|PID\|e236571 | cell wall anchoring signal [Enterococcus faecalis] | 84 | 72 |
| 653 | 3 | 1023 | 736 | gi\|1408584 | LtrC [Lactococcus lactis lactis] | 84 | 72 |
| 674 | 1 | 763 | 254 | gi\|467452 | unknown [Bacillus subtilis] | 84 | 66 |
| 788 | 1 | 165 | 500 | gi\|1196907 | daunorubicin resistance protein [Streptomyces peucetius] | 84 | 66 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 796 | 1 | 1 | 366 | gi\|496504 | orf beta [Streptococcus pyogenes] | 84 | 67 |
| 812 | 1 | 2 | 415 | gi\|511075 | ORF2 [Streptococcus agalactiae] | 84 | 73 |
| 935 | 2 | 1317 | 949 | gnl\|PID\|e247026 | orf6 [Lactobacillus sake] | 84 | 73 |
| 954 | 1 | 3 | 470 | gi\|40019 | ORF 821 (aa 1-821) [Bacillus subtilis] | 84 | 67 |
| 17 | 3 | 2922 | 3311 | gi\|532555 | ORF22 [Enterococcus faecalis] | 83 | 69 |
| 17 | 12 | 8919 | 10130 | gi\|532553 | ORF20 [Enterococcus faecalis] | 83 | 64 |
| 17 | 30 | 30339 | 29137 | gi\|467416 | unknown [Bacillus subtilis] | 83 | 69 |
| 22 | 4 | 3208 | 3453 | gi\|467469 | unknown [Bacillus subtilis] | 83 | 64 |
| 28 | 3 | 6158 | 3471 | pir\|A26738\|SYBSVS | valine--tRNA ligase (EC 6.1.1.9) - Bacillus stearothermophilus | 83 | 70 |
| 75 | 2 | 359 | 1405 | gi\|310628 | phosphoenolpyruvate:sugar phosphotransferase system enzyme I Streptococcus mutans] | 83 | 72 |
| 78 | 4 | 6971 | 5841 | gi\|155571 | alcohol dehydrogenase I (adhA) (EC 1.1.1.1) [Zymomonas mobilis] pir\|A35260\|A35260 alcohol dehydrogenase (EC 1.1.1.1) I - Zymomonas obilis | 83 | 72 |
| 95 | 9 | 6859 | 7521 | gi\|487280 | Na+ -ATPase subunit D [Enterococcus hirae] | 83 | 66 |
| 98 | 3 | 2785 | 4008 | gi\|984803 | ATPase [Bacillus subtilis] | 83 | 71 |
| 107 | 3 | 1467 | 988 | sp\|P37214\|ERA_STRMU | GTP-BINDING PROTEIN ERA HOMOLOG. | 83 | 73 |
| 122 | 4 | 2781 | 3047 | gi\|467436 | unknown [Bacillus subtilis] | 83 | 60 |
| 128 | 3 | 1572 | 2633 | gi\|559471 | pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum] pir\|S49497\|S49497 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - ommon ice plant | 83 | 64 |
| 128 | 34 | 28154 | 26844 | gi\|142941 | ftsZ [Bacillus subtilis] | 83 | 69 |
| 141 | 2 | 555 | 809 | pir\|S03556\|R3BS18 | ribosomal protein S18 - Bacillus stearothermophilus | 83 | 71 |
| 173 | 8 | 6237 | 7241 | gi\|451216 | Mannosephosphate Isomerase [Streptococcus mutans] | 83 | 70 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 190 | 6 | 3124 | 2738 | gi\|532555 | ORF22 [Enterococcus faecalis] | 83 | 69 |
| 273 | 1 | 29 | 436 | gnl\|PID\|e269878 | ribosomal protein S15 [Bacillus subtilis] | 83 | 71 |
| 334 | 1 | 3 | 920 | gnl\|PID\|e248484 | X-1 [Homo sapiens] | 83 | 71 |
| 350 | 4 | 2723 | 2941 | gi\|511015 | dihydroorotate dehydrogenase A [Lactococcus lactis] sp\|P54321\|PYDA_LACLC DIHYDROOROTATE DEHYDROGENASE A (EC 1.3.3.1) DIHYDROOROTATE OXIDASE A) (DHODEHASE A). | 83 | 66 |
| 367 | 2 | 1218 | 529 | gi\|142463 | RNA polymerase alpha-core-subunit [Bacillus subtilis] | 83 | 70 |
| 399 | 23 | 21538 | 22989 | gi\|40025 | homologous to E.coli 50K [Bacillus subtilis] | 83 | 67 |
| 399 | 25 | 25046 | 25879 | gi\|43939 | D-glucitol-6-P-Dehydrogenase [Klebsiella pneumoniae] ir\|S50186\|S50186 sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.140) - Klebsiella pneumoniae | 83 | 61 |
| 401 | 7 | 5097 | 5864 | gi\|755153 | ATP-binding protein [Bacillus subtilis] | 83 | 64 |
| 438 | 2 | 217 | 681 | gi\|530798 | LysB [Bacteriophage phi-LC3] | 83 | 67 |
| 497 | 4 | 2191 | 3402 | gi\|532553 | ORF20 [Enterococcus faecalis] | 83 | 63 |
| 539 | 2 | 2182 | 782 | gi\|467475 | unknown [Bacillus subtilis] | 83 | 67 |
| 563 | 1 | 2 | 1084 | gi\|142521 | deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl\|PID\|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis] | 83 | 68 |
| 565 | 4 | 1018 | 1206 | gi\|1123066 | weak similarity to bovine cAMP-dependant protein kinase II-B-binding protein (PIR:A39782) [Caenorhabditis elegans] | 83 | 58 |
| 577 | 1 | 1 | 561 | gi\|1303854 | YqgG [Bacillus subtilis] | 83 | 63 |
| 635 | 3 | 1210 | 1527 | gi\|1402526 | ORF5 [Enterococcus faecalis] | 83 | 65 |
| 644 | 1 | 2 | 442 | gi\|153801 | enzyme scr-II [Streptococcus mutans] | 83 | 69 |
| 655 | 3 | 848 | 1246 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 83 | 66 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 675 | 1 | 1 | 621 | gi\|467470 | lysyl-tRNA thynthetase [Bacillus subtilis] | 83 | 71 |
| 763 | 2 | 374 | 640 | gi\|145851 | envM [Escherichia coli] | 83 | 61 |
| 774 | 1 | 658 | 2 | gi\|1256145 | YbbP [Bacillus subtilis] | 83 | 60 |
| 3 | 1 | 58 | 327 | gi\|312443 | carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus] | 82 | 70 |
| 5 | 10 | 6389 | 7708 | sp\|P30053\|SYH_STREQ | HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS). | 82 | 71 |
| 27 | 4 | 1906 | 1145 | gi\|1303960 | YqjI [Bacillus subtilis] | 82 | 71 |
| 32 | 2 | 1333 | 965 | gi\|1303839 | YqfR [Bacillus subtilis] | 82 | 60 |
| 34 | 1 | 1643 | 324 | gnl\|PID\|e218042 | pyruvate kinase [Lactobacillus delbrueckii] | 82 | 68 |
| 55 | 9 | 4182 | 5054 | gi\|1685110 | tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus] | 82 | 70 |
| 62 | 7 | 4644 | 4210 | gi\|143723 | putative [Bacillus subtilis] | 82 | 66 |
| 88 | 2 | 995 | 1624 | gi\|535349 | CodW [Bacillus subtilis] | 82 | 66 |
| 94 | 7 | 4790 | 3432 | gi\|1146247 | asparaginyl-tRNA synthetase [Bacillus subtilis] | 82 | 67 |
| 110 | 23 | 21590 | 20742 | gi\|467403 | seryl-tRNA synthetase [Bacillus subtilis] | 82 | 69 |
| 114 | 7 | 8623 | 9228 | gi\|703442 | thymidine kinase [Streptococcus gordonii] | 82 | 68 |
| 123 | 6 | 4499 | 4996 | gi\|467356 | unknown [Bacillus subtilis] | 82 | 68 |
| 130 | 3 | 1413 | 2381 | gi\|308851 | ATP binding protein [Lactococcus lactis] | 82 | 64 |
| 144 | 3 | 3292 | 2339 | gnl\|PID\|e183449 | putative ATP-binding protein of ABC-type [Bacillus subtilis] | 82 | 62 |
| 144 | 7 | 5331 | 5110 | gi\|335495 | A23R; putative [Vaccinia virus] | 82 | 47 |
| 159 | 4 | 2533 | 5010 | gi\|143148 | transfer RNA-Leu synthetase [Bacillus subtilis] | 82 | 71 |
| 159 | 6 | 5845 | 5387 | gi\|467354 | unknown [Bacillus subtilis] | 82 | 55 |
| 171 | 8 | 8510 | 9349 | gi\|1591672 | phosphate transport system ATP-binding protein [Methanococcus jannaschii] | 82 | 61 |
| 222 | 5 | 2158 | 3402 | gi\|143444 | RNase PH [Bacillus subtilis] | 82 | 66 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 254 | 6 | 1621 | 1112 | gi\|49316 | ORF2 gene product [Bacillus subtilis] | 82 | 61 |
| 279 | 12 | 9839 | 8442 | gi\|1237019 | Srb [Bacillus subtilis] | 82 | 67 |
| 288 | 1 | 22 | 546 | gi\|149393 | lacA [Lactococcus lactis] | 82 | 73 |
| 345 | 8 | 5608 | 8118 | gi\|442360 | ClpC adenosine triphosphatase [Bacillus subtilis] | 82 | 63 |
| 367 | 3 | 1472 | 1110 | gi\|142463 | RNA polymerase alpha-core-subunit [Bacillus subtilis] | 82 | 75 |
| 367 | 9 | 4961 | 3660 | gi\|44073 | SecY protein [Lactococcus lactis] | 82 | 65 |
| 367 | 28 | 12719 | 12411 | pir\|A02815\|R5BS23 | ribosomal protein L23 - Bacillus stearothermophilus | 82 | 66 |
| 367 | 29 | 13330 | 12701 | gi\|1165304 | L4 [Bacillus subtilis] | 82 | 67 |
| 379 | 5 | 4396 | 3107 | gi\|887820 | UUG start; possible frameshift at end? [Escherichia coli] | 82 | 71 |
| 393 | 2 | 1145 | 711 | gi\|1303993 | YqkL [Bacillus subtilis] | 82 | 67 |
| 416 | 1 | 3 | 650 | gi\|475113 | sucrase [Pediococcus pentosaceus] | 82 | 69 |
| 477 | 1 | 1 | 1209 | gi\|309663 | signaling protein [Plasmid pCF10] | 82 | 62 |
| 497 | 7 | 3760 | 4275 | gi\|532551 | ORF18 [Enterococcus faecalis] | 82 | 67 |
| 535 | 3 | 4275 | 1666 | gi\|1747434 | KdpD [Clostridium acetobutylicum] | 82 | 62 |
| 587 | 1 | 488 | 108 | gi\|1303840 | YqfS [Bacillus subtilis] | 82 | 71 |
| 623 | 2 | 122 | 1348 | gi\|460259 | enolase [Bacillus subtilis] | 82 | 67 |
| 656 | 1 | 1 | 1908 | gi\|1184680 | polynucleotide phosphorylase [Bacillus subtilis] | 82 | 69 |
| 687 | 1 | 227 | 1252 | gi\|40218 | PRPP synthetase (AA 1-317) [Bacillus subtilis] | 82 | 64 |
| 728 | 1 | 3 | 527 | gi\|1146183 | putative [Bacillus subtilis] | 82 | 65 |
| 741 | 1 | 3 | 704 | gi\|153804 | sucrose-6-phosphate hydrolase [Streptococcus mutans] | 82 | 66 |
| 846 | 1 | 458 | 3 | gnl\|PID\|e221400 | tex gene product [Bordetella pertussis] | 82 | 76 |
| 865 | 1 | 18 | 308 | gi\|416006 | orf CJO1.2 [Campylobacter jejuni] | 82 | 57 |
| 876 | 1 | 207 | 689 | gi\|1064795 | function unknown [Bacillus subtilis] | 82 | 62 |
| 925 | 1 | 436 | 128 | gi\|1773195 | hypothetical [Escherichia coli] | 82 | 74 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 983 | 2 | 280 | 474 | gi\|40026 | homologous to E.coli gidA [Bacillus subtilis] | 82 | 78 |
| 12 | 3 | 4778 | 5788 | gi\|1100074 | tryptophanyl-tRNA synthetase [Clostridium longisporum] | 81 | 68 |
| 31 | 4 | 2984 | 4456 | gi\|849026 | hypothetical 54.6-kDa protein [Bacillus subtilis] | 81 | 68 |
| 34 | 6 | 6707 | 6910 | gi\|606067 | ORF_f444 [Escherichia coli] | 81 | 54 |
| 37 | 1 | 1 | 144 | gi\|1303854 | YqgG [Bacillus subtilis] | 81 | 59 |
| 37 | 3 | 2671 | 1958 | gi\|40056 | phoP gene product [Bacillus subtilis] | 81 | 61 |
| 57 | 3 | 1733 | 3220 | gi\|1657506 | hypothetical protein [Escherichia coli] | 81 | 66 |
| 60 | 5 | 5564 | 4440 | gi\|143370 | phosphoribosylpyrophosphate amidotransferase (PUR-F; EC 2.4.2.14) Bacillus subtilis] | 81 | 63 |
| 73 | 3 | 2706 | 1450 | gi\|853767 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus ubtilis] | 81 | 61 |
| 88 | 4 | 1977 | 2732 | gnl\|PID\|e137596 | heat shock induced protein HtpO [Lactobacillus leichmannii] | 81 | 67 |
| 88 | 5 | 2723 | 3040 | gi\|535350 | CodX [Bacillus subtilis] | 81 | 65 |
| 101 | 4 | 3091 | 2435 | gi\|1109687 | ProZ [Bacillus subtilis] | 81 | 60 |
| 101 | 7 | 5884 | 4661 | gi\|1109684 | ProV [Bacillus subtilis] | 81 | 64 |
| 101 | 9 | 7501 | 7965 | gi\|1001768 | queuosine biosynthesis protein QueA [Synechocystis sp.] | 81 | 47 |
| 116 | 5 | 2766 | 3395 | gi\|1146234 | dihydrodipicolinate reductase [Bacillus subtilis] | 81 | 66 |
| 121 | 5 | 4811 | 5074 | gi\|153765 | DNA polymerase I [Streptococcus pneumoniae] | 81 | 64 |
| 121 | 7 | 5203 | 7488 | gi\|153765 | DNA polymerase I [Streptococcus pneumoniae] | 81 | 70 |
| 127 | 5 | 5103 | 3826 | gi\|290561 | o188 [Escherichia coli] | 81 | 48 |
| 147 | 1 | 299 | 1279 | gi\|467462 | cysteine synthetase A [Bacillus subtilis] | 81 | 65 |
| 147 | 2 | 1370 | 1861 | gnl\|PID\|e281583 | hypothetical 16.4 kd protein [Bacillus | 81 | 63 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | subtilis] | | |
| 154 | 1 | 168 | 638 | gi\|149533 | conjugated bile acid hydrolase [Lactobacillus plantarum] | 81 | 66 |
| 154 | 2 | 1074 | 1277 | gnl\|PID\|e242898 | aBIR [Lactococcus lactis] | 81 | 59 |
| 158 | 14 | 13790 | 12324 | gi\|558559 | pyrimidine nucleoside phosphorylase [Bacillus subtilis] | 81 | 71 |
| 164 | 5 | 2469 | 3035 | gi\|727436 | putative 20-kDa protein [Lactococcus lactis] | 81 | 61 |
| 223 | 8 | 5293 | 6153 | gnl\|PID\|e254976 | hypothetical protein [Bacillus subtilis] | 81 | 66 |
| 238 | 1 | 185 | 937 | gi\|622991 | mannitol transport protein [Bacillus stearothermophilus] sp\|P50852\|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL). | 81 | 68 |
| 276 | 7 | 3109 | 2819 | pir\|A41207\|A41207 | collagen 13, nonfibrillar - freshwater sponge (Ephydatia muelleri) (fragment) | 81 | 77 |
| 307 | 2 | 1983 | 3617 | gi\|153742 | dextran glucosidase [Streptococcus mutans] | 81 | 69 |
| 322 | 2 | 122 | 286 | gi\|296147 | Asd protein [Bacillus subtilis] | 81 | 63 |
| 326 | 6 | 5352 | 4513 | gi\|40041 | pyruvate dehydrogenase (lipoamide) [Bacillus stearothermophilus] ir\|S10798\|DEBSPF pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pha chain - Bacillus stearothermophilus | 81 | 69 |
| 329 | 3 | 1774 | 1448 | gi\|1117994 | surface antigen A variant precursor [Streptococcus pneumoniae] | 81 | 72 |
| 346 | 3 | 1056 | 1199 | gi\|536970 | ORF_f543 [Escherichia coli] | 81 | 43 |
| 362 | 4 | 1131 | 2213 | gi\|1001826 | cadmium-transporting ATPase [Synechocystis sp.] | 81 | 64 |
| 391 | 3 | 1345 | 575 | gi\|1184967 | ScrR [Streptococcus mutans] | 81 | 66 |
| 441 | 3 | 1873 | 3447 | gi\|1742675 | Phosphotransferase system enzyme II (EC 2.7.1.69) MalX [Escherichia coli] | 81 | 64 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 556 | 2 | 1062 | 493 | gi\|1553037 | RecN [Bacillus subtilis] | 81 | 66 |
| 710 | 2 | 361 | 816 | gi\|1303840 | YqfS [Bacillus subtilis] | 81 | 68 |
| 804 | 1 | 403 | 2 | gi\|149533 | conjugated bile acid hydrolase [Lactobacillus plantarum] | 81 | 68 |
| 5 | 7 | 3311 | 4255 | gi\|407881 | stringent response-like protein [Streptococcus equisimilis] pir\|S39975\|S39975 stringent response-like protein - Streptococcus quisimilis | 80 | 62 |
| 17 | 10 | 8283 | 8438 | gi\|1326394 | B0218.7 gene product [Caenorhabditis elegans] | 80 | 53 |
| 17 | 15 | 12258 | 12776 | gi\|532551 | ORF18 [Enterococcus faecalis] | 80 | 63 |
| 22 | 1 | 3 | 2180 | gi\|44027 | Tma protein [Lactococcus lactis] | 80 | 70 |
| 37 | 6 | 3707 | 5140 | pir\|B47154\|B47154 | signal recognition particle 54K chain homolog Ffh - Bacillus subtilis | 80 | 64 |
| 42 | 1 | 2 | 259 | gi\|1066157 | chaperonin-10 [Thermus aquaticus thermophilus] | 80 | 66 |
| 49 | 16 | 11106 | 11309 | gi\|1136430 | similar to hypothetical protein YM9959.11C of S.cerevisiae. [Homo sapiens] | 80 | 53 |
| 60 | 4 | 4465 | 3407 | gi\|143371 | phosphoribosyl aminoimidazole synthetase (PUR-M) [Bacillus subtilis] pir\|H29326\|AJBSCL phosphoribosylformylglycinamidine cyclo-ligase EC 6.3.3.1) - Bacillus subtilis | 80 | 62 |
| 60 | 9 | 9023 | 8745 | pir\|E29326\|E29326 | hypothetical protein (pur operon) - Bacillus subtilis | 80 | 50 |
| 66 | 1 | 1 | 783 | gi\|520753 | DNA topoisomerase I [Bacillus subtilis] | 80 | 66 |
| 80 | 3 | 2519 | 1821 | gnl\|PID\|e236074 | beta-phosphoglucomutase [Lactococcus lactis] | 80 | 62 |
| 83 | 9 | 6268 | 5378 | gi\|1070079 | R08B4.1 [Caenorhabditis elegans] | 80 | 72 |
| 89 | 18 | 19093 | 18845 | gi\|39451 | type III restriction endonuclease [Bacillus cereus] ir\|S15518\|JC1116 type III site-specific deoxyribonuclease (EC | 80 | 72 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | 1.21.5) - Bacillus cereus (fragment) | | |
| 97 | 1 | 366 | 4 | gi\|148506 | dnaJ [Erysipelothrix rhusiopathiae] | 80 | 70 |
| 107 | 2 | 1094 | 591 | sp\|P37214\|ERA_STRMU | GTP-BINDING PROTEIN ERA HOMOLOG. | 80 | 64 |
| 114 | 3 | 1474 | 5076 | gi\|43863 | pyruvate-flavodoxin oxidoreductase [Klebsiella pneumoniae] ir\|S01997\|QQKBFP pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) Klebsiella pneumoniae | 80 | 62 |
| 117 | 3 | 1456 | 2367 | gi\|40031 | spoOJ93 gene product [Bacillus subtilis] | 80 | 56 |
| 126 | 3 | 1857 | 709 | gi\|551854 | ORF2 [Erwinia herbicola] | 80 | 68 |
| 128 | 28 | 23265 | 22447 | gi\|437916 | isoleucyl-tRNA synthetase [Staphylococcus aureus] | 80 | 63 |
| 133 | 10 | 9128 | 9856 | gi\|520844 | orf4 [Bacillus subtilis] | 80 | 63 |
| 158 | 4 | 3926 | 2703 | gi\|944943 | phosphopentomutase [Bacillus subtilis] | 80 | 64 |
| 172 | 5 | 3732 | 3920 | sp\|P20182\|YT14_STRFR | HYPOTHETICAL 29.1 KD PROTEIN IN TRANSPOSON TN4556. | 80 | 63 |
| 180 | 16 | 15548 | 16393 | gi\|1773200 | hypothetical protein [Escherichia coli] | 80 | 66 |
| 181 | 10 | 8597 | 7407 | gi\|143806 | AroF [Bacillus subtilis] | 80 | 64 |
| 194 | 4 | 1580 | 1957 | gi\|47394 | 5-oxoprolyl-peptidase [Streptococcus pyogenes] | 80 | 66 |
| 213 | 5 | 3515 | 4078 | gnl\|PID\|e199384 | pyrR gene product [Lactobacillus plantarum] | 80 | 65 |
| 217 | 11 | 7724 | 8395 | gi\|1561567 | Unknown [Bacillus subtilis] | 80 | 65 |
| 218 | 6 | 4843 | 5331 | gi\|1574120 | branched-chain-amino-acid transaminase [Haemophilus influenzae] | 80 | 64 |
| 225 | 8 | 6092 | 5829 | gi\|530459 | similar to phosphotransferase EII [Mycoplasma capricolum] | 80 | 52 |
| 229 | 2 | 1170 | 178 | gi\|1502419 | PlsX [Bacillus subtilis] | 80 | 59 |
| 243 | 3 | 2545 | 2150 | gi\|1732315 | transport system permease homolog [Listeria monocytogenes] | 80 | 64 |
| 275 | 2 | 694 | 939 | gi\|1256629 | cold-shock protein [Bacillus subtilis] | 80 | 65 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 307 | 3 | 3607 | 3888 | gi\|1321625 | exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus] | 80 | 73 |
| 322 | 3 | 284 | 1090 | gi\|142828 | aspartate semialdehyde dehydrogenase [Bacillus subtilis] sp\|Q04797\|DHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC .2.1.11) (ASA DEHYDROGENASE). | 80 | 62 |
| 349 | 1 | 2 | 616 | gi\|495089 | recombinase [Staphylococcus aureus] | 80 | 65 |
| 367 | 7 | 3511 | 2924 | gi\|44074 | adenylate kinase [Lactococcus lactis] | 80 | 64 |
| 386 | 7 | 4305 | 5306 | gi\|149396 | lacD [Lactococcus lactis] | 80 | 64 |
| 394 | 3 | 2642 | 3757 | pir\|B39096\|B39096 | alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis | 80 | 64 |
| 399 | 17 | 12070 | 13488 | gi\|1591862 | oxaloacetate decarboxylase, alpha subunit [Methanococcus jannaschii] | 80 | 61 |
| 399 | 24 | 22979 | 24907 | gi\|40026 | homologous to E.coli gidA [Bacillus subtilis] | 80 | 67 |
| 435 | 3 | 2217 | 2032 | gi\|559863 | clyA [Plasmid pAD1] | 80 | 78 |
| 466 | 1 | 3 | 1208 | gi\|467330 | replicative DNA helicase [Bacillus subtilis] | 80 | 61 |
| 475 | 4 | 3402 | 2947 | gi\|532547 | ORF14 [Enterococcus faecalis] | 80 | 68 |
| 491 | 4 | 3844 | 4392 | gi\|473892 | large-conductance mechanosensitive channel [Escherichia coli] gi\|473420 yhdC [Escherichia coli] | 80 | 56 |
| 605 | 2 | 1252 | 338 | gi\|580875 | ipa-57d gene product [Bacillus subtilis] | 80 | 69 |
| 615 | 1 | 760 | 14 | gi\|467469 | unknown [Bacillus subtilis] | 80 | 66 |
| 668 | 1 | 117 | 587 | pir\|S16974\|R5BS7F | ribosomal protein L9 - Bacillus stearothermophilus | 80 | 71 |
| 684 | 2 | 694 | 464 | gi\|786314 | Highly similar to Glycogen debranching enzyme 4-alpha-glucanotransferase, Swiss Prot. accession number P35573) Saccharomyces cerevisiae] | 80 | 33 |
| 767 | 1 | 1 | 480 | gi\|41828 | istB gene product [Escherichia coli] | 80 | 52 |
| 818 | 1 | 1 | 357 | gi\|1743856 | intrageneric coaggregation-relevant | 80 | 66 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | adhesin [Streptococcus gordonii] | | |
| 833 | 1 | 325 | 95 | gi\|1561567 | Unknown [Bacillus subtilis] | 80 | 68 |
| 934 | 1 | 394 | 56 | gi\|1001706 | ABC transporter subunit [Synechocystis sp.] | 80 | 63 |
| 948 | 1 | 465 | 4 | gi\|1773196 | similar to B. stearothermophilus N-carbamyl-L-amino acid amidohydrolase [Escherichia coli] | 80 | 59 |
| 949 | 1 | 61 | 411 | gi\|1330380 | Similar to cystathionine gamma-lyase [Caenorhabditis elegans] | 80 | 61 |
| 20 | 2 | 468 | 1262 | gi\|1256698 | chitinase [Serratia marcescens] | 79 | 67 |
| 22 | 3 | 2420 | 3238 | gi\|467460 | unknown [Bacillus subtilis] | 79 | 59 |
| 24 | 1 | 39 | 1109 | gi\|1303821 | YqfE [Bacillus subtilis] | 79 | 61 |
| 26 | 1 | 214 | 873 | gi\|403984 | deoxyguanosine kinase/deoxyadenosine kinase(I) subunit Lactobacillus acidophilus] | 79 | 68 |
| 47 | 8 | 10268 | 8106 | gi\|153657 | mismatch repair protein [Streptococcus pneumoniae] pir\|A33589\|A33589 mismatch repair protein hexB - Streptococcus neumoniae | 79 | 63 |
| 48 | 9 | 9905 | 9198 | gi\|290566 | f213 [Escherichia coli] | 79 | 53 |
| 58 | 4 | 4677 | 3694 | gi\|1653179 | hydrogenase subunit [Synechocystis sp.] | 79 | 52 |
| 63 | 6 | 3605 | 5443 | gi\|1064813 | homologous to sp:PHOR_BACSU [Bacillus subtilis] | 79 | 55 |
| 88 | 8 | 5493 | 4771 | gnl\|PID\|e208252 | unidentified [Streptococcus pneumoniae] | 79 | 57 |
| 146 | 8 | 6649 | 5609 | gi\|153676 | tagatose 1,6-aldolase [Streptococcus mutans] | 79 | 63 |
| 149 | 4 | 2554 | 1976 | gi\|1216490 | DNA/pantothenate metabolism flavoprotein [Streptococcus mutans] | 79 | 64 |
| 158 | 2 | 1859 | 1143 | gi\|1276873 | DeoD [Streptococcus thermophilus] | 79 | 67 |
| 179 | 19 | 19022 | 18417 | gi\|467372 | 3'-exo-deoxyribonuclease [Bacillus subtilis] | 79 | 61 |
| 222 | 2 | 982 | 230 | gi\|142988 | membrane transport protein [Bacillus | 79 | 59 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | stearothermophilus] pir\|A42478\|A42478 glutamine transport protein glnQ - Bacillus tearothermophilus | | |
| 228 | 6 | 4060 | 3401 | gi\|413950 | ipa-26d gene product [Bacillus subtilis] | 79 | 55 |
| 229 | 3 | 3270 | 1219 | gnl\|PID\|e186699 | MmsA [Streptococcus pneumoniae] | 79 | 62 |
| 238 | 7 | 5750 | 5100 | gi\|596046 | L8003.16 gene product [Saccharomyces cerevisiae] | 79 | 55 |
| 269 | 10 | 6664 | 5489 | gi\|1303788 | YqeH [Bacillus subtilis] | 79 | 63 |
| 274 | 1 | 1 | 1143 | gi\|153062 | helicase [Staphylococcus aureus] | 79 | 65 |
| 290 | 9 | 7364 | 8779 | gi\|466882 | pps1; B1496_C2_189 [Mycobacterium leprae] | 79 | 64 |
| 292 | 22 | 18122 | 17595 | gi\|1303951 | YqiZ [Bacillus subtilis] | 79 | 61 |
| 316 | 3 | 864 | 2003 | gi\|1146207 | putative [Bacillus subtilis] | 79 | 58 |
| 326 | 2 | 1772 | 360 | gi\|40044 | dihydrolipoamide dehydrogenase [Bacillus stearothermophilus] ir\|S13839\|S13839 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - cillus stearothermophilus | 79 | 65 |
| 363 | 5 | 5738 | 7180 | gi\|1657519 | hypothetical protein [Escherichia coli] | 79 | 63 |
| 367 | 11 | 5668 | 5447 | gi\|216337 | ORF for L30 ribosomal protein [Bacillus subtilis] | 79 | 63 |
| 375 | 5 | 4346 | 3393 | gi\|1644203 | unknown [Bacillus subtilis] | 79 | 62 |
| 406 | 2 | 666 | 1481 | gi\|49316 | ORF2 gene product [Bacillus subtilis] | 79 | 58 |
| 460 | 7 | 4973 | 5860 | gi\|1276664 | acetyl-CoA carboxylase carboxytransferase beta subunit [Porphyra purpurea] | 79 | 62 |
| 486 | 1 | 380 | 3 | gi\|1256618 | transport protein [Bacillus subtilis] | 79 | 63 |
| 488 | 3 | 987 | 1997 | gi\|532547 | ORF14 [Enterococcus faecalis] | 79 | 69 |
| 500 | 2 | 1358 | 681 | gi\|535662 | transposase [Insertion sequence IS1251] | 79 | 75 |
| 523 | 3 | 1803 | 820 | gi\|142981 | ORF5; This ORF includes a region (aa23-103) containing a potential ron-sulphur centre homologous to a region of Rhodospirillum rubrum nd Chromatium vinosum; putative [Bacillus stearothermophilus] pir\|PQ0299\|PQ0299 | 79 | 62 |

**Table 2:** ***E. faecalis*** **- Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | hypothetical protein 5 (gldA 3' region) - | | |
| 552 | 2 | 2401 | 902 | gi\|887851 | ORF_o479 [Escherichia coli] | 79 | 63 |
| 587 | 2 | 622 | 434 | gi\|1303840 | YqfS [Bacillus subtilis] | 79 | 66 |
| 612 | 1 | 1 | 378 | gi\|1064791 | function umknown [Bacillus subtilis] | 79 | 56 |
| 654 | 1 | 2 | 286 | pir\|A47079\|A47079 | heat shock protein DnaJ - Lactococcus lactis | 79 | 75 |
| 701 | 2 | 325 | 534 | gi\|143793 | tyrosyl-tRNA synthetase [Bacillus caldotenax] | 79 | 63 |
| 708 | 2 | 369 | 566 | gi\|488430 | alcohol dehydrogenase 2 [Entamoeba histolytica] | 79 | 66 |
| 840 | 1 | 140 | 1078 | gi\|1573250 | aspartate aminotransferase (aspC) [Haemophilus influenzae] | 79 | 65 |
| 5 | 9 | 5555 | 6049 | gi\|407880 | ORF1 [Streptococcus equisimilis] | 78 | 58 |
| 33 | 4 | 3755 | 4597 | gi\|1742846 | NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1) (Nitrogen-regulatory protein). [Escherichia coli] | 78 | 64 |
| 60 | 7 | 8100 | 5854 | gi\|143369 | phosphoribosylformyl glycinamidine synthetase II (PUR-Q) [Bacillus ubtilis] | 78 | 62 |
| 65 | 4 | 3407 | 2625 | gi\|1661179 | high affinity branched chain amino acid transport protein [Streptococcus mutans] | 78 | 67 |
| 76 | 7 | 5760 | 4747 | gi\|1161061 | dioxygenase [Methylobacterium extorquens] | 78 | 62 |
| 81 | 11 | 7141 | 6824 | gi\|1072380 | ORF3 [Lactococcus lactis] | 78 | 67 |
| 83 | 5 | 2559 | 2843 | gi\|1256896 | L9606.1 gene product [Saccharomyces cerevisiae] | 78 | 52 |
| 85 | 4 | 4298 | 3288 | gi\|142612 | branched chain alpha-keto acid dehydrogenase E1-beta [Bacillus ubtilis] | 78 | 61 |
| 85 | 8 | 6723 | 6307 | gi\|1303941 | YqiV [Bacillus subtilis] | 78 | 62 |
| 88 | 10 | 6477 | 6689 | gi\|222585 | nucleocapsid protein [Sialodacryoadenitis virus] | 78 | 57 |
| 93 | 5 | 1838 | 2641 | gi\|405133 | putative [Bacillus subtilis] | 78 | 51 |
| 117 | 1 | 3 | 707 | gi\|40027 | homologous to E.coli gidB [Bacillus | 78 | 64 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | subtilis] | | |
| 117 | 11 | 9624 | 8338 | gi\|467403 | seryl-tRNA synthetase [Bacillus subtilis] | 78 | 63 |
| 132 | 2 | 2323 | 2024 | gi\|683484 | fusion protein [Mumps virus] | 78 | 63 |
| 133 | 3 | 2241 | 3413 | gi\|405622 | unknown [Bacillus subtilis] | 78 | 63 |
| 150 | 2 | 568 | 1425 | gnl\|PID\|e185373 | ceuD gene product [Campylobacter coli] | 78 | 52 |
| 155 | 2 | 604 | 1182 | gi\|285628 | transcription antitermination factor NusG [Bacillus subtilis] pir\|S39859\|S39859 transcription antitermination factor NusG - acillus subtilis | 78 | 61 |
| 156 | 2 | 308 | 2629 | gi\|1573874 | ATP-dependent protease binding subunit (clpB) [Haemophilus influenzae] | 78 | 59 |
| 158 | 3 | 2719 | 1868 | gi\|1638804 | purine nucleoside phosphorylase [Bacillus stearothermophilus] | 78 | 64 |
| 160 | 5 | 2058 | 3050 | gi\|1161061 | dioxygenase [Methylobacterium extorquens] | 78 | 60 |
| 161 | 3 | 1466 | 3295 | gnl\|PID\|e280490 | unknown [Streptococcus pneumoniae] | 78 | 62 |
| 169 | 1 | 2 | 2206 | gi\|1072361 | pyruvate-formate-lyase [Clostridium pasteurianum] | 78 | 61 |
| 171 | 2 | 2833 | 3897 | sp\|P28367\|RF2_BACSU | PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT). | 78 | 64 |
| 180 | 15 | 14851 | 15567 | gi\|1773199 | hypothetical protein [Escherichia coli] | 78 | 67 |
| 185 | 1 | 1142 | 3 | pir\|C33496\|C33496 | hisC homolog - Bacillus subtilis | 78 | 59 |
| 188 | 3 | 1863 | 4178 | gnl\|PID\|e256969 | nifJ gene product [Enterobacter agglomerans] | 78 | 62 |
| 216 | 7 | 5136 | 5600 | gnl\|PID\|e276830 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis] | 78 | 60 |
| 216 | 8 | 5531 | 6508 | gnl\|PID\|e276830 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis] | 78 | 63 |
| 238 | 26 | 24515 | 25387 | gi\|396681 | rhamnulose-1-phosphate aldolase [Escherichia coli] | 78 | 56 |
| 256 | 6 | 4189 | 6237 | gi\|467427 | methionyl-tRNA synthetase [Bacillus | 78 | 67 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | subtilis] | | |
| 292 | 4 | 2063 | 2353 | gi\|1742823 | Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli] | 78 | 62 |
| 305 | 1 | 268 | 1872 | gi\|143582 | spoIIIEA protein [Bacillus subtilis] | 78 | 58 |
| 337 | 2 | 2332 | 1448 | gi\|308861 | GTG start codon [Lactococcus lactis] | 78 | 63 |
| 338 | 2 | 606 | 1466 | gi\|1773142 | similar to the 20.2kd protein in TETB-EXOA region of B. subtilis [Escherichia coli] | 78 | 66 |
| 362 | 1 | 109 | 429 | gi\|150719 | cadmium resistance protein [Plasmid pI258] | 78 | 51 |
| 379 | 3 | 2878 | 1922 | gi\|887824 | ORF_o310 [Escherichia coli] | 78 | 60 |
| 446 | 2 | 962 | 1636 | gi\|537235 | Kenn Rudd identifies as gpmB [Escherichia coli] | 78 | 43 |
| 495 | 5 | 3038 | 3502 | gi\|634107 | kdpB [Escherichia coli] | 78 | 58 |
| 502 | 3 | 3077 | 1470 | gi\|1652592 | peptide-chain-release factor 3 [Synechocystis sp.] | 78 | 58 |
| 523 | 1 | 2 | 616 | gi\|289288 | lexA [Bacillus subtilis] | 78 | 59 |
| 571 | 1 | 99 | 365 | gnl\|PID\|e249644 | YneF [Bacillus subtilis] | 78 | 65 |
| 573 | 3 | 1258 | 1971 | gi\|1731683 | component II of heptaprenyl diphosphate synthase [Bacillus stearothermophilus] | 78 | 50 |
| 575 | 2 | 434 | 168 | gi\|58831 | The experimental evidence that this sequence codes for a complete gag otein is that transfection of the viral genome results in oduction of infectious virus [Cas-Br-E murine leukemia virus] p\|P27460\|GAG_MLVCB GAG POLYPROTEIN (CONTAINS: CORE PROTEIN P15; N | 78 | 47 |
| 607 | 1 | 148 | 708 | gi\|530410 | Ala-tRNA synthetase [Mycoplasma capricolum] | 78 | 63 |
| 655 | 2 | 300 | 899 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 78 | 60 |
| 704 | 1 | 181 | 2 | gi\|467430 | unknown [Bacillus subtilis] | 78 | 63 |
| 708 | 1 | 1 | 378 | gi\|443985 | alcohol dehydrogenase [Entamoeba | 78 | 61 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | histolytica] | | |
| 732 | 1 | 661 | 2 | gi\|1064791 | function umknown [Bacillus subtilis] | 78 | 55 |
| 785 | 1 | 2 | 679 | gi\|556014 | UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis] | 78 | 59 |
| 786 | 1 | 2 | 172 | gi\|536992 | SugES [Escherichia coli] | 78 | 60 |
| 820 | 2 | 1602 | 1144 | gi\|153749 | UDPglucose 4-epimerase [Streptococcus thermophilus] pir\|A44509\|A44509 UDPglucose 4-epimerase (EC 5.1.3.2) - treptococcus thermophilus | 78 | 60 |
| 887 | 1 | 337 | 2 | gi\|495046 | tripeptidase [Lactococcus lactis] | 78 | 70 |
| 970 | 2 | 395 | 234 | gi\|1652190 | Fat protein [Synechocystis sp.] | 78 | 51 |
| 4 | 7 | 6069 | 5656 | gi\|1573482 | high affinity ribose transport protein (rbsD) [Haemophilus influenzae] | 77 | 51 |
| 45 | 16 | 12065 | 14047 | gi\|666069 | orf2 gene product [Lactobacillus leichmannii] | 77 | 51 |
| 49 | 13 | 8199 | 9992 | gnl\|PID\|e228615 | homologous to yqcC of the skin element [Bacillus subtilis] | 77 | 59 |
| 60 | 2 | 2895 | 1300 | gi\|143373 | phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis] | 77 | 63 |
| 70 | 6 | 5118 | 3874 | gi\|912464 | No definition line found [Escherichia coli] | 77 | 53 |
| 70 | 7 | 5172 | 5756 | gi\|288413 | glutamate dehydrogenase (NADP+) [Corynebacterium glutamicum] pir\|S32227\|S32227 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - orynebacterium glutamicum | 77 | 65 |
| 74 | 10 | 7303 | 5864 | gi\|289284 | cysteinyl-tRNA synthetase [Bacillus subtilis] | 77 | 62 |
| 74 | 12 | 9559 | 8078 | gi\|289282 | glutamyl-tRNA synthetase [Bacillus subtilis] | 77 | 57 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 88 | 6 | 3013 | 3843 | gi\|535351 | CodY [Bacillus subtilis] | 77 | 57 |
| 89 | 6 | 5749 | 2510 | gi\|1695686 | pyruvate carboxylase [Bacillus stearothermophilus] | 77 | 62 |
| 91 | 1 | 396 | 728 | gi\|1184044 | L-glutamine:D-fructose-6-P amidotransferase precursor [Thermus aquaticus thermophilus] | 77 | 66 |
| 98 | 4 | 3992 | 5710 | gi\|984804 | transmembrane protein [Bacillus subtilis] | 77 | 56 |
| 124 | 1 | 2 | 940 | gnl\|PID\|e199002 | prolidase PepQ [Lactobacillus delbrueckii] | 77 | 60 |
| 158 | 5 | 4845 | 4171 | gi\|435297 | unknown [Lactococcus lactis] | 77 | 48 |
| 162 | 6 | 7426 | 5882 | gi\|142992 | glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir\|B45868\|B45868 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp\|P18157\|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL - PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK). | 77 | 60 |
| 164 | 1 | 179 | 1102 | gi\|882532 | ORF_o294 [Escherichia coli] | 77 | 57 |
| 164 | 22 | 24158 | 23646 | gi\|1573564 | hypothetical [Haemophilus influenzae] | 77 | 36 |
| 171 | 6 | 6656 | 7639 | gi\|1303855 | YqgH [Bacillus subtilis] | 77 | 59 |
| 171 | 9 | 9198 | 9683 | gi\|1591672 | phosphate transport system ATP-binding protein [Methanococcus jannaschii] | 77 | 57 |
| 202 | 4 | 2967 | 3422 | gi\|147782 | ruvA protein (gtg start) [Escherichia coli] | 77 | 50 |
| 202 | 6 | 3662 | 4693 | gi\|147783 | ruvB protein [Escherichia coli] | 77 | 58 |
| 213 | 1 | 3 | 1046 | gi\|1103865 | formyl-tetrahydrofolate synthetase [Streptococcus mutans] | 77 | 63 |
| 217 | 10 | 6870 | 7742 | gi\|414014 | ipa-90d gene product [Bacillus subtilis] | 77 | 50 |
| 223 | 5 | 4171 | 4902 | gnl\|PID\|e254974 | autolysin response regulator [Bacillus subtilis] | 77 | 55 |
| 223 | 7 | 5024 | 5473 | gnl\|PID\|e254975 | hypothetical protein [Bacillus subtilis] | 77 | 58 |
| 228 | 10 | 7747 | 6035 | gi\|467409 | DNA polymerase III subunit [Bacillus subtilis] | 77 | 61 |
| 229 | 15 | 16711 | 14261 | gnl\|PID\|e290286 | priA [Bacillus subtilis] | 77 | 62 |

**Table 2:** ***E. faecalis*** **- Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 232 | 3 | 1742 | 1437 | gi\|142708 | comG3 gene product [Bacillus subtilis] | 77 | 50 |
| 238 | 25 | 23174 | 24511 | pir\|B48649\|B48649 | L-rhamnose isomerase (EC 5.3.1.14) - Escherichia coli | 77 | 59 |
| 238 | 32 | 29472 | 28708 | gi\|451072 | di-tripeptide transporter [Lactococcus lactis] | 77 | 56 |
| 244 | 4 | 3591 | 2809 | gi\|1773173 | similar to M. jannaschii MJ0938 [Escherichia coli] | 77 | 60 |
| 269 | 5 | 3890 | 3522 | gi\|1303793 | YqeL [Bacillus subtilis] | 77 | 55 |
| 276 | 6 | 2840 | 2328 | pir\|PC1127\|PC1127 | hypothetical 110 protein (lytA 5' region) - Lactococcus lactis phage US3 (fragment) | 77 | 50 |
| 291 | 1 | 119 | 916 | gi\|556014 | UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis] | 77 | 63 |
| 304 | 2 | 941 | 2020 | gnl\|PID\|e285001 | CTORF239 [Staphylococcus aureus] | 77 | 62 |
| 305 | 4 | 3618 | 4394 | gi\|709993 | hypothetical protein [Bacillus subtilis] | 77 | 54 |
| 327 | 8 | 5697 | 6005 | gi\|153570 | H+ ATPase [Enterococcus faecalis] | 77 | 61 |
| 341 | 4 | 1206 | 1937 | gi\|1303951 | YqiZ [Bacillus subtilis] | 77 | 62 |
| 360 | 1 | 429 | 4 | gi\|897754 | nonstructural protein NSP3 [Human rotavirus] | 77 | 38 |
| 362 | 3 | 541 | 1239 | gi\|1001826 | cadmium-transporting ATPase [Synechocystis sp.] | 77 | 60 |
| 363 | 9 | 13917 | 12652 | gi\|1574390 | C4-dicarboxylate transport protein [Haemophilus influenzae] | 77 | 55 |
| 367 | 14 | 7218 | 6679 | pir\|A02766\|R5BS0F | ribosomal protein L6 - Bacillus stearothermophilus | 77 | 63 |
| 386 | 8 | 5456 | 5776 | gnl\|PID\|e281578 | hypothetical 12.2 kd protein [Bacillus subtilis] | 77 | 61 |
| 394 | 4 | 3706 | 4167 | pir\|B39096\|B39096 | alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis | 77 | 55 |
| 402 | 1 | 710 | 3 | gi\|533105 | unknown [Bacillus subtilis] | 77 | 59 |
| 408 | 2 | 1357 | 584 | gi\|666983 | putative ATP binding subunit [Bacillus subtilis] | 77 | 58 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 460 | 6 | 3562 | 4938 | gi\|1055246 | biotin carboxylase [Bacillus subtilis] | 77 | 60 |
| 466 | 7 | 8657 | 9253 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 77 | 61 |
| 475 | 5 | 3794 | 3234 | gi\|532547 | ORF14 [Enterococcus faecalis] | 77 | 68 |
| 498 | 1 | 1 | 603 | gi\|410137 | ORFX13 [Bacillus subtilis] | 77 | 58 |
| 515 | 1 | 107 | 574 | gi\|1303815 | YqeY [Bacillus subtilis] | 77 | 60 |
| 518 | 6 | 2980 | 4518 | gi\|1402515 | membrane-spanning transporter protein [Clostridium perfringens] | 77 | 56 |
| 523 | 5 | 2527 | 2333 | gi\|149601 | thymidylate synthase (EC 2.1.1.45) [Lactobacillus casei] | 77 | 66 |
| 526 | 2 | 1782 | 436 | gi\|1750124 | xylose isomerase [Bacillus subtilis] | 77 | 62 |
| 552 | 7 | 6809 | 6135 | gi\|534045 | antiterminator [Bacillus subtilis] | 77 | 51 |
| 607 | 3 | 778 | 936 | gi\|1015321 | alanyl-tRNA synthetase [Homo sapiens] | 77 | 51 |
| 624 | 3 | 2289 | 2555 | gnl\|PID\|e187971 | orf121 gene product [Lactococcus lactis] | 77 | 57 |
| 781 | 1 | 15 | 485 | gi\|580883 | ipa-88d gene product [Bacillus subtilis] | 77 | 65 |
| 850 | 2 | 895 | 572 | gi\|142520 | thioredoxin [Bacillus subtilis] | 77 | 59 |
| 853 | 1 | 186 | 4 | gi\|39962 | ribosomal protein L35 (AA 1-66) [Bacillus stearothermophilus] ir\|S05347\|R5BS35 ribosomal protein L35 - Bacillus earothermophilus | 77 | 66 |
| 944 | 1 | 2 | 172 | gi\|425467 | transposase [Lactobacillus helveticus] | 77 | 50 |
| 10 | 1 | 1 | 258 | gnl\|PID\|e234078 | hom [Lactococcus lactis] | 76 | 63 |
| 12 | 4 | 7650 | 5842 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 76 | 57 |
| 17 | 29 | 29022 | 28153 | gi\|1500003 | mutator mutT protein [Methanococcus jannaschii] | 76 | 47 |
| 23 | 15 | 8897 | 10285 | gi\|153960 | ethanolamine ammonia-lyase (eutB) [Salmonella typhimurium] pir\|A36570\|A36570 ethanolamine ammonia-lyase (EC 4.3.1.7) 55K chain Salmonella typhimurium | 76 | 64 |
| 29 | 2 | 1024 | 500 | gi\|40011 | ORF17 (AA 1-161) [Bacillus subtilis] | 76 | 61 |
| 33 | 1 | 14 | 1552 | gi\|148304 | beta-1,4-N-acetylmuramoylhydrolase | 76 | 60 |

Table 2: E. *faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Enterococcus hirae] pir\|A42296\|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790) | | |
| 34 | 7 | 7432 | 6965 | gi\|44067 | ORF1 C-terminal [Lactococcus lactis] | 76 | 59 |
| 45 | 8 | 3708 | 4166 | gi\|1303698 | BltD [Bacillus subtilis] | 76 | 56 |
| 47 | 9 | 12849 | 10270 | gi\|1002520 | MutS [Bacillus subtilis] | 76 | 59 |
| 55 | 8 | 3614 | 4105 | gi\|1303915 | YqhZ [Bacillus subtilis] | 76 | 53 |
| 55 | 11 | 6385 | 6642 | gi\|216583 | ORF1 [Escherichia coli] | 76 | 45 |
| 57 | 14 | 17283 | 16597 | gi\|1183887 | integral membrane protein [Bacillus subtilis] | 76 | 56 |
| 59 | 6 | 3112 | 2426 | gi\|392872 | repressor protein [Pasteurella multocida] | 76 | 47 |
| 64 | 1 | 1242 | 46 | gi\|483941 | blt gene product [Bacillus subtilis] | 76 | 55 |
| 67 | 3 | 1370 | 2146 | gnl\|PID\|e199390 | orotate phosphoribosyltransferase [Lactobacillus plantarum] | 76 | 57 |
| 69 | 2 | 837 | 334 | gi\|1377831 | unknown [Bacillus subtilis] | 76 | 57 |
| 70 | 1 | 164 | 1588 | gi\|895751 | putative 6-phospho-beta-glucosidase [Bacillus subtilis] pir\|S57762\|S57762 probable 6-phospho-beta-glucosidase - Bacillus ubtilis | 76 | 60 |
| 74 | 11 | 7826 | 7269 | pir\|E53402\|E53402 | serine O-acetyltransferase (EC 2.3.1.30) - Bacillus stearothermophilus | 76 | 54 |
| 74 | 13 | 10073 | 9588 | gi\|289281 | unknown [Bacillus subtilis] | 76 | 60 |
| 85 | 11 | 7809 | 7102 | gi\|457634 | butyrate kinase [Clostridium acetobutylicum] | 76 | 61 |
| 94 | 8 | 6036 | 4801 | gi\|142538 | aspartate aminotransferase [Bacillus sp.] | 76 | 57 |
| 94 | 14 | 17174 | 12801 | gi\|40060 | DNA polymerase III (AA 1-1437) [Bacillus subtilis] p\|P13267\|DP3A_BACSU DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7). | 76 | 62 |
| 94 | 15 | 19140 | 17407 | gi\|1573733 | prolyl-tRNA synthetase (proS) [Haemophilus influenzae] | 76 | 54 |
| 95 | 1 | 1 | 1290 | gi\|472918 | v-type Na-ATPase [Enterococcus hirae] | 76 | 59 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 95 | 4 | 2367 | 3194 | gi\|487276 | Na+ -ATPase subunit C [Enterococcus hirae] | 76 | 48 |
| 99 | 1 | 1 | 171 | gi\|1353874 | unknown [Rhodobacter capsulatus] | 76 | 52 |
| 100 | 5 | 5414 | 5064 | gi\|1591962 | M. jannaschii predicted coding region MJ1322 [Methanococcus jannaschii] | 76 | 46 |
| 100 | 27 | 23165 | 21198 | gi\|216151 | DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi\|579197 SPO2 DNA polymerase (aa 1-648) [Bacteriophage SPO2] pir\|A21498\|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2 | 76 | 62 |
| 106 | 1 | 1511 | 264 | gi\|1750108 | YnbA [Bacillus subtilis] | 76 | 61 |
| 116 | 4 | 2480 | 2854 | gi\|755602 | unknown [Bacillus subtilis] | 76 | 60 |
| 116 | 6 | 3299 | 3625 | gi\|1146234 | dihydrodipicolinate reductase [Bacillus subtilis] | 76 | 56 |
| 122 | 5 | 3029 | 3619 | gi\|467436 | unknown [Bacillus subtilis] | 76 | 52 |
| 123 | 10 | 9109 | 10389 | gi\|1773196 | similar to B. stearothermophilus N-carbamyl-L-amino acid amidohydrolase [Escherichia coli] | 76 | 61 |
| 124 | 5 | 4087 | 3182 | gi\|974332 | NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus ubtilis] | 76 | 58 |
| 130 | 5 | 3341 | 4294 | gi\|308853 | transmembrane protein [Lactococcus lactis] | 76 | 55 |
| 132 | 3 | 2265 | 5117 | gi\|1673889 | (AE000022) Mycoplasma pneumoniae, excinuclease ABC subunit A; similar to Swiss-Prot Accession Number P07671, from E. coli [Mycoplasma pneumoniae] | 76 | 59 |
| 138 | 34 | 25849 | 25409 | gi\|143795 | transfer RNA-Tyr synthetase [Bacillus subtilis] | 76 | 56 |
| 139 | 1 | 3 | 350 | gnl\|PID\|e191395 | mobilisation protein [Lactococcus lactis] | 76 | 65 |
| 141 | 1 | 2 | 544 | gi\|662792 | single-stranded DNA binding protein [unidentified eubacterium] | 76 | 64 |
| 155 | 9 | 7612 | 7058 | gnl\|PID\|e247026 | orf6 [Lactobacillus sake] | 76 | 57 |
| 164 | 4 | 1889 | 2416 | gi\|727436 | putative 20-kDa protein [Lactococcus lactis] | 76 | 55 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 181 | 5 | 3475 | 2288 | gi\|1147744 | PSR [Enterococcus hirae] | 76 | 53 |
| 181 | 8 | 6281 | 4986 | gi\|683583 | 5-enolpyruvylshikimate-3-phosphate synthase [Lactococcus lactis] pir\|S52580\|S52580 3-phosphoshikimate 1-carboxyvinyltransferase (EC .5.1.19) - Lactococcus lactis | 76 | 62 |
| 197 | 7 | 7662 | 8102 | gi\|1783253 | homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis] | 76 | 58 |
| 222 | 16 | 10780 | 11298 | gi\|1591856 | hypothetical protein (SP:P15889) [Methanococcus jannaschii] | 76 | 64 |
| 229 | 1 | 1 | 138 | gi\|148316 | NaH-antiporter protein [Enterococcus hirae] | 76 | 47 |
| 233 | 6 | 3946 | 3341 | gi\|1591652 | hypothetical protein (SP:P31065) [Methanococcus jannaschii] | 76 | 60 |
| 238 | 2 | 844 | 1848 | gi\|622991 | mannitol transport protein [Bacillus stearothermophilus] sp\|P50852\|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL). | 76 | 64 |
| 238 | 9 | 7235 | 7957 | gi\|1592142 | ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii] | 76 | 49 |
| 249 | 2 | 543 | 1235 | gi\|143156 | membrane bound protein [Bacillus subtilis] | 76 | 45 |
| 262 | 3 | 4131 | 2692 | gnl\|PID\|e281591 | catalase [Bacillus subtilis] | 76 | 65 |
| 265 | 1 | 2 | 400 | gi\|141858 | replication-associated protein [Plasmid pAD1] | 76 | 52 |
| 271 | 13 | 8175 | 10844 | gi\|397973 | Mg2+ transport ATPase [Salmonella typhimurium] | 76 | 57 |
| 323 | 4 | 4128 | 4568 | gnl\|PID\|e249023 | T19B10.3 [Caenorhabditis elegans] | 76 | 60 |
| 329 | 5 | 3270 | 2560 | gi\|310631 | ATP binding protein [Streptococcus gordonii] | 76 | 54 |
| 356 | 1 | 971 | 3 | gi\|971479 | orf3 gene product [Lactobacillus | 76 | 52 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | delbrueckii] | | |
| 371 | 1 | 1564 | 944 | gi\|1750125 | xylulose kinase [Bacillus subtilis] | 76 | 57 |
| 375 | 6 | 5137 | 4238 | gi\|1644202 | unknown [Bacillus subtilis] | 76 | 58 |
| 382 | 2 | 508 | 2769 | gi\|442360 | ClpC adenosine triphosphatase [Bacillus subtilis] | 76 | 60 |
| 399 | 11 | 7811 | 8845 | gi\|1572970 | acetate:SH-citrate lyase ligase (AMP) [Haemophilus influenzae] | 76 | 54 |
| 399 | 13 | 9126 | 10034 | gi\|1572968 | citrate lyase beta chain (acyl lyase subunit) (citE) [Haemophilus influenzae] | 76 | 57 |
| 485 | 1 | 3 | 1262 | gi\|564018 | dihydrofolate synthetase [Streptococcus pneumoniae] | 76 | 54 |
| 486 | 2 | 970 | 344 | gi\|1256617 | adenine phosphoribosyltransferase [Bacillus subtilis] | 76 | 61 |
| 536 | 1 | 220 | 2 | gi\|437389 | transposase [Lactococcus lactis] | 76 | 59 |
| 552 | 3 | 3969 | 2491 | gi\|882609 | 6-phospho-beta-glucosidase [Escherichia coli] | 76 | 63 |
| 634 | 2 | 697 | 918 | gi\|1022725 | unknown [Staphylococcus haemolyticus] | 76 | 52 |
| 684 | 3 | 1191 | 688 | gi\|1256653 | DNA-binding protein [Bacillus subtilis] | 76 | 65 |
| 752 | 1 | 1111 | 929 | gi\|407907 | ORF2 [Staphylococcus xylosus] | 76 | 46 |
| 822 | 1 | 548 | 237 | gi\|144313 | 6.0 kd ORF [Plasmid ColE1] | 76 | 73 |
| 923 | 1 | 2 | 421 | gi\|153843 | trypsin-resistant surface T6 protein (tee6) precursor [Streptococcus yogenes] | 76 | 57 |
| 953 | 2 | 534 | 187 | gi\|1592339 | hypothetical protein (PIR:S52522) [Methanococcus jannaschii] | 76 | 44 |
| 965 | 2 | 564 | 343 | gi\|1098898 | CTRP [Plasmodium falciparum] | 76 | 69 |
| 7 | 4 | 3754 | 4161 | gi\|495046 | tripeptidase [Lactococcus lactis] | 75 | 61 |
| 25 | 1 | 2 | 580 | gi\|1575577 | DNA-binding response regulator [Thermotoga maritima] | 75 | 57 |
| 45 | 7 | 3090 | 3350 | gi\|1673663 | (AE000003) Mycoplasma pneumoniae, E07_orf166 Protein [Mycoplasma pneumoniae] | 75 | 35 |
| 47 | 6 | 7526 | 6957 | gi\|1673843 | (AE000019) Mycoplasma pneumoniae, pilB | 75 | 58 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | homolog; similar to GenBank Accession Number E64124, from H. influenzae [Mycoplasma pneumoniae] | | |
| 51 | 1 | 15 | 1520 | sp\|P39168\|ATMA_ECOLI | MG(2+) TRANSPORT ATPASE, P-TYPE 1 (EC 3.6.1.-). | 75 | 58 |
| 54 | 11 | 3761 | 3579 | gi\|1504026 | similar to C.elegans protein (Z37093) [Homo sapiens] | 75 | 56 |
| 55 | 5 | 1648 | 2562 | gi\|1303901 | YqhT [Bacillus subtilis] | 75 | 58 |
| 56 | 8 | 5873 | 5358 | gi\|895749 | putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis] | 75 | 49 |
| 58 | 2 | 2707 | 1916 | gi\|1658403 | formate dehydrogenase alpha subunit [Moorella thermoacetica] | 75 | 58 |
| 71 | 1 | 110 | 1429 | gi\|1304007 | LysA [Bacillus subtilis] | 75 | 58 |
| 74 | 5 | 3436 | 3074 | gi\|467433 | unknown [Bacillus subtilis] | 75 | 61 |
| 74 | 8 | 5491 | 4631 | gi\|467483 | unknown [Bacillus subtilis] | 75 | 60 |
| 77 | 1 | 3 | 992 | gi\|1653966 | 47 kD protein [Synechocystis sp.] | 75 | 34 |
| 81 | 1 | 26 | 862 | gi\|1064809 | homologous to sp:HTRA_ECOLI [Bacillus subtilis] | 75 | 55 |
| 89 | 11 | 11651 | 9801 | gi\|1573881 | hypothetical [Haemophilus influenzae] | 75 | 51 |
| 96 | 3 | 2521 | 1643 | gi\|1531619 | NodB [Rhizobium sp.] | 75 | 54 |
| 98 | 9 | 11494 | 10199 | gi\|1573043 | hypothetical [Haemophilus influenzae] | 75 | 53 |
| 110 | 12 | 11326 | 10283 | gi\|1184121 | auxin-induced protein [Vigna radiata] | 75 | 51 |
| 117 | 13 | 11200 | 9944 | gi\|457635 | vancomycin histidine protein kinase [Enterococcus faecium] gi\|801884 vanS [Transposon Tn1546] | 75 | 51 |
| 122 | 6 | 3812 | 5206 | gi\|467439 | temperature sensitive cell division [Bacillus subtilis] | 75 | 59 |
| 128 | 12 | 8262 | 7921 | gi\|466473 | cellobiose phosphotransferase enzyme II' [Bacillus tearothermophilus] | 75 | 48 |
| 128 | 38 | 31848 | 30733 | gi\|216300 | peptidoglycan synthesis enzyme [Bacillus subtilis] sp\|P37585\|MURG_BACSU MURG PROTEIN UPD-N-ACETYLGLUCOSAMINE--N- | 75 | 56 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | ACETYLMURAMYL-PENTAPEPTIDE)PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE RANSFERASE). | | |
| 129 | 2 | 1916 | 2134 | gnl\|PID\|e267624 | Unknown, highly similar to Pseudomonas putida 4-oxalocrotonate tautomerase [Bacillus subtilis] | 75 | 47 |
| 130 | 4 | 2375 | 3343 | gi\|495179 | transmembrane protein [Lactococcus lactis] | 75 | 55 |
| 133 | 1 | 3 | 1514 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 75 | 54 |
| 158 | 13 | 12326 | 11634 | gi\|809660 | deoxyribose-phosphate aldolase [Bacillus subtilis] pir\|S49455\|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis | 75 | 66 |
| 162 | 13 | 14285 | 12543 | gi\|1653222 | cation-transporting ATPase PacL [Synechocystis sp.] | 75 | 60 |
| 170 | 2 | 1280 | 921 | sp\|P07999\|DHGB_BACME | GLUCOSE 1-DEHYDROGENASE B (EC 1.1.1.47). | 75 | 62 |
| 171 | 7 | 7618 | 8523 | gi\|1303856 | YqgI [Bacillus subtilis] | 75 | 52 |
| 179 | 14 | 14668 | 15255 | gi\|457177 | alkyl hydroperoxide reductase [Salmonella typhimurium] sp\|P19479\|AHPC_SALTY ALKYL HYDROPEROXIDE REDUCTASE C22 PROTEIN (EC .6.4.-). {SUB 2-187} | 75 | 55 |
| 181 | 6 | 4470 | 3604 | gi\|683585 | prephenate dehydratase [Lactococcus lactis] | 75 | 49 |
| 191 | 1 | 183 | 560 | gnl\|PID\|e261991 | putative orf [Bacillus subtilis] | 75 | 57 |
| 197 | 3 | 2117 | 3592 | gi\|1783250 | homologous to cytochrome d ubiquinol oxidase subunit I; hypothetical [Bacillus subtilis] | 75 | 60 |
| 215 | 3 | 2545 | 2201 | gnl\|PID\|e284996 | ORF136 [Staphylococcus aureus] | 75 | 54 |
| 216 | 1 | 2 | 256 | gi\|153570 | H+ ATPase [Enterococcus faecalis] | 75 | 53 |
| 223 | 4 | 2406 | 4193 | gi\|862312 | lytS gene product [Staphylococcus aureus] | 75 | 56 |
| 227 | 5 | 3004 | 3567 | gi\|144729 | butanol dehydrogenase [Clostridium acetobutylicum] sp\|Q04944\|ADHA_CLOAB NADH- | 75 | 53 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | DEPENDENT BUTANOL DEHYDROGENASE A (EC .1.1.-) (BDH I). | | |
| 228 | 9 | 6032 | 5700 | gi\|467410 | unknown [Bacillus subtilis] | 75 | 59 |
| 229 | 16 | 17081 | 16848 | gi\|207398 | tropomyosin T class IVd alpha-3 [Rattus norvegicus] | 75 | 42 |
| 238 | 8 | 6038 | 7237 | gi\|141927 | czcB gene product [Alcaligenes eutrophus] | 75 | 39 |
| 244 | 10 | 7795 | 7460 | gi\|467419 | unknown [Bacillus subtilis] | 75 | 56 |
| 247 | 1 | 7 | 1431 | gi\|577569 | PepV [Lactobacillus delbrueckii] | 75 | 54 |
| 250 | 5 | 3416 | 3201 | gi\|1580783 | sperm receptor [Strongylocentrotus purpuratus] | 75 | 50 |
| 256 | 1 | 2 | 562 | gi\|709991 | hypothetical protein [Bacillus subtilis] | 75 | 56 |
| 262 | 2 | 1031 | 2479 | gi\|142783 | DNA photolyase [Bacillus firmus] | 75 | 59 |
| 263 | 1 | 222 | 890 | gi\|148304 | beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir\|A42296\|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790) | 75 | 60 |
| 266 | 5 | 2224 | 1982 | gnl\|PID\|e253211 | ORF YDL065c [Saccharomyces cerevisiae] | 75 | 50 |
| 269 | 2 | 1477 | 707 | gi\|1736647 | ORF_ID:o347#4; similar to [SwissProt Accession Number P44634] [Escherichia coli] | 75 | 61 |
| 276 | 11 | 7415 | 4593 | gnl\|PID\|e221269 | tail protein [Bacteriophage CP-1] | 75 | 54 |
| 279 | 17 | 14992 | 14651 | gi\|1389549 | ORF3 [Bacillus subtilis] | 75 | 61 |
| 292 | 11 | 7829 | 8470 | gi\|160693 | sporozoite surface protein [Plasmodium yoelii] | 75 | 50 |
| 295 | 2 | 489 | 1157 | gi\|533099 | endonuclease III [Bacillus subtilis] | 75 | 59 |
| 307 | 4 | 3804 | 4889 | gi\|1321625 | exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus] | 75 | 60 |
| 322 | 4 | 1088 | 1996 | gi\|310303 | mosA [Rhizobium meliloti] | 75 | 63 |
| 331 | 1 | 1 | 294 | gi\|1016092 | ribosomal protein S14 [Cyanophora paradoxa] | 75 | 57 |
| 334 | 7 | 6860 | 7969 | gi\|409286 | bmrU [Bacillus subtilis] | 75 | 45 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 340 | 1 | 3 | 743 | gi\|288413 | glutamate dehydrogenase (NADP+) [Corynebacterium glutamicum] pir\|S32227\|S32227 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - orynebacterium glutamicum | 75 | 60 |
| 343 | 2 | 1497 | 778 | gi\|46602 | putative transposase (AA 1 - 224) [Staphylococcus aureus] ir\|S12093\|S12093 probable IS431mec protein - Staphylococcus aureus p\|P19380\|TRA2_STAAU TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT 431MEC. | 75 | 54 |
| 372 | 3 | 865 | 1629 | gi\|146282 | gut operon repressor (gutR) [Escherichia coli] | 75 | 58 |
| 372 | 7 | 6614 | 5307 | gnl\|PID\|e255128 | trigger factor [Bacillus subtilis] | 75 | 62 |
| 387 | 3 | 1721 | 1353 | gi\|580902 | ORF6 gene product [Bacillus subtilis] | 75 | 53 |
| 399 | 30 | 28774 | 29805 | gi\|146278 | glucitol-specific enzyme II (gutA) [Escherichia coli] pir\|A26725\|WQEC2S phosphotransferase system enzyme II (EC .7.1.69), sorbitol-specific, factor II - Escherichia coli sp\|P05705\|PTHB_ECOLI PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC OMPONENT (EIIBC-GUT) | 75 | 61 |
| 399 | 33 | 31077 | 32768 | gi\|517205 | 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes] | 75 | 59 |
| 404 | 6 | 4994 | 4332 | gi\|1303921 | YqiF [Bacillus subtilis] | 75 | 64 |
| 404 | 7 | 4984 | 4829 | gi\|1303921 | YqiF [Bacillus subtilis] | 75 | 60 |
| 419 | 1 | 320 | 3 | gi\|496283 | lysin [Bacteriophage Tuc2009] | 75 | 67 |
| 431 | 3 | 1139 | 759 | sp\|P46351\|YZGD_BACSU | HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION. | 75 | 60 |
| 473 | 1 | 166 | 2 | gnl\|PID\|e229299 | R04D3.8 [Caenorhabditis elegans] | 75 | 35 |
| 481 | 1 | 1 | 351 | gi\|1573766 | phosphoglyceromutase (gpmA) [Haemophilus influenzae] | 75 | 64 |
| 492 | 1 | 440 | 3 | gi\|806487 | ORF211; putative [Lactococcus lactis] | 75 | 57 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 595 | 1 | 705 | 181 | gi\|147485 | queA [Escherichia coli] | 75 | 51 |
| 619 | 2 | 879 | 319 | gi\|1063246 | low homology to P14 protein of Heamophilus influenzar and 14.2 kDa protein of Escherichia coli [Bacillus subtilis] | 75 | 59 |
| 663 | 1 | 15 | 1544 | gi\|475112 | enzyme IIabc [Pediococcus pentosaceus] | 75 | 54 |
| 701 | 4 | 662 | 946 | gi\|143793 | tyrosyl-tRNA synthetase [Bacillus caldotenax] | 75 | 60 |
| 719 | 1 | 970 | 419 | gi\|727436 | putative 20-kDa protein [Lactococcus lactis] | 75 | 56 |
| 886 | 1 | 101 | 409 | gi\|143150 | levR [Bacillus subtilis] | 75 | 59 |
| 939 | 1 | 403 | 191 | gi\|425467 | transposase [Lactobacillus helveticus] | 75 | 53 |
| 984 | 2 | 66 | 227 | gi\|1652190 | Fat protein [Synechocystis sp.] | 75 | 48 |
| 17 | 2 | 2592 | 2924 | gi\|532556 | ORF23 [Enterococcus faecalis] | 74 | 53 |
| 17 | 25 | 24449 | 25639 | gi\|1458228 | mutY homolog [Homo sapiens] | 74 | 50 |
| 21 | 7 | 4729 | 5229 | gi\|726320 | putative protein of unknown function encoded by the IS200-like lement [Yersinia pestis] | 74 | 57 |
| 32 | 9 | 5819 | 4488 | gi\|1498962 | M. jannaschii predicted coding region MJ0188 [Methanococcus jannaschii] | 74 | 41 |
| 38 | 1 | 707 | 3 | gi\|142152 | sulfate permease (gtg start codon) [Synechococcus PCC6301] pir\|A30301\|GRYCS7 sulfate transport protein - Synechococcus sp. PCC 7942) | 74 | 53 |
| 44 | 1 | 1 | 927 | gi\|1377823 | aminopeptidase [Bacillus subtilis] | 74 | 63 |
| 60 | 8 | 8747 | 8070 | gi\|143368 | phosphoribosylformyl glycinamidine synthetase I (PUR-L; gtg start odon) [Bacillus subtilis] | 74 | 63 |
| 72 | 8 | 7388 | 7119 | gnl\|PID\|e209004 | glutaredoxin-like protein [Lactococcus lactis] | 74 | 53 |
| 91 | 4 | 1031 | 2257 | gi\|726480 | L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis] | 74 | 58 |
| 105 | 7 | 5553 | 5855 | gi\|467418 | unknown [Bacillus subtilis] | 74 | 63 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 110 | 18 | 16903 | 15842 | gi\|45288 | arcB (AA 1-336) [Pseudomonas aeruginosa] | 74 | 57 |
| 112 | 3 | 1112 | 636 | gi\|887824 | ORF_o310 [Escherichia coli] | 74 | 53 |
| 123 | 8 | 6105 | 7619 | gi\|1773191 | similar to Pseudomonas sp. ORF5 [Escherichia coli] | 74 | 60 |
| 128 | 1 | 2 | 1315 | gi\|143961 | pyruvate phosphate dikinase [Clostridium symbiosum] pir\|A36231\|KIQAPO pyruvate,orthophosphate dikinase (EC 2.7.9.1) - lostridium symbiosum | 74 | 58 |
| 128 | 26 | 18866 | 20401 | gi\|1303961 | YqjJ [Bacillus subtilis] | 74 | 57 |
| 150 | 5 | 4653 | 5303 | gi\|495046 | tripeptidase [Lactococcus lactis] | 74 | 53 |
| 159 | 8 | 7500 | 6850 | gi\|581098 | GlnQ (AA 1-240); gtg start [Escherichia coli] | 74 | 53 |
| 179 | 1 | 1259 | 57 | gi\|537080 | ribonucleoside triphosphate reductase [Escherichia coli] pir\|A47331\|A47331 oxygen-sensitive ribonucleoside-triphosphate eductase (EC 1.17.4.-) - Escherichia coli | 74 | 62 |
| 183 | 2 | 1669 | 224 | gi\|1146200 | DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis] | 74 | 53 |
| 213 | 4 | 2265 | 3200 | gi\|1373157 | orf-X; hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis] | 74 | 63 |
| 229 | 13 | 13774 | 12806 | gnl\|PID\|e290288 | Met-tRNAi formyl transferase [Bacillus subtilis] | 74 | 55 |
| 238 | 31 | 28648 | 28052 | gi\|451072 | di-tripeptide transporter [Lactococcus lactis] | 74 | 56 |
| 244 | 8 | 6409 | 5552 | gi\|467422 | unknown [Bacillus subtilis] | 74 | 60 |
| 249 | 1 | 7 | 411 | gi\|1591758 | diaminopimelate epimerase [Methanococcus jannaschii] | 74 | 51 |
| 270 | 3 | 1832 | 3955 | gi\|1303829 | YqfK [Bacillus subtilis] | 74 | 55 |
| 276 | 3 | 1668 | 1357 | gi\|496282 | holin [Bacteriophage Tuc2009] | 74 | 54 |
| 288 | 9 | 5807 | 5076 | gi\|530063 | glycerol uptake facilitator [Streptococcus | 74 | 60 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | pneumoniae] sp\|P52281\|GLPF_STRPN GLYCEROL UPTAKE FACILITATOR PROTEIN. | | |
| 292 | 21 | 16780 | 17547 | gi\|1573646 | Mg(2+) transport ATPase protein C (mgtC) (SP:P22037) [Haemophilus influenzae] | 74 | 42 |
| 297 | 1 | 682 | 11 | gnl\|PID\|e255093 | hypothetical protein [Bacillus subtilis] | 74 | 54 |
| 298 | 3 | 3562 | 3095 | gi\|1303970 | YqjS [Bacillus subtilis] | 74 | 46 |
| 321 | 10 | 5081 | 6028 | pir\|A32950\|A32950 | probable reductase protein - Leishmania major | 74 | 56 |
| 327 | 2 | 904 | 3285 | gi\|1573876 | virulence associated protein homolog (vacB) [Haemophilus influenzae] | 74 | 53 |
| 334 | 5 | 3942 | 5432 | gi\|1652678 | amidase [Synechocystis sp.] | 74 | 57 |
| 341 | 13 | 13007 | 12069 | gi\|39881 | ORF 311 (AA 1-311) [Bacillus subtilis] | 74 | 53 |
| 362 | 7 | 3529 | 5274 | gnl\|PID\|e255093 | hypothetical protein [Bacillus subtilis] | 74 | 58 |
| 376 | 3 | 1282 | 2346 | gi\|1773090 | transfer RNA-guanine transglycosylase [Escherichia coli] | 74 | 59 |
| 421 | 2 | 48 | 1400 | gi\|710632 | beta-glucosidase [Bacillus subtilis] | 74 | 58 |
| 471 | 1 | 815 | 3 | gi\|854234 | cymG gene product [Klebsiella oxytoca] | 74 | 53 |
| 480 | 2 | 263 | 607 | gi\|1303994 | YqkM [Bacillus subtilis] | 74 | 48 |
| 518 | 7 | 4409 | 5002 | gi\|145821 | EBG enzyme alpha subunit [Escherichia coli] | 74 | 47 |
| 539 | 8 | 6607 | 7179 | gi\|1165295 | D3703.8p [Saccharomyces cerevisiae] | 74 | 57 |
| 542 | 1 | 750 | 4 | gi\|1064810 | function unknown [Bacillus subtilis] | 74 | 56 |
| 559 | 1 | 1204 | 5 | gi\|43821 | nifJ protein (AA 1-1171) [Klebsiella pneumoniae] p\|P03833\|NIFJ_KLEPN PYRUVATE-FLAVODOXIN OXIDOREDUCTASE (EC -.-.-). | 74 | 58 |
| 579 | 3 | 1373 | 1624 | gi\|1237013 | ORF2 [Bacillus subtilis] | 74 | 46 |
| 624 | 4 | 2518 | 3669 | gi\|467394 | recombination protein [Bacillus subtilis] | 74 | 56 |
| 688 | 1 | 623 | 3 | gi\|662880 | novel hemolytic factor [Bacillus cereus] | 74 | 48 |
| 763 | 1 | 106 | 441 | gi\|153955 | envM protein [Salmonella typhimurium] | 74 | 46 |
| 811 | 1 | 3 | 158 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 74 | 57 |
| 852 | 1 | 2 | 601 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 74 | 53 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 935 | 1 | 976 | 2 | gi\|467403 | seryl-tRNA synthetase [Bacillus subtilis] | 74 | 59 |
| 22 | 2 | 2178 | 2471 | gi\|467460 | unknown [Bacillus subtilis] | 73 | 61 |
| 24 | 2 | 1126 | 3150 | gi\|1303822 | YqfF [Bacillus subtilis] | 73 | 54 |
| 33 | 6 | 6638 | 6970 | gi\|536971 | ORF_o76 [Escherichia coli] | 73 | 56 |
| 48 | 1 | 621 | 1241 | gnl\|PID\|e274111 | aggregation promoting protein [Lactobacillus gasseri] | 73 | 67 |
| 48 | 6 | 5327 | 7225 | gi\|1185289 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus subtilis] | 73 | 56 |
| 50 | 2 | 1097 | 2008 | gi\|1498295 | homoserine kinase homolog [Streptococcus pneumoniae] | 73 | 55 |
| 52 | 4 | 2793 | 4334 | gi\|473902 | alpha-acetolactate synthase [Lactococcus lactis] | 73 | 59 |
| 55 | 1 | 1 | 261 | gi\|396365 | alternate name yjbA [Escherichia coli] | 73 | 36 |
| 60 | 6 | 5935 | 5549 | gi\|551881 | amidophosphoribosyltransferase [Lactobacillus casei] pir\|PC1136\|PC1136 purF protein - Lactobacillus casei (fragment) sp\|P35853\|PUR1_LACCA AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14) GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) FRAGMENT | 73 | 57 |
| 74 | 2 | 477 | 1355 | gnl\|PID\|e233567 | unknown [Mycobacterium tuberculosis] | 73 | 54 |
| 81 | 19 | 14213 | 13845 | gi\|606073 | ORF_o169 [Escherichia coli] | 73 | 52 |
| 93 | 7 | 2861 | 4075 | gi\|405134 | acetate kinase [Bacillus subtilis] | 73 | 56 |
| 100 | 1 | 1057 | 2 | gi\|1353561 | ORF44 [Bacteriophage r1t] | 73 | 52 |
| 100 | 41 | 28872 | 28627 | gi\|188492 | heat shock-induced protein [Homo sapiens] | 73 | 42 |
| 104 | 4 | 5558 | 5274 | gi\|312440 | aspartate carbamoyltransferase [Bacillus caldolyticus] pir\|S34318\|S34318 aspartate carbamoyltransferase (EC 2.1.3.2) - acillus caldolyticus | 73 | 55 |
| 119 | 5 | 3264 | 3638 | gi\|473707 | positive regulator for virulence factors [Clostridium perfringens] | 73 | 39 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 123 | 17 | 16156 | 15665 | gi\|1303703 | YrkD [Bacillus subtilis] | 73 | 37 |
| 123 | 18 | 16133 | 16465 | gi\|1303893 | YqhL [Bacillus subtilis] | 73 | 43 |
| 124 | 3 | 2165 | 1722 | gi\|486661 | TMnm related protein [Saccharomyces cerevisiae] | 73 | 45 |
| 127 | 6 | 5778 | 5101 | gi\|290561 | o188 [Escherichia coli] | 73 | 48 |
| 128 | 10 | 6896 | 7201 | pir\|S37387\|S37387 | internalin A precursor - Listeria monocytogenes | 73 | 53 |
| 137 | 2 | 980 | 1954 | gi\|1276882 | EpsI [Streptococcus thermophilus] | 73 | 56 |
| 141 | 3 | 942 | 2777 | gi\|467336 | unknown [Bacillus subtilis] | 73 | 49 |
| 146 | 7 | 5611 | 4739 | gi\|149395 | lacC [Lactococcus lactis] | 73 | 56 |
| 154 | 6 | 3566 | 4621 | gi\|1354775 | pfoS/R [Treponema pallidum] | 73 | 46 |
| 155 | 8 | 7136 | 6726 | gnl\|PID\|e247026 | orf6 [Lactobacillus sake] | 73 | 61 |
| 158 | 8 | 8693 | 7119 | gi\|1674275 | (AE000056) Mycoplasma pneumoniae, hypothetical ABC transporter (yjcW) homolog; similar to Swiss-Prot Accession Number P32721, from E. coli [Mycoplasma pneumoniae] | 73 | 45 |
| 162 | 4 | 4039 | 3305 | gi\|142997 | glycerol uptake facilitator [Bacillus subtilis] | 73 | 55 |
| 165 | 4 | 3962 | 3105 | gi\|882736 | ORF_f278 [Escherichia coli] | 73 | 58 |
| 171 | 3 | 3952 | 4689 | gnl\|PID\|e63527 | FtsE [Mycobacterium tuberculosis] | 73 | 56 |
| 171 | 5 | 5673 | 6596 | gi\|1303854 | YqgG [Bacillus subtilis] | 73 | 59 |
| 179 | 9 | 9302 | 10414 | gnl\|PID\|e254984 | hypothetical protein [Bacillus subtilis] | 73 | 55 |
| 180 | 1 | 24 | 1151 | gi\|43985 | nifS-like gene [Lactobacillus delbrueckii] | 73 | 56 |
| 181 | 12 | 10036 | 9674 | gnl\|PID\|e220317 | chorismate mutase [Staphylococcus xylosus] | 73 | 50 |
| 181 | 13 | 10713 | 10003 | gi\|39813 | phospho-2-dehydro-3-deoxyheptonate aldolase [Bacillus subtilis] ir\|S21418\|S21418 phospho-2-dehydro-3-deoxyheptonate aldolase (EC 1.2.15) - Bacillus subtilis | 73 | 56 |
| 183 | 3 | 2716 | 1667 | gi\|1146199 | putative [Bacillus subtilis] | 73 | 36 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 198 | 1 | 869 | 108 | gi\|142854 | homologous to E. coli radC gene product and to unidentified protein rom Staphylococcus aureus [Bacillus subtilis] | 73 | 47 |
| 210 | 1 | 956 | 3 | gnl\|PID\|e281310 | acetyl coenzyme A acetyltransferase (thiolase) [Thermoanaerobacterium thermosaccharolyticum] | 73 | 54 |
| 230 | 1 | 1 | 171 | gi\|304143 | S-layer protein [Bacillus circulans] | 73 | 46 |
| 235 | 1 | 715 | 2 | gi\|1732315 | transport system permease homolog [Listeria monocytogenes] | 73 | 49 |
| 235 | 2 | 888 | 676 | gi\|551726 | sporulation protein [Bacillus subtilis] | 73 | 54 |
| 242 | 4 | 3290 | 3517 | gnl\|PID\|e236570 | orf6 gene product [Enterococcus faecalis] | 73 | 30 |
| 242 | 8 | 5914 | 6492 | gi\|1742340 | HipB protein. [Escherichia coli] | 73 | 49 |
| 250 | 3 | 3037 | 2411 | gi\|1174238 | TipB [Pseudomonas fluorescens] | 73 | 57 |
| 254 | 5 | 1124 | 792 | gi\|580900 | ORF3 gene product [Bacillus subtilis] | 73 | 52 |
| 269 | 9 | 5507 | 5154 | gi\|1303790 | YqeI [Bacillus subtilis] | 73 | 60 |
| 269 | 12 | 7989 | 7345 | gi\|285621 | undefined open reading frame [Bacillus stearothermophilus] | 73 | 54 |
| 284 | 1 | 1 | 915 | gi\|455528 | ORF2 [Streptococcus thermophilus bacteriophage] | 73 | 54 |
| 290 | 3 | 1932 | 2678 | gnl\|PID\|e248883 | unknown [Mycobacterium tuberculosis] | 73 | 57 |
| 295 | 8 | 4521 | 4739 | gi\|145478 | putative [Escherichia coli] | 73 | 56 |
| 296 | 1 | 2 | 1846 | gnl\|PID\|e249642 | transketolase [Bacillus subtilis] | 73 | 59 |
| 310 | 4 | 3488 | 3036 | gi\|1591900 | nucleoside diphosphate kinase [Methanococcus jannaschii] | 73 | 48 |
| 313 | 1 | 17 | 778 | gi\|1658371 | cyclic beta-1,2-glucan modification protein [Rhizobium meliloti] | 73 | 60 |
| 314 | 3 | 2642 | 2067 | gi\|1330343 | C34D4.12 gene product [Caenorhabditis elegans] | 73 | 56 |
| 325 | 1 | 492 | 4 | gi\|407908 | EIIscr [Staphylococcus xylosus] | 73 | 56 |
| 345 | 19 | 20549 | 21901 | gi\|443691 | glutathione reductase [Streptococcus thermophilus] | 73 | 59 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 359 | 4 | 3280 | 2252 | gi\|1001478 | hypothetical protein [Synechocystis sp.] | 73 | 50 |
| 374 | 1 | 884 | 3 | gi\|435123 | PacL [Synechococcus sp.] | 73 | 58 |
| 379 | 6 | 5676 | 4339 | gi\|887822 | possible frameshift at end to join to next ORF? [Escherichia coli] | 73 | 57 |
| 383 | 4 | 3815 | 3387 | gi\|1651732 | mutator MutT protein [Synechocystis sp.] | 73 | 52 |
| 392 | 4 | 3454 | 5202 | gi\|294587 | minimal change nephritis transmembrane glycoprotein [Rattus orvegicus] | 73 | 56 |
| 394 | 5 | 4267 | 5250 | gi\|49011 | amidinotransferase II [Streptomyces griseus] | 73 | 42 |
| 395 | 10 | 4252 | 4608 | gi\|1591139 | M. jannaschii predicted coding region MJ0435 [Methanococcus jannaschii] | 73 | 48 |
| 397 | 1 | 885 | 4 | gnl\|PID\|e249658 | GrlA [Bacillus subtilis] | 73 | 56 |
| 399 | 15 | 10007 | 11569 | gi\|565619 | citrate lyase alpha-subunit [Klebsiella pneumoniae] pir\|S60776\|S60776 citrate (pro-3S)-lyase (EC 4.1.3.6) alpha chain - lebsiella pneumoniae | 73 | 54 |
| 416 | 2 | 660 | 1649 | gi\|475114 | regulatory protein [Pediococcus pentosaceus] | 73 | 50 |
| 436 | 6 | 4124 | 3540 | gi\|727436 | putative 20-kDa protein [Lactococcus lactis] | 73 | 53 |
| 446 | 3 | 1618 | 4260 | gi\|882711 | exonuclease V alpha-subunit [Escherichia coli] | 73 | 48 |
| 462 | 1 | 819 | 43 | gi\|1399011 | immunogenic secreted protein precursor [Streptococcus pyogenes] | 73 | 63 |
| 482 | 5 | 3181 | 2501 | gi\|1072419 | glcB gene product [Staphylococcus carnosus] | 73 | 55 |
| 495 | 4 | 1340 | 3031 | gi\|146547 | kdpA [Escherichia coli] | 73 | 55 |
| 523 | 4 | 2354 | 1821 | pir\|A00392\|RDSODF | dihydrofolate reductase (EC 1.5.1.3) - Enterococcus faecium | 73 | 54 |
| 543 | 5 | 3099 | 2893 | gi\|19743 | nsGRP-2 [Nicotiana sylvestris] | 73 | 53 |
| 567 | 1 | 9 | 740 | gi\|1147601 | cyclophilin isoform 4 [Caenorhabditis elegans] | 73 | 54 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 629 | 1 | 945 | 4 | gi\|1006620 | ABC transporter [Synechocystis sp.] | 73 | 46 |
| 714 | 2 | 344 | 556 | gi\|1045872 | ATP-binding protein [Mycoplasma genitalium] | 73 | 61 |
| 747 | 1 | 320 | 3 | gi\|437389 | transposase [Lactococcus lactis] | 73 | 56 |
| 764 | 1 | 3 | 515 | gi\|532554 | ORF21 [Enterococcus faecalis] | 73 | 50 |
| 766 | 1 | 683 | 3 | gi\|1673788 | (AE000015) Mycoplasma pneumoniae, fructose-bisphosphate aldolase; similar to Swiss-Prot Accession Number P13243, from B. subtilis [Mycoplasma pneumoniae] | 73 | 52 |
| 880 | 1 | 198 | 4 | gi\|309661 | regulatory protein [Plasmid pCF10] | 73 | 50 |
| 897 | 1 | 3 | 170 | gi\|807976 | unknown [Saccharomyces cerevisiae] | 73 | 57 |
| 5 | 1 | 223 | 2 | gnl\|PID\|e255315 | unknown [Mycobacterium tuberculosis] | 72 | 56 |
| 8 | 5 | 4158 | 4799 | gi\|587088 | shikimate kinase [Bacillus subtilis] | 72 | 54 |
| 19 | 6 | 2600 | 2833 | gi\|34844 | embryonic myosin heavy chain (AA 1 - 1940) [Homo sapiens] ir\|S04090\|S04090 myosin heavy chain, skeletal muscle, embryonic - man | 72 | 38 |
| 19 | 25 | 12872 | 14605 | gnl\|PID\|e242896 | orf5 [Bacteriophage A2] | 72 | 52 |
| 21 | 4 | 2777 | 2598 | gi\|54115 | skeletal muscle chloride channel [Mus musculus domesticus] | 72 | 45 |
| 23 | 7 | 3702 | 4847 | gi\|144714 | NADPH-dependent butanol dehydrogenase [Clostridium acetobutylicum] pir\|JU0053\|JU0053 NADPH-dependent butanol dehydrogenase - lostridium acetobutylicum | 72 | 48 |
| 32 | 1 | 1073 | 3 | gi\|1303839 | YqfR [Bacillus subtilis] | 72 | 50 |
| 39 | 8 | 4137 | 3244 | pir\|A32950\|A32950 | probable reductase protein - Leishmania major | 72 | 55 |
| 43 | 3 | 969 | 1919 | gi\|290494 | o287 [Escherichia coli] | 72 | 46 |
| 45 | 2 | 911 | 1567 | gi\|1039479 | ORFU [Lactococcus lactis] | 72 | 50 |
| 55 | 6 | 2549 | 2896 | gi\|755602 | unknown [Bacillus subtilis] | 72 | 51 |
| 55 | 7 | 3178 | 3660 | gi\|1303914 | YqhY [Bacillus subtilis] | 72 | 49 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 60 | 1 | 1302 | 34 | gi\|143374 | phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) Bacillus subtilis] | 72 | 59 |
| 60 | 3 | 3422 | 2838 | gi\|143372 | phosphoribosyl glycinamide formyltransferase (PUR-N) [Bacillus ubtilis] | 72 | 48 |
| 60 | 10 | 9771 | 9010 | gi\|143367 | phosphoribosyl aminoidazole succinocarboxamide synthetase (PUR-C; tg start codon) [Bacillus subtilis] | 72 | 57 |
| 70 | 5 | 3615 | 3833 | sp\|P43672\|YCBH_ECOLI | HYPOTHETICAL 14.4 KD PROTEIN IN PYRD-PQIA INTERGENIC REGION. | 72 | 48 |
| 79 | 2 | 632 | 841 | gi\|1652343 | ABC transporter [Synechocystis sp.] | 72 | 47 |
| 85 | 2 | 1843 | 770 | gi\|1354775 | pfoS/R [Treponema pallidum] | 72 | 45 |
| 87 | 1 | 2 | 745 | gi\|42029 | ORF1 gene product [Escherichia coli] | 72 | 47 |
| 88 | 1 | 124 | 1047 | gi\|535348 | CodV [Bacillus subtilis] | 72 | 50 |
| 88 | 7 | 3862 | 4752 | gi\|149413 | ORF [Lactococcus lactis] | 72 | 51 |
| 91 | 2 | 611 | 877 | gi\|726480 | L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis] | 72 | 57 |
| 98 | 16 | 16302 | 15163 | gi\|147326 | transport protein [Escherichia coli] | 72 | 57 |
| 101 | 6 | 4676 | 4023 | gi\|1109685 | ProW [Bacillus subtilis] | 72 | 53 |
| 104 | 3 | 5331 | 3982 | gi\|312441 | dihydroorotase [Bacillus caldolyticus] | 72 | 58 |
| 114 | 10 | 11165 | 12205 | gi\|556881 | Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] pir\|S49358\|S49358 ipc-29d protein - Bacillus subtilis sp\|P39153\|YWLC_BACSU HYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC NTERGENIC REGION. | 72 | 60 |
| 128 | 19 | 14325 | 11560 | gi\|143150 | levR [Bacillus subtilis] | 72 | 58 |
| 130 | 2 | 382 | 1437 | gi\|308850 | ATP binding protein [Lactococcus lactis] | 72 | 55 |
| 135 | 4 | 5012 | 3693 | gi\|413940 | ipa-16d gene product [Bacillus subtilis] | 72 | 56 |
| 150 | 6 | 5114 | 5878 | gi\|495046 | tripeptidase [Lactococcus lactis] | 72 | 54 |
| 154 | 9 | 5850 | 5677 | gi\|425467 | transposase [Lactobacillus helveticus] | 72 | 52 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 168 | 4 | 1375 | 1563 | gi\|1652869 | NADH dehydrogenase [Synechocystis sp.] | 72 | 55 |
| 173 | 5 | 2879 | 4024 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 72 | 57 |
| 179 | 2 | 1608 | 2399 | gi\|709993 | hypothetical protein [Bacillus subtilis] | 72 | 45 |
| 179 | 6 | 7584 | 7844 | gi\|1161934 | DltC [Lactobacillus casei] | 72 | 54 |
| 180 | 21 | 19948 | 21105 | gi\|1773197 | similar to M. fervidus malate dehydrogenase [Escherichia coli] | 72 | 55 |
| 182 | 1 | 3 | 413 | gi\|1146182 | putative [Bacillus subtilis] | 72 | 48 |
| 200 | 23 | 13106 | 12789 | gi\|1707358 | polyprotein precurser [Soybean mosaic virus] | 72 | 34 |
| 204 | 6 | 2462 | 2289 | gi\|1200525 | dihydrolipoamide acetyltransferase [Pseudomonas aeruginosa] | 72 | 61 |
| 204 | 9 | 6374 | 5187 | gi\|1732040 | alcohol dehydrogenase [Actinobacillus pleuropneumoniae] | 72 | 56 |
| 205 | 1 | 463 | 71 | gi\|42029 | ORF1 gene product [Escherichia coli] | 72 | 57 |
| 210 | 7 | 6433 | 5279 | gi\|142978 | glycerol dehydrogenase [Bacillus stearothermophilus] pir\|JQ1474\|JQ1474 glycerol dehydrogenase (EC 1.1.1.6) - Bacillus tearothermophilus | 72 | 46 |
| 213 | 6 | 4086 | 5141 | gi\|431231 | uracil permease [Bacillus caldolyticus] | 72 | 51 |
| 223 | 1 | 99 | 833 | gi\|1573615 | ATP-binding protein (abc) [Haemophilus influenzae] | 72 | 47 |
| 227 | 1 | 26 | 886 | gi\|1070015 | protein-dependent [Bacillus subtilis] | 72 | 52 |
| 228 | 4 | 2047 | 2481 | gi\|467339 | unknown [Bacillus subtilis] | 72 | 50 |
| 238 | 17 | 14728 | 15582 | gi\|882736 | ORF_f278 [Escherichia coli] | 72 | 59 |
| 250 | 6 | 4169 | 4765 | gi\|437389 | transposase [Lactococcus lactis] | 72 | 56 |
| 258 | 7 | 5296 | 7089 | gi\|192185 | acid beta-galactosidase [Mus musculus] | 72 | 53 |
| 266 | 3 | 2024 | 1773 | gi\|145149 | ORFd [Escherichia coli] | 72 | 50 |
| 269 | 8 | 5142 | 4477 | gi\|1303791 | YqeJ [Bacillus subtilis] | 72 | 45 |
| 276 | 13 | 9843 | 8152 | gnl\|PID\|e59644 | predicted 86.4kd protein; 52Kd observed [Mycobacteriophage 15] | 72 | 48 |
| 278 | 2 | 965 | 1573 | gi\|425467 | transposase [Lactobacillus helveticus] | 72 | 52 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 279 | 2 | 1305 | 340 | gnl\|PID\|e198981 | ttg start [Campylobacter coli] | 72 | 47 |
| 283 | 4 | 1668 | 2045 | gi\|1353563 | ORF46 [Bacteriophage r1t] | 72 | 48 |
| 286 | 2 | 789 | 2606 | gi\|1651216 | Pz-peptidase [Bacillus licheniformis] | 72 | 52 |
| 290 | 4 | 2676 | 3239 | gi\|1653645 | ribosome releasing factor [Synechocystis sp.] | 72 | 56 |
| 301 | 2 | 1762 | 899 | gi\|606013 | CG Site No. 829 [Escherichia coli] | 72 | 57 |
| 362 | 2 | 377 | 688 | gi\|1001826 | cadmium-transporting ATPase [Synechocystis sp.] | 72 | 53 |
| 369 | 1 | 582 | 142 | gi\|153745 | mannitol-specific enzyme III [Streptococcus mutans] pir\|B44798\|B44798 mannitol-specific factor III, MtlF - treptococcus mutans | 72 | 47 |
| 379 | 2 | 1934 | 1527 | gi\|1055071 | C23G10.2 gene product [Caenorhabditis elegans] | 72 | 51 |
| 384 | 2 | 694 | 1098 | gi\|1208474 | hypothetical protein [Synechocystis sp.] | 72 | 49 |
| 388 | 1 | 291 | 4 | gi\|1673836 | (AE000018) Mycoplasma pneumoniae, osmotically inducible protein; similar to Swiss-Prot Accession Number P23929, from E. coli [Mycoplasma pneumoniae] | 72 | 43 |
| 401 | 6 | 3995 | 5137 | gi\|508242 | ORF 6, putative Galf synthesis pathway protein [Escherichia coli] gi\|510253 orf6 [Escherichia coli] | 72 | 62 |
| 404 | 2 | 2119 | 776 | gi\|466474 | cellobiose phosphotransferase enzyme II'' [Bacillus tearothermophilus] | 72 | 48 |
| 416 | 4 | 3461 | 1980 | gi\|710632 | beta-glucosidase [Bacillus subtilis] | 72 | 55 |
| 416 | 7 | 6285 | 5551 | gnl\|PID\|e269549 | Unknown [Bacillus subtilis] | 72 | 52 |
| 419 | 3 | 759 | 505 | gi\|928830 | ORF75; putative [Lactococcus lactis phage BK5-T] | 72 | 47 |
| 441 | 4 | 3420 | 4676 | gi\|1732195 | beta-cystathionase [Vibrio furnissii] | 72 | 54 |
| 460 | 3 | 1385 | 2641 | gi\|1652389 | beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.] | 72 | 55 |
| 460 | 5 | 3129 | 3560 | gnl\|PID\|e289141 | similar to hydroxymyristoyl-(acyl carrier | 72 | 54 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | protein) dehydratase [Bacillus subtilis] | | |
| 460 | 8 | 5817 | 6023 | gi\|285621 | undefined open reading frame [Bacillus stearothermophilus] | 72 | 57 |
| 462 | 2 | 1591 | 785 | gi\|148304 | beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir\|A42296\|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus irae (ATCC 9790) | 72 | 51 |
| 467 | 1 | 2 | 706 | gi\|148711 | 6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium sp.] gi\|488343 6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium p.] | 72 | 50 |
| 469 | 3 | 1144 | 1419 | gi\|466474 | cellobiose phosphotransferase enzyme II'' [Bacillus tearothermophilus] | 72 | 48 |
| 493 | 1 | 1124 | 240 | sp\|P50848\|YPWA_BACSU | HYPOTHETICAL 58.2 KD PROTEIN IN KDGT-XPT INTERGENIC REGION. | 72 | 58 |
| 536 | 2 | 379 | 218 | gi\|437389 | transposase [Lactococcus lactis] | 72 | 58 |
| 543 | 1 | 574 | 86 | gi\|290513 | f470 [Escherichia coli] | 72 | 47 |
| 592 | 1 | 57 | 680 | gi\|987092 | ABC-transporter [Streptomyces hygroscopicus] | 72 | 55 |
| 666 | 2 | 551 | 967 | gi\|1064786 | function unknown [Bacillus subtilis] | 72 | 48 |
| 762 | 1 | 974 | 273 | gi\|304928 | pantothenate synthetase [Escherichia coli] | 72 | 55 |
| 792 | 1 | 401 | 3 | pir\|A36933\|A36933 | diacylglycerol kinase homolog - Streptococcus mutans | 72 | 50 |
| 873 | 1 | 183 | 4 | gnl\|PID\|e258329 | oxaloacetate decarboxylase alpha-chain [Legionella pneumophila] | 72 | 55 |
| 4 | 4 | 3799 | 3155 | gi\|496943 | ORF [Saccharomyces cerevisiae] | 71 | 45 |
| 10 | 2 | 180 | 977 | gnl\|PID\|e234078 | hom [Lactococcus lactis] | 71 | 49 |
| 16 | 7 | 4922 | 6097 | gi\|534982 | phosphoglucomutase [Spinacia oleracea] | 71 | 54 |
| 21 | 6 | 4148 | 3972 | gi\|1736645 | Proline/betaine transporter (Proline porter II) (PPII). [Escherichia coli] | 71 | 50 |
| 23 | 27 | 16452 | 17459 | gi\|1408503 | yxeR gene product [Bacillus subtilis] | 71 | 52 |
| 25 | 7 | 5812 | 6669 | gi\|413943 | ipa-19d gene product [Bacillus subtilis] | 71 | 58 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 31 | 1 | 80 | 946 | gi\|534045 | antiterminator [Bacillus subtilis] | 71 | 47 |
| 39 | 3 | 755 | 1297 | sp\|P09997\|YIDA_ECOLI | HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION. | 71 | 50 |
| 39 | 7 | 2537 | 3193 | pir\|C43748\|C43748 | hypothetical protein (pepX 3' region) - Lactococcus lactis subsp. lactis | 71 | 54 |
| 45 | 10 | 5119 | 5484 | gi\|606044 | ORF_o130; Geneplot suggests frameshift, none found [Escherichia oli] | 71 | 51 |
| 48 | 10 | 11722 | 10148 | gi\|20432 | 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum] ir\|S01667\|S01667 4-coumarate--CoA ligase (EC 6.2.1.12) (clone 4CL-1) - parsley | 71 | 39 |
| 55 | 4 | 1470 | 1709 | gi\|1303901 | YqhT [Bacillus subtilis] | 71 | 54 |
| 57 | 10 | 12899 | 13060 | gi\|40053 | phenylalanyl-tRNA synthetase alpha subunit [Bacillus subtilis] ir\|S11730\|YFBSA phenylalanine--tRNA ligase (EC 6.1.1.20) alpha ain - Bacillus subtilis | 71 | 45 |
| 58 | 3 | 3743 | 2571 | gi\|1658403 | formate dehydrogenase alpha subunit [Moorella thermoacetica] | 71 | 51 |
| 68 | 11 | 8225 | 8602 | gi\|793910 | surface antigen [Homo sapiens] | 71 | 49 |
| 74 | 4 | 2908 | 2042 | gi\|467435 | unknown [Bacillus subtilis] | 71 | 55 |
| 85 | 3 | 3267 | 1966 | gi\|142613 | branched chain alpha-keto acid dehydrogenase E2 [Bacillus subtilis] gi\|1303944 BfmBB [Bacillus subtilis] | 71 | 56 |
| 111 | 8 | 5737 | 4253 | gi\|1256135 | YbbF [Bacillus subtilis] | 71 | 50 |
| 111 | 9 | 6590 | 5730 | gi\|1573762 | glucokinase regulator [Haemophilus influenzae] | 71 | 53 |
| 120 | 1 | 111 | 353 | gnl\|PID\|e235823 | unknown [Schizosaccharomyces pombe] | 71 | 52 |
| 123 | 11 | 10387 | 11196 | gi\|1773195 | hypothetical [Escherichia coli] | 71 | 55 |
| 151 | 3 | 4045 | 3098 | gi\|1256618 | transport protein [Bacillus subtilis] | 71 | 51 |
| 172 | 6 | 3949 | 4806 | gi\|1262288 | CdsA [Brucella abortus] | 71 | 56 |
| 172 | 7 | 5264 | 6448 | gi\|40100 | rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir\|S06049\|S06049 rodC | 71 | 52 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | protein - Bacillus subtilis p\|P13485\|TAGF_BACSU TEICHOIC ACID BIOSYNTHESIS PROTEIN F. | | |
| 190 | 7 | 3454 | 3122 | gi\|532556 | ORF23 [Enterococcus faecalis] | 71 | 52 |
| 195 | 24 | 9850 | 11871 | gi\|405564 | traE [Plasmid pSK41] | 71 | 45 |
| 215 | 4 | 3361 | 2711 | gi\|1573086 | uridine kinase (uridine monophosphokinase) (udk) [Haemophilus influenzae] | 71 | 51 |
| 218 | 2 | 1456 | 2613 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 71 | 41 |
| 222 | 3 | 1205 | 2053 | gnl\|PID\|e255114 | glutamate racemase [Bacillus subtilis] | 71 | 56 |
| 222 | 4 | 1611 | 1387 | gi\|1001195 | phosphate transport system permease protein PstA [Synechocystis sp.] | 71 | 57 |
| 222 | 14 | 8852 | 9853 | gi\|466720 | No definition line found [Escherichia coli] | 71 | 53 |
| 238 | 22 | 19256 | 20578 | gi\|595299 | YgiK [Salmonella typhimurium] | 71 | 50 |
| 255 | 3 | 2692 | 1061 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 71 | 55 |
| 265 | 5 | 2960 | 1581 | gi\|1039479 | ORFU [Lactococcus lactis] | 71 | 58 |
| 276 | 2 | 1359 | 538 | gi\|496283 | lysin [Bacteriophage Tuc2009] | 71 | 63 |
| 290 | 5 | 3552 | 4379 | gi\|1016162 | ABC transporter subunit [Cyanophora paradoxa] | 71 | 49 |
| 290 | 7 | 5659 | 6912 | gi\|1001708 | NifS [Synechocystis sp.] | 71 | 56 |
| 292 | 3 | 948 | 2156 | gnl\|PID\|e233874 | hypothetical protein [Bacillus subtilis] | 71 | 55 |
| 318 | 4 | 3229 | 2285 | gi\|1256138 | YbbI [Bacillus subtilis] | 71 | 54 |
| 333 | 1 | 145 | 741 | gi\|293011 | unknown protein [Lactococcus lactis] | 71 | 50 |
| 344 | 1 | 76 | 396 | gi\|853775 | unknown [Bacillus subtilis] | 71 | 53 |
| 350 | 1 | 138 | 1394 | gi\|1652389 | beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.] | 71 | 57 |
| 363 | 4 | 4184 | 5674 | gi\|1657518 | similar to fdrA gene of E. coli [Escherichia coli] | 71 | 54 |
| 364 | 5 | 5319 | 6563 | gi\|1657522 | hypothetical protein [Escherichia coli] | 71 | 46 |
| 367 | 13 | 6539 | 6162 | gi\|44225 | ribosomal protein L18 (AA 1-116) | 71 | 51 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Mycoplasma capricolum] ir\|S02847\|R5YM18 ribosomal protein L18 - Mycoplasma capricolum GC3) | | |
| 379 | 7 | 6884 | 5655 | gi\|887821 | ORF_o398 [Escherichia coli] | 71 | 50 |
| 399 | 9 | 6528 | 7664 | gi\|154198 | oxaloacetate decarboxylase [Salmonella typhimurium] pir\|C44465\|C44465 sodium ion pump oxaloacetate decarboxylase ubunit beta - Salmonella typhimurium | 71 | 50 |
| 399 | 18 | 13540 | 14778 | gi\|143165 | malic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] pir\|A33307\|DEBSXS malate dehydrogenase oxaloacetate-decarboxylating) (EC 1.1.1.38) - Bacillus tearothermophilus | 71 | 46 |
| 404 | 4 | 3769 | 3029 | gi\|143402 | recombination protein (ttg start codon) [Bacillus subtilis] gi\|1303923 RecN [Bacillus subtilis] | 71 | 48 |
| 464 | 1 | 1532 | 216 | gi\|895749 | putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis] | 71 | 40 |
| 464 | 3 | 2088 | 2846 | gi\|1486242 | unknown [Bacillus subtilis] | 71 | 39 |
| 481 | 2 | 954 | 409 | gi\|144729 | butanol dehydrogenase [Clostridium acetobutylicum] sp\|Q04944\|ADHA_CLOAB NADH-DEPENDENT BUTANOL DEHYDROGENASE A (EC .1.1.-) (BDH I). | 71 | 58 |
| 482 | 4 | 2503 | 1841 | gi\|1072418 | glcA gene product [Staphylococcus carnosus] | 71 | 58 |
| 496 | 2 | 1636 | 848 | gi\|1001226 | methionine aminopeptidase [Synechocystis sp.] | 71 | 51 |
| 503 | 2 | 1624 | 650 | gi\|39478 | ATP binding protein of transport ATPases [Bacillus firmus] ir\|S15486\|S15486 ATP-binding protein - Bacillus firmus p\|P26946\|YATR_BACFI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING OTEIN. | 71 | 49 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 513 | 2 | 1590 | 982 | gnl\|PID\|e202290 | unknown [Lactobacillus sake] | 71 | 46 |
| 530 | 1 | 2 | 1534 | gi\|1542974 | AbcA [Thermoanaerobacterium thermosulfurigenes] | 71 | 52 |
| 537 | 1 | 706 | 365 | gi\|929972 | ORFB; similar to B. anthracis SterneL element ORFB; putative S150-like transposase [Bacillus anthracis] | 71 | 57 |
| 553 | 1 | 304 | 1287 | gi\|1653479 | regulatory components of sensory transduction system [Synechocystis sp.] | 71 | 48 |
| 573 | 9 | 5560 | 5090 | gi\|143799 | MtrA [Bacillus subtilis] | 71 | 59 |
| 583 | 1 | 21 | 341 | gi\|1064791 | function umknown [Bacillus subtilis] | 71 | 50 |
| 584 | 2 | 638 | 276 | gi\|662792 | single-stranded DNA binding protein [unidentified eubacterium] | 71 | 58 |
| 585 | 1 | 282 | 809 | gi\|666972 | ORF 168 [Synechococcus sp.] | 71 | 46 |
| 611 | 1 | 985 | 2 | gi\|1039479 | ORFU [Lactococcus lactis] | 71 | 55 |
| 616 | 1 | 350 | 3 | gi\|1088272 | nitrogen fixation protein [Bacillus cereus] | 71 | 52 |
| 624 | 1 | 61 | 399 | gi\|40014 | pot. ORF 446 (aa 1-446) [Bacillus subtilis] | 71 | 53 |
| 624 | 2 | 608 | 1732 | gi\|40015 | pot. ORF 378 (aa 1-378) [Bacillus subtilis] | 71 | 51 |
| 659 | 1 | 76 | 582 | gi\|1591045 | hypothetical protein (SP:P31466) [Methanococcus jannaschii] | 71 | 51 |
| 668 | 2 | 836 | 1030 | gi\|467330 | replicative DNA helicase [Bacillus subtilis] | 71 | 60 |
| 683 | 1 | 582 | 118 | gnl\|PID\|e264663 | CinA [Streptococcus pneumoniae] | 71 | 55 |
| 701 | 3 | 411 | 797 | gi\|143795 | transfer RNA-Tyr synthetase [Bacillus subtilis] | 71 | 51 |
| 720 | 1 | 1 | 351 | gi\|1595810 | type-I signal peptidase SpsB [Staphylococcus aureus] | 71 | 55 |
| 724 | 2 | 1020 | 415 | gnl\|PID\|e239621 | ORF YNL218w [Saccharomyces cerevisiae] | 71 | 51 |
| 790 | 2 | 658 | 383 | gi\|1783253 | homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis] | 71 | 48 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 799 | 1 | 505 | 906 | gi\|580866 | ipa-12d gene product [Bacillus subtilis] | 71 | 45 |
| 974 | 2 | 139 | 333 | gi\|1778531 | HI0021 homolog [Escherichia coli] | 71 | 42 |
| 980 | 1 | 156 | 497 | gi\|437389 | transposase [Lactococcus lactis] | 71 | 57 |
| 4 | 3 | 3170 | 2418 | gi\|1001805 | hypothetical protein [Synechocystis sp.] | 70 | 55 |
| 17 | 21 | 18642 | 21527 | gi\|145821 | EBG enzyme alpha subunit [Escherichia coli] | 70 | 53 |
| 19 | 8 | 2894 | 3952 | gi\|1353527 | ORF10 [Bacteriophage r1t] | 70 | 58 |
| 23 | 6 | 2640 | 3230 | gi\|699336 | C. freundii orfW homologue [Mycobacterium leprae] sp\|P53523\|Y02Y_MYCLE HYPOTHETICAL 20.9 KD PROTEIN U471A. | 70 | 43 |
| 27 | 3 | 1011 | 493 | gi\|1001644 | regulatory components of sensory transduction system [Synechocystis sp.] | 70 | 44 |
| 31 | 2 | 1095 | 1337 | gi\|1100076 | PTS-dependent enzyme II [Clostridium longisporum] | 70 | 55 |
| 32 | 10 | 6527 | 5817 | gi\|1591789 | M. jannaschii predicted coding region MJ1163 [Methanococcus jannaschii] | 70 | 51 |
| 33 | 7 | 6930 | 7235 | gi\|536972 | ORF_o90a [Escherichia coli] | 70 | 45 |
| 35 | 2 | 500 | 2533 | gi\|43819 | nagE gene product [Klebsiella pneumoniae] | 70 | 50 |
| 47 | 13 | 15837 | 14512 | gi\|150209 | ORF 1 [Mycoplasma mycoides] | 70 | 44 |
| 49 | 15 | 10409 | 11179 | gi\|853751 | N-acetylmuramoyl-L-alanine amidase [Bacteriophage A511] | 70 | 54 |
| 57 | 7 | 8365 | 12189 | gi\|142440 | ATP-dependent nuclease [Bacillus subtilis] | 70 | 48 |
| 57 | 16 | 18656 | 18033 | gi\|388565 | major cell-binding factor [Campylobacter jejuni] | 70 | 52 |
| 59 | 9 | 4985 | 7060 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 70 | 49 |
| 72 | 6 | 6771 | 4600 | gi\|557567 | ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis] sp\|P50640\|RIR1_MYCTU RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA HAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) (R1 SUBUNIT) FRAGMENT). | 70 | 53 |
| 76 | 8 | 5960 | 6343 | gi\|1063251 | no homologous protein [Bacillus subtilis] | 70 | 52 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 81 | 16 | 12529 | 11723 | gi\|1732200 | PTS permease for mannose subunit IIPMan [Vibrio furnissii] | 70 | 52 |
| 98 | 7 | 8974 | 7874 | gi\|1573045 | hypothetical [Haemophilus influenzae] | 70 | 46 |
| 110 | 2 | 1353 | 502 | gi\|1399848 | unknown [Synechococcus PCC7942] | 70 | 52 |
| 123 | 7 | 5009 | 5527 | gi\|143284 | negative regulator pai 1 [Bacillus subtilis] | 70 | 51 |
| 123 | 22 | 19729 | 20412 | gi\|1591493 | glutamine transport ATP-binding protein Q [Methanococcus jannaschii] | 70 | 48 |
| 133 | 6 | 5905 | 6498 | gi\|746399 | transcription elongation factor [Escherichia coli] | 70 | 50 |
| 134 | 1 | 1 | 384 | gi\|1146242 | aspartate 1-decarboxylase [Bacillus subtilis] | 70 | 49 |
| 138 | 10 | 8543 | 7953 | gi\|467371 | LACI family of transcriptional repreesor (probable) [Bacillus ubtilis] | 70 | 50 |
| 160 | 3 | 1263 | 1520 | gi\|1468939 | meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiella pneumoniae] | 70 | 45 |
| 174 | 3 | 2279 | 1572 | gi\|413931 | ipa-7d gene product [Bacillus subtilis] | 70 | 44 |
| 177 | 2 | 2104 | 1022 | gnl\|PID\|e186242 | D-mannonate hydrolase [Thermotoga neapolitana] | 70 | 52 |
| 178 | 2 | 1320 | 532 | gi\|499659 | K+ channel protein [Panulirus interruptus] | 70 | 51 |
| 180 | 18 | 17770 | 18729 | gi\|887824 | ORF_o310 [Escherichia coli] | 70 | 50 |
| 180 | 22 | 21072 | 22526 | gi\|1573294 | hypothetical [Haemophilus influenzae] | 70 | 40 |
| 181 | 9 | 7409 | 6279 | sp\|P20692\|TYRA_BACSU | PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH). | 70 | 49 |
| 197 | 5 | 4529 | 6340 | gi\|1783252 | homologous to many ATP-binding transport proteins including SwissProt:CYDD_ECOLI; hypothetical [Bacillus subtilis] | 70 | 47 |
| 200 | 21 | 12419 | 11820 | gi\|290943 | HindIII modification methyltransferase [Haemophilus influenzae] sp\|P43871\|MTH3_HAEIN MODIFICATION METHYLASE HINDIII (EC 2.1.1.72) ADENINE-SPECIFIC METHYLTRANSFERASE HINDIII) | 70 | 47 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | (M.HINDIII). | | |
| 210 | 4 | 3877 | 3269 | gi\|602683 | orfC [Mycoplasma capricolum] | 70 | 47 |
| 217 | 2 | 405 | 707 | gi\|153767 | ORF [Streptococcus pneumoniae] | 70 | 56 |
| 222 | 8 | 4940 | 6046 | gi\|537033 | ORF_f356 [Escherichia coli] | 70 | 54 |
| 222 | 15 | 9825 | 10553 | gi\|537039 | ORF_o228a [Escherichia coli] | 70 | 56 |
| 227 | 4 | 1871 | 2893 | gi\|1070014 | protein-dependent [Bacillus subtilis] | 70 | 44 |
| 228 | 2 | 1343 | 792 | gi\|1742730 | Protein AraJ precursor. [Escherichia coli] | 70 | 50 |
| 228 | 5 | 3470 | 2574 | gi\|1573390 | hypothetical [Haemophilus influenzae] | 70 | 54 |
| 231 | 2 | 2470 | 1238 | gi\|1574085 | H. influenzae predicted coding region HI1048 [Haemophilus influenzae] | 70 | 48 |
| 235 | 4 | 2779 | 2138 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 70 | 46 |
| 239 | 4 | 5807 | 6409 | gi\|682765 | mccB gene product [Escherichia coli] | 70 | 41 |
| 248 | 1 | 3 | 350 | gi\|143725 | putative [Bacillus subtilis] | 70 | 52 |
| 254 | 4 | 838 | 497 | gi\|49318 | ORF4 gene product [Bacillus subtilis] | 70 | 48 |
| 256 | 3 | 1737 | 2612 | gi\|596092 | putative multiple membrane domain protein; possible TTG initiation odon at position 1064, near putative RBS at position 1052 Streptococcus pyogenes] | 70 | 51 |
| 279 | 15 | 14547 | 14224 | gi\|1389549 | ORF3 [Bacillus subtilis] | 70 | 50 |
| 283 | 6 | 2279 | 3190 | gi\|853751 | N-acetylmuramoyl-L-alanine amidase [Bacteriophage A511] | 70 | 52 |
| 292 | 8 | 5557 | 6534 | gi\|474195 | This ORF is homologous to a 40.0 kd hypothetical protein in the htrB ' region from E. coli, Accession Number X61000 [Mycoplasma-like rganism] | 70 | 50 |
| 294 | 8 | 2776 | 3375 | gi\|1750126 | YncB [Bacillus subtilis] | 70 | 47 |
| 294 | 10 | 3742 | 4020 | gi\|984581 | YafQ [Escherichia coli] | 70 | 50 |
| 299 | 1 | 905 | 132 | gi\|606309 | ORF_o265; gtg start [Escherichia coli] | 70 | 40 |
| 300 | 3 | 3200 | 2784 | gi\|289260 | comE ORF1 [Bacillus subtilis] | 70 | 50 |
| 301 | 9 | 8564 | 7590 | gi\|1303865 | YqgR [Bacillus subtilis] | 70 | 52 |
| 336 | 2 | 661 | 921 | gi\|202864 | [Rat alternatively spliced mRNA.], gene | 70 | 47 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | product [Rattus norvegicus] | | |
| 339 | 1 | 269 | 3 | gi\|786163 | Ribosomal Protein L10 [Bacillus subtilis] | 70 | 50 |
| 351 | 9 | 4760 | 4359 | gi\|799235 | dTDP-6-deoxy-L-lyxo-4-hexulose reductase [Escherichia coli] | 70 | 45 |
| 399 | 28 | 28203 | 28793 | gi\|146278 | glucitol-specific enzyme II (gutA) [Escherichia coli] pir\|A26725\|WQEC2S phosphotransferase system enzyme II (EC .7.1.69), sorbitol-specific, factor II - Escherichia coli sp\|P05705\|PTHB_ECOLI PTS SYSTEM, GLUCITOL/SORBITOL-SPECIFIC IIBC OMPONENT (EIIBC-GUT) | 70 | 52 |
| 406 | 1 | 1 | 552 | gi\|49315 | ORF1 gene product [Bacillus subtilis] | 70 | 50 |
| 436 | 5 | 2417 | 2193 | gi\|773665 | transposase [Lactococcus lactis] | 70 | 36 |
| 482 | 3 | 1887 | 1660 | gi\|48680 | ptsG-like product [Bacillus subtilis] | 70 | 47 |
| 529 | 3 | 6587 | 7030 | gi\|1022726 | unknown [Staphylococcus haemolyticus] | 70 | 44 |
| 535 | 2 | 1702 | 965 | gi\|1747435 | KdpE [Clostridium acetobutylicum] | 70 | 52 |
| 543 | 2 | 1248 | 547 | gi\|1591045 | hypothetical protein (SP:P31466) [Methanococcus jannaschii] | 70 | 47 |
| 543 | 8 | 4084 | 3878 | gi\|511976 | SERP gene gene product [Plasmodium falciparum] | 70 | 60 |
| 560 | 3 | 1037 | 876 | gi\|558458 | acidic 82 kDa protein [Homo sapiens] | 70 | 40 |
| 573 | 4 | 1920 | 2258 | gi\|336639 | prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] gi\|1016130 prenyl transferase [Cyanophora paradoxa] pir\|A40433\|A40433 prephytoene pyrophosphatase dehydrogenase (crtE) omolog - Cyanophora paradoxa | 70 | 32 |
| 599 | 2 | 244 | 573 | gi\|42029 | ORF1 gene product [Escherichia coli] | 70 | 49 |
| 608 | 3 | 867 | 556 | gi\|475032 | formamidopyrimidine-DNA glycosylase [Streptococcus mutans] sp\|P55045\|FPG_STRMU FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC .2.2.23) (FAPY-DNA GLYCOSYLASE). | 70 | 53 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 636 | 1 | 2 | 628 | gi\|606309 | ORF_o265; gtg start [Escherichia coli] | 70 | 50 |
| 670 | 2 | 2157 | 1828 | gi\|1657698 | hyaluronan receptor [Homo sapiens] | 70 | 41 |
| 702 | 1 | 103 | 870 | gi\|149490 | sucrose-6-phosphate hydrolase [Lactococcus lactis] pir\|JH0754\|JH0754 sucrose-6-phosphate hydrolase (EC 3.2.1.-) - actococcus lactis | 70 | 51 |
| 726 | 2 | 725 | 480 | gnl\|PID\|e240103 | unknown ORF [Saccharomyces cerevisiae] | 70 | 41 |
| 854 | 1 | 1 | 207 | gi\|532653 | thermonuclease [Staphylococcus hyicus] | 70 | 51 |
| 901 | 1 | 238 | 447 | gi\|172022 | myosin 1 isoform (MYO2) [Saccharomyces cerevisiae] | 70 | 20 |
| 940 | 1 | 1 | 318 | gi\|1039479 | ORFU [Lactococcus lactis] | 70 | 56 |
| 1 | 2 | 2112 | 1213 | gi\|413976 | ipa-52r gene product [Bacillus subtilis] | 69 | 51 |
| 8 | 2 | 2196 | 778 | gi\|1510108 | ORF-1 [Agrobacterium tumefaciens] | 69 | 50 |
| 8 | 9 | 7949 | 6654 | gi\|1196907 | daunorubicin resistance protein [Streptomyces peucetius] | 69 | 44 |
| 16 | 3 | 1618 | 2574 | gi\|1109684 | ProV [Bacillus subtilis] | 69 | 53 |
| 17 | 26 | 25781 | 26944 | gi\|485275 | 53.6 kDa protein [Streptococcus pneumoniae] | 69 | 44 |
| 17 | 35 | 32300 | 32770 | gi\|1574146 | pfs protein (pfs) [Haemophilus influenzae] | 69 | 53 |
| 23 | 30 | 18107 | 18538 | gnl\|PID\|e249656 | YneT [Bacillus subtilis] | 69 | 59 |
| 25 | 8 | 6653 | 6994 | gi\|413943 | ipa-19d gene product [Bacillus subtilis] | 69 | 46 |
| 37 | 2 | 2042 | 186 | gi\|143331 | alkaline phosphatase regulatory protein [Bacillus subtilis] pir\|A27650\|A27650 regulatory protein phoR - Bacillus subtilis sp\|P23545\|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-). | 69 | 52 |
| 39 | 2 | 528 | 767 | gi\|1408493 | homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis] | 69 | 52 |
| 56 | 6 | 4809 | 3457 | gi\|1591610 | probable ATP-dependent helicase [Methanococcus jannaschii] | 69 | 45 |
| 67 | 5 | 3042 | 3938 | gi\|1658188 | oxidative stress transcriptional regulator | 69 | 39 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Erwinia carotovora] | | |
| 68 | 3 | 684 | 1529 | gnl\|PID\|e214719 | PlcR protein [Bacillus thuringiensis] | 69 | 45 |
| 72 | 4 | 2099 | 3394 | gi\|882672 | ORF_o313 [Escherichia coli] | 69 | 37 |
| 81 | 15 | 11820 | 10915 | gi\|1732201 | PTS permease for mannose subunit IIBMan [Vibrio furnissii] | 69 | 44 |
| 83 | 20 | 14001 | 15800 | gi\|1230668 | Similar to Arginyl-tRNA synthetase (Swiss Prot. accession number P11875) [Saccharomyces cerevisiae] | 69 | 44 |
| 85 | 6 | 6309 | 5299 | sp\|P54533\|DLD2_BACSU | LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4) (DIHYDROLIPOAMIDE DEHYDROGENASE) (LPD-VAL). | 69 | 46 |
| 86 | 3 | 2084 | 3367 | gi\|143318 | phosphoglycerate kinase [Bacillus megaterium] | 69 | 53 |
| 94 | 2 | 1401 | 751 | gi\|755216 | N-acetylmuramidase [Lactococcus lactis] | 69 | 41 |
| 94 | 16 | 20498 | 19197 | gi\|1208948 | unknown [Escherichia coli] | 69 | 47 |
| 98 | 8 | 10201 | 9029 | gi\|563934 | similar to E. coli hypothetical protein: PIR Accession Number Q0614] [Bacillus subtilis] | 69 | 51 |
| 109 | 4 | 2350 | 1316 | gi\|396501 | aspartyl-tRNA synthetase [Thermus aquaticus thermophilus] pir\|S33743\|S33743 aspartate--tRNA ligase (EC 6.1.1.12) - Thermus quaticus | 69 | 56 |
| 114 | 1 | 83 | 1522 | gi\|1658402 | formate dehydrogenase beta subunit [Moorella thermoacetica] | 69 | 45 |
| 123 | 9 | 7617 | 8984 | gi\|1773192 | similar to S. cerevisiae dal1 [Escherichia coli] | 69 | 50 |
| 128 | 11 | 7940 | 7578 | gi\|895750 | putative cellobiose phosphotransferase enzyme III [Bacillus ubtilis] | 69 | 53 |
| 130 | 10 | 8764 | 9036 | gi\|1641 | put. Na(+)/glucose co-transporter (AA 1-662) [Oryctolagus cuniculus] \|1717 | 69 | 47 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | cortical sodium-D-glucose cotransporter [Oryctolagus iculus] | | |
| 138 | 26 | 16721 | 17545 | pir\|A25805\|A25805 | L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis | 69 | 55 |
| 139 | 2 | 310 | 1083 | gi\|1408587 | relaxase [Lactococcus lactis lactis] | 69 | 46 |
| 139 | 9 | 5196 | 4984 | gi\|473955 | DNA-binding protein [Lactobacillus sp.] | 69 | 34 |
| 142 | 9 | 5559 | 4564 | gi\|623073 | ORF360; putative [Bacteriophage LL-H] | 69 | 47 |
| 155 | 6 | 4658 | 5818 | gi\|1591260 | endoglucanase [Methanococcus jannaschii] | 69 | 48 |
| 158 | 12 | 11671 | 11201 | gi\|606744 | cytidine deaminase [Bacillus subtilis] | 69 | 52 |
| 162 | 5 | 5888 | 4032 | gi\|142993 | glycerol-3-phosphate dehydrogenase (glpD) (EC 1.1.99.5) [Bacillus ubtilis] | 69 | 54 |
| 180 | 2 | 1901 | 1203 | gi\|1575577 | DNA-binding response regulator [Thermotoga maritima] | 69 | 49 |
| 197 | 4 | 3571 | 4602 | gi\|1783251 | homologous to cytochrome d ubiquinol oxidase subunit II; hypothetical [Bacillus subtilis] | 69 | 46 |
| 197 | 6 | 6283 | 7701 | gi\|1783253 | homologous to many ATP-binding transport proteins; hypothetical [Bacillus subtilis] | 69 | 49 |
| 222 | 1 | 201 | 10 | gi\|149901 | gene codes for a 19 kDa protein [Mycobacterium avium] sp\|P46733\|19KD_MYCAV 19 KD LIPOPROTEIN ANTIGEN PRECURSOR. | 69 | 50 |
| 223 | 28 | 23857 | 24567 | gnl\|PID\|e269548 | Unknown [Bacillus subtilis] | 69 | 53 |
| 228 | 3 | 2031 | 1285 | gi\|1742730 | Protein AraJ precursor. [Escherichia coli] | 69 | 45 |
| 229 | 8 | 7390 | 6698 | gi\|1162980 | ribulose-5-phosphate 3-epimerase [Spinacia oleracea] | 69 | 52 |
| 238 | 27 | 25243 | 25695 | gi\|305005 | ORF_f104 [Escherichia coli] | 69 | 53 |
| 253 | 3 | 1067 | 921 | gi\|1591278 | aspartokinase I [Methanococcus jannaschii] | 69 | 39 |
| 260 | 4 | 2110 | 3105 | gi\|580841 | F1 [Bacillus subtilis] | 69 | 45 |
| 268 | 3 | 2287 | 1910 | gi\|460026 | repressor protein [Streptococcus pneumoniae] | 69 | 48 |
| 269 | 7 | 4532 | 4083 | gi\|1303792 | YqeK [Bacillus subtilis] | 69 | 50 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 271 | 15 | 11040 | 12236 | gi\|1303805 | YqeR [Bacillus subtilis] | 69 | 48 |
| 271 | 16 | 12444 | 12809 | gi\|435490 | orf1 gene product [Lactococcus lactis] | 69 | 46 |
| 281 | 3 | 1277 | 2068 | gi\|1303968 | YqjQ [Bacillus subtilis] | 69 | 50 |
| 281 | 6 | 5004 | 5534 | gi\|1773151 | adenine phosphoribosyltransferase [Escherichia coli] | 69 | 54 |
| 292 | 24 | 19939 | 18398 | gi\|1652664 | glutamine-binding periplasmic protein [Synechocystis sp.] | 69 | 45 |
| 323 | 3 | 2708 | 4243 | gi\|179401 | beta-D-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] gi\|179423 beta-galactosidase precursor (EC 3.2.1.23) [Homo sapiens] pir\|A32688\|A32611 beta-galactosidase (EC 3.2.1.23) precursor - uman | 69 | 56 |
| 330 | 2 | 1388 | 2353 | gi\|1303783 | YqeC [Bacillus subtilis] | 69 | 48 |
| 332 | 1 | 2 | 223 | gi\|1653594 | hemolysin [Synechocystis sp.] | 69 | 50 |
| 338 | 9 | 7035 | 7607 | gi\|467442 | stage V sporulation [Bacillus subtilis] | 69 | 55 |
| 341 | 1 | 1 | 408 | gi\|1477741 | histidine periplasmic binding protein P29 [Campylobacter jejuni] | 69 | 50 |
| 368 | 2 | 972 | 598 | gi\|516826 | rat GCP360 [Rattus rattus] | 69 | 33 |
| 375 | 4 | 3405 | 2599 | gi\|1215693 | putative orf; GT9_orf434 [Mycoplasma pneumoniae] | 69 | 38 |
| 386 | 1 | 2 | 166 | gi\|1549376 | putative protein [Synechococcus PCC7942] | 69 | 42 |
| 396 | 4 | 1248 | 1715 | gi\|410132 | ORFX8 [Bacillus subtilis] | 69 | 50 |
| 398 | 4 | 2763 | 2927 | gi\|466475 | putative phospho-beta-glucosidase [Bacillus stearothermophilus] pir\|D49898\|D49898 cellobiose phosphotransferase system celC - acillus stearothermophilus | 69 | 55 |
| 421 | 5 | 2950 | 3471 | gi\|1574625 | H. influenzae predicted coding region HI1074 [Haemophilus influenzae] | 69 | 45 |
| 423 | 4 | 2408 | 2893 | gnl\|PID\|e163522 | rnhB [Haemophilus influenzae] | 69 | 55 |
| 436 | 3 | 1763 | 1521 | gi\|155032 | ORF B [Plasmid pEa34] | 69 | 37 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 452 | 1 | 3 | 341 | gi\|1591139 | M. jannaschii predicted coding region MJ0435 [Methanococcus jannaschii] | 69 | 52 |
| 470 | 3 | 1816 | 2181 | gi\|437389 | transposase [Lactococcus lactis] | 69 | 56 |
| 471 | 2 | 2003 | 813 | gi\|854233 | cymF gene product [Klebsiella oxytoca] | 69 | 49 |
| 478 | 1 | 822 | 4 | gi\|142521 | deoxyribodipyrimidine photolyase [Bacillus subtilis] gnl\|PID\|e255102 deoxyribodipyrimidine photolyase [Bacillus ubtilis] | 69 | 63 |
| 490 | 4 | 1447 | 1289 | gi\|699379 | glvr-1 protein [Mycobacterium leprae] | 69 | 41 |
| 518 | 2 | 213 | 605 | pir\|S00076\|R5BS12 | ribosomal protein L12 - Bacillus stearothermophilus | 69 | 59 |
| 536 | 4 | 1471 | 1653 | gi\|1146240 | ketopantoate hydroxymethyltransferase [Bacillus subtilis] | 69 | 53 |
| 539 | 5 | 3796 | 5091 | gi\|973231 | gamma-glutamyl phosphate reductase [Lycopersicon esculentum] | 69 | 54 |
| 566 | 1 | 1 | 231 | gi\|45741 | ORFE [Enterococcus faecalis] | 69 | 50 |
| 579 | 5 | 2729 | 3595 | gi\|145887 | malonyl coenzyme A-acyl carrier protein transacylase [Escherichia oli] | 69 | 49 |
| 583 | 2 | 373 | 912 | gi\|1064791 | function umknown [Bacillus subtilis] | 69 | 55 |
| 605 | 1 | 254 | 3 | pir\|S39743\|S39743 | hypothetical protein - Bacillus subtilis | 69 | 37 |
| 630 | 2 | 1659 | 1231 | gi\|153672 | lactose repressor [Streptococcus mutans] | 69 | 47 |
| 634 | 1 | 36 | 731 | gi\|1022725 | unknown [Staphylococcus haemolyticus] | 69 | 53 |
| 662 | 1 | 486 | 73 | gi\|467431 | high level kasgamycin resistance [Bacillus subtilis] sp\|P37468\|KSGA_BACSU DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) 16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESISTANCE PROTEIN SGA) (K | 69 | 55 |
| 689 | 1 | 340 | 26 | gi\|1017817 | membrane spanning protein [Streptomyces coelicolor] | 69 | 41 |
| 756 | 2 | 300 | 500 | gi\|520596 | Mre2 protein [Saccharomyces cerevisiae] | 69 | 46 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 792 | 2 | 855 | 460 | gi\|1303823 | YqfG [Bacillus subtilis] | 69 | 55 |
| 916 | 1 | 4 | 789 | gnl\|PID\|e253114 | ornithine carbamoyltransferase [Pyrococcus furiosus] | 69 | 57 |
| 7 | 3 | 2609 | 3748 | gi\|1303836 | YqfO [Bacillus subtilis] | 68 | 50 |
| 16 | 5 | 4165 | 4689 | gi\|142450 | ahrC protein [Bacillus subtilis] | 68 | 46 |
| 17 | 16 | 12826 | 13071 | gi\|222681 | RNA polymerase [Tomato spotted wilt virus] | 68 | 50 |
| 17 | 32 | 31402 | 31572 | gi\|1303984 | YqkG [Bacillus subtilis] | 68 | 44 |
| 17 | 33 | 31509 | 32009 | gi\|1303984 | YqkG [Bacillus subtilis] | 68 | 50 |
| 29 | 1 | 19 | 282 | gi\|1234787 | up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region [Xenopus laevis] | 68 | 37 |
| 29 | 3 | 1087 | 1950 | gi\|407878 | leucine rich protein [Streptococcus equisimilis] | 68 | 45 |
| 45 | 1 | 204 | 959 | gi\|1039479 | ORFU [Lactococcus lactis] | 68 | 50 |
| 47 | 7 | 8108 | 7527 | gi\|142853 | homologous to unidentified E. coli protein [Bacillus subtilis] gi\|143161 maf [Bacillus subtilis] | 68 | 46 |
| 52 | 6 | 4304 | 5050 | gnl\|PID\|e124050 | alpha-acetolactate decarboxylase [Lactococcus lactis] | 68 | 53 |
| 58 | 5 | 5961 | 4807 | gi\|466365 | potential NAD-reducing hydrogenase subunit [Desulfovibrio ructosovorans] | 68 | 49 |
| 68 | 8 | 4036 | 4743 | gi\|1673727 | (AE000009) Mycoplasma pneumoniae, glutamine transport ATP-binding protein; similar to Swiss-Prot Accession Number P10346, from E. coli [Mycoplasma pneumoniae] | 68 | 44 |
| 72 | 5 | 4441 | 3434 | gi\|1395209 | ribonucleotide reductase R2-2 small subunit [Mycobacterium tuberculosis] | 68 | 52 |
| 80 | 1 | 836 | 3 | gi\|474176 | regulator protein [Staphylococcus xylosus] | 68 | 48 |
| 81 | 2 | 793 | 1359 | gi\|1064809 | homologous to sp:HTRA_ECOLI [Bacillus | 68 | 48 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | subtilis] | | |
| 85 | 9 | 6911 | 6711 | gi\|144893 | butyrate kinase [Clostridium acetobutylicum] | 68 | 55 |
| 89 | 8 | 7184 | 5970 | gi\|1469784 | putative cell division protein ftsW [Enterococcus hirae] | 68 | 44 |
| 91 | 3 | 828 | 1076 | gi\|726480 | L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis] | 68 | 53 |
| 103 | 1 | 1019 | 3 | gi\|143365 | phosphoribosyl aminoimidazole carboxylase II (PUR-K; ttg start odon) [Bacillus subtilis] | 68 | 50 |
| 106 | 2 | 2441 | 1509 | gi\|146860 | delta-2-isopentenyl pyrophosphate transferase [Escherichia coli] gi\|537012 tRNA delta-2-isopentenylpyrophosphate (IPP) transferase Escherichia coli] | 68 | 47 |
| 112 | 1 | 558 | 100 | gnl\|PID\|e242290 | carbamate kinase [Clostridium perfringens] | 68 | 50 |
| 116 | 3 | 2383 | 1496 | gi\|755601 | unknown [Bacillus subtilis] | 68 | 42 |
| 119 | 3 | 2136 | 1201 | gi\|1171125 | thioredoxin reductase [Clostridium litorale] | 68 | 49 |
| 121 | 4 | 3697 | 4650 | gi\|790945 | aryl-alcohol dehydrogenase [Bacillus subtilis] | 68 | 48 |
| 123 | 26 | 24262 | 24801 | gi\|537235 | Kenn Rudd identifies as gpmB [Escherichia coli] | 68 | 51 |
| 123 | 27 | 24887 | 25888 | gi\|143150 | levR [Bacillus subtilis] | 68 | 51 |
| 126 | 4 | 2773 | 1844 | gi\|551854 | ORF2 [Erwinia herbicola] | 68 | 54 |
| 131 | 1 | 150 | 1058 | gi\|1387979 | 44% identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtil | 68 | 44 |
| 134 | 3 | 2154 | 1804 | sp\|P39213\|YI91_SHI | INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 | 68 | 43 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | DY | KD PROTEIN. | | |
| 138 | 19 | 12285 | 12656 | gi\|1438847 | homologue of hypothetical 17.6 kDa protein in rplI-cpdB intergenic region of E. coli [Bacillus subtilis] | 68 | 43 |
| 151 | 2 | 2784 | 1654 | gi\|143365 | phosphoribosyl aminoimidazole carboxylase II (PUR-K; ttg start odon) [Bacillus subtilis] | 68 | 45 |
| 164 | 23 | 24352 | 24119 | gi\|1573564 | hypothetical [Haemophilus influenzae] | 68 | 40 |
| 166 | 2 | 970 | 1260 | gi\|151968 | nifS [Rhodobacter sphaeroides] | 68 | 41 |
| 172 | 2 | 1320 | 2015 | gi\|1208965 | hypothetical 23.3 kd protein [Escherichia coli] | 68 | 46 |
| 175 | 1 | 900 | 451 | gi\|468207 | Submitter comments: A Mg2+ transporting P-type ATPase highly omologous with mgtB ATPase at 80 min on Salmonella chromosome. ediates the influx of Mg2+ only. Transcription regulated by xtracellular Mg2+ [Salmonella typhimurium] | 68 | 47 |
| 180 | 14 | 12551 | 14956 | gi\|565641 | FdrA protein [Escherichia coli] | 68 | 49 |
| 186 | 1 | 3 | 686 | gi\|405804 | transposase [Streptococcus thermophilus] | 68 | 51 |
| 200 | 1 | 239 | 3 | gi\|468016 | immunoglobulin heavy chain binding protein [Giardia intestinalis] | 68 | 42 |
| 201 | 4 | 4468 | 3686 | gi\|304013 | abcA [Aeromonas salmonicida] | 68 | 50 |
| 204 | 10 | 6833 | 6468 | gi\|488430 | alcohol dehydrogenase 2 [Entamoeba histolytica] | 68 | 51 |
| 214 | 3 | 3360 | 2491 | gi\|928834 | integrase [Lactococcus lactis phage BK5-T] | 68 | 50 |
| 229 | 9 | 8277 | 7375 | gi\|1574569 | hypothetical [Haemophilus influenzae] | 68 | 41 |
| 229 | 14 | 14288 | 13740 | gnl\|PID\|e290287 | polypeptide deformylase [Bacillus subtilis] | 68 | 50 |
| 230 | 5 | 4593 | 3532 | gi\|143002 | proton glutamate symport protein [Bacillus caldotenax] pir\|S26246\|S26246 glutamate/aspartate transport protein - Bacillus aldotenax | 68 | 29 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 244 | 1 | 1 | 891 | gi\|537080 | ribonucleoside triphosphate reductase [Escherichia coli] pir\|A47331\|A47331 oxygen-sensitive ribonucleoside-triphosphate eductase (EC 1.17.4.-) - Escherichia coli | 68 | 54 |
| 244 | 5 | 4249 | 3551 | gi\|1773172 | hypothetical protein [Escherichia coli] | 68 | 46 |
| 244 | 7 | 5670 | 5212 | gi\|467423 | unknown [Bacillus subtilis] | 68 | 43 |
| 264 | 9 | 3925 | 3734 | gi\|914991 | Similar to hemoglobinase [Saccharomyces cerevisiae] pir\|S59796\|S59796 hypothetical protein D9798.2 - yeast Saccharomyces cerevisiae) | 68 | 44 |
| 271 | 7 | 3484 | 4686 | gi\|1469784 | putative cell division protein ftsW [Enterococcus hirae] | 68 | 50 |
| 271 | 11 | 6817 | 6548 | gi\|413948 | ipa-24d gene product [Bacillus subtilis] | 68 | 50 |
| 288 | 3 | 1638 | 1333 | gi\|562039 | NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii] pir\|S53835\|S53835 *NADH dehydrogenase* chain 2 - Acanthamoeba astellanii mitochondrion (SGC6) | 68 | 50 |
| 295 | 6 | 3537 | 4472 | gi\|555668 | glycosylasparaginase precursor [Flavobacterium meningosepticum] | 68 | 41 |
| 296 | 2 | 3143 | 1950 | gi\|1742630 | Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli] | 68 | 34 |
| 301 | 3 | 3271 | 1760 | gi\|413960 | ipa-36d galT gene product [Bacillus subtilis] | 68 | 53 |
| 315 | 3 | 2230 | 905 | gi\|1653498 | ABC transporter [Synechocystis sp.] | 68 | 47 |
| 318 | 2 | 1285 | 854 | gi\|43940 | EIII-F Sor PTS [Klebsiella pneumoniae] | 68 | 39 |
| 320 | 2 | 1178 | 621 | gi\|664842 | sister of P-glycoprotein [Sus scrofa domestica] | 68 | 46 |
| 331 | 2 | 342 | 566 | pir\|B48396\|B48396 | ribosomal protein L33 - Bacillus stearothermophilus | 68 | 59 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 336 | 1 | 1 | 663 | gi\|1006591 | cation-transporting ATPase PacL [Synechocystis sp.] | 68 | 44 |
| 338 | 6 | 4004 | 5035 | gi\|155276 | aldehyde dehydrogenase [Vibrio cholerae] | 68 | 51 |
| 338 | 12 | 10404 | 11165 | gi\|467444 | transcription-repair coupling factor [Bacillus subtilis] sp\|P37474\|MFD_BACSU TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF). | 68 | 46 |
| 341 | 3 | 743 | 1222 | gi\|1183886 | integral membrane protein [Bacillus subtilis] | 68 | 45 |
| 351 | 6 | 2992 | 2561 | gi\|580881 | ipa-73d gene product [Bacillus subtilis] | 68 | 53 |
| 363 | 8 | 12517 | 9950 | gi\|1652980 | H(+)-transporting ATPase [Synechocystis sp.] | 68 | 46 |
| 368 | 3 | 1269 | 1736 | gnl\|PID\|e209005 | homologous to ORF2 in nrdEF operons of E.coli and S.typhimurium [Lactococcus lactis] | 68 | 37 |
| 386 | 11 | 6564 | 6115 | gi\|765072 | ORF3 [Staphylococcus aureus] | 68 | 46 |
| 395 | 3 | 935 | 729 | gi\|15521 | ORF 3 (AA 1-90) [Bacteriophage phi-105] | 68 | 34 |
| 399 | 8 | 6073 | 6519 | gi\|153584 | biotin carboxyl carrier protein [Streptococcus mutans] sp\|P29337\|BCCP_STRMU BIOTIN CARBOXYL CARRIER PROTEIN (BCCP). | 68 | 53 |
| 408 | 3 | 2289 | 1336 | gi\|41572 | GlnP (AA 1-219) [Escherichia coli] | 68 | 40 |
| 420 | 1 | 559 | 2 | gi\|1592142 | ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii] | 68 | 51 |
| 423 | 2 | 254 | 1294 | gi\|1773109 | similar to S. typhimurium apbA [Escherichia coli] | 68 | 47 |
| 423 | 3 | 1465 | 2421 | gi\|1653032 | hypothetical protein [Synechocystis sp.] | 68 | 40 |
| 428 | 1 | 859 | 2 | gi\|1652454 | hypothetical protein [Synechocystis sp.] | 68 | 48 |
| 432 | 7 | 4626 | 3901 | gi\|1573285 | hypothetical [Haemophilus influenzae] | 68 | 55 |
| 434 | 1 | 90 | 1889 | gi\|1542975 | AbcB [Thermoanaerobacterium thermosulfurigenes] | 68 | 50 |
| 441 | 5 | 4674 | 5156 | gi\|467437 | unknown [Bacillus subtilis] | 68 | 48 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 455 | 4 | 3835 | 4080 | gi\|19815 | luminal binding protein (BiP) [Nicotiana tabacum] | 68 | 40 |
| 530 | 2 | 394 | 546 | gi\|763326 | unknown [Saccharomyces cerevisiae] | 68 | 42 |
| 531 | 2 | 810 | 622 | gi\|1146183 | putative [Bacillus subtilis] | 68 | 51 |
| 537 | 3 | 1353 | 1192 | gi\|929968 | ORFA; similar to B. anthracis WeyAR element ORFA; putative ransposase [Bacillus anthracis] | 68 | 56 |
| 539 | 3 | 2725 | 2231 | gi\|1353537 | dUTPase [Bacteriophage r1t] | 68 | 53 |
| 569 | 1 | 3 | 446 | gi\|146544 | 18 kD protein [Escherichia coli] | 68 | 47 |
| 591 | 2 | 656 | 174 | gi\|1039479 | ORFU [Lactococcus lactis] | 68 | 42 |
| 652 | 2 | 739 | 1032 | gi\|1303715 | YrkP [Bacillus subtilis] | 68 | 50 |
| 671 | 2 | 436 | 1617 | gi\|413959 | ipa-35d galK gene product [Bacillus subtilis] | 68 | 50 |
| 684 | 1 | 466 | 2 | gnl\|PID\|e248400 | orfRM1 gene product [Bacillus subtilis] | 68 | 40 |
| 693 | 1 | 2 | 787 | gi\|405804 | transposase [Streptococcus thermophilus] | 68 | 46 |
| 700 | 2 | 772 | 596 | gi\|153801 | enzyme scr-II [Streptococcus mutans] | 68 | 50 |
| 735 | 1 | 118 | 609 | gi\|969027 | gamma-aminobutyrate permease [Bacillus subtilis] sp\|P46349\|GABP_BACSU GABA PERMEASE (4-AMINO BUTYRATE TRANSPORT ARRIER) (GAMA-AMINOBUTYRATE PERMEASE). | 68 | 40 |
| 750 | 1 | 2 | 529 | gi\|893358 | PgsA [Bacillus subtilis] | 68 | 54 |
| 762 | 2 | 1588 | 950 | gi\|1146240 | ketopantoate hydroxymethyltransferase [Bacillus subtilis] | 68 | 49 |
| 790 | 1 | 407 | 3 | gi\|142224 | attachment protein ChvA (ttg strart codon) [Agrobacterium umefaciens] | 68 | 55 |
| 882 | 1 | 3 | 278 | gi\|57572 | glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) attus rattus] | 68 | 48 |
| 950 | 1 | 140 | 568 | gi\|882736 | ORF_f278 [Escherichia coli] | 68 | 53 |
| 969 | 2 | 554 | 339 | gi\|1118031 | similar to neural cell adhesion molecules and neuroglians in their IG-like C2-type domains [Caenorhabditis elegans] | 68 | 47 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 970 | 1 | 297 | 73 | gi\|474404 | cyclophilin [Tolypocladium inflatum] | 68 | 40 |
| 1 | 1 | 1103 | 3 | gi\|48790 | ORF 3 [Pseudomonas putida] | 67 | 50 |
| 29 | 10 | 7156 | 6614 | sp\|P36672\|PTTB_ECOLI | PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-TRE). | 67 | 52 |
| 48 | 8 | 8035 | 9141 | gi\|975627 | N-acylamino acid racemase [Amycolatopsis sp.] | 67 | 48 |
| 55 | 12 | 6621 | 7439 | gi\|391610 | farnesyl diphosphate synthase [Bacillus stearothermophilus] pir\|JX0257\|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus tearothermophilus | 67 | 47 |
| 57 | 13 | 13972 | 16401 | gnl\|PID\|e255138 | phenylalanyl-tRNA synthetase beta subunit [Bacillus subtilis] | 67 | 47 |
| 63 | 4 | 1917 | 2729 | gi\|1321629 | MIP related protein of E. coli [Escherichia coli] | 67 | 47 |
| 68 | 12 | 8600 | 8923 | gi\|793910 | surface antigen [Homo sapiens] | 67 | 43 |
| 72 | 7 | 7138 | 6740 | gnl\|PID\|e209005 | homologous to ORF2 in nrdEF operons of E.coli and S.typhimurium [Lactococcus lactis] | 67 | 39 |
| 72 | 10 | 8309 | 9433 | gi\|1199515 | ferrous iron transport protein B [Escherichia coli] | 67 | 41 |
| 85 | 5 | 5315 | 4296 | gi\|142611 | branched chain alpha-keto acid dehydrogenase E1-alpha [Bacillus ubtilis] | 67 | 52 |
| 101 | 5 | 4149 | 3100 | gi\|1109686 | ProX [Bacillus subtilis] | 67 | 48 |
| 110 | 4 | 2335 | 1292 | gi\|1066343 | mu-crystallin [Homo sapiens] | 67 | 48 |
| 114 | 12 | 12936 | 13520 | gi\|146218 | serine hydroxymethyltransferase [Escherichia coli] | 67 | 50 |
| 115 | 5 | 3137 | 2010 | gi\|1256150 | YbaR [Bacillus subtilis] | 67 | 47 |
| 115 | 6 | 3199 | 2792 | gi\|1652593 | hypothetical protein [Synechocystis sp.] | 67 | 45 |
| 123 | 25 | 22739 | 24208 | gi\|148711 | 6-aminohexanoate-cyclic-dimer hydrolase [Flavobacterium sp.] gi\|488343 6- | 67 | 50 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | aminohexanoate-cyclic-dimer hydrolase [Flavobacterium p.] | | |
| 124 | 6 | 5139 | 4267 | gi\|1016770 | prolipoprotein diacylglyceryl transferase [Staphylococcus aureus] | 67 | 50 |
| 125 | 2 | 1306 | 221 | gi\|853743 | L-alanoyl-D-glutamate peptidase [Bacteriophage A118] | 67 | 50 |
| 128 | 36 | 29462 | 28737 | gi\|142940 | ftsA [Bacillus subtilis] | 67 | 46 |
| 138 | 27 | 17602 | 18183 | gi\|1256639 | putative [Bacillus subtilis] | 67 | 50 |
| 138 | 31 | 21578 | 20097 | gi\|143245 | Na+/H+ antiporter [Bacillus firmus] | 67 | 42 |
| 138 | 33 | 25165 | 23249 | gi\|1498811 | M. jannaschii predicted coding region MJ0050 [Methanococcus jannaschii] | 67 | 45 |
| 138 | 36 | 28690 | 27362 | gnl\|PID\|e269549 | Unknown [Bacillus subtilis] | 67 | 47 |
| 144 | 4 | 3271 | 3717 | gi\|1753229 | PKCI [Borrelia burgdorferi] | 67 | 52 |
| 145 | 3 | 1435 | 2511 | gi\|1573615 | ATP-binding protein (abc) [Haemophilus influenzae] | 67 | 47 |
| 146 | 5 | 4657 | 2804 | gi\|1045034 | beta-galactosidase [Xanthomonas campestris pv. manihotis] | 67 | 51 |
| 149 | 3 | 1978 | 1367 | gi\|806536 | membrane protein [Bacillus acidopullulyticus] | 67 | 51 |
| 156 | 1 | 3 | 365 | gnl\|PID\|e265539 | ClpB-homologue [Thermus aquaticus thermophilus] | 67 | 42 |
| 158 | 15 | 14863 | 13766 | gi\|1573487 | rbs repressor (rbsR) [Haemophilus influenzae] | 67 | 40 |
| 158 | 17 | 16483 | 15959 | gi\|677850 | hypothetical protein [Staphylococcus aureus] | 67 | 51 |
| 159 | 7 | 6872 | 6006 | gi\|1303949 | YqiX [Bacillus subtilis] | 67 | 41 |
| 159 | 9 | 8103 | 7498 | gi\|1303950 | YqiY [Bacillus subtilis] | 67 | 41 |
| 165 | 11 | 9846 | 9004 | gi\|606079 | ORF_o267 [Escherichia coli] | 67 | 36 |
| 169 | 2 | 2151 | 3047 | gi\|42371 | pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia li] | 67 | 44 |
| 179 | 13 | 13648 | 14451 | gnl\|PID\|e257631 | methyltransferase [Lactococcus lactis] | 67 | 45 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 180 | 28 | 28656 | 29801 | gi\|666005 | hypothetical protein [Bacillus subtilis] | 67 | 48 |
| 194 | 6 | 2774 | 4231 | gi\|143245 | Na+/H+ antiporter [Bacillus firmus] | 67 | 41 |
| 194 | 10 | 6472 | 8259 | gi\|622991 | mannitol transport protein [Bacillus stearothermophilus] sp\|P50852\|PTMB_BACST PTS SYSTEM, MANNITOL-SPECIFIC IIBC COMPONENT EIIBC-MTL) (MANNITOL- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE NZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-MTL). | 67 | 50 |
| 204 | 5 | 1924 | 3006 | gi\|1235684 | mevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae] | 67 | 50 |
| 214 | 1 | 42 | 1196 | gi\|606013 | CG Site No. 829 [Escherichia coli] | 67 | 36 |
| 219 | 2 | 524 | 850 | gnl\|PID\|e257628 | ORF [Lactococcus lactis] | 67 | 42 |
| 223 | 15 | 13640 | 14407 | gi\|496520 | orf iota [Streptococcus pyogenes] | 67 | 54 |
| 227 | 3 | 1011 | 1892 | gi\|1070013 | protein-dependent [Bacillus subtilis] | 67 | 37 |
| 233 | 12 | 9340 | 8339 | gi\|507880 | xanthine dehydrogenase [Gallus gallus] | 67 | 50 |
| 238 | 10 | 7951 | 9183 | gi\|1653948 | hypothetical protein [Synechocystis sp.] | 67 | 45 |
| 246 | 3 | 783 | 1430 | gnl\|PID\|e233869 | hypothetical protein [Bacillus subtilis] | 67 | 47 |
| 256 | 2 | 570 | 1601 | gi\|709992 | hypothetical protein [Bacillus subtilis] | 67 | 36 |
| 266 | 2 | 1266 | 835 | gi\|963038 | ArpU [Enterococcus hirae] | 67 | 42 |
| 285 | 1 | 3 | 809 | gi\|40014 | pot. ORF 446 (aa 1-446) [Bacillus subtilis] | 67 | 53 |
| 288 | 10 | 6838 | 5801 | gi\|1651806 | hypothetical protein [Synechocystis sp.] | 67 | 45 |
| 301 | 10 | 8822 | 8562 | gi\|1303864 | YqgQ [Bacillus subtilis] | 67 | 43 |
| 312 | 5 | 2377 | 2595 | gi\|709991 | hypothetical protein [Bacillus subtilis] | 67 | 52 |
| 353 | 1 | 3 | 1472 | gi\|151259 | HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir\|A44756\|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp. | 67 | 48 |
| 359 | 2 | 984 | 439 | gi\|1773190 | similar to E. coli yhaE [Escherichia coli] | 67 | 45 |
| 359 | 3 | 2244 | 982 | gi\|1001478 | hypothetical protein [Synechocystis sp.] | 67 | 30 |
| 364 | 8 | 8469 | 7816 | gi\|496943 | ORF [Saccharomyces cerevisiae] | 67 | 50 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 386 | 12 | 6625 | 7833 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 67 | 36 |
| 394 | 2 | 497 | 2635 | gnl\|PID\|e255093 | hypothetical protein [Bacillus subtilis] | 67 | 45 |
| 399 | 6 | 5410 | 3971 | gi\|665994 | hypothetical protein [Bacillus subtilis] | 67 | 45 |
| 414 | 1 | 1 | 1227 | gi\|1621027 | high affinity potassium transporter [Debaryomyces occidentalis] | 67 | 40 |
| 453 | 2 | 618 | 391 | gi\|537189 | ORF_f132 [Escherichia coli] | 67 | 45 |
| 458 | 1 | 825 | 226 | gnl\|PID\|e189917 | ORF 28.5 [Escherichia coli] | 67 | 45 |
| 460 | 2 | 644 | 1387 | gi\|1502421 | 3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis] | 67 | 48 |
| 460 | 4 | 2622 | 3131 | gi\|1399830 | biotin carboxyl carrier protein [Synechococcus PCC7942] | 67 | 53 |
| 474 | 1 | 1456 | 77 | gi\|495277 | histidine kinase [Streptococcus pneumoniae] | 67 | 54 |
| 488 | 6 | 3892 | 3032 | gi\|437389 | transposase [Lactococcus lactis] | 67 | 47 |
| 490 | 1 | 460 | 2 | gi\|1742830 | ORF_ID:o326#2; similar to [SwissProt Accession Number P37794] [Escherichia coli] | 67 | 43 |
| 582 | 1 | 2 | 787 | gi\|1408485 | yxdM gene product [Bacillus subtilis] | 67 | 38 |
| 629 | 2 | 1280 | 915 | gi\|1006620 | ABC transporter [Synechocystis sp.] | 67 | 50 |
| 633 | 2 | 941 | 390 | gnl\|PID\|e221400 | tex gene product [Bordetella pertussis] | 67 | 54 |
| 655 | 1 | 47 | 313 | gi\|147403 | mannose permease subunit II-P-Man [Escherichia coli] | 67 | 48 |
| 671 | 3 | 1630 | 2415 | sp\|P13226\|GALE_STRLI | UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE). | 67 | 52 |
| 682 | 2 | 1428 | 595 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 67 | 42 |
| 704 | 3 | 977 | 411 | gi\|467428 | unknown [Bacillus subtilis] | 67 | 45 |
| 711 | 1 | 590 | 168 | gi\|471236 | orf3 [Haemophilus influenzae] | 67 | 37 |
| 784 | 1 | 253 | 2 | gnl\|PID\|e236287 | site-specific DNA-methyltransferase [Bacillus stearothermophilus] | 67 | 44 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 907 | 1 | 209 | 3 | gi\|5119 | topoisomerase I [Schizosaccharomyces pombe] | 67 | 42 |
| 908 | 1 | 275 | 96 | gi\|1591045 | hypothetical protein (SP:P31466) [Methanococcus jannaschii] | 67 | 46 |
| 960 | 1 | 499 | 98 | gi\|405804 | transposase [Streptococcus thermophilus] | 67 | 50 |
| 963 | 1 | 259 | 2 | pir\|S34632\|S34632 | dnaJ protein homolog - human | 67 | 54 |
| 964 | 1 | 164 | 628 | bbs\|173803 | CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167, Peptide Partial, 268 aa] [Listeria monocytogenes] | 67 | 49 |
| 5 | 4 | 1438 | 2403 | gi\|1303810 | YqeT [Bacillus subtilis] | 66 | 50 |
| 7 | 1 | 24 | 1727 | gi\|145220 | alanyl-tRNA synthetase [Escherichia coli] | 66 | 50 |
| 7 | 2 | 1858 | 2646 | gi\|687599 | orfA1; transposon insertion into orfA1 impairs growth and virulence f L. monocytogenes [Listeria monocytogenes] | 66 | 58 |
| 8 | 1 | 3 | 707 | gi\|1303830 | YqfL [Bacillus subtilis] | 66 | 45 |
| 9 | 1 | 182 | 1051 | gi\|467399 | IMP dehydrogenase [Bacillus subtilis] | 66 | 51 |
| 17 | 11 | 8383 | 8598 | gi\|457336 | Pv200 [Plasmodium vivax] | 66 | 42 |
| 18 | 14 | 5903 | 6136 | gi\|294706 | trfA [Plasmid RK2] | 66 | 50 |
| 23 | 12 | 5951 | 6895 | gi\|1652472 | ethylene response sensor protein [Synechocystis sp.] | 66 | 51 |
| 23 | 17 | 11198 | 11881 | gi\|466517 | pduB [Salmonella typhimurium] | 66 | 44 |
| 23 | 19 | 12395 | 13501 | gi\|145206 | alcohol dehydrogenase (adhE) [Escherichia coli] | 66 | 47 |
| 34 | 5 | 5987 | 6232 | gi\|397360 | yNucR endo-exonuclease [Saccharomyces cerevisiae] | 66 | 46 |
| 43 | 2 | 782 | 1018 | gi\|513417 | non-structural polyprotein of pSP6-SFV4 [unidentified] | 66 | 46 |
| 43 | 5 | 3757 | 2324 | gnl\|PID\|e154145 | penicillin binding protein 4 [Staphylococcus aureus] | 66 | 44 |
| 56 | 4 | 2351 | 1662 | gi\|49272 | Asparaginase [Bacillus licheniformis] | 66 | 44 |
| 57 | 2 | 950 | 1735 | gi\|1657505 | hypothetical protein [Escherichia coli] | 66 | 46 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 57 | 4 | 3117 | 3932 | gi\|1657507 | hypothetical protein [Escherichia coli] | 66 | 41 |
| 57 | 8 | 12269 | 12646 | gi\|1622733 | orf108; unknown function [Butyrivibrio fibrisolvens] | 66 | 44 |
| 62 | 2 | 547 | 1302 | gi\|413967 | ipa-43d gene product [Bacillus subtilis] | 66 | 50 |
| 62 | 5 | 2633 | 1905 | gi\|475110 | fructokinase [Pediococcus pentosaceus] | 66 | 51 |
| 74 | 7 | 4661 | 4086 | gi\|467484 | unknown [Bacillus subtilis] | 66 | 47 |
| 81 | 18 | 13878 | 13717 | gi\|146724 | enzyme III-Man function protein (manX (ptsL)) [Escherichia coli] gi\|41976 manX gene product (AA 1-315) [Escherichia coli] | 66 | 35 |
| 94 | 17 | 20780 | 21253 | gi\|142955 | glucose dehydrogenase (EC 1.1.1.47) [Bacillus subtilis] pir\|S36090\|S36090 glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus ubtilis | 66 | 47 |
| 98 | 15 | 15165 | 14338 | gi\|147327 | transport protein [Escherichia coli] | 66 | 34 |
| 105 | 3 | 1726 | 3183 | gnl\|PID\|e205173 | orf1 gene product [Lactobacillus helveticus] | 66 | 45 |
| 110 | 17 | 15811 | 14804 | gi\|887824 | ORF_o310 [Escherichia coli] | 66 | 52 |
| 112 | 2 | 712 | 443 | gnl\|PID\|e242290 | carbamate kinase [Clostridium perfringens] | 66 | 51 |
| 123 | 1 | 1 | 540 | gi\|1573538 | H. influenzae predicted coding region HI0552 [Haemophilus influenzae] | 66 | 39 |
| 123 | 33 | 30312 | 31460 | gi\|1498930 | M. jannaschii predicted coding region MJ0158 [Methanococcus jannaschii] | 66 | 48 |
| 125 | 8 | 4914 | 4474 | gi\|1736749 | Exopolysaccharide production protein PSS. [Escherichia coli] | 66 | 54 |
| 128 | 25 | 18201 | 18878 | gnl\|PID\|e255543 | putative iron dependant repressor [Staphylococcus epidermidis] | 66 | 48 |
| 131 | 3 | 2311 | 3213 | gi\|38969 | lacF gene product [Agrobacterium radiobacter] | 66 | 37 |
| 131 | 5 | 3588 | 3394 | gi\|1303823 | YqfG [Bacillus subtilis] | 66 | 29 |
| 135 | 1 | 1214 | 45 | gi\|1498930 | M. jannaschii predicted coding region MJ0158 [Methanococcus jannaschii] | 66 | 48 |
| 135 | 10 | 7764 | 7405 | gi\|530825 | OVT1 [Onchocerca volvulus] | 66 | 47 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 144 | 13 | 12859 | 10739 | pir\|A40614\|A40614 | penicillin-binding protein pbpF - Bacillus subtilis | 66 | 47 |
| 145 | 5 | 3224 | 4063 | gi\|349531 | lipoprotein [Pasteurella haemolytica] | 66 | 45 |
| 146 | 2 | 1497 | 619 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 66 | 38 |
| 149 | 2 | 1097 | 1282 | gi\|1762962 | FemA [Staphylococcus simulans] | 66 | 38 |
| 150 | 3 | 1443 | 2417 | gnl\|PID\|e185374 | ceuE gene product [Campylobacter coli] | 66 | 46 |
| 150 | 8 | 6487 | 6903 | gi\|1377842 | unknown [Bacillus subtilis] | 66 | 43 |
| 164 | 20 | 21846 | 22646 | gi\|1279769 | FdhC [Methanobacterium thermoformicicum] | 66 | 57 |
| 164 | 25 | 24555 | 25688 | pir\|A43577\|A43577 | regulatory protein pfoR - Clostridium perfringens | 66 | 47 |
| 178 | 1 | 383 | 3 | gi\|763052 | integrase [Bacteriophage T270] | 66 | 47 |
| 195 | 19 | 8698 | 8516 | bbs\|169008 | homeobox gene [Drosophila sp.] | 66 | 55 |
| 207 | 1 | 166 | 1554 | gi\|619724 | MgtE [Bacillus firmus] | 66 | 39 |
| 207 | 3 | 2312 | 2010 | gi\|1204258 | soluble protein [Escherichia coli] | 66 | 44 |
| 211 | 3 | 1523 | 1729 | gi\|289932 | MHC class II beta chain [Cyphotilapia frontosa] | 66 | 66 |
| 213 | 3 | 1811 | 2308 | gi\|153045 | prolipoprotein signal peptidase [Staphylococcus aureus] pir\|S20433\|S20433 lsp protein - Staphylococcus aureus sp\|P31024\|LSPA_STAAU LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36) PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II). | 66 | 40 |
| 221 | 7 | 2524 | 3468 | gi\|1353527 | ORF10 [Bacteriophage r1t] | 66 | 44 |
| 222 | 13 | 8272 | 8988 | gi\|466719 | No definition line found [Escherichia coli] | 66 | 48 |
| 223 | 18 | 15210 | 15971 | gi\|496520 | orf iota [Streptococcus pyogenes] | 66 | 57 |
| 232 | 5 | 3494 | 2715 | gi\|142706 | comG1 gene product [Bacillus subtilis] | 66 | 41 |
| 235 | 3 | 1774 | 734 | gi\|580897 | OppB gene product [Bacillus subtilis] | 66 | 47 |
| 244 | 2 | 906 | 1520 | gi\|15354 | ORF 55.9 [Bacteriophage T4] | 66 | 46 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 259 | 3 | 2355 | 1867 | gi\|56312 | Gephyrin [Rattus norvegicus] | 66 | 55 |
| 271 | 1 | 1 | 675 | gi\|1574748 | tRNA pseudouridine 55 synthase (truB) [Haemophilus influenzae] | 66 | 53 |
| 277 | 1 | 1 | 927 | gi\|1303799 | YqeN [Bacillus subtilis] | 66 | 45 |
| 291 | 5 | 4587 | 3547 | gnl\|PID\|e257609 | sugar-binding transport protein [Anaerocellum thermophilum] | 66 | 46 |
| 292 | 25 | 20451 | 19912 | gi\|1649035 | high-affinity periplasmic glutamine binding protein [Salmonella typhimurium] | 66 | 50 |
| 300 | 1 | 2302 | 77 | gi\|289262 | comE ORF3 [Bacillus subtilis] | 66 | 46 |
| 301 | 4 | 4290 | 3265 | sp\|P13226\|GALE_STRLI | UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE). | 66 | 51 |
| 301 | 5 | 4516 | 4689 | gnl\|PID\|e212164 | PSII, protein N [Odontella sinensis] | 66 | 58 |
| 314 | 1 | 360 | 4 | gi\|467452 | unknown [Bacillus subtilis] | 66 | 43 |
| 315 | 4 | 2559 | 2209 | gi\|1653498 | ABC transporter [Synechocystis sp.] | 66 | 44 |
| 320 | 3 | 2406 | 1081 | gnl\|PID\|e250352 | unknown [Mycobacterium tuberculosis] | 66 | 35 |
| 332 | 2 | 157 | 921 | gi\|1303875 | YqhB [Bacillus subtilis] | 66 | 44 |
| 334 | 2 | 1001 | 3076 | gi\|1651660 | DNA ligase [Synechocystis sp.] | 66 | 48 |
| 338 | 1 | 2 | 616 | gi\|845686 | ORF-27 [Staphylococcus aureus] | 66 | 54 |
| 338 | 7 | 5011 | 5496 | gi\|912476 | No definition line found [Escherichia coli] | 66 | 48 |
| 341 | 5 | 1935 | 3107 | gi\|142538 | aspartate aminotransferase [Bacillus sp.] | 66 | 44 |
| 343 | 3 | 2548 | 2045 | gnl\|PID\|e289147 | similar to single strand binding protein [Bacillus subtilis] | 66 | 44 |
| 345 | 20 | 22093 | 22461 | gi\|1657795 | dihydroneopterin aldolase [Methylobacterium extorquens] | 66 | 45 |
| 353 | 3 | 2621 | 2379 | gnl\|PID\|e257628 | ORF [Lactococcus lactis] | 66 | 52 |
| 365 | 4 | 5117 | 4779 | gi\|1742868 | Mutator MutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (8-oxo-dgtpase) (EC 3.6.1.-) (DGTP pyrophosphohydrolase). [Escherichia coli] | 66 | 54 |
| 376 | 1 | 3 | 1076 | gi\|1778517 | glycerol dehydrogenase homolog | 66 | 45 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Escherichia coli] | | |
| 394 | 7 | 5980 | 5648 | gi\|486358 | ORF YKL202w [Saccharomyces cerevisiae] | 66 | 38 |
| 421 | 4 | 1469 | 2539 | gi\|606375 | ORF_f345 [Escherichia coli] | 66 | 48 |
| 475 | 6 | 3978 | 3763 | gi\|532547 | ORF14 [Enterococcus faecalis] | 66 | 48 |
| 491 | 8 | 7710 | 7081 | gi\|1000453 | TreR [Bacillus subtilis] | 66 | 49 |
| 526 | 1 | 392 | 3 | gi\|1750125 | xylulose kinase [Bacillus subtilis] | 66 | 49 |
| 552 | 6 | 6147 | 5917 | gi\|1432152 | PTS antiterminator [Klebsiella oxytoca] | 66 | 37 |
| 571 | 2 | 560 | 1153 | gi\|1773132 | multidrug resistance-like ATP-binding protein Mdl [Escherichia coli] | 66 | 38 |
| 575 | 3 | 1075 | 539 | gi\|1651722 | guanylate kinase [Synechocystis sp.] | 66 | 48 |
| 608 | 2 | 631 | 113 | gi\|1213334 | OrfX; hypothetical 22.5 KD protein downstream of type IV prepilin leader peptidase gene; Method: conceptual translation supplied by author [Vibrio vulnificus] | 66 | 41 |
| 640 | 1 | 877 | 2 | sp\|P50487\|YCPX_CLOPE | HYPOTHETICAL PROTEIN IN CPE 5'REGION (FRAGMENT). | 66 | 36 |
| 734 | 1 | 2 | 343 | gi\|1653602 | hypothetical protein [Synechocystis sp.] | 66 | 43 |
| 802 | 1 | 2 | 292 | gnl\|PID\|e280516 | voltage-gated sodium channel [Mus musculus] | 66 | 58 |
| 812 | 2 | 343 | 531 | gi\|511075 | ORF2 [Streptococcus agalactiae] | 66 | 51 |
| 823 | 1 | 1 | 393 | gi\|1303843 | YqfV [Bacillus subtilis] | 66 | 42 |
| 891 | 1 | 82 | 402 | gi\|567769 | ORF5; predicted protein shows similarity to ATP-binding transport roteins AmiE and AmiF of Streptococcus pneumoniae; disruptuion of RF5 leads to aminopterin resistance [Streptococcus parasanguis] | 66 | 52 |
| 5 | 6 | 2630 | 3154 | gi\|1303811 | YqeU [Bacillus subtilis] | 65 | 50 |
| 6 | 1 | 2 | 628 | gi\|1742303 | Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment). [Escherichia coli] | 65 | 43 |
| 18 | 6 | 3360 | 2518 | gi\|601880 | rep protein [Bacillus borstelensis] | 65 | 40 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 21 | 11 | 7933 | 7706 | gi\|1500521 | M. jannaschii predicted coding region MJ1623 [Methanococcus jannaschii] | 65 | 32 |
| 23 | 20 | 13459 | 13881 | gi\|488430 | alcohol dehydrogenase 2 [Entamoeba histolytica] | 65 | 43 |
| 23 | 25 | 15987 | 16178 | gnl\|PID\|e248966 | F32D8.5 [Caenorhabditis elegans] | 65 | 50 |
| 27 | 2 | 526 | 302 | gi\|1001644 | regulatory components of sensory transduction system [Synechocystis sp.] | 65 | 44 |
| 29 | 9 | 6770 | 5727 | sp\|P36672\|PTTB_ECOLI | PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE- PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-TRE). | 65 | 45 |
| 31 | 5 | 4611 | 5207 | gi\|171625 | guanylate kinase [Saccharomyces cerevisiae] | 65 | 39 |
| 32 | 7 | 4085 | 3915 | gi\|150158 | 29 kD protein [Mycoplasma genitalium] | 65 | 51 |
| 33 | 8 | 7396 | 7638 | gi\|1573421 | protein translocation protein, low temperature (secG) [Haemophilus influenzae] | 65 | 26 |
| 35 | 1 | 2 | 499 | gi\|1737500 | transcription antiterminator [Bacillus stearothermophilus] | 65 | 40 |
| 45 | 6 | 2537 | 3037 | gi\|511455 | unknown [Coxiella burnetii] | 65 | 37 |
| 46 | 3 | 1028 | 2254 | gi\|1001642 | dGTP triphosphohydrolase [Synechocystis sp.] | 65 | 43 |
| 47 | 12 | 14524 | 14264 | gi\|150209 | ORF 1 [Mycoplasma mycoides] | 65 | 34 |
| 50 | 3 | 2866 | 2051 | gi\|1303830 | YqfL [Bacillus subtilis] | 65 | 40 |
| 57 | 11 | 12955 | 13332 | gnl\|PID\|e254999 | phenylalany-tRNA synthetase beta subunit [Bacillus subtilis] | 65 | 51 |
| 62 | 1 | 2 | 484 | gi\|1573470 | H. influenzae predicted coding region HI0491 [Haemophilus influenzae] | 65 | 57 |
| 68 | 1 | 49 | 282 | gi\|1573250 | aspartate aminotransferase (aspC) [Haemophilus influenzae] | 65 | 52 |
| 72 | 2 | 567 | 1325 | gi\|466645 | alternate name yhiD [Escherichia coli] | 65 | 40 |
| 81 | 5 | 3711 | 2938 | gi\|1732200 | PTS permease for mannose subunit IIPMan | 65 | 43 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Vibrio furnissii] | | |
| 83 | 18 | 12506 | 12745 | pir\|D64042\|D64042 | ribosomal-protein-alanine acetyltransferase (rimI) homolog - Haemophilus influenzae (strain Rd KW20) | 65 | 50 |
| 100 | 38 | 28229 | 28032 | gi\|183075 | glial fibrillary acidic protein [Homo sapiens] | 65 | 43 |
| 105 | 1 | 912 | 106 | pir\|S15248\|YQBZCD | fimC protein - Dichelobacter nodosus (serotype D) | 65 | 46 |
| 106 | 5 | 6097 | 5102 | gi\|1143204 | ORF2; Method: conceptual translation supplied by author [Shigella sonnei] | 65 | 44 |
| 109 | 3 | 1165 | 899 | gi\|1573390 | hypothetical [Haemophilus influenzae] | 65 | 55 |
| 110 | 7 | 5579 | 4257 | pir\|B44514\|B44514 | hypothetical protein 1 (vnfA 5' region) - Azotobacter vinelandii | 65 | 43 |
| 120 | 3 | 1249 | 1632 | sp\|P54746\|YBGB_ECOLI | HYPOTHETICAL PROTEIN IN HRSA 3'REGION (FRAGMENT). | 65 | 48 |
| 122 | 2 | 896 | 1654 | gi\|1335913 | unknown [Erysipelothrix rhusiopathiae] | 65 | 48 |
| 145 | 4 | 2509 | 3210 | gi\|1208965 | hypothetical 23.3 kd protein [Escherichia coli] | 65 | 40 |
| 149 | 7 | 4407 | 3502 | gi\|145173 | 35 kDa protein [Escherichia coli] | 65 | 46 |
| 154 | 8 | 5738 | 4926 | gi\|405804 | transposase [Streptococcus thermophilus] | 65 | 47 |
| 155 | 1 | 306 | 512 | gi\|285627 | E.coli SecE homologous protein [Bacillus subtilis] pir\|S39858\|S39858 secE protein homolog - Bacillus subtilis sp\|Q06799\|SECE_BACSU PREPROTEIN TRANSLOCASE SECE SUBUNIT. | 65 | 48 |
| 158 | 1 | 150 | 1103 | gi\|289272 | ferrichrome-binding protein [Bacillus subtilis] | 65 | 40 |
| 158 | 16 | 14885 | 15946 | gi\|467172 | add; L308_C2_206 [Mycobacterium leprae] | 65 | 36 |
| 173 | 4 | 2103 | 2912 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 65 | 41 |
| 173 | 12 | 9749 | 9054 | gi\|1652864 | hypothetical protein [Synechocystis sp.] | 65 | 50 |
| 179 | 16 | 15674 | 17035 | gi\|1171125 | thioredoxin reductase [Clostridium litorale] | 65 | 41 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 180 | 26 | 26911 | 28266 | sp\|P13692\|P54_ENTFC | P54 PROTEIN PRECURSOR. | 65 | 39 |
| 193 | 6 | 2893 | 3795 | gi\|39787 | adaA [Bacillus subtilis] | 65 | 45 |
| 194 | 5 | 1843 | 2238 | gi\|47394 | 5-oxoprolyl-peptidase [Streptococcus pyogenes] | 65 | 48 |
| 199 | 1 | 894 | 82 | gi\|1591118 | nitrate transport ATP-binding protein [Methanococcus jannaschii] | 65 | 46 |
| 200 | 24 | 13441 | 13136 | gi\|144926 | toxin A [Clostridium difficile] | 65 | 39 |
| 202 | 3 | 2925 | 1846 | gi\|413968 | ipa-44d gene product [Bacillus subtilis] | 65 | 46 |
| 203 | 1 | 797 | 3 | gi\|1377832 | unknown [Bacillus subtilis] | 65 | 45 |
| 204 | 3 | 1065 | 1472 | gi\|1008996 | unknown [Schizosaccharomyces pombe] | 65 | 51 |
| 205 | 4 | 1029 | 1685 | gi\|148989 | truncated tetracycline resistance repressor (non-functional) Haemophilus parainfluenzae] | 65 | 42 |
| 206 | 8 | 5037 | 4807 | pir\|D60110\|D60110 | repetitive protein antigen 3 - Trypanosoma cruzi (fragment) | 65 | 41 |
| 217 | 1 | 411 | 4 | gi\|1146181 | putative [Bacillus subtilis] | 65 | 43 |
| 217 | 4 | 1092 | 3065 | gi\|984229 | penicillin-binding protein 1a [Streptococcus pneumoniae] | 65 | 48 |
| 223 | 27 | 23445 | 23879 | gnl\|PID\|e269486 | Unknown [Bacillus subtilis] | 65 | 47 |
| 225 | 6 | 5138 | 3984 | gi\|39956 | IIGlc [Bacillus subtilis] | 65 | 47 |
| 229 | 5 | 5528 | 5130 | gi\|1303914 | YqhY [Bacillus subtilis] | 65 | 33 |
| 229 | 10 | 10697 | 8517 | gnl\|PID\|e266933 | unknown [Mycobacterium tuberculosis] | 65 | 46 |
| 233 | 3 | 2413 | 1526 | gi\|887825 | ORF_f541 [Escherichia coli] | 65 | 46 |
| 236 | 4 | 6975 | 4789 | gi\|405863 | yohA [Escherichia coli] | 65 | 43 |
| 237 | 4 | 1460 | 1816 | gi\|305080 | myosin heavy chain [Entamoeba histolytica] | 65 | 42 |
| 238 | 24 | 21690 | 23228 | gi\|305008 | rhamnulokinase [Escherichia coli] | 65 | 49 |
| 242 | 3 | 2192 | 3280 | gnl\|PID\|e221269 | tail protein [Bacteriophage CP-1] | 65 | 37 |
| 244 | 6 | 5172 | 4228 | gi\|1653197 | hypothetical protein [Synechocystis sp.] | 65 | 51 |
| 259 | 5 | 3684 | 2779 | gi\|559900 | F49E2.1 [Caenorhabditis elegans] | 65 | 39 |
| 259 | 6 | 4243 | 3749 | gi\|1743887 | molybdopterin cofactor biosynthesis enzyme | 65 | 50 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Bradyrhizobium japonicum] | | |
| 260 | 1 | 140 | 478 | gi\|895748 | putative cellobiose phosphotransferase enzyme II' [Bacillus ubtilis] | 65 | 55 |
| 269 | 6 | 4113 | 3907 | gi\|1303792 | YqeK [Bacillus subtilis] | 65 | 39 |
| 271 | 12 | 7731 | 6772 | gi\|1657534 | cyn operon transcriptional activator [Escherichia coli] | 65 | 45 |
| 275 | 9 | 6413 | 5361 | gi\|1773132 | multidrug resistance-like ATP-binding protein Mdl [Escherichia coli] | 65 | 48 |
| 276 | 4 | 1813 | 1583 | gi\|1504014 | similar to myosin heavy chain: Containing ATP/GTP-binding site motif A(P-loop) [Homo sapiens] | 65 | 34 |
| 279 | 14 | 14254 | 10625 | gi\|1237015 | ORF4 [Bacillus subtilis] | 65 | 45 |
| 281 | 2 | 692 | 1279 | gi\|1303962 | YqjK [Bacillus subtilis] | 65 | 50 |
| 295 | 5 | 2279 | 3388 | gi\|436965 | [malA] gene products [Bacillus stearothermophilus] pir\|S43914\|S43914 hypothetical protein 1 - Bacillus tearothermophilus | 65 | 41 |
| 298 | 1 | 63 | 1142 | gi\|928834 | integrase [Lactococcus lactis phage BK5-T] | 65 | 44 |
| 301 | 8 | 7592 | 7176 | gi\|1303893 | YqhL [Bacillus subtilis] | 65 | 50 |
| 311 | 3 | 4658 | 5701 | gnl\|PID\|e221269 | tail protein [Bacteriophage CP-1] | 65 | 40 |
| 326 | 1 | 2 | 247 | gi\|466520 | pocR [Salmonella typhimurium] | 65 | 38 |
| 329 | 1 | 789 | 523 | gi\|1303895 | YqhN [Bacillus subtilis] | 65 | 36 |
| 345 | 5 | 3363 | 3641 | gi\|895749 | putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis] | 65 | 51 |
| 369 | 3 | 1635 | 1207 | gi\|1480429 | putative transcriptional regulator [Bacillus stearothermophilus] | 65 | 45 |
| 373 | 2 | 815 | 1630 | gi\|1277032 | unknown [Bacillus subtilis] | 65 | 41 |
| 379 | 9 | 11301 | 8275 | gi\|887828 | was o492p and o826p before splice [Escherichia coli] | 65 | 49 |
| 386 | 13 | 7903 | 8145 | gnl\|PID\|e217382 | M7.9 [Caenorhabditis elegans] | 65 | 39 |
| 395 | 4 | 1028 | 1231 | gi\|1592033 | M. jannaschii predicted coding region | 65 | 30 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | MJ1387 [Methanococcus jannaschii] | | |
| 396 | 3 | 1000 | 1272 | gi\|1045900 | hypothetical protein (GB:L09228_17) [Mycoplasma genitalium] | 65 | 44 |
| 422 | 3 | 2050 | 1262 | gi\|405907 | yejD [Escherichia coli] | 65 | 50 |
| 438 | 1 | 44 | 358 | gi\|530798 | LysB [Bacteriophage phi-LC3] | 65 | 39 |
| 460 | 1 | 119 | 646 | gi\|1502420 | malonyl-CoA:Acyl carrier protein transacylase [Bacillus subtilis] | 65 | 46 |
| 463 | 1 | 870 | 121 | gi\|1651917 | tRNA(m1G37)methyltransferase [Synechocystis sp.] | 65 | 47 |
| 468 | 1 | 2 | 823 | gi\|216457 | ORF [Escherichia coli] | 65 | 46 |
| 470 | 1 | 34 | 816 | gi\|530798 | LysB [Bacteriophage phi-LC3] | 65 | 47 |
| 476 | 1 | 21 | 830 | gi\|1006591 | cation-transporting ATPase PacL [Synechocystis sp.] | 65 | 46 |
| 510 | 7 | 4875 | 6092 | gi\|143150 | levR [Bacillus subtilis] | 65 | 46 |
| 565 | 2 | 686 | 339 | gi\|143833 | PBSX repressor [Bacillus subtilis] | 65 | 51 |
| 566 | 2 | 198 | 743 | gi\|496501 | RepS [Streptococcus pyogenes] | 65 | 34 |
| 604 | 5 | 1875 | 2078 | gi\|1590997 | M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii] | 65 | 49 |
| 608 | 1 | 194 | 3 | gnl\|PID\|e290940 | unknown [Mycobacterium tuberculosis] | 65 | 35 |
| 648 | 1 | 60 | 953 | gi\|1591145 | hypothetical protein (HI0902) [Methanococcus jannaschii] | 65 | 31 |
| 657 | 4 | 2531 | 1620 | gi\|1500015 | amidase [Methanococcus jannaschii] | 65 | 46 |
| 691 | 1 | 2 | 718 | gnl\|PID\|e248400 | orfRM1 gene product [Bacillus subtilis] | 65 | 48 |
| 704 | 2 | 474 | 175 | gi\|467428 | unknown [Bacillus subtilis] | 65 | 50 |
| 758 | 2 | 408 | 683 | gi\|451201 | ORF1 [Bacillus subtilis] | 65 | 44 |
| 778 | 1 | 833 | 3 | gi\|410137 | ORFX13 [Bacillus subtilis] | 65 | 40 |
| 793 | 1 | 1 | 564 | gi\|912436 | oligo-1,6-glucosidase [Bacillus thermoglucosidasius] pir\|A41707\|A41707 oligo-1,6-glucosidase (EC 3.2.1.10) - Bacillus hermoglucosidasius | 65 | 40 |
| 827 | 1 | 364 | 2 | gi\|852076 | MrgA [Bacillus subtilis] | 65 | 33 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 856 | 1 | 209 | 3 | gi\|1575605 | 4-methyl-5-nitrocatechol oxygenase [Burkholderia sp.] | 65 | 45 |
| 890 | 1 | 966 | 745 | pir\|A44803\|A44803 | pG1 protein - human (fragment) | 65 | 63 |
| 4 | 1 | 2 | 958 | gnl\|PID\|e265530 | yorfE [Streptococcus pneumoniae] | 64 | 43 |
| 5 | 8 | 4212 | 5579 | gi\|407881 | stringent response-like protein [Streptococcus equisimilis] pir\|S39975\|S39975 stringent response-like protein - Streptococcus quisimilis | 64 | 47 |
| 8 | 4 | 4047 | 3304 | gi\|1573150 | dihydrolipoamide acetyltransferase (acoC) [Haemophilus influenzae] | 64 | 37 |
| 17 | 14 | 11709 | 10393 | gi\|155109 | ORF 1B [Thermus aquaticus thermophilus] | 64 | 37 |
| 19 | 12 | 6499 | 6801 | gi\|1303755 | YqbO [Bacillus subtilis] | 64 | 32 |
| 23 | 1 | 1 | 303 | gi\|1022963 | dextransucrase [Leuconostoc mesenteroides] | 64 | 50 |
| 28 | 4 | 7059 | 6505 | gi\|1568609 | 18kDA protein [Streptococcus pneumoniae] | 64 | 45 |
| 31 | 3 | 1316 | 2986 | gi\|1100076 | PTS-dependent enzyme II [Clostridium longisporum] | 64 | 47 |
| 47 | 2 | 2665 | 3408 | gi\|1742154 | Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] | 64 | 52 |
| 48 | 2 | 1699 | 1310 | gi\|142702 | A competence protein 2 [Bacillus subtilis] | 64 | 41 |
| 54 | 8 | 2750 | 2352 | gi\|951052 | ORF9, putative [Streptococcus pneumoniae] | 64 | 31 |
| 57 | 15 | 18035 | 17274 | gi\|1183886 | integral membrane protein [Bacillus subtilis] | 64 | 40 |
| 62 | 4 | 1968 | 1699 | gi\|475110 | fructokinase [Pediococcus pentosaceus] | 64 | 52 |
| 100 | 42 | 29329 | 29039 | gi\|951048 | excisionase [Streptococcus pneumoniae] | 64 | 37 |
| 102 | 4 | 3726 | 4805 | gi\|215331 | morphogenesis protein [Bacteriophage phi-29] | 64 | 43 |
| 106 | 3 | 3296 | 2439 | gi\|1303930 | YqiK [Bacillus subtilis] | 64 | 44 |
| 123 | 12 | 12960 | 11314 | sp\|P37047\|YAEG_ECOLI | HYPOTHETICAL 44.3 KD PROTEIN IN HTRA-DAPD INTERGENIC REGION. | 64 | 40 |
| 128 | 2 | 1285 | 1614 | gi\|143961 | pyruvate phosphate dikinase [Clostridium symbiosum] pir\|A36231\|KIQAPO | 64 | 52 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | pyruvate,orthophosphate dikinase (EC 2.7.9.1) - lostridium symbiosum | | |
| 128 | 8 | 6178 | 4757 | gi\|40665 | beta-glucosidase [Clostridium thermocellum] | 64 | 41 |
| 133 | 2 | 1748 | 2248 | gi\|1591027 | ferripyochelin binding protein [Methanococcus jannaschii] | 64 | 46 |
| 150 | 1 | 35 | 673 | gnl\|PID\|e185372 | ceuC gene product [Campylobacter coli] | 64 | 38 |
| 158 | 6 | 6038 | 5040 | gi\|1045801 | hypothetical protein (SP:P32720) [Mycoplasma genitalium] | 64 | 35 |
| 164 | 7 | 3620 | 4903 | gnl\|PID\|e283116 | unknown similar to quinolon resistance protein NorA [Bacillus subtilis] | 64 | 41 |
| 171 | 11 | 10107 | 10784 | gi\|1591668 | phosphate transport system regulatory protein [Methanococcus jannaschii] | 64 | 40 |
| 179 | 4 | 4826 | 6373 | gi\|149535 | D-alanine activating enzyme [Lactobacillus casei] | 64 | 51 |
| 181 | 4 | 2251 | 1364 | gi\|671632 | unknown [Staphylococcus aureus] | 64 | 38 |
| 190 | 11 | 11302 | 10355 | gi\|599850 | orf1 gene product [Lactobacillus sake] | 64 | 33 |
| 195 | 37 | 15344 | 16033 | gi\|1736499 | Lysostaphin precursor (EC 3.5.1.-). [Escherichia coli] | 64 | 49 |
| 199 | 4 | 4000 | 5631 | gi\|746574 | similar to M. musculus transport system membrane protein, Nramp PIR:A40739) and S. cerevisiae SMF1 protein (PIR:A45154) Caenorhabditis elegans] | 64 | 37 |
| 202 | 1 | 1 | 1560 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 64 | 45 |
| 204 | 7 | 3000 | 4115 | gi\|1591731 | melvalonate kinase [Methanococcus jannaschii] | 64 | 41 |
| 208 | 1 | 308 | 1090 | gi\|473821 | 'tetrahydrodipicolinate N-succinyltransferase' [Escherichia coli] gi\|1552743 tetrahydrodipicolinate N-succinyltransferase Escherichia coli] | 64 | 42 |
| 216 | 9 | 6501 | 6698 | gi\|47373 | 7 kDa protein [Streptococcus pneumoniae] | 64 | 35 |
| 221 | 18 | 8268 | 8513 | gi\|1389837 | complement regulatory protein [Trypanosoma | 64 | 28 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | cruzi] | | |
| 231 | 4 | 2964 | 2632 | gnl\|PID\|e279941 | muconate cycloisomerase [Rhodococcus erythropolis] | 64 | 37 |
| 234 | 2 | 751 | 302 | gnl\|PID\|e194709 | N-terminal part of a protein of unknown function [Chlamydia psittaci] | 64 | 42 |
| 238 | 18 | 15580 | 16392 | gi\|537108 | ORF_f254 [Escherichia coli] | 64 | 44 |
| 245 | 1 | 14 | 868 | gi\|153247 | endo-beta-N-acetylglucosaminidase H [Streptomyces plicatus] pir\|A00903\|RBSMHP mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) H precursor - treptomyces plicatus | 64 | 51 |
| 272 | 2 | 584 | 1144 | gi\|580781 | signal peptidase [Bacillus licheniformis] | 64 | 47 |
| 281 | 5 | 2659 | 5019 | gi\|147550 | recJ [Escherichia coli] | 64 | 46 |
| 290 | 12 | 9496 | 10371 | gi\|45713 | P.putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, gidB, uncI and uncB seudomonas putida] | 64 | 42 |
| 298 | 4 | 4029 | 3466 | gi\|147780 | rts gene product [Escherichia coli] | 64 | 43 |
| 301 | 20 | 16216 | 15977 | gi\|170482 | prosystemin [Solanum lycopersicum] | 64 | 57 |
| 301 | 21 | 17732 | 17391 | gi\|405804 | transposase [Streptococcus thermophilus] | 64 | 52 |
| 307 | 1 | 198 | 1964 | gi\|1255196 | BSMA [Bacillus stearothermophilus] | 64 | 48 |
| 320 | 5 | 3441 | 3070 | gi\|972900 | ArtP [Haemophilus influenzae] | 64 | 38 |
| 341 | 9 | 7690 | 6413 | gi\|1161380 | IcaA [Staphylococcus epidermidis] | 64 | 30 |
| 345 | 6 | 3589 | 4848 | gi\|902932 | L-methionine gamma-lyase [Pseudomonas putida] | 64 | 45 |
| 348 | 1 | 453 | 22 | gi\|1591957 | M. jannaschii predicted coding region MJ1318 [Methanococcus jannaschii] | 64 | 32 |
| 350 | 2 | 1372 | 1830 | gnl\|PID\|e289141 | similar to hydroxymyristoyl-(acyl carrier protein) dehydratase [Bacillus subtilis] | 64 | 44 |
| 351 | 7 | 3291 | 2917 | gi\|49013 | dTDP-dihydrostreptose synthase [Streptomyces griseus] ir\|S18618\|SYSMPG dTDP-dihydrostreptose synthase - Streptomyces iseus | 64 | 46 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 352 | 2 | 780 | 1028 | gi\|173431 | H+-ATPase [Schizosaccharomyces pombe] | 64 | 38 |
| 386 | 10 | 5952 | 6161 | gnl\|PID\|e243284 | ORF YGL056c [Saccharomyces cerevisiae] | 64 | 50 |
| 398 | 2 | 1233 | 1808 | gi\|147920 | 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] | 64 | 47 |
| 399 | 12 | 8761 | 9159 | gi\|1778534 | HI0024 homolog [Escherichia coli] | 64 | 40 |
| 409 | 1 | 657 | 1607 | gi\|1773157 | ferrochelatase [Escherichia coli] | 64 | 41 |
| 446 | 1 | 266 | 775 | gi\|563845 | orf gene product [Bacillus circulans] | 64 | 53 |
| 462 | 4 | 1714 | 1959 | gi\|169461 | serine proteinase inhibitor [Populus trichocarpa x Populus eltoides] | 64 | 50 |
| 466 | 6 | 5621 | 8539 | gi\|143150 | levR [Bacillus subtilis] | 64 | 43 |
| 501 | 2 | 891 | 1469 | gi\|467109 | rim; 30S Ribosomal protein S18 alanine acetyltransferase; 229_C1_170 [Mycobacterium leprae] | 64 | 44 |
| 512 | 1 | 1 | 279 | gi\|1651948 | hypothetical protein [Synechocystis sp.] | 64 | 35 |
| 516 | 1 | 466 | 2 | gi\|155027 | 6'-N-acetyltransferase [Transposon Tn2426] | 64 | 35 |
| 516 | 2 | 556 | 759 | gi\|1653387 | nitrogen assimilation regulatory protein [Synechocystis sp.] | 64 | 58 |
| 523 | 2 | 904 | 662 | gi\|159464 | armadillo protein [Musca domestica] | 64 | 45 |
| 537 | 2 | 1083 | 844 | gi\|929966 | truncated ORFB due to a basepair deletion; similar to B. anthracis terneR element ORFB [Bacillus anthracis] | 64 | 42 |
| 549 | 1 | 309 | 4 | gi\|1279769 | FdhC [Methanobacterium thermoformicicum] | 64 | 48 |
| 552 | 4 | 5960 | 3945 | gi\|1100076 | PTS-dependent enzyme II [Clostridium longisporum] | 64 | 47 |
| 556 | 1 | 3 | 224 | gi\|727437 | putative 37-kDa protein [Lactococcus lactis] | 64 | 49 |
| 557 | 2 | 767 | 1120 | gnl\|PID\|e257629 | transcription factor [Lactococcus lactis] | 64 | 44 |
| 602 | 1 | 428 | 156 | gi\|520407 | orf2; GTG start codon [Bacillus thuringiensis] | 64 | 50 |
| 603 | 1 | 1 | 165 | gi\|1621445 | sporulation protein Cse15 [Bacillus subtilis] | 64 | 32 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 626 | 1 | 3 | 992 | gi\|1574715 | thioredoxin reductase (trxB) [Haemophilus influenzae] | 64 | 40 |
| 628 | 2 | 240 | 446 | gi\|1165281 | Smg [Borrelia burgdorferi] | 64 | 41 |
| 723 | 1 | 23 | 829 | gi\|1620648 | surface protein Rib [Streptococcus agalactiae] | 64 | 50 |
| 739 | 1 | 4 | 378 | gi\|143835 | PBSX repressor [Bacillus subtilis] | 64 | 37 |
| 748 | 1 | 139 | 765 | gi\|498816 | ORF7; homology to regions 4.1 and 4.2 of sigma factors [Bacillus ubtilis] | 64 | 35 |
| 758 | 1 | 3 | 410 | gi\|451201 | ORF1 [Bacillus subtilis] | 64 | 34 |
| 808 | 1 | 368 | 3 | gi\|142833 | ORF2 [Bacillus subtilis] | 64 | 47 |
| 818 | 2 | 415 | 663 | gi\|854020 | U41, major DNA binding protein [Human herpesvirus 6] | 64 | 40 |
| 906 | 1 | 2 | 433 | gi\|1303865 | YqgR [Bacillus subtilis] | 64 | 44 |
| 17 | 28 | 28175 | 27612 | gi\|151824 | ORF5 [Plasmid R46] | 63 | 34 |
| 19 | 18 | 9546 | 9722 | gi\|288661 | ORF5 product [Bacteriophage P2] | 63 | 45 |
| 39 | 5 | 1841 | 2329 | gi\|1573292 | hypothetical [Haemophilus influenzae] | 63 | 47 |
| 41 | 1 | 1531 | 2 | gi\|580896 | nodB protein (aa 1-219) [Bradyrhizobium sp.] | 63 | 43 |
| 55 | 10 | 5052 | 6410 | gi\|1303917 | YqiB [Bacillus subtilis] | 63 | 42 |
| 80 | 2 | 1852 | 824 | gi\|38722 | precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir\|A29277\|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus | 63 | 42 |
| 81 | 10 | 6724 | 6221 | gi\|1591234 | hypothetical protein (SP:P42297) [Methanococcus jannaschii] | 63 | 40 |
| 81 | 14 | 9175 | 10848 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 63 | 44 |
| 86 | 1 | 2 | 1006 | gi\|143316 | [gap] gene products [Bacillus megaterium] | 63 | 43 |
| 89 | 13 | 12929 | 12639 | gi\|1377841 | unknown [Bacillus subtilis] | 63 | 44 |
| 98 | 14 | 14365 | 13502 | sp\|P45169\|POTC_HAEIN | SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC. | 63 | 37 |
| 100 | 24 | 20444 | 17985 | gi\|563258 | virulence-associated protein E | 63 | 44 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Dichelobacter nodosus] | | |
| 102 | 2 | 2441 | 2599 | gi\|1619835 | MOB [Bacillus thuringiensis israelensis] | 63 | 28 |
| 110 | 22 | 19725 | 20705 | gi\|1763011 | lysophospholipase homolog [Homo sapiens] | 63 | 48 |
| 115 | 1 | 481 | 92 | gi\|467360 | unknown [Bacillus subtilis] | 63 | 38 |
| 128 | 30 | 25257 | 24397 | gi\|1518679 | orf [Bacillus subtilis] | 63 | 39 |
| 138 | 18 | 12236 | 11580 | gi\|405516 | This ORF is homologous to nitroreductase from Enterobacter cloacae, ccession Number A38686, and Salmonella, Accession Number P15888 Mycoplasma-like organism] | 63 | 39 |
| 143 | 2 | 167 | 1096 | pir\|S39416\|S39416 | metallothionein 10-I - blue mussel | 63 | 63 |
| 158 | 9 | 10023 | 8893 | bbs\|173803 | CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167, Peptide Partial, 268 aa] [Listeria monocytogenes] | 63 | 48 |
| 164 | 6 | 3041 | 3301 | gi\|1573583 | H. influenzae predicted coding region HI0594 [Haemophilus influenzae] | 63 | 31 |
| 164 | 18 | 18502 | 21708 | gi\|1015903 | ORF YJR151c [Saccharomyces cerevisiae] | 63 | 45 |
| 165 | 3 | 3084 | 2278 | gi\|537108 | ORF_f254 [Escherichia coli] | 63 | 45 |
| 166 | 1 | 83 | 1045 | gi\|762778 | NifS gene product [Anabaena azollae] | 63 | 49 |
| 168 | 3 | 638 | 1489 | gi\|805022 | Ndi1p [Saccharomyces cerevisiae] | 63 | 32 |
| 171 | 12 | 10655 | 10810 | gi\|152403 | phosphate regulatory protein [Rhizobium meliloti] | 63 | 50 |
| 172 | 1 | 242 | 1336 | gi\|1552775 | ATP-binding protein [Escherichia coli] | 63 | 45 |
| 179 | 11 | 11236 | 12111 | gnl\|PID\|e245033 | unknown [Mycobacterium tuberculosis] | 63 | 42 |
| 179 | 15 | 15289 | 15765 | gi\|1353197 | thioredoxin reductase [Eubacterium acidaminophilum] | 63 | 44 |
| 180 | 3 | 3412 | 1892 | gi\|1064813 | homologous to sp:PHOR_BACSU [Bacillus subtilis] | 63 | 40 |
| 180 | 7 | 7063 | 7926 | gi\|1657516 | hypothetical protein [Escherichia coli] | 63 | 41 |
| 187 | 1 | 1 | 729 | gi\|1651957 | hypothetical protein [Synechocystis sp.] | 63 | 34 |
| 195 | 17 | 7717 | 8280 | gi\|431928 | MunI methyltransferase [Mycoplasma sp.] | 63 | 44 |
| 202 | 8 | 5311 | 6165 | gi\|606162 | ORF_f229 [Escherichia coli] | 63 | 48 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 202 | 10 | 7848 | 8681 | gi\|606018 | ORF_o783 [Escherichia coli] | 63 | 47 |
| 208 | 3 | 2979 | 2341 | gi\|1006613 | hypothetical protein [Synechocystis sp.] | 63 | 40 |
| 221 | 3 | 874 | 1146 | gnl\|PID\|e265530 | yorfE [Streptococcus pneumoniae] | 63 | 42 |
| 227 | 2 | 856 | 1254 | gi\|438459 | homologous to E. coli hydrophobic Fe-uptake components FepD, FecD; utative [Bacillus subtilis] | 63 | 41 |
| 231 | 3 | 2618 | 2448 | gi\|606248 | 30S ribosomal subunit protein S3 [Escherichia coli] | 63 | 42 |
| 233 | 9 | 6773 | 6144 | gi\|887827 | ORF_o192 [Escherichia coli] | 63 | 41 |
| 234 | 1 | 348 | 70 | gi\|494958 | ExpZ [Bacillus subtilis] | 63 | 32 |
| 240 | 2 | 1230 | 721 | gnl\|PID\|e252616 | DcuC protein [Escherichia coli] | 63 | 38 |
| 244 | 9 | 7512 | 6508 | gi\|467421 | similar to B. subtilis DnaH [Bacillus subtilis] sp\|P37540\|YAAS_BACSU HYPOTHETICAL 37.6 KD PROTEIN IN XPAC-ABRB NTERGENIC REGION. | 63 | 43 |
| 255 | 5 | 3600 | 2818 | gi\|1486244 | unknown [Bacillus subtilis] | 63 | 47 |
| 258 | 1 | 3 | 449 | gi\|1041115 | TRAC [Plasmid pPD1] | 63 | 38 |
| 259 | 4 | 2842 | 2342 | gnl\|PID\|e290788 | unknown [Mycobacterium tuberculosis] | 63 | 42 |
| 265 | 8 | 3313 | 3480 | gi\|694074 | emml gene product [Streptococcus pyogenes] | 63 | 42 |
| 276 | 18 | 12505 | 11654 | gi\|601878 | beta-1,3-glucanase bglH [Bacillus circulans] | 63 | 36 |
| 294 | 5 | 2012 | 2275 | gi\|288661 | ORF5 product [Bacteriophage P2] | 63 | 40 |
| 301 | 7 | 7063 | 6704 | gnl\|PID\|e290998 | unknown [Mycobacterium tuberculosis] | 63 | 41 |
| 345 | 2 | 2279 | 2725 | gi\|413940 | ipa-16d gene product [Bacillus subtilis] | 63 | 39 |
| 351 | 8 | 4361 | 3306 | gi\|398120 | TDP-glucose oxireductase [Xanthomonas campestris] | 63 | 47 |
| 359 | 1 | 526 | 14 | gi\|1001605 | 3-hydroxyisobutyrate dehydrogenase [Synechocystis sp.] | 63 | 36 |
| 364 | 6 | 6741 | 7277 | gi\|1736473 | ORF_ID:o335#13; similar to [SwissProt Accession Number P36088] [Escherichia coli] | 63 | 42 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 378 | 2 | 683 | 1414 | gi\|529016 | aminoglycoside 6-adenylyltransferase [Bacillus subtilis] pir\|JU0059\|XXBSG aminoglycoside 6-adenylyltransferase (EC 2.7.7.-) Bacillus subtilis | 63 | 41 |
| 392 | 2 | 783 | 1646 | gi\|1772644 | orfR gene product [Bacillus subtilis] | 63 | 34 |
| 399 | 2 | 574 | 1407 | gi\|40023 | B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] i\|467388 stage III sporulation [Bacillus subtilis] ir\|S18073\|S18073 spoIIIJ protein - Bacillus subtilis | 63 | 42 |
| 403 | 1 | 754 | 2 | gi\|1303938 | YqiS [Bacillus subtilis] | 63 | 52 |
| 404 | 5 | 4149 | 3745 | gi\|142450 | ahrC protein [Bacillus subtilis] | 63 | 42 |
| 430 | 1 | 2 | 1222 | gi\|1046082 | M. genitalium predicted coding region MG372 [Mycoplasma genitalium] | 63 | 40 |
| 432 | 1 | 3 | 1241 | gi\|1001328 | UDP-MurNac-tripeptide synthetase [Synechocystis sp.] | 63 | 33 |
| 432 | 4 | 1970 | 3016 | gi\|1161061 | dioxygenase [Methylobacterium extorquens] | 63 | 41 |
| 463 | 2 | 1324 | 851 | gi\|1573163 | hypothetical [Haemophilus influenzae] | 63 | 40 |
| 466 | 4 | 2843 | 3730 | gnl\|PID\|e261988 | putative ORF [Bacillus subtilis] | 63 | 41 |
| 472 | 1 | 527 | 3 | gi\|556885 | Unknown [Bacillus subtilis] | 63 | 50 |
| 517 | 3 | 2803 | 1646 | gi\|531265 | lipophilic protein which affects bacterial lysis rate and ethicillin resistance level [Staphylococcus aureus] pir\|A55856\|A55856 llm protein - Staphylococcus aureus | 63 | 38 |
| 538 | 1 | 206 | 3 | gi\|172657 | serine-protein kinase [Saccharomyces cerevisiae] | 63 | 47 |
| 539 | 4 | 2997 | 3851 | gi\|973230 | gamma-glutamyl kinase [Lycopersicon esculentum] | 63 | 43 |
| 565 | 3 | 756 | 1010 | gi\|1303724 | YqaF [Bacillus subtilis] | 63 | 51 |
| 573 | 7 | 4518 | 3709 | gi\|1652352 | dihydropteroate pyrophosphorylase [Synechocystis sp.] | 63 | 45 |
| 579 | 2 | 361 | 1344 | gi\|1573114 | beta-ketoacyl-acyl carrier protein | 63 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | synthase III (fabH) [Haemophilus influenzae] | | |
| 593 | 2 | 390 | 1037 | gi\|409286 | bmrU [Bacillus subtilis] | 63 | 33 |
| 707 | 1 | 647 | 171 | gi\|511596 | interleukin-2 [Canis familiaris] | 63 | 33 |
| 714 | 1 | 2 | 268 | gnl\|PID\|e213832 | putative inner membrane protein [Bacillus licheniformis] | 63 | 38 |
| 724 | 1 | 562 | 239 | gnl\|PID\|e255315 | unknown [Mycobacterium tuberculosis] | 63 | 49 |
| 759 | 1 | 681 | 4 | gi\|437639 | [Plasmodium falciparum 3' end.], gene product [Plasmodium alciparum] | 63 | 28 |
| 794 | 1 | 981 | 313 | gi\|451201 | ORF1 [Bacillus subtilis] | 63 | 37 |
| 811 | 2 | 609 | 184 | gi\|150553 | regulatory protein [Plasmid pCF10] | 63 | 30 |
| 835 | 1 | 2 | 262 | gi\|1736496 | RpiR protein. [Escherichia coli] | 63 | 41 |
| 11 | 1 | 2 | 1144 | gi\|143150 | levR [Bacillus subtilis] | 62 | 48 |
| 12 | 5 | 8710 | 7673 | gi\|1486244 | unknown [Bacillus subtilis] | 62 | 43 |
| 15 | 3 | 1167 | 2957 | gi\|1592101 | adenine deaminase [Methanococcus jannaschii] | 62 | 40 |
| 16 | 4 | 2572 | 4092 | gi\|1109685 | ProW [Bacillus subtilis] | 62 | 37 |
| 23 | 4 | 1279 | 2067 | gi\|41432 | fepC gene product [Escherichia coli] | 62 | 35 |
| 23 | 26 | 16176 | 16454 | gi\|154499 | carbon dioxide concentrating mechanism protein [Synechococcus sp.] pir\|C36904\|C36904 carbon dioxide concentrating mechanism protein cmL - Synechococcus sp. (PCC 7942) | 62 | 41 |
| 31 | 6 | 5322 | 5774 | gi\|532309 | 25 kDa protein [Escherichia coli] | 62 | 38 |
| 68 | 4 | 1606 | 2778 | gi\|1732203 | GlcNAc 6-P deacetylase [Vibrio furnissii] | 62 | 44 |
| 72 | 1 | 1 | 540 | gi\|1573097 | glucosamine-6-phosphate deaminase protein (nagB) [Haemophilus influenzae] | 62 | 26 |
| 76 | 3 | 1937 | 2227 | gi\|928830 | ORF75; putative [Lactococcus lactis phage BK5-T] | 62 | 34 |
| 83 | 16 | 11700 | 12272 | gi\|1592161 | N-terminal acetyltransferase complex, subunit ARD1 [Methanococcus jannaschii] | 62 | 33 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 83 | 19 | 12685 | 13737 | gi\|1653193 | sialoglycoprotease [Synechocystis sp.] | 62 | 42 |
| 91 | 6 | 3232 | 3789 | gi\|1762962 | FemA [Staphylococcus simulans] | 62 | 37 |
| 100 | 43 | 29676 | 29317 | gi\|963033 | orf1 gene product [Enterococcus hirae] | 62 | 45 |
| 101 | 8 | 7410 | 6481 | gi\|1161061 | dioxygenase [Methylobacterium extorquens] | 62 | 45 |
| 110 | 3 | 653 | 871 | gi\|992683 | mdm2-D [Homo sapiens] | 62 | 37 |
| 110 | 8 | 8440 | 5810 | gi\|784897 | beta-N-acetylhexosaminidase [Streptococcus pneumoniae] pir\|A56390\|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae | 62 | 46 |
| 111 | 2 | 1057 | 287 | gnl\|PID\|e253280 | ORF YDL238c [Saccharomyces cerevisiae] | 62 | 45 |
| 114 | 5 | 6886 | 7662 | gi\|152719 | flavocytochrome c [Shewanella putrefaciens] | 62 | 37 |
| 115 | 4 | 1401 | 1994 | gi\|1303978 | YqkA [Bacillus subtilis] | 62 | 46 |
| 118 | 1 | 545 | 225 | gi\|39431 | oligo-1,6-glucosidase [Bacillus cereus] | 62 | 40 |
| 119 | 8 | 4625 | 4356 | gi\|1522673 | type I restriction enzyme [Methanococcus jannaschii] | 62 | 33 |
| 120 | 2 | 257 | 1270 | gnl\|PID\|e235823 | unknown [Schizosaccharomyces pombe] | 62 | 41 |
| 121 | 8 | 7543 | 8034 | gi\|39475 | formamidopyrimidine-DNA glycosylase [Bacillus firmus] ir\|S11489\|S11489 formamidopyrimidine-DNA glycosidase (EC 3.2.2.23) Bacillus firmus | 62 | 48 |
| 123 | 2 | 1677 | 592 | gi\|882252 | conjugated bile acid hydrolase [Clostridium perfringens] sp\|P54965\|CBH_CLOPE CHOLOYLGLYCINE HYDROLASE (EC 3.5.1.24) CONJUGATED BILE ACID HYDROLASE) (CBAH) (BILE SALT HYDROLASE). | 62 | 40 |
| 128 | 16 | 10895 | 9408 | gi\|1742834 | PTS system, cellobiose-specific IIC component (EIIC-CEL) (Cellobiose- permease IIC component) (Phosphotransferase enzyme II, C component). [Escherichia coli] | 62 | 43 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 128 | 29 | 24254 | 23544 | gi\|1518680 | minicell-associated protein DivIVA [Bacillus subtilis] | 62 | 37 |
| 128 | 35 | 28843 | 28103 | gi\|142940 | ftsA [Bacillus subtilis] | 62 | 42 |
| 133 | 4 | 3434 | 4165 | gnl\|PID\|e235174 | unknown [Mycobacterium tuberculosis] | 62 | 38 |
| 134 | 2 | 1679 | 933 | gi\|155032 | ORF B [Plasmid pEa34] | 62 | 36 |
| 146 | 6 | 4923 | 4651 | gi\|153675 | tagatose 6-P kinase [Streptococcus mutans] | 62 | 48 |
| 149 | 5 | 3318 | 2527 | gi\|1591587 | pantothenate metabolism flavoprotein [Methanococcus jannaschii] | 62 | 35 |
| 152 | 9 | 4830 | 5747 | gi\|1652461 | lactose transport system permease protein LacF [Synechocystis sp.] | 62 | 39 |
| 163 | 2 | 1341 | 544 | gi\|533098 | DnaD protein [Bacillus subtilis] | 62 | 41 |
| 164 | 14 | 9567 | 9322 | gi\|1118060 | coded for by C. elegans cDNA yk3d11.5; coded for by C. elegans cDNA yk5f4.5 [Caenorhabditis elegans] | 62 | 27 |
| 172 | 8 | 6613 | 7146 | gi\|915199 | ggaB [Bacillus subtilis] | 62 | 33 |
| 173 | 13 | 11127 | 9736 | gi\|1653484 | hypothetical protein [Synechocystis sp.] | 62 | 44 |
| 177 | 1 | 1077 | 364 | gi\|1572994 | 2-keto-3-deoxy-6-phosphogluconate aldolase (eda) [Haemophilus influenzae] | 62 | 38 |
| 178 | 4 | 1683 | 1318 | gnl\|PID\|e155310 | Orf2 [Bacteriophage TP901-1] | 62 | 51 |
| 179 | 5 | 6425 | 7576 | gi\|1161933 | DltB [Lactobacillus casei] | 62 | 44 |
| 180 | 13 | 12470 | 10842 | sp\|P37047\|YAEG_ECOLI | HYPOTHETICAL 44.3 KD PROTEIN IN HTRA-DAPD INTERGENIC REGION. | 62 | 38 |
| 181 | 14 | 11649 | 10735 | gi\|1742758 | Shikimate 5-dehydrogenase (EC 1.1.1.25). [Escherichia coli] | 62 | 41 |
| 197 | 2 | 516 | 1442 | gi\|623476 | transcriptional activator [Providencia stuartii] sp\|P43463\|AARP_PROST TRANSCRIPTIONAL ACTIVATOR AARP. | 62 | 34 |
| 206 | 5 | 2728 | 1790 | gnl\|PID\|e265638 | unknown [Mycobacterium tuberculosis] | 62 | 37 |
| 210 | 2 | 938 | 2290 | gi\|528991 | unknown [Bacillus subtilis] | 62 | 41 |
| 221 | 15 | 7083 | 7280 | gnl\|PID\|e219154 | K08F4.5 [Caenorhabditis elegans] | 62 | 44 |
| 222 | 11 | 7141 | 8022 | gi\|537034 | ORF_o488 [Escherichia coli] | 62 | 39 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 223 | 9 | 6924 | 6358 | gnl\|PID\|e283128 | unknown, highly similar to E. coli YecD hypothtical 21.8 KD protein in aspS 5'region and to isochorismatase [Bacillus subtilis] | 62 | 42 |
| 225 | 4 | 2055 | 2885 | gi\|18724 | pyrroline-5-carboxylate reductase (AA 1-274) [Glycine max] ir\|S10186\|S10186 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - ybean | 62 | 39 |
| 229 | 11 | 11428 | 10670 | gnl\|PID\|e235745 | hypothetical protein [Mycobacterium leprae] | 62 | 36 |
| 231 | 1 | 1244 | 3 | gi\|48808 | dciAE gene product [Bacillus subtilis] | 62 | 45 |
| 233 | 1 | 801 | 4 | gi\|143391 | ORF2 [Bacillus subtilis] | 62 | 42 |
| 233 | 13 | 10471 | 9431 | gi\|887825 | ORF_f541 [Escherichia coli] | 62 | 35 |
| 242 | 1 | 3 | 149 | gi\|532549 | ORF16 [Enterococcus faecalis] | 62 | 44 |
| 255 | 2 | 443 | 1009 | gi\|639789 | ORF9 [Mycoplasma pneumoniae] | 62 | 44 |
| 266 | 6 | 2349 | 2158 | gnl\|PID\|e194945 | yeast sds22 homolog [Homo sapiens] | 62 | 37 |
| 270 | 1 | 3 | 314 | gi\|1303827 | YqfI [Bacillus subtilis] | 62 | 35 |
| 270 | 7 | 5136 | 4447 | gi\|1303958 | YqjG [Bacillus subtilis] | 62 | 41 |
| 279 | 1 | 271 | 2 | gnl\|PID\|e185372 | ceuC gene product [Campylobacter coli] | 62 | 44 |
| 301 | 11 | 9598 | 8798 | gi\|1303863 | YqgP [Bacillus subtilis] | 62 | 45 |
| 306 | 2 | 750 | 1202 | gi\|148771 | ribosomal protein HmaS4 [Haloarcula marismortui] | 62 | 41 |
| 308 | 3 | 2328 | 1684 | gnl\|PID\|e238666 | hypothetical protein [Bacillus subtilis] | 62 | 40 |
| 309 | 5 | 8806 | 8573 | gi\|1591861 | M. jannaschii predicted coding region MJ1230 [Methanococcus jannaschii] | 62 | 37 |
| 318 | 3 | 2278 | 1283 | gi\|1256134 | YbbE [Bacillus subtilis] | 62 | 37 |
| 321 | 3 | 1433 | 1792 | gi\|606080 | ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli] | 62 | 37 |
| 338 | 13 | 11175 | 12770 | gi\|467446 | similar to SpoVB [Bacillus subtilis] | 62 | 38 |
| 345 | 11 | 10519 | 11793 | gi\|1736789 | Collagenase precursor (EC 3.4.-.-). | 62 | 40 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Escherichia coli] | | |
| 345 | 21 | 22459 | 22947 | gi\|1657794 | 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase [Methylobacterium extorquens] | 62 | 47 |
| 358 | 1 | 902 | 36 | gi\|409241 | penicillin-binding protein 2 [Staphylococcus aureus] | 62 | 44 |
| 362 | 6 | 2930 | 3493 | gnl\|PID\|e255091 | hypothetical protein [Bacillus subtilis] | 62 | 37 |
| 363 | 2 | 3242 | 1581 | gnl\|PID\|e254997 | hypothetical protein [Bacillus subtilis] | 62 | 40 |
| 365 | 2 | 400 | 1770 | gi\|143150 | levR [Bacillus subtilis] | 62 | 42 |
| 372 | 5 | 2525 | 4489 | gi\|1045736 | fructose-permease IIBC component [Mycoplasma genitalium] | 62 | 43 |
| 373 | 1 | 3 | 851 | gi\|438462 | transmembrane protein [Bacillus subtilis] | 62 | 36 |
| 375 | 1 | 2 | 1336 | gi\|732813 | branched-chain amino acid carrier [Lactobacillus delbrueckii] pir\|S60180\|S60180 branched-chain amino acid carrier brnQ - actobacillus delbrueckii | 62 | 43 |
| 375 | 3 | 2592 | 1831 | gi\|1644206 | unknown [Bacillus subtilis] | 62 | 43 |
| 391 | 2 | 142 | 510 | gi\|151776 | ORF3 [Escherichia coli] | 62 | 31 |
| 396 | 2 | 254 | 1051 | gi\|410131 | ORFX7 [Bacillus subtilis] | 62 | 41 |
| 423 | 1 | 197 | 6 | pir\|A33592\|A33592 | repressor protein catM - Acinetobacter calcoaceticus | 62 | 38 |
| 436 | 1 | 704 | 3 | gi\|455376 | unidentified reading frame L (ORFL) (putative); putative [Transposon n10] | 62 | 32 |
| 466 | 8 | 9320 | 10480 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 62 | 44 |
| 488 | 5 | 2175 | 2927 | gi\|532546 | ORF13 [Enterococcus faecalis] | 62 | 40 |
| 510 | 4 | 2572 | 3078 | gi\|43941 | EIII-B Sor PTS [Klebsiella pneumoniae] | 62 | 35 |
| 517 | 2 | 1533 | 736 | gi\|559388 | epsX gene product [Acinetobacter calcoaceticus] | 62 | 53 |
| 519 | 1 | 2 | 1084 | gi\|1652876 | hypothetical protein [Synechocystis sp.] | 62 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 535 | 1 | 353 | 69 | gi\|1196922 | unknown protein [Insertion sequence IS861] | 62 | 33 |
| 579 | 1 | 1 | 363 | gi\|535052 | involved in protein secretion [Bacillus subtilis] | 62 | 22 |
| 656 | 5 | 5351 | 5956 | gnl\|PID\|e290931 | unknown [Mycobacterium tuberculosis] | 62 | 40 |
| 666 | 1 | 445 | 128 | gi\|483940 | transcription regulator [Bacillus subtilis] | 62 | 42 |
| 682 | 1 | 597 | 172 | gi\|146724 | enzyme III-Man function protein (manX (ptsL)) [Escherichia coli] gi\|41976 manX gene product (AA 1-315) [Escherichia coli] | 62 | 37 |
| 771 | 1 | 3 | 365 | gi\|1773086 | similar to S. typhimurium ProY [Escherichia coli] | 62 | 44 |
| 831 | 1 | 390 | 94 | gnl\|PID\|e255000 | hypothetical protein [Bacillus subtilis] | 62 | 55 |
| 15 | 5 | 4421 | 5260 | gnl\|PID\|e214719 | PlcR protein [Bacillus thuringiensis] | 61 | 38 |
| 16 | 6 | 4705 | 4938 | gi\|758425 | complement component C3 [Xenopus laevis/gilli] | 61 | 44 |
| 23 | 16 | 10279 | 11214 | sp\|P19265\|EUTC_SALTY | ETHANOLAMINE AMMONIA-LYASE LIGHT CHAIN (EC 4.3.1.7). | 61 | 46 |
| 33 | 2 | 1789 | 2205 | gi\|413958 | ipa-34d gene product [Bacillus subtilis] | 61 | 36 |
| 33 | 5 | 4756 | 6594 | gi\|1001823 | cadmium-transporting ATPase [Synechocystis sp.] | 61 | 38 |
| 37 | 4 | 2813 | 3295 | gi\|1256140 | YbbK [Bacillus subtilis] | 61 | 51 |
| 37 | 7 | 5973 | 5215 | gnl\|PID\|e269488 | Unknown [Bacillus subtilis] | 61 | 33 |
| 49 | 4 | 1567 | 1839 | gnl\|PID\|e139445 | major tail protein [Bacteriophage B1] | 61 | 43 |
| 56 | 1 | 108 | 641 | gi\|1574067 | H. influenzae predicted coding region HI1034 [Haemophilus influenzae] | 61 | 35 |
| 59 | 1 | 1 | 1002 | gi\|763513 | ORF4; putative [Streptomyces violaceoruber] | 61 | 37 |
| 69 | 7 | 4837 | 5523 | gnl\|PID\|e254877 | unknown [Mycobacterium tuberculosis] | 61 | 34 |
| 72 | 11 | 9262 | 10476 | gi\|1591272 | ferrous iron transport protein B [Methanococcus jannaschii] | 61 | 45 |
| 83 | 2 | 731 | 1549 | gi\|755152 | highly hydrophobic integral membrane | 61 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | protein [Bacillus subtilis] sp\|P42953\|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG. | | |
| 87 | 2 | 2067 | 925 | gi\|1573129 | hypothetical [Haemophilus influenzae] | 61 | 46 |
| 103 | 5 | 2689 | 3495 | gi\|1685111 | orf1091 [Streptococcus thermophilus] | 61 | 45 |
| 110 | 13 | 11455 | 11820 | gi\|1001825 | transcriptional repressor SmtB [Synechocystis sp.] | 61 | 42 |
| 110 | 15 | 14048 | 12588 | gi\|1573583 | H. influenzae predicted coding region HI0594 [Haemophilus influenzae] | 61 | 38 |
| 111 | 3 | 1675 | 1055 | gnl\|PID\|e253280 | ORF YDL238c [Saccharomyces cerevisiae] | 61 | 34 |
| 111 | 4 | 1838 | 2518 | gi\|1574513 | hypothetical [Haemophilus influenzae] | 61 | 50 |
| 111 | 5 | 2535 | 3158 | gi\|537235 | Kenn Rudd identifies as gpmB [Escherichia coli] | 61 | 40 |
| 121 | 1 | 3 | 1397 | gi\|290643 | ATPase [Enterococcus hirae] | 61 | 50 |
| 123 | 28 | 25608 | 27734 | gi\|143150 | levR [Bacillus subtilis] | 61 | 39 |
| 125 | 5 | 3455 | 2589 | gi\|148921 | LicD protein [Haemophilus influenzae] | 61 | 47 |
| 128 | 14 | 9382 | 9146 | gi\|575361 | protein kinase PkpA [Phycomyces blakesleeanus] | 61 | 38 |
| 138 | 32 | 23151 | 21628 | gi\|1184262 | GadC [Shigella flexneri] | 61 | 34 |
| 144 | 8 | 6311 | 5325 | gi\|710422 | cmp-binding-factor 1 [Staphylococcus aureus] | 61 | 39 |
| 171 | 4 | 4601 | 5566 | gi\|41500 | ORF 3 (AA 1-352); 38 kD (put. ftsX) [Escherichia coli] | 61 | 31 |
| 172 | 3 | 2006 | 2848 | gi\|303560 | ORF271 [Escherichia coli] | 61 | 42 |
| 173 | 7 | 5146 | 6228 | gi\|1256134 | YbbE [Bacillus subtilis] | 61 | 31 |
| 197 | 8 | 9183 | 8182 | gi\|143803 | GerC3 [Bacillus subtilis] | 61 | 33 |
| 217 | 5 | 3007 | 3462 | gi\|1749414 | unnamed protein product [Schizosaccharomyces pombe] | 61 | 43 |
| 217 | 8 | 6099 | 5464 | gi\|143456 | rpoE protein (ttg start codon) [Bacillus subtilis] | 61 | 37 |
| 222 | 6 | 3400 | 3927 | gnl\|PID\|e255118 | hypothetical protein [Bacillus subtilis] | 61 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 225 | 3 | 1946 | 981 | gi\|1574660 | xylose operon regluatory protein (xylR) [Haemophilus influenzae] | 61 | 43 |
| 237 | 2 | 203 | 952 | gi\|1019108 | alternate start at bp 59; ORF [Bacteriophage phi-80] | 61 | 52 |
| 237 | 7 | 3058 | 3279 | gnl\|PID\|e246904 | ORF YPL169c [Saccharomyces cerevisiae] | 61 | 32 |
| 262 | 1 | 20 | 913 | gnl\|PID\|e214719 | PlcR protein [Bacillus thuringiensis] | 61 | 35 |
| 271 | 17 | 12725 | 13504 | gi\|143057 | ORF39 [Bacillus subtilis] | 61 | 31 |
| 275 | 8 | 5370 | 3697 | gi\|1542975 | AbcB [Thermoanaerobacterium thermosulfurigenes] | 61 | 41 |
| 280 | 2 | 692 | 3079 | gi\|1001352 | ABC transporter [Synechocystis sp.] | 61 | 42 |
| 294 | 7 | 2276 | 2767 | gi\|662792 | single-stranded DNA binding protein [unidentified eubacterium] | 61 | 44 |
| 301 | 12 | 9965 | 9519 | gi\|1303861 | YqgN [Bacillus subtilis] | 61 | 41 |
| 308 | 1 | 1471 | 26 | gi\|1276882 | EpsI [Streptococcus thermophilus] | 61 | 36 |
| 314 | 2 | 475 | 1662 | gi\|975351 | PatB [Bacillus subtilis] | 61 | 42 |
| 321 | 9 | 3762 | 4193 | gi\|1732202 | PTS permease for mannose subunit IIIMan N terminal domain [Vibrio furnissii] | 61 | 40 |
| 323 | 5 | 5118 | 5537 | gi\|532540 | ORF7 [Enterococcus faecalis] | 61 | 28 |
| 324 | 7 | 4800 | 5156 | gi\|146122 | H-protein [Escherichia coli] | 61 | 39 |
| 338 | 3 | 1456 | 1989 | pir\|A47071\|A47071 | orf1 immediately 5' of nifS - Bacillus subtilis | 61 | 43 |
| 341 | 2 | 342 | 947 | gi\|1736577 | Octopine transport system permease protein OccM. [Escherichia coli] | 61 | 41 |
| 349 | 3 | 1788 | 1363 | pir\|G64143\|G64143 | hypothetical protein HI0143 - Haemophilus influenzae (strain Rd KW20) | 61 | 38 |
| 369 | 2 | 1261 | 587 | gi\|153744 | ORF X; putative [Streptococcus mutans] | 61 | 33 |
| 371 | 2 | 1801 | 1562 | gi\|48836 | xylulokinase [Staphylococcus xylosus] | 61 | 40 |
| 372 | 4 | 1575 | 2543 | gi\|149395 | lacC [Lactococcus lactis] | 61 | 43 |
| 379 | 11 | 12683 | 11727 | gi\|887829 | D21141 uses 2nd start; frame determined by Lac fusion [Escherichia oli] | 61 | 40 |
| 383 | 5 | 5625 | 3820 | gi\|624072 | similar to Escherichia coli | 61 | 36 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | glycerophosphoryl diester hosphodiesterase, Swiss-Prot Accession Number P10908 [Paramecium ursaria Chlorella virus 1] | | |
| 395 | 2 | 771 | 517 | gnl\|PID\|e276251 | T23G11.6 [Caenorhabditis elegans] | 61 | 42 |
| 399 | 20 | 15621 | 15812 | gi\|472527 | protein phosphatase 1 [Schizosaccharomyces pombe] | 61 | 44 |
| 413 | 1 | 3 | 749 | gnl\|PID\|e289144 | ywpE [Bacillus subtilis] | 61 | 42 |
| 427 | 1 | 1079 | 288 | gi\|403373 | glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir\|S37251\|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis | 61 | 42 |
| 436 | 4 | 2045 | 1761 | gi\|48669 | pot. ORF B [Shigella sonnei] | 61 | 38 |
| 437 | 1 | 1158 | 244 | gi\|580866 | ipa-12d gene product [Bacillus subtilis] | 61 | 47 |
| 482 | 2 | 1676 | 1167 | bbs\|158786 | 4A11 antigen, sperm tail membrane antigen=putative sucrose-specific phosphotransferase enzyme II homolog [mice, testis, Peptide Partial, 172 aa] [Mus sp.] | 61 | 42 |
| 490 | 3 | 1291 | 1094 | gnl\|PID\|e248473 | putative phosphate permease [Arabidopsis thaliana] | 61 | 35 |
| 514 | 1 | 687 | 142 | gi\|1742775 | msm operon regulatory protein. [Escherichia coli] | 61 | 36 |
| 541 | 1 | 758 | 3 | gi\|1591732 | cobalt transport ATP-binding protein O [Methanococcus jannaschii] | 61 | 39 |
| 551 | 3 | 2163 | 1600 | gi\|671632 | unknown [Staphylococcus aureus] | 61 | 38 |
| 603 | 2 | 163 | 564 | gi\|1408587 | relaxase [Lactococcus lactis lactis] | 61 | 39 |
| 637 | 8 | 4539 | 4769 | gi\|143559 | subtilin [Bacillus subtilis] | 61 | 38 |
| 765 | 1 | 34 | 681 | gi\|408888 | orfA 5' of intG [Lactobacillus bacteriophage phi adh] pir\|PN0468\|PN0468 hypothetical protein 106 - Lactobacillus | 61 | 40 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | gasseri fragment) | | |
| 773 | 1 | 53 | 1207 | gi\|143841 | xylose repressor [Bacillus subtilis] | 61 | 36 |
| 798 | 1 | 175 | 381 | gi\|187572 | located at OATL1 [Homo sapiens] | 61 | 32 |
| 5 | 2 | 303 | 998 | gi\|1783264 | homologous to DNA glycosylases; hypothetical [Bacillus subtilis} | 60 | 50 |
| 8 | 8 | 5891 | 6550 | gi\|1777939 | Pfs [Treponema pallidum] | 60 | 40 |
| 11 | 7 | 4096 | 4935 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 60 | 41 |
| 11 | 8 | 4919 | 5254 | gi\|467125 | glmS; L-Glucosamine:D-fructose-6-phosphate aminotransferase; 229_C3_238 [Mycobacterium leprae] | 60 | 30 |
| 17 | 9 | 7736 | 8203 | gi\|496514 | orf zeta [Streptococcus pyogenes] | 60 | 42 |
| 20 | 1 | 3 | 443 | gi\|861137 | chitin binding protein [Streptomyces olivaceoviridis] pir\|S55001\|S55001 CHB1 protein - Streptomyces olivaceoviridis {SUB -30} | 60 | 40 |
| 21 | 3 | 1970 | 684 | gi\|1778520 | hypothetical protein [Escherichia coli] | 60 | 43 |
| 23 | 11 | 5357 | 5953 | gi\|619066 | NAST [Azotobacter vinelandii] | 60 | 31 |
| 34 | 4 | 6662 | 3279 | gi\|153952 | polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] pir\|A45915\|A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain - Salmonella typhimurium | 60 | 37 |
| 39 | 1 | 47 | 466 | gi\|1561567 | Unknown [Bacillus subtilis] | 60 | 35 |
| 39 | 4 | 1855 | 1361 | gi\|298045 | Orf154 [Streptomyces ambofaciens] | 60 | 41 |
| 48 | 4 | 2554 | 4128 | gi\|1255259 | o-succinylbenzoic acid (OSB) CoA ligase [Staphylococcus aureus] | 60 | 40 |
| 56 | 9 | 6682 | 5795 | gi\|413940 | ipa-16d gene product [Bacillus subtilis] | 60 | 40 |
| 65 | 3 | 2105 | 2593 | gi\|1573061 | hypothetical [Haemophilus influenzae] | 60 | 34 |
| 72 | 9 | 7854 | 8330 | gi\|606343 | CG Site No. 28964 [Escherichia coli] | 60 | 39 |
| 81 | 3 | 2053 | 1406 | gi\|1574770 | phenylalanyl-tRNA synthetase beta-subunit (pheT) [Haemophilus influenzae] | 60 | 46 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 81 | 4 | 2987 | 2130 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 60 | 34 |
| 81 | 12 | 8280 | 7150 | gnl\|PID\|e254984 | hypothetical protein [Bacillus subtilis] | 60 | 44 |
| 83 | 22 | 16887 | 16537 | gi\|509672 | repressor protein [Bacteriophage Tuc2009] | 60 | 33 |
| 89 | 1 | 698 | 60 | gi\|840838 | hypothetical 21.7 kDa protein in ftsY 5' region [Pseudomonas eruginosa] | 60 | 36 |
| 89 | 12 | 12641 | 11856 | gi\|1377843 | unknown [Bacillus subtilis] | 60 | 40 |
| 89 | 17 | 18879 | 15844 | gi\|666069 | orf2 gene product [Lactobacillus leichmannii] | 60 | 37 |
| 94 | 6 | 2281 | 3384 | gi\|468760 | ORF334 [Rhizobium meliloti] | 60 | 36 |
| 98 | 1 | 12 | 1970 | gi\|1652892 | ABC transporter [Synechocystis sp.] | 60 | 38 |
| 99 | 3 | 978 | 1460 | gi\|473955 | DNA-binding protein [Lactobacillus sp.] | 60 | 31 |
| 100 | 35 | 26818 | 26333 | gi\|347851 | junctional sarcoplasmic reticulum glycoprotein [Oryctolagus uniculus] | 60 | 48 |
| 100 | 45 | 30072 | 30449 | gi\|143547 | Sin regulatory protein (ttg start codon) [Bacillus subtilis] gi\|1303886 SinR [Bacillus subtilis] | 60 | 43 |
| 102 | 8 | 5923 | 6561 | gi\|1633572 | Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] | 60 | 25 |
| 109 | 1 | 362 | 3 | pir\|S10655\|S10655 | hypothetical protein X - Pyrococcus woesei (fragment) | 60 | 33 |
| 110 | 16 | 14806 | 14087 | pir\|JH0364\|JH0364 | hypothetical protein 176 (SAGP 5' region) - Streptococcus pyogenes | 60 | 35 |
| 110 | 20 | 18929 | 18414 | gi\|142450 | ahrC protein [Bacillus subtilis] | 60 | 39 |
| 110 | 21 | 19124 | 19624 | gi\|142450 | ahrC protein [Bacillus subtilis] | 60 | 40 |
| 111 | 1 | 289 | 2 | gi\|1256618 | transport protein [Bacillus subtilis] | 60 | 31 |
| 122 | 7 | 5627 | 9589 | gi\|217191 | 5'-nucleotidase precursor [Vibrio parahaemolyticus] | 60 | 39 |
| 123 | 5 | 4390 | 3659 | gi\|1197667 | vitellogenin [Anolis pulchellus] | 60 | 27 |
| 123 | 20 | 18102 | 18407 | gi\|1303705 | YrkF [Bacillus subtilis] | 60 | 34 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 128 | 32 | 26229 | 25492 | gi\|1652485 | hypothetical protein [Synechocystis sp.] | 60 | 29 |
| 129 | 5 | 4421 | 6259 | gi\|1303853 | YqgF [Bacillus subtilis] | 60 | 36 |
| 131 | 2 | 1112 | 2338 | gi\|699112 | ugpC gene product [Mycobacterium leprae] | 60 | 41 |
| 131 | 4 | 3194 | 4036 | gi\|296356 | putative membrane transport protein [Clostridium perfringens]<br>pir\|A56641\|A56641 probable membrane transport protein - Clostridium erfringens | 60 | 32 |
| 131 | 8 | 6669 | 7901 | gi\|537054 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli]<br>pir\|S56438\|S56438 2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC .1.4.16) - Escherichia coli | 60 | 40 |
| 133 | 11 | 9854 | 10240 | gnl\|PID\|e249654 | YneR [Bacillus subtilis] | 60 | 37 |
| 138 | 7 | 6793 | 6263 | gi\|1486247 | unknown [Bacillus subtilis] | 60 | 48 |
| 146 | 4 | 2831 | 2328 | gi\|39979 | P18 [Bacillus subtilis] | 60 | 38 |
| 149 | 6 | 3504 | 3316 | gi\|145173 | 35 kDa protein [Escherichia coli] | 60 | 47 |
| 154 | 5 | 2599 | 3558 | gi\|1773109 | similar to S. typhimurium apbA [Escherichia coli] | 60 | 41 |
| 155 | 5 | 3061 | 4701 | gi\|388269 | traC [Plasmid pAD1] | 60 | 38 |
| 155 | 11 | 8565 | 8927 | gi\|1197460 | MtfB [Escherichia coli] | 60 | 39 |
| 158 | 10 | 11123 | 10032 | gi\|581809 | tmbC gene product [Treponema pallidum] | 60 | 39 |
| 165 | 7 | 6131 | 5700 | gi\|1439527 | EIIA-man [Lactobacillus curvatus] | 60 | 35 |
| 172 | 4 | 3169 | 3810 | gi\|1001342 | hypothetical protein [Synechocystis sp.] | 60 | 42 |
| 174 | 2 | 1574 | 762 | gi\|1045808 | hypothetical protein (GB:U00021_19) [Mycoplasma genitalium] | 60 | 35 |
| 181 | 7 | 4975 | 4460 | gi\|683584 | shikimate kinase [Lactococcus lactis] | 60 | 33 |
| 183 | 6 | 2719 | 2955 | gi\|1146198 | ferredoxin [Bacillus subtilis] | 60 | 37 |
| 189 | 2 | 3528 | 2221 | gi\|396301 | matches PS00041: Bacterial regulatory proteins, araC family ignature [Escherichia coli] | 60 | 35 |
| 193 | 5 | 3121 | 2600 | gi\|39788 | adaB [Bacillus subtilis] | 60 | 49 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 195 | 11 | 4623 | 6569 | gnl\|PID\|e250887 | potential coding region [Clostridium difficile] | 60 | 39 |
| 202 | 2 | 1837 | 1607 | gi\|693939 | membrane ATPase [Haloferax volcanii] | 60 | 32 |
| 206 | 7 | 4794 | 3754 | gi\|1574702 | hypothetical [Haemophilus influenzae] | 60 | 42 |
| 209 | 2 | 1308 | 433 | pir\|A38587\|A38587 | collagen, corneal - chicken (fragment) | 60 | 51 |
| 220 | 3 | 4263 | 1213 | gi\|437706 | alternative truncated translation product from E.coli [Streptococcus neumoniae] | 60 | 41 |
| 222 | 9 | 6019 | 6522 | gi\|882463 | protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia oli] | 60 | 47 |
| 222 | 12 | 8001 | 8336 | gi\|537035 | ORF_o101 [Escherichia coli] | 60 | 33 |
| 233 | 2 | 1294 | 827 | gi\|145091 | flavodoxin [Desulfovibrio salexigens] | 60 | 39 |
| 242 | 11 | 7370 | 7627 | gi\|1353404 | cytochrome oxidase subunit I [Metridium senile] | 60 | 28 |
| 249 | 3 | 1109 | 1768 | gi\|143156 | membrane bound protein [Bacillus subtilis] | 60 | 41 |
| 251 | 3 | 4053 | 1933 | gi\|1235662 | RfbC [Myxococcus xanthus] | 60 | 42 |
| 256 | 4 | 2614 | 3867 | gi\|532612 | ecotropic retrovirus receptor [Mus musculus] | 60 | 37 |
| 260 | 2 | 1539 | 802 | gi\|1208447 | metalloprotease transporter [Serratia marcescens] | 60 | 35 |
| 261 | 5 | 4528 | 3179 | gnl\|PID\|e246728 | histidine kinase [Streptococcus gordonii] | 60 | 25 |
| 269 | 3 | 2723 | 1563 | gi\|1591618 | M. jannaschii predicted coding region MJ0951 [Methanococcus jannaschii] | 60 | 39 |
| 269 | 4 | 3541 | 2780 | gi\|1303794 | YqeM [Bacillus subtilis] | 60 | 36 |
| 269 | 11 | 7164 | 6595 | gi\|1303787 | YqeG [Bacillus subtilis] | 60 | 38 |
| 271 | 2 | 677 | 1651 | gnl\|PID\|e269877 | riboflavin kinase [Bacillus subtilis] | 60 | 43 |
| 271 | 3 | 1639 | 2247 | gi\|537148 | ORF_f181 [Escherichia coli] | 60 | 41 |
| 271 | 18 | 13502 | 13762 | pir\|S39341\|S39341 | grpE protein - Lactococcus lactis | 60 | 40 |
| 277 | 2 | 1662 | 979 | gi\|1773109 | similar to S. typhimurium apbA [Escherichia coli] | 60 | 41 |
| 279 | 13 | 10627 | 9773 | gi\|290545 | f270 [Escherichia coli] | 60 | 41 |
| 290 | 2 | 790 | 1695 | gi\|152886 | elongation factor Ts (tsf) [Spiroplasma | 60 | 38 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | citri] | | |
| 291 | 4 | 3571 | 2612 | gnl\|PID\|e257610 | sugar-binding transport protein [Anaerocellum thermophilum] | 60 | 40 |
| 295 | 3 | 1309 | 2094 | gi\|1000453 | TreR [Bacillus subtilis] | 60 | 37 |
| 301 | 15 | 11063 | 11344 | gi\|535274 | ORF1 [Streptococcus thermophilus] | 60 | 36 |
| 310 | 3 | 2903 | 1266 | gi\|809765 | aspartate aminotransferase (AA 1-402) [Sulfolobus solfataricus] pir\|S07088\|S07088 aspartate transaminase (EC 2.6.1.1) - Sulfolobus olfataricus | 60 | 44 |
| 316 | 2 | 319 | 119 | bbs\|115298 | polyprotein(coat protein) [raspberry ringspot virus RRV, Peptide, 1107 aa] [Raspberry ringspot virus] | 60 | 28 |
| 320 | 4 | 3085 | 2483 | gi\|143002 | proton glutamate symport protein [Bacillus caldotenax] pir\|S26246\|S26246 glutamate/aspartate transport protein - Bacillus aldotenax | 60 | 26 |
| 323 | 1 | 1 | 681 | gi\|1477486 | transposase [Burkholderia cepacia] | 60 | 44 |
| 330 | 4 | 3361 | 4488 | gi\|1778517 | glycerol dehydrogenase homolog [Escherichia coli] | 60 | 48 |
| 356 | 3 | 2471 | 2205 | gi\|57633 | neuronal myosin heavy chain [Rattus rattus] | 60 | 40 |
| 362 | 5 | 2458 | 2925 | gnl\|PID\|e255090 | hypothetical protein [Bacillus subtilis] | 60 | 36 |
| 364 | 4 | 4096 | 5349 | gi\|1657522 | hypothetical protein [Escherichia coli] | 60 | 41 |
| 383 | 1 | 654 | 4 | gnl\|PID\|e288399 | F56H6.k [Caenorhabditis elegans] | 60 | 39 |
| 383 | 2 | 2208 | 853 | gi\|143536 | sigma factor 54 [Bacillus subtilis] | 60 | 37 |
| 386 | 2 | 130 | 510 | gi\|1046053 | hypothetical protein (SP:P32049) [Mycoplasma genitalium] | 60 | 42 |
| 399 | 26 | 25892 | 27757 | gi\|895747 | putative cel operon regulator [Bacillus subtilis] | 60 | 30 |
| 399 | 27 | 27721 | 28239 | gi\|146281 | gut operon activator (gutM) [Escherichia coli] | 60 | 35 |
| 401 | 4 | 2081 | 3523 | gi\|142833 | ORF2 [Bacillus subtilis] | 60 | 36 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 405 | 2 | 1353 | 763 | gi\|633113 | ORF3 [Streptococcus sobrinus] | 60 | 42 |
| 407 | 7 | 4380 | 4589 | gi\|1674126 | (AE000043) Mycoplasma pneumoniae, MG280 homolog, from M. genitalium [Mycoplasma pneumoniae] | 60 | 39 |
| 408 | 1 | 12 | 539 | gi\|455006 | orf6 [Rhodococcus fascians] | 60 | 42 |
| 421 | 7 | 4113 | 3925 | gi\|60020 | ORF31 (AA1-868) [Human herpesvirus 3] | 60 | 43 |
| 452 | 3 | 712 | 2223 | gi\|532554 | ORF21 [Enterococcus faecalis] | 60 | 38 |
| 462 | 3 | 2066 | 1551 | gi\|1015903 | ORF YJR151c [Saccharomyces cerevisiae] | 60 | 37 |
| 480 | 1 | 12 | 272 | gi\|468715 | sss gene product [Pseudomonas aeruginosa] | 60 | 34 |
| 487 | 1 | 1091 | 3 | gi\|388269 | traC [Plasmid pAD1] | 60 | 39 |
| 490 | 5 | 2108 | 1479 | gi\|699379 | glvr-1 protein [Mycobacterium leprae] | 60 | 29 |
| 507 | 1 | 221 | 751 | gi\|1303952 | YqjA [Bacillus subtilis] | 60 | 37 |
| 511 | 1 | 449 | 63 | gi\|391610 | farnesyl diphosphate synthase [Bacillus stearothermophilus] pir\|JX0257\|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus tearothermophilus | 60 | 42 |
| 551 | 2 | 1521 | 604 | gi\|1256648 | putative [Bacillus subtilis] | 60 | 37 |
| 552 | 1 | 887 | 63 | gi\|537235 | Kenn Rudd identifies as gpmB [Escherichia coli] | 60 | 40 |
| 610 | 1 | 1 | 792 | gi\|1321625 | exo-alpha-1, 4-glucosidase [Bacillus stearothermophilus] | 60 | 45 |
| 642 | 1 | 402 | 214 | gi\|992964 | thioredoxin [Arabidopsis thaliana] | 60 | 36 |
| 646 | 1 | 642 | 265 | gi\|1041115 | TRAC [Plasmid pPD1] | 60 | 32 |
| 661 | 2 | 305 | 943 | gi\|1651536 | 3-oxoacyl-[acyl-carrier-protein] reductase [Escherichia coli] | 60 | 37 |
| 678 | 1 | 536 | 3 | gi\|532554 | ORF21 [Enterococcus faecalis] | 60 | 39 |
| 716 | 1 | 799 | 305 | gi\|886040 | ORFtxe1 [Clostridium difficile] | 60 | 38 |
| 717 | 1 | 2 | 472 | gi\|1402529 | ORF8 [Enterococcus faecalis] | 60 | 31 |
| 727 | 1 | 516 | 82 | gi\|471283 | ORF [Synechococcus PCC6301] | 60 | 41 |
| 770 | 1 | 327 | 4 | gi\|467451 | unknown [Bacillus subtilis] | 60 | 33 |
| 843 | 1 | 234 | 4 | gi\|2819 | transferase (GAL10) (AA 1 - 687) | 60 | 37 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Kluyveromyces lactis] r\|S01407\|XUVKG UDPglucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis) | | |
| 21 | 1 | 341 | 3 | gi\|1778519 | hypothetical protein [Escherichia coli] | 59 | 47 |
| 23 | 2 | 290 | 1303 | gi\|1407800 | ABC-type permease [Yersinia pestis] | 59 | 36 |
| 23 | 13 | 6720 | 7388 | gi\|1652472 | ethylene response sensor protein [Synechocystis sp.] | 59 | 37 |
| 23 | 18 | 11892 | 12413 | gi\|825627 | major carboxysome shell protein [Thiobacillus neapolitanus] pir\|S60136\|S60136 major carboxysome shell protein - Thiobacillus eapolitanus | 59 | 42 |
| 29 | 4 | 1989 | 2852 | gi\|1742383 | ORF_ID:o276#3; similar to [PIR Accession Number S11432] [Escherichia coli] | 59 | 48 |
| 32 | 8 | 4504 | 4064 | gi\|1046081 | hypothetical protein (GB:D26185_10) [Mycoplasma genitalium] | 59 | 33 |
| 37 | 9 | 6670 | 6284 | gi\|290561 | o188 [Escherichia coli] | 59 | 44 |
| 47 | 1 | 2 | 2743 | gnl\|PID\|e248792 | unknown [Mycobacterium tuberculosis] | 59 | 46 |
| 48 | 5 | 4017 | 5492 | gi\|1185288 | isochorismate synthase [Bacillus subtilis] | 59 | 40 |
| 49 | 5 | 1797 | 2093 | gi\|496280 | structural protein [Bacteriophage Tuc2009] | 59 | 41 |
| 59 | 8 | 3324 | 5057 | gi\|1486244 | unknown [Bacillus subtilis] | 59 | 35 |
| 72 | 14 | 13937 | 13434 | gi\|532540 | ORF7 [Enterococcus faecalis] | 59 | 25 |
| 81 | 20 | 14659 | 14219 | gi\|39978 | P16 [Bacillus subtilis] | 59 | 38 |
| 98 | 2 | 1961 | 2617 | gi\|41519 | P30 protein (AA 1-240) [Escherichia coli] | 59 | 39 |
| 102 | 3 | 2542 | 3774 | gi\|1674376 | (AE000062) Mycoplasma pneumoniae, MG148 homolog, from M. genitalium [Mycoplasma pneumoniae] | 59 | 30 |
| 116 | 2 | 907 | 1458 | gi\|1146225 | putative [Bacillus subtilis] | 59 | 37 |
| 116 | 7 | 3532 | 4842 | gi\|1146238 | poly(A) polymerase [Bacillus subtilis] | 59 | 41 |
| 128 | 20 | 15626 | 14310 | gi\|1001719 | ATP-dependent RNA helicase DeaD [Synechocystis sp.] | 59 | 34 |
| 134 | 4 | 3158 | 3850 | gi\|1477486 | transposase [Burkholderia cepacia] | 59 | 40 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 137 | 1 | 1 | 999 | gi\|1065948 | similar to thymidine diphosphoglucose 4,6-dehydratase [Caenorhabditis elegans] | 59 | 40 |
| 138 | 8 | 7489 | 6827 | gnl\|PID\|e264435 | Putative orf YCLX8c, len:192 [Saccharomyces cerevisiae] | 59 | 36 |
| 140 | 1 | 3 | 656 | gnl\|PID\|e254943 | unknown [Mycobacterium tuberculosis] | 59 | 32 |
| 165 | 13 | 10427 | 9849 | gi\|1732199 | PTS permease for mannose subunit IIIMan C terminal domain [Vibrio furnissii] | 59 | 37 |
| 167 | 1 | 2 | 1045 | gi\|1573128 | hypothetical [Haemophilus influenzae] | 59 | 38 |
| 173 | 2 | 430 | 2160 | gi\|1486244 | unknown [Bacillus subtilis] | 59 | 31 |
| 179 | 10 | 10432 | 11199 | gi\|288299 | ORF1 gene product [Bacillus megaterium] | 59 | 34 |
| 179 | 12 | 12117 | 13148 | gi\|1045964 | hypothetical protein (GB:U14003_297) [Mycoplasma genitalium] | 59 | 41 |
| 181 | 11 | 9684 | 8575 | gi\|1653152 | 3-dehydroquinate synthase [Synechocystis sp.] | 59 | 41 |
| 223 | 24 | 20736 | 21974 | gi\|1573051 | succinyl-diaminopimelate desuccinylase (dapE) [Haemophilus influenzae] | 59 | 48 |
| 229 | 12 | 12818 | 11421 | gi\|1652035 | fmu and fmv protein [Synechocystis sp.] | 59 | 39 |
| 244 | 3 | 2836 | 1565 | gi\|1303959 | YqjH [Bacillus subtilis] | 59 | 45 |
| 265 | 9 | 4116 | 3868 | gi\|311100 | translational activator [Saccharomyces cerevisiae] | 59 | 28 |
| 272 | 1 | 1 | 546 | gi\|490320 | Y gene product [unidentified] | 59 | 41 |
| 279 | 16 | 14774 | 14370 | gi\|1389549 | ORF3 [Bacillus subtilis] | 59 | 46 |
| 283 | 8 | 3222 | 3401 | gi\|153047 | lysostaphin (ttg start codon) [Staphylococcus simulans] pir\|A25881\|A25881 lysostaphin precursor - Staphylococcus simulans sp\|P10547\|LSTP_STASI LYSOSTAPHIN PRECURSOR (EC 3.5.1.-). | 59 | 43 |
| 288 | 5 | 2617 | 3144 | gi\|1142714 | phosphoenolpyruvate:mannose phosphotransferase element IIB [Lactobacillus curvatus] | 59 | 45 |
| 292 | 19 | 14837 | 16792 | gi\|495646 | ATPase [Transposon Tn5422] | 59 | 40 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 295 | 1 | 49 | 495 | gi\|533098 | DnaD protein [Bacillus subtilis] | 59 | 39 |
| 315 | 2 | 907 | 653 | gi\|1574802 | hypothetical [Haemophilus influenzae] | 59 | 38 |
| 318 | 6 | 4549 | 4058 | gi\|43941 | EIII-B Sor PTS [Klebsiella pneumoniae] | 59 | 35 |
| 345 | 3 | 2707 | 3507 | gi\|895749 | putative cellobiose phosphotransferase enzyme II'' [Bacillus ubtilis] | 59 | 38 |
| 351 | 5 | 2646 | 2371 | gi\|1666506 | RfbC [Leptospira interrogans] | 59 | 30 |
| 355 | 21 | 15237 | 17222 | gi\|515738 | ORF2; putative [Oenococcus oeni] | 59 | 35 |
| 384 | 1 | 14 | 754 | gi\|1162959 | homologous to HI0365 in Haemophilus influenzae; ORF1 [Pseudomonas aeruginosa] | 59 | 34 |
| 385 | 1 | 3 | 533 | gi\|1146197 | putative [Bacillus subtilis] | 59 | 36 |
| 394 | 13 | 13137 | 12160 | gnl\|PID\|e243582 | ORF YGR263c [Saccharomyces cerevisiae] | 59 | 36 |
| 399 | 1 | 224 | 580 | gi\|580904 | homologous to E.coli rnpA [Bacillus subtilis] | 59 | 38 |
| 412 | 1 | 3 | 2927 | gi\|1620648 | surface protein Rib [Streptococcus agalactiae] | 59 | 43 |
| 412 | 2 | 2918 | 3559 | gi\|1620648 | surface protein Rib [Streptococcus agalactiae] | 59 | 43 |
| 416 | 6 | 5283 | 3940 | gi\|1100076 | PTS-dependent enzyme II [Clostridium longisporum] | 59 | 38 |
| 437 | 2 | 1561 | 1136 | gi\|580866 | ipa-12d gene product [Bacillus subtilis] | 59 | 44 |
| 495 | 2 | 438 | 614 | gi\|1500472 | M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii] | 59 | 45 |
| 502 | 1 | 853 | 188 | gi\|1063248 | No homologous protein [Bacillus subtilis] | 59 | 25 |
| 573 | 8 | 5092 | 4493 | gi\|1573226 | hypothetical [Haemophilus influenzae] | 59 | 39 |
| 579 | 4 | 1716 | 2717 | gnl\|PID\|e280724 | unknown [Mycobacterium tuberculosis] | 59 | 41 |
| 600 | 1 | 1 | 504 | gi\|49386 | internal region of the penicillin-binding protein 2B gene treptococcus pneumoniae] | 59 | 40 |
| 616 | 3 | 904 | 533 | gi\|289265 | [Bacillus sp. (KSM 64) endo-1,4-beta-glucanase gene, complete cds.], ene products [Bacillus sp.] | 59 | 44 |
| 657 | 1 | 432 | 4 | gi\|1651338 | PnuC protein [Escherichia coli] | 59 | 37 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 699 | 1 | 416 | 165 | gnl\|PID\|e199096 | PepR1 [Lactobacillus delbrueckii] | 59 | 23 |
| 713 | 4 | 3709 | 2660 | gi\|515738 | ORF2; putative [Oenococcus oeni] | 59 | 37 |
| 715 | 1 | 698 | 84 | gi\|1176399 | EpiF [Staphylococcus epidermidis] | 59 | 42 |
| 737 | 2 | 660 | 199 | gi\|666000 | hypothetical protein [Bacillus subtilis] | 59 | 43 |
| 744 | 1 | 395 | 3 | gi\|1732057 | MUC.CL-1 [Trypanosoma cruzi] | 59 | 45 |
| 746 | 1 | 3 | 554 | gi\|141858 | replication-associated protein [Plasmid pAD1] | 59 | 36 |
| 869 | 1 | 2 | 250 | gi\|1432153 | cellobiose-specific PTS permease [Klebsiella oxytoca] | 59 | 40 |
| 4 | 8 | 6948 | 6067 | gi\|147516 | ribokinase [Escherichia coli] | 58 | 42 |
| 11 | 6 | 3312 | 4121 | gi\|1732200 | PTS permease for mannose subunit IIPMan [Vibrio furnissii] | 58 | 35 |
| 16 | 9 | 7684 | 6932 | gnl\|PID\|e233879 | hypothetical protein [Bacillus subtilis] | 58 | 48 |
| 23 | 14 | 7440 | 8903 | gi\|142940 | ftsA [Bacillus subtilis] | 58 | 39 |
| 30 | 2 | 570 | 1283 | gi\|1644202 | unknown [Bacillus subtilis] | 58 | 37 |
| 48 | 7 | 7186 | 8037 | gi\|1573247 | hypothetical [Haemophilus influenzae] | 58 | 35 |
| 49 | 7 | 2395 | 2871 | gnl\|PID\|e210884 | c2 gene product [Bacteriophage B1] | 58 | 34 |
| 54 | 1 | 1014 | 91 | gi\|46645 | ORF (rlx) [Staphylococcus aureus] | 58 | 46 |
| 55 | 3 | 1221 | 511 | gi\|726443 | No definition line found [Caenorhabditis elegans] | 58 | 41 |
| 58 | 1 | 1904 | 696 | gi\|1591564 | molybdenum cofactor biosynthesis moeA protein [Methanococcus jannaschii] | 58 | 39 |
| 58 | 8 | 7238 | 6996 | gi\|1279769 | FdhC [Methanobacterium thermoformicicum] | 58 | 54 |
| 72 | 12 | 12117 | 10897 | gi\|763052 | integrase [Bacteriophage T270] | 58 | 37 |
| 77 | 2 | 1155 | 1910 | gi\|1245464 | YfeA [Yersinia pestis] | 58 | 34 |
| 78 | 1 | 2589 | 49 | gi\|40663 | sialidase [Clostridium septicum] | 58 | 40 |
| 88 | 9 | 5854 | 6528 | gi\|1619623 | hemin binding protein [Yersinia enterocolitica] | 58 | 37 |
| 93 | 6 | 2639 | 2863 | gi\|405133 | putative [Bacillus subtilis] | 58 | 33 |
| 98 | 13 | 13523 | 12432 | gi\|147329 | transport protein [Escherichia coli] | 58 | 41 |
| 100 | 12 | 8550 | 8224 | gi\|1736642 | Invasin. [Escherichia coli] | 58 | 47 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 102 | 7 | 5688 | 5969 | gi\|808869 | human gcp372 [Homo sapiens] | 58 | 30 |
| 105 | 5 | 3716 | 4501 | gi\|143729 | transcription activator [Bacillus subtilis] | 58 | 40 |
| 107 | 1 | 511 | 2 | gi\|1303827 | YqfI [Bacillus subtilis] | 58 | 34 |
| 108 | 2 | 1040 | 1732 | gi\|1592142 | ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii] | 58 | 37 |
| 114 | 6 | 7608 | 8444 | gi\|152719 | flavocytochrome c [Shewanella putrefaciens] | 58 | 40 |
| 117 | 14 | 11813 | 11115 | gi\|1575577 | DNA-binding response regulator [Thermotoga maritima] | 58 | 42 |
| 122 | 1 | 1 | 936 | gi\|393269 | adhesion protein [Streptococcus pneumoniae] | 58 | 38 |
| 123 | 23 | 20379 | 21617 | gi\|1653948 | hypothetical protein [Synechocystis sp.] | 58 | 38 |
| 133 | 8 | 7362 | 8480 | gi\|143498 | degS protein [Bacillus subtilis] | 58 | 38 |
| 133 | 9 | 8437 | 9087 | gi\|143089 | iep protein [Bacillus subtilis] | 58 | 31 |
| 138 | 3 | 3551 | 2898 | gi\|216114 | DNA polymerase [Bacteriophage SPO1] | 58 | 41 |
| 138 | 5 | 5819 | 5049 | gnl\|PID\|e289148 | highly similar to phosphotransferase system regulator [Bacillus subtilis] | 58 | 38 |
| 138 | 17 | 11419 | 10379 | gi\|1674137 | (AE000044) Mycoplasma pneumoniae, lipoate protein ligase; similar to Swiss-Prot Accession Number P32099, from E. coli [Mycoplasma pneumoniae] | 58 | 37 |
| 139 | 8 | 5002 | 4808 | gi\|153607 | dpnD gene product [Streptococcus pneumoniae] | 58 | 43 |
| 146 | 9 | 7817 | 6627 | gi\|606076 | ORF_o384 [Escherichia coli] | 58 | 43 |
| 150 | 10 | 7529 | 7894 | gi\|141852 | sialidase [Actinomyces viscosus] | 58 | 28 |
| 152 | 10 | 5717 | 6637 | gi\|296356 | putative membrane transport protein [Clostridium perfringens] pir\|A56641\|A56641 probable membrane transport protein - Clostridium erfringens | 58 | 36 |
| 162 | 10 | 11009 | 11185 | gi\|42655 | pi protein [Escherichia coli] | 58 | 37 |
| 164 | 3 | 1793 | 1608 | gi\|881499 | parathion hydrolase (phosphotriesterase)- | 58 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | related protein [Mus usculus] | | |
| 165 | 6 | 5640 | 4975 | gi\|1146190 | 2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis] | 58 | 39 |
| 165 | 10 | 9038 | 8199 | gi\|606080 | ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli] | 58 | 35 |
| 168 | 1 | 1 | 657 | gi\|413930 | ipa-6d gene product [Bacillus subtilis] | 58 | 41 |
| 170 | 1 | 923 | 234 | gi\|1573505 | hypothetical [Haemophilus influenzae] | 58 | 30 |
| 176 | 1 | 1 | 1101 | gi\|1652379 | cation-transporting P-ATPase [Synechocystis sp.] | 58 | 30 |
| 180 | 12 | 10237 | 10410 | gi\|408123 | V-ATPase 14kD subunit peptide [Drosophila melanogaster] pir\|S38436\|S38436 H+-transporting ATPase (EC 3.6.1.35) 14K chain - ruit fly (Drosophila melanogaster) | 58 | 33 |
| 193 | 3 | 2077 | 1388 | gi\|1256633 | putative [Bacillus subtilis] | 58 | 39 |
| 193 | 4 | 2602 | 2075 | gi\|147920 | 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] | 58 | 33 |
| 194 | 9 | 6492 | 5500 | sp\|P09997\|YIDA_ECOLI | HYPOTHETICAL 29.7 KD PROTEIN IN IBPA-GYRB INTERGENIC REGION. | 58 | 38 |
| 201 | 5 | 5152 | 4466 | gi\|755152 | highly hydrophobic integral membrane protein [Bacillus subtilis] sp\|P42953\|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG. | 58 | 28 |
| 210 | 9 | 6546 | 7265 | gi\|466520 | pocR [Salmonella typhimurium] | 58 | 36 |
| 220 | 1 | 3 | 569 | gi\|467441 | expressed at the end of exponential growyh under condtions in which he enzymes of the TCA cycle are repressed [Bacillus subtilis] sp\|P14194\|CTC_BACSU GENERAL STRESS PROTEIN CTC. {SUB 2-204} gi\|40219 partial ctc gene product (AA 1-186) [Bacillus subtilis] | 58 | 38 |
| 222 | 10 | 6520 | 7143 | gi\|1674024 | (AE000033) Mycoplasma pneumoniae, | 58 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | hypothetical protein (yjfS) homolog; similar to Swiss-Prot Accession Number P39301, from E. coli [Mycoplasma pneumoniae] | | |
| 233 | 7 | 4984 | 3944 | gi\|147806 | selenium metabolism protein [Escherichia coli] | 58 | 45 |
| 238 | 14 | 12128 | 12910 | gi\|1736468 | Pectin degradation repressor protein KdgR. [Escherichia coli] | 58 | 37 |
| 244 | 11 | 8102 | 7809 | gi\|467418 | unknown [Bacillus subtilis] | 58 | 37 |
| 246 | 1 | 1 | 276 | gi\|65291 | receptor tyrosine kiase preprotein [Xiphophorus sp.} ir\|S06142\|S06142 kinase-related transforming protein (Tu) (EC 7.1.-) precursor - southern platyfish | 58 | 32 |
| 255 | 4 | 2927 | 2559 | gi\|1652384 | ABC transporter [Synechocystis sp.] | 58 | 41 |
| 258 | 9 | 8025 | 8966 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 58 | 35 |
| 259 | 2 | 1801 | 893 | gi\|1591564 | molybdenum cofactor biosynthesis moeA protein [Methanococcus jannaschii] | 58 | 39 |
| 260 | 3 | 1754 | 2254 | gi\|580841 | F1 [Bacillus subtilis] | 58 | 38 |
| 271 | 4 | 2382 | 2738 | gi\|40067 | X gene product [Bacillus sphaericus] | 58 | 37 |
| 279 | 8 | 6237 | 6536 | gi\|1783243 | homologous to jojC gene product (B. subtilis; prf:2111327a); hypothetical [Bacillus subtilis] | 58 | 34 |
| 301 | 1 | 753 | 175 | gi\|499196 | ORF1 [Streptomyces lincolnensis] | 58 | 37 |
| 304 | 1 | 100 | 849 | gi\|1653322 | hypothetical protein [Synechocystis sp.] | 58 | 41 |
| 313 | 2 | 748 | 1650 | gi\|1658371 | cyclic beta-1,2-glucan modification protein [Rhizobium meliloti] | 58 | 36 |
| 321 | 11 | 6033 | 6533 | gi\|1573292 | hypothetical [Haemophilus influenzae] | 58 | 34 |
| 322 | 6 | 3819 | 5069 | gi\|23897 | 5'-nucleotidase [Homo sapiens] | 58 | 34 |
| 324 | 5 | 3259 | 4452 | gi\|1469784 | putative cell division protein ftsW [Enterococcus hirae] | 58 | 37 |
| 328 | 1 | 1 | 270 | gi\|882579 | CG Site No. 29739 [Escherichia coli] | 58 | 43 |

Table 2: E. *faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 330 | 8 | 6228 | 6758 | gi\|43941 | EIII-B Sor PTS [Klebsiella pneumoniae] | 58 | 37 |
| 334 | 4 | 3634 | 3963 | gi\|1001306 | hypothetical protein [Synechocystis sp.] | 58 | 34 |
| 345 | 17 | 18899 | 20044 | gi\|853809 | ORF3 [Clostridium perfringens] | 58 | 30 |
| 363 | 7 | 8475 | 9944 | gi\|348056 | trans-acting positive regulator [Bacillus anthracis] | 58 | 33 |
| 375 | 7 | 6472 | 5279 | gi\|1408501 | homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis] | 58 | 42 |
| 394 | 12 | 10689 | 12095 | gi\|537034 | ORF_o488 [Escherichia coli] | 58 | 32 |
| 399 | 3 | 1383 | 2198 | gi\|580905 | B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis] gi\|580919 Jag [Bacillus subtilis] | 58 | 36 |
| 399 | 16 | 11544 | 12098 | gi\|1572965 | hypothetical [Haemophilus influenzae] | 58 | 39 |
| 399 | 19 | 14776 | 15654 | gi\|1778530 | CitG homolog [Escherichia coli] | 58 | 40 |
| 407 | 2 | 738 | 553 | gi\|170553 | pyruvate kinase [Trichoderma reesei] | 58 | 38 |
| 416 | 5 | 4045 | 3389 | gi\|475112 | enzyme IIabc [Pediococcus pentosaceus] | 58 | 41 |
| 449 | 4 | 1421 | 879 | gi\|928834 | integrase [Lactococcus lactis phage BK5-T] | 58 | 32 |
| 497 | 1 | 3 | 458 | gi\|160628 | reticulocyte binding protein 2 [Plasmodium vivax] | 58 | 30 |
| 594 | 1 | 285 | 4 | gi\|1353874 | unknown [Rhodobacter capsulatus] | 58 | 39 |
| 637 | 6 | 3451 | 2765 | pir\|D61615\|D61615 | sericin MG-1 - greater wax moth (fragment) | 58 | 52 |
| 653 | 1 | 595 | 245 | gi\|1408585 | LtrD [Lactococcus lactis lactis] | 58 | 41 |
| 656 | 4 | 3713 | 5209 | sp\|P13692\|P54_ENTFC | P54 PROTEIN PRECURSOR. | 58 | 37 |
| 656 | 6 | 5988 | 6467 | gi\|1017818 | phosphotyrosine protein phosphatase [Streptomyces coelicolor] | 58 | 48 |
| 667 | 1 | 88 | 1467 | bbs\|177441 | OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] | 58 | 40 |
| 686 | 1 | 892 | 233 | pir\|A24255\|A24255 | chorion class A protein L11 precursor - | 58 | 38 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | silkworm | | |
| 706 | 1 | 1002 | 607 | gi\|1001762 | hypothetical protein [Synechocystis sp.] | 58 | 32 |
| 801 | 1 | 254 | 12 | gnl\|PID\|e243641 | unknown [Mycobacterium tuberculosis] | 58 | 29 |
| 848 | 1 | 212 | 3 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 58 | 37 |
| 975 | 1 | 3 | 422 | gi\|290545 | f270 [Escherichia coli] | 58 | 35 |
| 11 | 4 | 2345 | 2833 | gi\|1439527 | EIIA-man [Lactobacillus curvatus] | 57 | 46 |
| 16 | 2 | 1426 | 365 | gi\|780550 | acetyl transferase [Rhizobium loti] | 57 | 35 |
| 18 | 3 | 1593 | 925 | gnl\|PID\|e137594 | xerC recombinase [Lactobacillus leichmannii] | 57 | 36 |
| 19 | 15 | 8058 | 8267 | gi\|1590922 | cell division inhibitor [Methanococcus jannaschii] | 57 | 42 |
| 19 | 23 | 11938 | 12318 | gi\|1294760 | structural protein; orfL3; putative [Bacteriophage phi-41] | 57 | 46 |
| 25 | 9 | 7743 | 6958 | gnl\|PID\|e255000 | hypothetical protein [Bacillus subtilis] | 57 | 40 |
| 47 | 3 | 3857 | 4462 | gi\|1353540 | ORF23 [Bacteriophage r1t] | 57 | 35 |
| 65 | 10 | 7180 | 8919 | gi\|496254 | fibronectin/fibrinogen-binding protein [Streptococcus pyogenes] | 57 | 40 |
| 68 | 7 | 3923 | 3705 | gi\|336656 | ribosomal protein secY [Cyanophora paradoxa] | 57 | 28 |
| 70 | 4 | 2317 | 3645 | pir\|S11158\|YESAEE | erythromycin resistance protein - Staphylococcus epidermidis plasmid pUL5050 | 57 | 40 |
| 76 | 1 | 55 | 1095 | gi\|1353562 | Structural protein [Bacteriophage r1t] | 57 | 41 |
| 91 | 11 | 9070 | 8849 | gi\|550321 | beta-fructofuranosidase [Chenopodium rubrum] | 57 | 30 |
| 94 | 4 | 1740 | 1495 | gi\|47406 | penicillin-binding protein 1a [Streptococcus pneumoniae] ir\|S28031\|S28031 penicillin-binding protein 1a - Streptococcus eumoniae (strain 456) (fragment) | 57 | 30 |
| 98 | 6 | 7766 | 6849 | gi\|409286 | bmrU [Bacillus subtilis] | 57 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 100 | 22 | 17294 | 15912 | gnl\|PID\|e289150 | member of the SNF2 helicase family [Bacillus subtilis] | 57 | 30 |
| 102 | 1 | 66 | 2465 | gi\|405564 | traE [Plasmid pSK41] | 57 | 28 |
| 110 | 14 | 11757 | 12497 | gi\|854601 | unknown [Schizosaccharomyces pombe] | 57 | 38 |
| 114 | 9 | 10291 | 11139 | gi\|853777 | product similar to E.coli PRFA2 protein [Bacillus subtilis] pir\|S55438\|S55438 ywkE protein - Bacillus subtilis sp\|P45873\|HEMK_BACSU POSSIBLE PROTOPORPHYRINOGEN OXIDASE (EC .3.3.-). | 57 | 38 |
| 115 | 3 | 955 | 1461 | gi\|396347 | alternate name yjaB [Escherichia coli] | 57 | 33 |
| 123 | 3 | 1925 | 2932 | gi\|1001731 | low affinity sulfate transporter [Synechocystis sp.] | 57 | 39 |
| 124 | 7 | 6026 | 5118 | gi\|1674310 | (AE000058) Mycoplasma pneumoniae, MG085 homolog, from M. genitalium [Mycoplasma pneumoniae] | 57 | 30 |
| 128 | 9 | 7530 | 6235 | gi\|413940 | ipa-16d gene product [Bacillus subtilis] | 57 | 36 |
| 128 | 31 | 25487 | 25206 | gi\|1651915 | hypothetical protein [Synechocystis sp.] | 57 | 42 |
| 128 | 33 | 26878 | 26150 | gi\|1001387 | hypothetical protein [Synechocystis sp.] | 57 | 30 |
| 128 | 37 | 30730 | 29600 | gi\|406877 | DivIB protein [Bacillus licheniformis] | 57 | 35 |
| 130 | 9 | 7408 | 8556 | gi\|343539 | NADH dehydrogenase subunit 4 [Trypanosoma brucei] | 57 | 27 |
| 144 | 1 | 1013 | 219 | gi\|1652518 | hypothetical protein [Synechocystis sp.] | 57 | 45 |
| 144 | 6 | 4145 | 5254 | gi\|149581 | maturation protein [Lactobacillus paracasei] | 57 | 38 |
| 146 | 1 | 617 | 192 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 57 | 33 |
| 153 | 1 | 83 | 991 | gi\|147336 | transmembrane protein [Escherichia coli] | 57 | 33 |
| 160 | 8 | 4718 | 4134 | gi\|305333 | zeta-crystallin [Cavia porcellus] | 57 | 39 |
| 167 | 8 | 14891 | 14688 | gi\|206354 | protein kinase C, zeta subspecies [Rattus norvegicus] pir\|A30314\|A30314 protein kinase C (EC 2.7.1.-) zeta - rat sp\|P09217\|KPCZ_RAT PROTEIN KINASE C, ZETA | 57 | 39 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | TYPE (EC 2.7.1.-) NPKC-ZETA). | | |
| 174 | 1 | 760 | 2 | gnl\|PID\|e191403 | ORFA gene product [Chloroflexus aurantiacus] | 57 | 42 |
| 176 | 4 | 3347 | 3568 | gi\|1236529 | cyclomaltodextrinase [Bacillus sp.] | 57 | 46 |
| 194 | 8 | 4786 | 5457 | gi\|405516 | This ORF is homologous to nitroreductase from Enterobacter cloacae, ccession Number A38686, and Salmonella, Accession Number P15888 Mycoplasma-like organism] | 57 | 26 |
| 199 | 3 | 3207 | 3764 | gi\|216350 | ORF [Bacillus subtilis] | 57 | 38 |
| 202 | 5 | 3356 | 3664 | gi\|1183841 | Holliday junction binding protein [Pseudomonas aeruginosa] | 57 | 34 |
| 202 | 12 | 10911 | 10192 | gi\|971338 | anaerobic regulatory protein [Bacillus subtilis] | 57 | 27 |
| 205 | 3 | 1022 | 468 | gi\|1783240 | hypothetical [Bacillus subtilis] | 57 | 38 |
| 223 | 2 | 779 | 1501 | gi\|1208965 | hypothetical 23.3 kd protein [Escherichia coli] | 57 | 32 |
| 223 | 3 | 1499 | 2332 | gi\|303560 | ORF271 [Escherichia coli] | 57 | 35 |
| 223 | 11 | 8404 | 12198 | gi\|158079 | period protein [Drosophila serrata] | 57 | 40 |
| 237 | 9 | 3685 | 3906 | gi\|514919 | phosphofructokinase [Drosophila melanogaster] | 57 | 31 |
| 242 | 7 | 5760 | 5020 | gi\|1574596 | H. influenzae predicted coding region HI1738 [Haemophilus influenzae] | 57 | 33 |
| 250 | 2 | 1243 | 1485 | gnl\|PID\|e275819 | K08G2.8 [Caenorhabditis elegans] | 57 | 47 |
| 276 | 28 | 16565 | 16332 | gi\|886375 | variant-specific surface protein [Plasmodium falciparum] | 57 | 47 |
| 288 | 6 | 3157 | 3363 | gi\|147403 | mannose permease subunit II-P-Man [Escherichia coli] | 57 | 39 |
| 289 | 1 | 141 | 818 | gi\|1742822 | Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] | 57 | 40 |
| 292 | 20 | 15930 | 15721 | gi\|854201 | putative polymerase [Infectious bursal disease virus] | 57 | 47 |
| 294 | 4 | 1454 | 2014 | gi\|454303 | LDJ2 gene product [Allium porrum] | 57 | 41 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 295 | 4 | 2052 | 2342 | pir\|S48588\|S48588 | hypothetical protein - Mycoplasma capricolum (SGC3) (fragment) | 57 | 39 |
| 301 | 14 | 10921 | 10148 | gnl\|PID\|e262045 | putative orf [Bacillus subtilis] | 57 | 38 |
| 306 | 1 | 2 | 793 | gi\|216715 | HpaI methyltransferase [Haemophilus parainfluenzae] pir\|S28681\|S28681 site-specific DNA-methyltransferase adenine-specific) (EC 2.1.1.72) HpaI - Haemophilus parainfluenzae sp\|P29538\|MTH1_HAEPA MODIFICATION METHYLASE HPAI (EC 2.1.1.72) ADENINE-SPECIFIC MET | 57 | 36 |
| 306 | 8 | 5418 | 5663 | gi\|1591542 | M. jannaschii predicted coding region MJ0857 [Methanococcus jannaschii] | 57 | 42 |
| 308 | 2 | 1732 | 1487 | gi\|1518045 | FlbF protein [Borrelia burgdorferi] | 57 | 28 |
| 321 | 2 | 1030 | 1458 | gi\|606080 | ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli] | 57 | 30 |
| 351 | 4 | 2342 | 1587 | gi\|1591853 | M. jannaschii predicted coding region MJ1222 [Methanococcus jannaschii] | 57 | 37 |
| 355 | 30 | 20619 | 20861 | gi\|1136394 | There are three putative hydrophobic domains in the central region. [Homo sapiens] | 57 | 42 |
| 364 | 10 | 9415 | 8852 | gi\|38722 | precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir\|A29277\|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus | 57 | 32 |
| 365 | 3 | 4715 | 1812 | gi\|914990 | Similar to DEAD box family helicases [Saccharomyces cerevisiae] pir\|S59797\|S59797 hypothetical protein D9798.1 - yeast Saccharomyces cerevisiae) | 57 | 35 |
| 378 | 1 | 615 | 10 | gi\|1652989 | hypothetical protein [Synechocystis sp.] | 57 | 35 |
| 379 | 1 | 1457 | 114 | gi\|1256618 | transport protein [Bacillus subtilis] | 57 | 36 |
| 390 | 1 | 1426 | 2 | gi\|387880 | collagen adhesin [Staphylococcus aureus] | 57 | 37 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 422 | 1 | 2 | 409 | gi\|1591837 | M. jannaschii predicted coding region MJ1207 [Methanococcus jannaschii] | 57 | 37 |
| 447 | 1 | 397 | 131 | gi\|214566 | keratin protein XK81 [Xenopus laevis] | 57 | 33 |
| 454 | 2 | 1095 | 889 | gi\|1783256 | sigma factor [Bacillus subtilis] | 57 | 28 |
| 504 | 2 | 641 | 1426 | gi\|42081 | nagD gene product (AA 1-250) [Escherichia coli] | 57 | 32 |
| 524 | 2 | 963 | 577 | gi\|143724 | putative [Bacillus subtilis] | 57 | 43 |
| 535 | 4 | 4862 | 4305 | gi\|146549 | kdpC [Escherichia coli] | 57 | 40 |
| 547 | 2 | 426 | 719 | gi\|533098 | DnaD protein [Bacillus subtilis] | 57 | 33 |
| 548 | 1 | 316 | 717 | gi\|397973 | Mg2+ transport ATPase [Salmonella typhimurium] | 57 | 33 |
| 639 | 2 | 359 | 105 | gnl\|PID\|e247390 | P-type ATPase [Dictyostelium discoideum] | 57 | 31 |
| 641 | 1 | 941 | 180 | gnl\|PID\|e261990 | putative orf [Bacillus subtilis] | 57 | 36 |
| 686 | 3 | 1298 | 3259 | gi\|496506 | orf gamma [Streptococcus pyogenes] | 57 | 37 |
| 686 | 6 | 2200 | 2847 | gi\|404800 | putative [Saccharopolyspora erythraea] | 57 | 47 |
| 782 | 2 | 591 | 860 | gi\|1591270 | alanyl-tRNA synthetase [Methanococcus jannaschii] | 57 | 32 |
| 844 | 1 | 3 | 182 | gi\|849217 | Weak similarity to Streptococcus Protein V, a type-II IgG receptor PIR accession number S17354) and Giardia lamblia median body rotein (PIR accession number S33821) [Saccharomyces cerevisiae] pir\|S61181\|S61181 hypothetical protein D9740.10 - yeast Sacchar | 57 | 34 |
| 859 | 1 | 174 | 4 | gi\|1762584 | polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana] | 57 | 28 |
| 967 | 1 | 381 | 4 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 57 | 40 |
| 11 | 5 | 2817 | 3314 | gi\|43941 | EIII-B Sor PTS [Klebsiella pneumoniae] | 56 | 30 |
| 15 | 1 | 80 | 892 | gi\|1574803 | spermidine/putrescine-binding periplasmic protein precursor (potD) [Haemophilus influenzae] | 56 | 32 |
| 37 | 8 | 6327 | 6088 | gi\|290561 | o188 [Escherichia coli] | 56 | 41 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 44 | 2 | 1169 | 1360 | gi\|16096 | peroxidase [Armoracia rusticana] | 56 | 37 |
| 56 | 3 | 1881 | 1363 | gi\|49272 | Asparaginase [Bacillus licheniformis] | 56 | 33 |
| 65 | 1 | 102 | 887 | gi\|1377832 | unknown [Bacillus subtilis] | 56 | 41 |
| 75 | 9 | 5817 | 4306 | gi\|1235712 | polyprotein [Infectious pancreatic necrosis virus] | 56 | 30 |
| 83 | 7 | 3260 | 4051 | gi\|1652645 | phosphoglycolate phosphatase [Synechocystis sp.] | 56 | 30 |
| 95 | 3 | 1793 | 2389 | pir\|C53610\|C53610 | ntpE protein - Enterococcus hirae | 56 | 28 |
| 100 | 3 | 5076 | 1915 | gi\|1353559 | ORF42 [Bacteriophage r1t] | 56 | 35 |
| 100 | 16 | 10581 | 10369 | gi\|868224 | No definition line found [Caenorhabditis elegans] | 56 | 35 |
| 100 | 48 | 31841 | 32770 | gi\|460025 | ORF2, putative [Streptococcus pneumoniae] | 56 | 38 |
| 108 | 5 | 4007 | 3336 | gi\|288301 | ORF2 gene product [Bacillus megaterium] | 56 | 34 |
| 109 | 2 | 1032 | 325 | gi\|413976 | ipa-52r gene product [Bacillus subtilis] | 56 | 36 |
| 119 | 7 | 3958 | 5304 | gi\|498842 | VirS [Clostridium perfringens] | 56 | 35 |
| 123 | 32 | 29479 | 30345 | gi\|39981 | P30 [Bacillus subtilis] | 56 | 38 |
| 126 | 1 | 521 | 3 | gi\|147403 | mannose permease subunit II-P-Man [Escherichia coli] | 56 | 29 |
| 130 | 6 | 4296 | 6104 | gi\|308854 | oligopeptide binding protein [Lactococcus lactis] | 56 | 33 |
| 131 | 7 | 5267 | 6613 | gi\|466589 | CG Site No. 39 [Escherichia coli] | 56 | 32 |
| 133 | 5 | 4358 | 5758 | gi\|1573431 | aminodeoxychorismate lyase (pabC) [Haemophilus influenzae] | 56 | 40 |
| 138 | 20 | 13680 | 12670 | gi\|1590951 | UDP-glucose 4-epimerase [Methanococcus jannaschii] | 56 | 40 |
| 138 | 29 | 19764 | 18823 | gi\|44864 | H.8 outer membrane protein (AA -17 to 71) [Neisseria gonorrhoeae] ir\|S02720\|S02720 outer membrane protein H.8 precursor - Neisseria norrhoeae | 56 | 33 |
| 145 | 7 | 5611 | 7179 | gi\|1652892 | ABC transporter [Synechocystis sp.] | 56 | 33 |
| 146 | 10 | 8545 | 7811 | gi\|41519 | P30 protein (AA 1-240) [Escherichia coli] | 56 | 28 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 150 | 4 | 2979 | 4637 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 56 | 32 |
| 159 | 5 | 5362 | 5066 | gi\|576733 | apocytochrome b [Trypanoplasma borreli] | 56 | 43 |
| 164 | 13 | 8864 | 15031 | gi\|1654116 | protein F2 [Streptococcus pyogenes] | 56 | 43 |
| 179 | 7 | 7790 | 9118 | gi\|413926 | ipa-2r gene product [Bacillus subtilis] | 56 | 33 |
| 187 | 4 | 2239 | 1667 | gi\|1573061 | hypothetical [Haemophilus influenzae] | 56 | 18 |
| 200 | 19 | 11473 | 10724 | gi\|498817 | ORF8; homologous to small subunit of phage terminases [Bacillus ubtilis] | 56 | 35 |
| 206 | 6 | 3766 | 2759 | gi\|474837 | ORF1 [Thermoanaerobacterium thermosulfurigenes] sp\|P38541\|YAMB_THETU HYPOTHETICAL 35.6 KD PROTEIN IN AMYB 5'REGION ORF1). | 56 | 34 |
| 207 | 2 | 2091 | 1672 | gi\|1204258 | soluble protein [Escherichia coli] | 56 | 40 |
| 217 | 9 | 6661 | 6158 | gi\|1017427 | elastic titin [Homo sapiens] | 56 | 28 |
| 225 | 7 | 6007 | 5099 | gi\|1742675 | Phosphotransferase system enzyme II (EC 2.7.1.69) MalX [Escherichia coli] | 56 | 46 |
| 230 | 3 | 595 | 3153 | gi\|437706 | alternative truncated translation product from E.coli [Streptococcus neumoniae] | 56 | 34 |
| 236 | 2 | 1486 | 515 | gi\|415664 | catabolite control protein [Bacillus megaterium] sp\|P46828\|CCPA_BACME GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN). | 56 | 35 |
| 236 | 7 | 9255 | 8599 | gi\|343544 | ATPase 6 [Trypanosoma brucei] | 56 | 48 |
| 238 | 15 | 13059 | 13718 | gi\|1146190 | 2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis] | 56 | 37 |
| 238 | 20 | 17734 | 18756 | gi\|1574060 | hypothetical [Haemophilus influenzae] | 56 | 32 |
| 238 | 23 | 21613 | 20726 | gi\|151361 | member of the AraC/XylS family of transcriptional regulators Pseudomonas aeruginosa] | 56 | 36 |
| 242 | 6 | 4103 | 4477 | gi\|886858 | nicotinic acetylcholine receptor [Caenorhabditis elegans] pir\|S57648\|S57648 nicotinic acetylcholine receptor - Caenorhabditis legans | 56 | 35 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 260 | 5 | 3170 | 3781 | gnl\|PID\|e58151 | F3 [Bacillus subtilis] | 56 | 43 |
| 279 | 6 | 5140 | 2831 | gi\|581100 | gamma-glutamylcysteine synthetase (aa 1-518) [Escherichia coli] pir\|A24136\|SYECEC glutamate--cysteine ligase (EC 6.3.2.2) - scherichia coli | 56 | 42 |
| 279 | 9 | 6434 | 7228 | gi\|1783243 | homologous to jojC gene product (B. subtilis; prf:2111327a); hypothetical [Bacillus subtilis] | 56 | 29 |
| 292 | 14 | 10719 | 11504 | gi\|45738 | ORFC [Enterococcus faecalis] | 56 | 37 |
| 313 | 3 | 3039 | 1831 | gi\|474915 | orf 337; translated orf similarity to SW: BCR_ECOLI bicyclomycin esistance protein of Escherichia coli [Coxiella burnetii] pir\|S44207\|S44207 hypothetical protein 337 - Coxiella burnetii (SUB -338) | 56 | 31 |
| 313 | 5 | 4233 | 3589 | gi\|405883 | yeiL [Escherichia coli] | 56 | 30 |
| 322 | 5 | 1994 | 3715 | gi\|1377831 | unknown [Bacillus subtilis] | 56 | 34 |
| 353 | 2 | 2353 | 1310 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 56 | 26 |
| 394 | 14 | 13289 | 14143 | gi\|142836 | repressor protein [Bacillus subtilis] | 56 | 30 |
| 399 | 32 | 30208 | 30891 | gi\|396293 | similar to Bacillus subtilis hypoth. 20 kDa protein, in tsr 3' egion [Escherichia coli] | 56 | 38 |
| 402 | 2 | 1267 | 914 | gi\|170710 | alpha-type gliadin precursor protein [Triticum aestivum] | 56 | 45 |
| 408 | 4 | 2825 | 2220 | gnl\|PID\|e257696 | collagen binding protein [Lactobacillus reuteri] | 56 | 36 |
| 432 | 5 | 3105 | 3302 | gi\|11678 | atpE gene product [Marchantia polymorpha] | 56 | 33 |
| 443 | 2 | 844 | 1089 | gi\|1256138 | YbbI [Bacillus subtilis] | 56 | 36 |
| 499 | 2 | 875 | 1666 | gi\|1499876 | magnesium and cobalt transport protein [Methanococcus jannaschii] | 56 | 30 |
| 510 | 6 | 3864 | 4733 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 56 | 34 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 543 | 6 | 3706 | 3113 | gi\|563812 | XCAP-C [Xenopus laevis] | 56 | 32 |
| 609 | 2 | 390 | 653 | gi\|48745 | principal sigma subunit (AA 1-442) [Streptomyces coelicolor] ir\|S11712\|S11712 translation initiation factor sigma hrdB - reptomyces coelicolor | 56 | 37 |
| 626 | 2 | 1124 | 2104 | gi\|950197 | unknown [Corynebacterium glutamicum] | 56 | 40 |
| 787 | 1 | 2 | 634 | gnl\|PID\|e283826 | orf c04012 [Sulfolobus solfataricus] | 56 | 26 |
| 820 | 1 | 1220 | 3 | gi\|44001 | galactose-1-P-uridyl transferase [Lactobacillus helveticus] ir\|B47032\|B47032 galactose-1-phosphate uridyl transferase - ctobacillus helveticus | 56 | 35 |
| 875 | 1 | 1 | 144 | gi\|455178 | 16K protein [Escherichia coli] | 56 | 46 |
| 906 | 2 | 307 | 846 | gi\|144858 | ORF A [Clostridium perfringens] | 56 | 34 |
| 941 | 1 | 3 | 335 | gi\|160299 | glutamic acid-rich protein [Plasmodium falciparum] pir\|A54514\|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum | 56 | 23 |
| 5 | 5 | 2451 | 2951 | gi\|1303811 | YqeU [Bacillus subtilis] | 55 | 39 |
| 8 | 10 | 8312 | 7947 | gi\|1196907 | daunorubicin resistance protein [Streptomyces peucetius] | 55 | 29 |
| 17 | 24 | 23626 | 24465 | gnl\|PID\|e285322 | RecX protein [Mycobacterium smegmatis] | 55 | 28 |
| 17 | 31 | 31027 | 30344 | gi\|143830 | xpaC [Bacillus subtilis] | 55 | 22 |
| 17 | 34 | 31991 | 32302 | gnl\|PID\|e229183 | C11G6.3 [Caenorhabditis elegans] | 55 | 34 |
| 30 | 1 | 2 | 478 | pir\|S10655\|S10655 | hypothetical protein X - Pyrococcus woesei (fragment) | 55 | 34 |
| 49 | 14 | 9998 | 10411 | gi\|455154 | ORF D [Clostridium perfringens] | 55 | 36 |
| 54 | 3 | 955 | 1332 | gnl\|PID\|e238660 | hypothetical protein [Bacillus subtilis] | 55 | 32 |
| 54 | 10 | 3527 | 3231 | pir\|JQ0405\|JQ0405 | hypothetical 119.5K protein (uvrA region) - Micrococcus luteus | 55 | 45 |
| 67 | 4 | 2313 | 3044 | gi\|555750 | unknown [Neisseria gonorrhoeae] | 55 | 42 |
| 69 | 4 | 2250 | 2020 | gnl\|PID\|e259955 | K04G11.5 [Caenorhabditis elegans] | 55 | 33 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 77 | 5 | 3954 | 2938 | gi\|1001634 | hypothetical protein [Synechocystis sp.] | 55 | 34 |
| 80 | 4 | 4806 | 2482 | gi\|466952 | B1620_F1_30 [Mycobacterium leprae] | 55 | 35 |
| 81 | 6 | 4212 | 3730 | gi\|606073 | ORF_o169 [Escherichia coli] | 55 | 34 |
| 83 | 1 | 66 | 737 | gi\|216064 | morphogenesis protein B [Bacteriophage PZA] | 55 | 36 |
| 89 | 10 | 9486 | 7714 | gi\|148221 | DNA-dependent ATPase, DNA helicase [Escherichia coli] pir\|JS0137\|BVECRQ recQ protein - Escherichia coli | 55 | 35 |
| 91 | 5 | 2507 | 3289 | gi\|153015 | FemA protein [Staphylococcus aureus] | 55 | 35 |
| 100 | 14 | 9974 | 9393 | gi\|558603 | synaptonemal complex protein 1 [Mus musculus] | 55 | 30 |
| 116 | 1 | 1 | 909 | gi\|473901 | ORF1 [Lactococcus lactis] | 55 | 33 |
| 122 | 3 | 1801 | 2655 | gi\|1016216 | putative protein of 299 amino acids [Cyanophora paradoxa] | 55 | 28 |
| 123 | 30 | 28191 | 28721 | gi\|1142714 | phosphoenolpyruvate:mannose phosphotransferase element IIB [Lactobacillus curvatus] | 55 | 29 |
| 128 | 22 | 16664 | 16029 | gi\|606025 | ORF_o221 [Escherichia coli] | 55 | 42 |
| 150 | 7 | 5949 | 6521 | gi\|39573 | P20 (AA 1-178) [Bacillus licheniformis] | 55 | 32 |
| 155 | 7 | 5767 | 6660 | gi\|1763974 | DPPA [Bacillus methanolicus] | 55 | 31 |
| 157 | 1 | 867 | 70 | gi\|1067010 | M153.1 [Caenorhabditis elegans] | 55 | 34 |
| 160 | 9 | 6090 | 4804 | gi\|1592141 | M. jannaschii predicted coding region MJ1507 [Methanococcus jannaschii] | 55 | 31 |
| 176 | 3 | 2060 | 3349 | gi\|153858 | wall-associated protein [Streptococcus mutans] | 55 | 37 |
| 201 | 2 | 3277 | 413 | gi\|1235662 | RfbC [Myxococcus xanthus] | 55 | 36 |
| 202 | 9 | 6199 | 8001 | gi\|606018 | ORF_o783 [Escherichia coli] | 55 | 42 |
| 222 | 7 | 4803 | 4021 | gnl\|PID\|e289148 | highly similar to phosphotransferase system regulator [Bacillus subtilis] | 55 | 40 |
| 238 | 12 | 11465 | 9942 | gnl\|PID\|e266573 | unknown [Mycobacterium tuberculosis] | 55 | 27 |
| 238 | 13 | 11527 | 12027 | gi\|1129093 | unknown protein [Bacillus sp.] | 55 | 36 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 240 | 4 | 1988 | 1215 | gnl\|PID\|e252616 | DcuC protein [Escherichia coli] | 55 | 34 |
| 246 | 2 | 433 | 792 | gnl\|PID\|e233868 | hypothetical protein [Bacillus subtilis] | 55 | 25 |
| 253 | 5 | 1827 | 1549 | gi\|142540 | aspartokinase II [Bacillus sp.] | 55 | 48 |
| 259 | 1 | 895 | 74 | gi\|1006621 | molybdate-binding periplasmic protein [Synechocystis sp.] | 55 | 37 |
| 267 | 1 | 1183 | 2 | gi\|882672 | ORF_o313 [Escherichia coli] | 55 | 27 |
| 292 | 16 | 12843 | 13325 | gi\|561746 | cyclin-dependent protein kinase [Mus musculus] | 55 | 26 |
| 294 | 9 | 3390 | 3752 | gi\|984582 | DinJ [Escherichia coli] | 55 | 26 |
| 300 | 5 | 3914 | 3582 | gi\|1591957 | M. jannaschii predicted coding region MJ1318 [Methanococcus jannaschii] | 55 | 38 |
| 305 | 3 | 2769 | 3527 | gi\|606309 | ORF_o265; gtg start [Escherichia coli] | 55 | 36 |
| 320 | 6 | 4479 | 3475 | gi\|1591732 | cobalt transport ATP-binding protein O [Methanococcus jannaschii] | 55 | 32 |
| 355 | 24 | 18149 | 18322 | gi\|344751 | MDV TK gene product [unidentified] | 55 | 40 |
| 364 | 2 | 2083 | 386 | gi\|1573045 | hypothetical [Haemophilus influenzae] | 55 | 40 |
| 364 | 9 | 8796 | 8575 | gnl\|PID\|e252108 | ORF YOR255w [Saccharomyces cerevisiae] | 55 | 27 |
| 379 | 8 | 8248 | 6872 | gi\|1330236 | dihydropyrimidinase [Homo sapiens] | 55 | 37 |
| 386 | 6 | 3847 | 4332 | gi\|976025 | HrsA [Escherichia coli] | 55 | 27 |
| 441 | 2 | 939 | 1730 | gi\|144859 | ORF B [Clostridium perfringens] | 55 | 28 |
| 482 | 6 | 3515 | 3156 | gi\|606162 | ORF_f229 [Escherichia coli] | 55 | 39 |
| 497 | 9 | 4885 | 5937 | gi\|1041637 | replication initiator protein [Staphylococcus xylosus] | 55 | 33 |
| 546 | 1 | 1 | 1104 | gi\|467446 | similar to SpoVB [Bacillus subtilis] | 55 | 36 |
| 634 | 4 | 2132 | 1524 | gi\|431950 | similar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium asteurianum] | 55 | 27 |
| 660 | 2 | 249 | 401 | gnl\|PID\|e254995 | hypothetical protein [Bacillus subtilis] | 55 | 35 |
| 671 | 1 | 288 | 58 | gi\|38722 | precursor (aa -20 to 381) [Acinetobacter calcoaceticus] ir\|A29277\|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lcoaceticus | 55 | 33 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 686 | 2 | 245 | 1141 | gi\|1633572 | Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] | 55 | 36 |
| 713 | 3 | 2742 | 1438 | gnl\|PID\|e8901 | RESA NF7 Ag13 [Plasmodium falciparum] | 55 | 25 |
| 815 | 1 | 2 | 226 | gi\|1113815 | histidine kinase [Borrelia burgdorferi] | 55 | 36 |
| 857 | 1 | 2 | 520 | gi\|143024 | glucose-resistance amylase regulator [Bacillus subtilis] pir\|S15318\|S15318 ccpA protein - Bacillus subtilis sp\|P25144\|CCPA_BACSU GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN). | 55 | 31 |
| 931 | 1 | 3 | 557 | gi\|1098508 | putative spore germination apparatus protein [Bacillus megaterium] | 55 | 32 |
| 17 | 7 | 6379 | 7218 | gnl\|PID\|e250887 | potential coding region [Clostridium difficile] | 54 | 35 |
| 21 | 9 | 7265 | 6348 | gi\|13441 | NADH dehydrogenase subunit 4L [Phoca vitulina] | 54 | 29 |
| 28 | 2 | 2727 | 3425 | gi\|1001792 | hypothetical protein [Synechocystis sp.] | 54 | 29 |
| 32 | 6 | 4044 | 3523 | gi\|1673660 | (AE000002) Mycoplasma pneumoniae, hypothetical 28K protein; similar to GenBank Accession Number JS0068, from M. pneumoniae [Mycoplasma pneumoniae] | 54 | 36 |
| 33 | 3 | 2274 | 3767 | gnl\|PID\|e245024 | unknown [Mycobacterium tuberculosis] | 54 | 36 |
| 40 | 1 | 1 | 915 | gi\|773349 | BirA protein [Bacillus subtilis] | 54 | 32 |
| 49 | 6 | 2120 | 2485 | gnl\|PID\|e139446 | a2 gene product [Bacteriophage B1] | 54 | 38 |
| 54 | 17 | 8969 | 8661 | gi\|334068 | ORF2 [Suid herpesvirus 1] | 54 | 51 |
| 65 | 2 | 1311 | 2120 | gi\|537207 | ORF_f277 [Escherichia coli] | 54 | 27 |
| 72 | 20 | 21986 | 22435 | gi\|928848 | ORF70'; putative [Lactococcus lactis phage BK5-T] | 54 | 34 |
| 105 | 4 | 3039 | 3827 | gnl\|PID\|e205174 | orf2 gene product [Lactobacillus helveticus] | 54 | 30 |
| 127 | 1 | 884 | 150 | gi\|726443 | No definition line found [Caenorhabditis | 54 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | elegans] | | |
| 148 | 1 | 1204 | 62 | gi\|467456 | unknown [Bacillus subtilis] | 54 | 37 |
| 156 | 4 | 4360 | 3167 | gi\|1032483 | unidentified ORF downstream of hydrogenase cluster; ORF5 [Anabaena variabilis] | 54 | 30 |
| 160 | 4 | 1523 | 2077 | gnl\|PID\|e255111 | hypothetical protein [Bacillus subtilis] | 54 | 27 |
| 160 | 7 | 4260 | 3745 | gi\|1184121 | auxin-induced protein [Vigna radiata] | 54 | 30 |
| 165 | 5 | 4996 | 3971 | gi\|1772652 | 2-keto-3-deoxygluconate kinase [Haloferax alicantei] | 54 | 36 |
| 176 | 2 | 1044 | 1937 | gi\|162201 | P-type ATPase [Trypanosoma brucei] | 54 | 38 |
| 180 | 29 | 30833 | 29853 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 54 | 29 |
| 200 | 16 | 7933 | 6656 | gi\|1574238 | traN protein (traN) [Haemophilus influenzae] | 54 | 31 |
| 206 | 1 | 232 | 2 | gi\|1220501 | Rickettsia tsutsugamushi (strain Kp47) gene, complete cds [Rickettsia tsutsugamushi] | 54 | 31 |
| 220 | 4 | 5235 | 4342 | gi\|606080 | ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli] | 54 | 31 |
| 220 | 5 | 5821 | 5135 | gi\|43942 | first subunit of EII-Sor [Klebsiella pneumoniae] | 54 | 36 |
| 223 | 20 | 17253 | 17747 | gi\|47932 | tonB protein [Salmonella typhimurium] | 54 | 38 |
| 228 | 7 | 4866 | 4033 | gi\|1736828 | Thi4 protein [Escherichia coli] | 54 | 34 |
| 229 | 4 | 5050 | 3371 | gi\|1046078 | M. genitalium predicted coding region MG369 [Mycoplasma genitalium] | 54 | 42 |
| 236 | 3 | 4777 | 1496 | gi\|152271 | 319-kDA protein [Rhizobium meliloti] | 54 | 28 |
| 236 | 5 | 7822 | 6944 | gnl\|PID\|e285031 | Hyp1 protein [Hydra vulgaris] | 54 | 20 |
| 238 | 30 | 27964 | 27746 | gnl\|PID\|e217586 | PlnM [Lactobacillus plantarum] | 54 | 42 |
| 242 | 5 | 3508 | 4050 | gi\|149502 | beta-lactamase [Lactococcus lactis] | 54 | 35 |
| 257 | 1 | 296 | 120 | gi\|1498064 | AtE1 [Arabidopsis thaliana] | 54 | 50 |
| 257 | 6 | 6745 | 5633 | gi\|343949 | var1(40.0) [Saccharomyces cerevisiae] | 54 | 42 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 258 | 8 | 7839 | 7114 | gi\|41519 | P30 protein (AA 1-240) [Escherichia coli] | 54 | 31 |
| 276 | 20 | 13101 | 12880 | gi\|155322 | icsB gene product [Plasmid pWR100] | 54 | 37 |
| 280 | 1 | 618 | 106 | gi\|467356 | unknown [Bacillus subtilis] | 54 | 21 |
| 288 | 4 | 2183 | 2632 | gi\|39978 | P16 [Bacillus subtilis] | 54 | 39 |
| 316 | 1 | 3 | 767 | gi\|143264 | membrane-associated protein [Bacillus subtilis] | 54 | 34 |
| 318 | 7 | 5035 | 4565 | gi\|606080 | ORF_o290; Geneplot suggests frameshift linking to o267, not found Escherichia coli] | 54 | 28 |
| 319 | 3 | 1393 | 2163 | gi\|148327 | vancomycin response regulator [Enterococcus faecium] | 54 | 34 |
| 323 | 2 | 1256 | 2560 | gi\|413940 | ipa-16d gene product [Bacillus subtilis] | 54 | 26 |
| 364 | 7 | 7335 | 7724 | gnl\|PID\|e250171 | F18C12.1 [Caenorhabditis elegans] | 54 | 31 |
| 386 | 5 | 2399 | 3844 | gi\|155369 | PTS enzyme-II fructose [Xanthomonas campestris] | 54 | 37 |
| 392 | 3 | 2004 | 3353 | gi\|872306 | integral membrane protein [Streptomyces pristinaespiralis] pir\|S57509\|S57509 integral membrane protein - Streptomyces ristinaespiralis | 54 | 32 |
| 424 | 5 | 1553 | 1371 | gi\|160316 | major merozoite surface antigen [Plasmodium falciparum] sp\|P50495\|MSP1_PLAFP MEROZOITE SURFACE PROTEIN 1 PRECURSOR MEROZOITE SURFACE ANTIGENS) (PMMSA) (GP195). | 54 | 37 |
| 445 | 2 | 1897 | 1178 | gi\|1781503 | MigA [Pseudomonas aeruginosa] | 54 | 31 |
| 452 | 5 | 2506 | 2805 | gi\|216292 | neopullulanase [Bacillus sp.] | 54 | 34 |
| 457 | 2 | 2178 | 1024 | gi\|405570 | TraK protein shares sequence similarity with a family of proteins ncoded on Gram-negative gene transfer systems such as TraD from the plasmid [Plasmid pSK41] | 54 | 35 |
| 461 | 3 | 627 | 1418 | gi\|797332 | MocD [Agrobacterium tumefaciens] | 54 | 38 |
| 466 | 5 | 5419 | 3770 | gi\|1652892 | ABC transporter [Synechocystis sp.] | 54 | 29 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 475 | 3 | 2745 | 1990 | gi\|532546 | ORF13 [Enterococcus faecalis] | 54 | 35 |
| 495 | 1 | 2 | 295 | gi\|304990 | ORF_o290 [Escherichia coli] | 54 | 21 |
| 502 | 4 | 3518 | 3216 | gi\|1573270 | hemolysin (tlyC) [Haemophilus influenzae] | 54 | 33 |
| 510 | 5 | 3089 | 3931 | gi\|1732200 | PTS permease for mannose subunit IIPMan [Vibrio furnissii] | 54 | 29 |
| 570 | 1 | 1 | 930 | gi\|1001582 | penicillin-binding protein 1A [Synechocystis sp.] | 54 | 31 |
| 573 | 6 | 2763 | 3164 | gi\|416197 | homologous to plasmid R100 pemK gene [Escherichia coli] | 54 | 35 |
| 590 | 1 | 433 | 2 | gi\|532309 | 25 kDa protein [Escherichia coli] | 54 | 33 |
| 643 | 2 | 1202 | 1477 | gnl\|PID\|e125689 | 256 kD golgin [Homo sapiens] | 54 | 29 |
| 705 | 1 | 2 | 682 | gi\|148921 | LicD protein [Haemophilus influenzae] | 54 | 39 |
| 730 | 1 | 370 | 167 | gnl\|PID\|e245531 | ORF YLR068w [Saccharomyces cerevisiae] | 54 | 29 |
| 745 | 1 | 502 | 209 | gi\|581140 | NADH dehydrogenase [Escherichia coli] | 54 | 37 |
| 749 | 1 | 413 | 3 | gi\|664840 | TagB [Dictyostelium discoideum] | 54 | 44 |
| 932 | 1 | 3 | 320 | gi\|537207 | ORF_f277 [Escherichia coli] | 54 | 27 |
| 4 | 6 | 5671 | 4748 | gi\|216267 | ORF2 [Bacillus megaterium] | 53 | 34 |
| 16 | 8 | 6231 | 6806 | gi\|517105 | spermidine acetyltransferase [Escherichia coli] | 53 | 35 |
| 17 | 1 | 2 | 2497 | gi\|387880 | collagen adhesin [Staphylococcus aureus] | 53 | 35 |
| 42 | 4 | 2942 | 3529 | gi\|1633572 | Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] | 53 | 20 |
| 69 | 6 | 3149 | 4879 | gi\|1486244 | unknown [Bacillus subtilis] | 53 | 30 |
| 72 | 3 | 1455 | 2063 | gi\|1592197 | M. jannaschii predicted coding region MJ1576 [Methanococcus jannaschii] | 53 | 32 |
| 79 | 1 | 83 | 592 | gi\|633757 | pr2 [Mycoplasma hyopneumoniae] | 53 | 28 |
| 83 | 8 | 5179 | 4412 | gi\|496100 | unknown function; putative [Bacteriophage phi-LC3] | 53 | 39 |
| 85 | 10 | 7180 | 6764 | gi\|1303940 | YqiU [Bacillus subtilis] | 53 | 35 |
| 92 | 2 | 789 | 986 | gi\|1372996 | Rho [Borrelia burgdorferi] | 53 | 28 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 95 | 10 | 7546 | 7734 | gi\|162379 | variant surface glycoprotein [Trypanosoma brucei] | 53 | 28 |
| 99 | 4 | 1391 | 1861 | gi\|1499620 | M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii] | 53 | 34 |
| 100 | 44 | 29982 | 29749 | gi\|1590997 | M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii] | 53 | 35 |
| 102 | 5 | 4787 | 5089 | gi\|1399011 | immunogenic secreted protein precursor [Streptococcus pyogenes] | 53 | 40 |
| 113 | 1 | 825 | 4 | gnl\|PID\|e264148 | unknown [Mycobacterium tuberculosis] | 53 | 24 |
| 114 | 4 | 6555 | 5113 | gi\|487282 | Na+ -ATPase subunit J [Enterococcus hirae] | 53 | 33 |
| 119 | 6 | 3581 | 3994 | gi\|473707 | positive regulator for virulence factors [Clostridium perfringens] | 53 | 31 |
| 123 | 19 | 16463 | 18115 | gi\|1591361 | NADH oxidase [Methanococcus jannaschii] | 53 | 33 |
| 136 | 1 | 381 | 4 | gi\|152744 | IpaD protein [Shigella flexneri] | 53 | 32 |
| 138 | 9 | 8079 | 7594 | gi\|467371 | LACI family of transcriptional repreesor (probable) [Bacillus ubtilis] | 53 | 29 |
| 142 | 8 | 4594 | 4007 | gi\|755216 | N-acetylmuramidase [Lactococcus lactis] | 53 | 38 |
| 162 | 12 | 12482 | 11937 | gi\|1063250 | low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticillus [Bacillus subtilis] | 53 | 36 |
| 163 | 1 | 546 | 31 | gi\|153767 | ORF [Streptococcus pneumoniae] | 53 | 34 |
| 163 | 7 | 4973 | 3453 | gi\|29468 | beta-myosin heavy chain (1151 AA) [Homo sapiens] | 53 | 36 |
| 167 | 2 | 1038 | 2006 | gi\|413930 | ipa-6d gene product [Bacillus subtilis] | 53 | 27 |
| 173 | 11 | 8865 | 7843 | gi\|1778569 | YaaF homolog [Escherichia coli] | 53 | 39 |
| 190 | 8 | 6842 | 3549 | gi\|387880 | collagen adhesin [Staphylococcus aureus] | 53 | 38 |
| 199 | 2 | 2725 | 950 | gi\|1652570 | nitrate transport protein NrtB [Synechocystis sp.] | 53 | 32 |
| 200 | 13 | 6184 | 5954 | gi\|1652679 | hypothetical protein [Synechocystis sp.] | 53 | 40 |
| 200 | 17 | 9287 | 7890 | gi\|1574246 | H. influenzae predicted coding region | 53 | 35 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | HI1409 [Haemophilus influenzae] | | |
| 205 | 6 | 2048 | 3229 | gi\|148026 | topoisomerase III [Escherichia coli] | 53 | 32 |
| 211 | 2 | 270 | 1052 | gi\|483940 | transcription regulator [Bacillus subtilis] | 53 | 30 |
| 221 | 10 | 5119 | 5994 | gi\|1353529 | ORF12 [Bacteriophage r1t] | 53 | 44 |
| 232 | 7 | 4344 | 3925 | gi\|1665759 | Similar to Schistosoma mansoni amino acid permease (L25068). [Homo sapiens] | 53 | 35 |
| 238 | 21 | 18705 | 19247 | gi\|1574062 | hypothetical [Haemophilus influenzae] | 53 | 30 |
| 239 | 1 | 2 | 1636 | gi\|433932 | activator of (R)-hydroxyglutaryl-CoA dehydratase [Acidaminococcus ermentans] | 53 | 35 |
| 250 | 1 | 1469 | 318 | gi\|987094 | membrane transport protein [Streptomyces hygroscopicus] | 53 | 22 |
| 253 | 4 | 1759 | 1028 | gi\|537245 | aspartokinase I-homoserine dehydrogenase I [Escherichia coli] pir\|S56629\|S56629 aspartate kinase (EC 2.7.2.4) / homoserine ehydrogenase (EC 1.1.1.3) - Escherichia coli | 53 | 35 |
| 271 | 8 | 4649 | 5800 | gi\|413966 | ipa-42d gene product [Bacillus subtilis] | 53 | 27 |
| 276 | 26 | 15786 | 15112 | gi\|1699017 | ErpB2 [Borrelia burgdorferi] | 53 | 26 |
| 279 | 11 | 8309 | 7797 | gi\|1651934 | hypothetical protein [Synechocystis sp.] | 53 | 35 |
| 288 | 8 | 3997 | 4872 | gi\|43943 | second subunit of EII-Sor [Klebsiella pneumoniae] | 53 | 32 |
| 290 | 6 | 4391 | 5680 | gi\|466882 | pps1; B1496_C2_189 [Mycobacterium leprae] | 53 | 29 |
| 294 | 3 | 1197 | 1481 | gi\|173004 | topoisomerase I [Saccharomyces cerevisiae] | 53 | 40 |
| 330 | 3 | 2351 | 3367 | gi\|466691 | No definition line found [Escherichia coli] | 53 | 34 |
| 334 | 8 | 8172 | 9182 | gi\|1652483 | hypothetical protein [Synechocystis sp.] | 53 | 29 |
| 368 | 1 | 620 | 102 | gi\|487273 | Na+ -ATPase subunit I [Enterococcus hirae] | 53 | 29 |
| 377 | 4 | 2424 | 2260 | gi\|221407 | FP5 [Fowlpox virus] | 53 | 35 |
| 382 | 1 | 257 | 36 | gi\|1592016 | M. jannaschii predicted coding region MJ1371 [Methanococcus jannaschii] | 53 | 32 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 387 | 1 | 2 | 460 | gi\|1574317 | repressor protein (GP:L22692_1) [Haemophilus influenzae] | 53 | 30 |
| 394 | 10 | 8379 | 10412 | gi\|882463 | protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia oli] | 53 | 34 |
| 399 | 4 | 2349 | 3098 | gi\|453287 | OmpR protein [Escherichia coli] | 53 | 27 |
| 420 | 2 | 1378 | 719 | gi\|1437473 | nitrate transporter [Bacillus subtilis] | 53 | 28 |
| 441 | 6 | 5361 | 7937 | gi\|1592205 | M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii] | 53 | 38 |
| 461 | 1 | 6 | 512 | gi\|1651800 | L-glutamine:D-fructose-6-P amidotransferase [Synechocystis sp.] | 53 | 29 |
| 497 | 3 | 1700 | 1960 | gi\|4328 | RIF1 gene product [Saccharomyces cerevisiae] | 53 | 33 |
| 503 | 1 | 669 | 4 | gnl\|PID\|e202290 | unknown [Lactobacillus sake] | 53 | 30 |
| 538 | 2 | 1053 | 262 | gi\|1613769 | response regulator [Streptococcus pneumoniae] | 53 | 30 |
| 539 | 6 | 6172 | 5183 | gi\|567887 | putative repressor [Streptomyces peucetius] | 53 | 32 |
| 551 | 1 | 629 | 162 | gi\|1256649 | putative [Bacillus subtilis] | 53 | 26 |
| 557 | 1 | 9 | 695 | gi\|143177 | putative [Bacillus subtilis] | 53 | 31 |
| 569 | 2 | 418 | 1158 | gi\|1184684 | MucD [Pseudomonas aeruginosa] | 53 | 26 |
| 614 | 1 | 99 | 581 | gi\|485280 | 28.2 kDa protein [Streptococcus pneumoniae] | 53 | 32 |
| 660 | 1 | 1 | 279 | gnl\|PID\|e288480 | R10E8.f [Caenorhabditis elegans] | 53 | 34 |
| 776 | 1 | 3 | 635 | gi\|151352 | mandelate racemase (EC 5.1.2.2) [Pseudomonas putida] | 53 | 33 |
| 11 | 2 | 1117 | 1656 | gi\|143150 | levR [Bacillus subtilis] | 52 | 29 |
| 17 | 6 | 5327 | 6559 | gnl\|PID\|e250887 | potential coding region [Clostridium difficile] | 52 | 37 |
| 19 | 31 | 17760 | 17978 | gi\|1079556 | dShc [Drosophila melanogaster] | 52 | 42 |
| 19 | 38 | 20306 | 22627 | gnl\|PID\|e139448 | host interacting protein [Bacteriophage B1] | 52 | 32 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 25 | 4 | 2662 | 2087 | gi\|1072067 | PepF [Rhodobacter sphaeroides] | 52 | 23 |
| 25 | 6 | 5596 | 3407 | gi\|1303866 | YqgS [Bacillus subtilis] | 52 | 34 |
| 49 | 3 | 1135 | 1569 | gi\|496279 | putative [Bacteriophage Tuc2009] | 52 | 25 |
| 53 | 1 | 850 | 2 | sp\|P52697\|YBHE_ECOLI | HYPOTHETICAL 30.2 KD PROTEIN IN MODC 3'REGION. | 52 | 35 |
| 54 | 9 | 10909 | 2687 | gi\|1633572 | Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] | 52 | 30 |
| 57 | 6 | 4779 | 8402 | gi\|142439 | ATP-dependent nuclease [Bacillus subtilis] | 52 | 31 |
| 58 | 6 | 6446 | 5949 | gnl\|PID\|e255921 | F53F4.10 [Caenorhabditis elegans] | 52 | 31 |
| 72 | 13 | 13446 | 13195 | gi\|532541 | ORF8 [Enterococcus faecalis] | 52 | 37 |
| 81 | 17 | 13692 | 12520 | gi\|1732203 | GlcNAc 6-P deacetylase [Vibrio furnissii] | 52 | 35 |
| 84 | 1 | 3 | 1355 | gi\|64288 | fast skeletal muscle Ca-ATPase [Rana esculenta] | 52 | 34 |
| 100 | 2 | 1917 | 1027 | gi\|1353560 | ORF43 [Bacteriophage r1t] | 52 | 34 |
| 101 | 1 | 30 | 1862 | gi\|405957 | yeeF [Escherichia coli] | 52 | 24 |
| 106 | 8 | 8517 | 7600 | gi\|454904 | rfbG gene product [Shigella flexneri] | 52 | 41 |
| 108 | 1 | 1 | 1059 | gnl\|PID\|e255337 | unknown [Mycobacterium tuberculosis] | 52 | 29 |
| 123 | 4 | 2899 | 3495 | gi\|1305720 | prs-associated putative membrane protein [Escherichia coli] | 52 | 24 |
| 128 | 23 | 17561 | 16740 | gi\|473805 | 'regulatory protein sfs1 involved in maltose metabolism' Escherichia coli] | 52 | 32 |
| 130 | 8 | 6693 | 7481 | gi\|1552775 | ATP-binding protein [Escherichia coli] | 52 | 30 |
| 138 | 1 | 40 | 1359 | gi\|1045867 | oligoendopeptidase F [Mycoplasma genitalium] | 52 | 31 |
| 138 | 2 | 2757 | 1384 | gi\|1591425 | hypothetical protein (GP:X91006_2) [Methanococcus jannaschii] | 52 | 26 |
| 138 | 6 | 6317 | 5940 | gi\|1486247 | unknown [Bacillus subtilis] | 52 | 36 |
| 142 | 10 | 7337 | 5466 | gi\|1151158 | repeat organellar protein [Plasmodium chabaudi] | 52 | 34 |
| 149 | 1 | 33 | 1133 | gi\|1762962 | FemA [Staphylococcus simulans] | 52 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 161 | 1 | 3 | 245 | gi\|151276 | histidine utilization genes repressor protein (hut) [Pseudomonas utida] | 52 | 35 |
| 163 | 4 | 2048 | 1320 | gi\|1064810 | function unknown [Bacillus subtilis] | 52 | 27 |
| 164 | 8 | 4882 | 5103 | gi\|57251 | precursor (AA -35 to 1766) [Rattus norvegicus] | 52 | 38 |
| 165 | 9 | 7247 | 7474 | gi\|1652671 | hypothetical protein [Synechocystis sp.] | 52 | 28 |
| 178 | 5 | 1887 | 1681 | gi\|220704 | cAMP-dependent protein kinase catalytic subunit-beta [Rattus sp.] gi\|191177 cAMP-dependent protein kinase beta-catalytic subunit Cricetulus sp.] | 52 | 36 |
| 180 | 24 | 22536 | 23774 | gi\|581052 | cytosine deaminase [Escherichia coli] | 52 | 28 |
| 190 | 9 | 8891 | 7056 | gi\|1592079 | M. jannaschii predicted coding region MJ1429 [Methanococcus jannaschii] | 52 | 39 |
| 195 | 8 | 2000 | 2272 | gi\|868024 | HIC-1 gene product [Homo sapiens] | 52 | 52 |
| 202 | 11 | 9189 | 10145 | gi\|141861 | traA gene product [Plasmid pAD1] | 52 | 33 |
| 204 | 4 | 1361 | 2011 | gi\|1184118 | mevalonate kinase [Methanobacterium thermoautotrophicum] | 52 | 33 |
| 204 | 8 | 4018 | 5142 | gnl\|PID\|e283860 | carotenoid biosynthetic gene ERWCRTS homolog [Sulfolobus solfataricus] | 52 | 31 |
| 208 | 2 | 1112 | 2296 | gi\|1408501 | homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis] | 52 | 35 |
| 215 | 1 | 772 | 2 | gi\|1480429 | putative transcriptional regulator [Bacillus stearothermophilus] | 52 | 26 |
| 218 | 4 | 4072 | 3425 | gi\|862630 | glyceraldehyde-3-phosphate dehydrogenase [Buchnera aphidicola] sp\|Q07234\|G3P_BUCAP GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC .2.1.12) (GAPDH). | 52 | 35 |
| 228 | 1 | 1 | 741 | gnl\|PID\|e264148 | unknown [Mycobacterium tuberculosis] | 52 | 29 |
| 230 | 2 | 149 | 634 | gi\|437705 | hyaluronidase [Streptococcus pneumoniae] | 52 | 28 |
| 233 | 8 | 6166 | 4982 | gi\|1001708 | NifS [Synechocystis sp.] | 52 | 31 |
| 240 | 3 | 725 | 967 | gi\|399655 | Ca2+ regulatory protein [Saccharomyces | 52 | 21 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | cerevisiae] sp\|P35206\|CSG2_YEAST CSG2 PROTEIN PRECURSOR. | | |
| 288 | 7 | 3171 | 4028 | gi\|147403 | mannose permease subunit II-P-Man [Escherichia coli] | 52 | 27 |
| 318 | 1 | 7 | 819 | gi\|1303849 | YqgB [Bacillus subtilis] | 52 | 33 |
| 330 | 1 | 1062 | 154 | gi\|144859 | ORF B [Clostridium perfringens] | 52 | 29 |
| 330 | 9 | 6815 | 7213 | gi\|1439527 | EIIA-man [Lactobacillus curvatus] | 52 | 31 |
| 345 | 9 | 8348 | 9397 | gi\|606292 | ORF_o696 [Escherichia coli] | 52 | 27 |
| 398 | 3 | 2671 | 1877 | gi\|144859 | ORF B [Clostridium perfringens] | 52 | 29 |
| 411 | 1 | 992 | 3 | gnl\|PID\|e283950 | daunorubicin resistance ATP-binding protein DrrA [Sulfolobus solfataricus] | 52 | 27 |
| 422 | 2 | 1292 | 585 | gi\|537214 | yjjG gene product [Escherichia coli] | 52 | 32 |
| 436 | 2 | 1669 | 1205 | gi\|507323 | ORF1 [Bacillus stearothermophilus] | 52 | 29 |
| 450 | 1 | 119 | 754 | gi\|1573916 | multidrug resistance protein (emrB) [Haemophilus influenzae] | 52 | 32 |
| 453 | 1 | 190 | 381 | gi\|182021 | elastin [Homo sapiens] | 52 | 40 |
| 455 | 7 | 5767 | 4634 | gnl\|PID\|e155312 | integrase [Bacteriophage TP901-1] | 52 | 34 |
| 479 | 1 | 138 | 758 | gi\|1742859 | ORF_ID:o327#7; similar to [SwissProt Accession Number P54449] [Escherichia coli] | 52 | 27 |
| 517 | 1 | 763 | 2 | gi\|152780 | rhamnosyl transferase II [Shigella dysenteriae] | 52 | 29 |
| 518 | 3 | 1735 | 848 | gi\|153858 | wall-associated protein [Streptococcus mutans] | 52 | 20 |
| 526 | 3 | 2297 | 1848 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 52 | 27 |
| 617 | 1 | 1 | 462 | gi\|142863 | replication initiation protein [Bacillus subtilis] | 52 | 35 |
| 639 | 3 | 1068 | 259 | gi\|1591153 | hypothetical protein (SP:P46348) [Methanococcus jannaschii] | 52 | 30 |
| 703 | 1 | 773 | 81 | gi\|793910 | surface antigen [Homo sapiens] | 52 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 737 | 1 | 235 | 2 | gi\|666000 | hypothetical protein [Bacillus subtilis] | 52 | 29 |
| 791 | 4 | 1368 | 1802 | gnl\|PID\|e269549 | Unknown [Bacillus subtilis] | 52 | 28 |
| 825 | 1 | 1 | 300 | gi\|732538 | No definition line found [Caenorhabditis elegans] | 52 | 28 |
| 981 | 1 | 226 | 2 | gi\|951100 | P45016a-ms1 [Mus spretus] | 52 | 36 |
| 17 | 23 | 23542 | 22163 | gi\|1652483 | hypothetical protein [Synechocystis sp.] | 51 | 32 |
| 65 | 6 | 4302 | 3691 | gi\|397498 | Membrane Ribose Binding Protein [Bacillus subtilis] pir\|S42714\|S42714 membrane ribose-binding protein - Bacillus ubtilis | 51 | 31 |
| 69 | 5 | 2926 | 2537 | gi\|1773150 | hypothetical 14.8kd protein [Escherichia coli] | 51 | 30 |
| 92 | 1 | 973 | 44 | gnl\|PID\|e243523 | ORF YGR130c [Saccharomyces cerevisiae] | 51 | 29 |
| 103 | 6 | 5272 | 3593 | gi\|312940 | threonine kinase [Streptococcus equisimilis] | 51 | 32 |
| 111 | 7 | 4195 | 3317 | pir\|G64143\|G64143 | hypothetical protein HI0143 - Haemophilus influenzae (strain Rd KW20) | 51 | 29 |
| 115 | 7 | 4526 | 3414 | gi\|405879 | yeiH [Escherichia coli] | 51 | 27 |
| 123 | 29 | 27788 | 28207 | gi\|147402 | mannose permease subunit III-Man [Escherichia coli] | 51 | 27 |
| 125 | 1 | 223 | 2 | gi\|4482 | SLY1 gene product [Saccharomyces cerevisiae] | 51 | 37 |
| 128 | 21 | 16156 | 15638 | gi\|606026 | ORF_o115 [Escherichia coli] | 51 | 27 |
| 137 | 4 | 3207 | 5369 | gi\|1673692 | (AE000005) Mycoplasma pneumoniae, C09_orf422 Protein [Mycoplasma pneumoniae] | 51 | 26 |
| 138 | 28 | 18295 | 18771 | gi\|149647 | ORFZ [Listeria monocytogenes] | 51 | 31 |
| 145 | 6 | 4054 | 5271 | gi\|1653860 | N-acyl-L-amino acid amidohydrolase [Synechocystis sp.] | 51 | 41 |
| 155 | 4 | 3019 | 2273 | gi\|1486242 | unknown [Bacillus subtilis] | 51 | 41 |
| 180 | 8 | 7951 | 9189 | gi\|1657522 | hypothetical protein [Escherichia coli] | 51 | 32 |
| 186 | 2 | 859 | 1620 | gi\|511497 | oleoyl-acyl carrier protein thioesterase [Coriandrum sativum] | 51 | 29 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 186 | 3 | 1644 | 2060 | sp\|P37348\|YECE_ECOLI | HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT). | 51 | 38 |
| 194 | 3 | 1521 | 1276 | gi\|332697 | fusion protein [Human parainfluenza virus 2] | 51 | 32 |
| 195 | 7 | 1986 | 3767 | gi\|405570 | TraK protein shares sequence similarity with a family of proteins ncoded on Gram-negative gene transfer systems such as TraD from the plasmid [Plasmid pSK41] | 51 | 28 |
| 197 | 1 | 3 | 494 | gi\|1592234 | DNA topoisomerase I [Methanococcus jannaschii] | 51 | 32 |
| 198 | 2 | 1521 | 862 | gi\|1196483 | unknown protein [Lactobacillus casei] | 51 | 32 |
| 238 | 16 | 13630 | 14730 | gi\|1772652 | 2-keto-3-deoxygluconate kinase [Haloferax alicantei] | 51 | 36 |
| 257 | 5 | 5646 | 4513 | pir\|S43367\|S43367 | metallothionein - Green crab, common shore crab | 51 | 38 |
| 261 | 6 | 4950 | 4519 | gi\|581545 | orf 4 [Staphylococcus aureus] | 51 | 26 |
| 270 | 5 | 4480 | 4220 | gi\|1066975 | F49E2.5a [Caenorhabditis elegans] | 51 | 28 |
| 306 | 10 | 5928 | 6905 | gi\|1752736 | gene required for phosphoylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae] | 51 | 28 |
| 324 | 3 | 1590 | 2405 | gi\|409925 | VirR positive regulator [Streptococcus pyogenes] | 51 | 25 |
| 328 | 2 | 632 | 309 | gi\|466475 | putative phospho-beta-glucosidase [Bacillus stearothermophilus] pir\|D49898\|D49898 cellobiose phosphotransferase system celC - acillus stearothermophilus | 51 | 30 |
| 340 | 2 | 898 | 1152 | gi\|40046 | phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus] ir\|S15936\|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus | 51 | 39 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 340 | 4 | 3617 | 2445 | gi\|763052 | integrase [Bacteriophage T270] | 51 | 33 |
| 379 | 10 | 11742 | 11311 | gi\|887829 | D21141 uses 2nd start; frame determined by Lac fusion [Escherichia oli] | 51 | 34 |
| 380 | 1 | 2 | 1123 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 51 | 34 |
| 395 | 1 | 526 | 95 | gi\|490986 | phi 105 repessor orf2 [unidentified] | 51 | 27 |
| 424 | 4 | 2512 | 995 | gi\|1633572 | Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] | 51 | 31 |
| 444 | 1 | 737 | 483 | gi\|1245376 | cardiac ryanodine receptor [Oryctolagus cuniculus] | 51 | 34 |
| 483 | 1 | 1 | 642 | gi\|1303981 | YqkD [Bacillus subtilis] | 51 | 29 |
| 500 | 1 | 2 | 550 | gi\|987094 | membrane transport protein [Streptomyces hygroscopicus] | 51 | 23 |
| 525 | 3 | 492 | 983 | pir\|A57438\|A57438 | tryptophan-rich sensory protein - Rhodobacter sphaeroides (strain 2.4.1) | 51 | 38 |
| 534 | 1 | 2 | 1165 | gi\|147516 | ribokinase [Escherichia coli] | 51 | 33 |
| 547 | 1 | 1 | 387 | gi\|1353528 | ORF11 [Bacteriophage r1t] | 51 | 33 |
| 553 | 2 | 1728 | 1330 | pir\|B55124\|B55124 | thioredoxin - Chlorobium sp. | 51 | 27 |
| 574 | 1 | 2291 | 2476 | bbs\|129435 | RprX=inner membrane signal-transducing protein [Bacteroides fragilis, Peptide, 519 aa] [Bacteroides fragilis] | 51 | 36 |
| 574 | 2 | 3145 | 3420 | gi\|1732202 | PTS permease for mannose subunit IIIMan N terminal domain [Vibrio furnissii] | 51 | 29 |
| 594 | 2 | 530 | 225 | gi\|1657696 | tryptophan hydroxylase [Gallus gallus] | 51 | 40 |
| 605 | 3 | 1220 | 1936 | gnl\|PID\|e289149 | similar to B. subtilis YcsE hypothetical protein [Bacillus subtilis] | 51 | 32 |
| 609 | 1 | 1027 | 74 | gi\|1226279 | strong similarity to Schistosoma amino acid permease (GB:L25068) [Caenorhabditis elegans] | 51 | 26 |
| 656 | 2 | 2033 | 2950 | gi\|143213 | putative [Bacillus subtilis] | 51 | 26 |
| 670 | 1 | 1508 | 369 | gi\|1652222 | hypothetical protein [Synechocystis sp.] | 51 | 25 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 673 | 1 | 2 | 1135 | gi\|532553 | ORF20 [Enterococcus faecalis] | 51 | 27 |
| 674 | 2 | 1158 | 778 | gi\|467451 | unknown [Bacillus subtilis] | 51 | 26 |
| 735 | 2 | 477 | 725 | gi\|757791 | aromatic amino acid permease [Corynebacterium glutamicum] pir\|S52754\|S52754 aromatic amino acid permease - Corynebacterium lutamicum | 51 | 38 |
| 924 | 1 | 794 | 3 | gi\|40663 | sialidase [Clostridium septicum] | 51 | 35 |
| 4 | 5 | 3811 | 4728 | gi\|413948 | ipa-24d gene product [Bacillus subtilis] | 50 | 29 |
| 8 | 3 | 3310 | 2180 | gi\|1592205 | M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii] | 50 | 28 |
| 11 | 9 | 5269 | 5520 | gi\|1651800 | L-glutamine:D-fructose-6-P amidotransferase [Synechocystis sp.] | 50 | 25 |
| 12 | 6 | 9045 | 8662 | gnl\|PID\|e254943 | unknown [Mycobacterium tuberculosis] | 50 | 23 |
| 15 | 4 | 2911 | 4269 | gi\|1592173 | N-ethylammeline chlorohydrolase [Methanococcus jannaschii] | 50 | 28 |
| 19 | 10 | 4934 | 5530 | gi\|825569 | unknown [Saccharomyces cerevisiae] | 50 | 20 |
| 28 | 5 | 7515 | 7057 | gi\|1230586 | orf10; Method: conceptual translation supplied by author [Vibrio cholerae O139] | 50 | 38 |
| 45 | 9 | 4279 | 5019 | gi\|1591029 | thioredoxin/glutaredoxin [Methanococcus jannaschii] | 50 | 32 |
| 54 | 16 | 7739 | 7590 | gi\|1589837 | cuticle preprocollagen [Meloidogyne incognita] | 50 | 46 |
| 59 | 5 | 1551 | 2345 | gi\|144297 | acetyl esterase (XynC) [Caldocellum saccharolyticum] pir\|B37202\|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum accharolyticum | 50 | 34 |
| 62 | 3 | 1650 | 1360 | gnl\|PID\|e205266 | LEA76 homologue type2 [Arabidopsis thaliana] | 50 | 31 |
| 91 | 10 | 8858 | 7521 | gi\|758229 | integrase [Bacteriophage phi-13] | 50 | 31 |
| 112 | 5 | 3548 | 2133 | gi\|1184262 | GadC [Shigella flexneri] | 50 | 25 |
| 123 | 13 | 13099 | 14319 | gi\|178273 | alanine:glyoxylate aminotransferase [Homo sapiens] | 50 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 123 | 15 | 14395 | 15675 | gi\|467342 | unknown [Bacillus subtilis] | 50 | 28 |
| 123 | 31 | 28700 | 29494 | gi\|43942 | first subunit of EII-Sor [Klebsiella pneumoniae] | 50 | 27 |
| 124 | 2 | 1666 | 1061 | gi\|556016 | similar to plant water stress proteins; ORF2 [Bacillus subtilis] gi\|556016 similar to plant water stress proteins; ORF2 [Bacillus ubtilis] | 50 | 34 |
| 128 | 39 | 32767 | 31829 | gi\|39993 | UDP-N-acetylmuramoylalanine--D-glutamate ligase [Bacillus subtilis] | 50 | 33 |
| 135 | 11 | 8803 | 7694 | gi\|895747 | putative cel operon regulator [Bacillus subtilis] | 50 | 26 |
| 138 | 21 | 14648 | 13653 | gi\|1591472 | malic acid transport protein [Methanococcus jannaschii] | 50 | 26 |
| 146 | 3 | 2338 | 1415 | gi\|1732200 | PTS permease for mannose subunit IIPMan [Vibrio furnissii] | 50 | 27 |
| 160 | 2 | 724 | 1302 | gnl\|PID\|e264218 | F54F3.4 [Caenorhabditis elegans] | 50 | 30 |
| 164 | 15 | 15432 | 16364 | gi\|409286 | bmrU [Bacillus subtilis] | 50 | 27 |
| 167 | 9 | 17082 | 15394 | gi\|143156 | membrane bound protein [Bacillus subtilis] | 50 | 30 |
| 179 | 3 | 2350 | 4485 | gi\|1408485 | yxdM gene product [Bacillus subtilis] | 50 | 24 |
| 180 | 30 | 31056 | 30643 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 50 | 27 |
| 184 | 1 | 2 | 1015 | gi\|854232 | cymE gene product [Klebsiella oxytoca] | 50 | 24 |
| 194 | 7 | 4335 | 4817 | gi\|1256652 | 25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis] | 50 | 30 |
| 195 | 29 | 11712 | 12422 | gi\|662263 | ORF5 [Plasmid pIP501] | 50 | 25 |
| 204 | 1 | 2 | 166 | gi\|328656 | envelope polyprotein [Human immunodeficiency virus type 1] | 50 | 45 |
| 205 | 7 | 3118 | 3861 | gi\|437697 | traE [Plasmid RP4] | 50 | 31 |
| 216 | 11 | 7181 | 7750 | gnl\|PID\|e254644 | membrane protein [Streptococcus pneumoniae] | 50 | 30 |
| 223 | 10 | 7036 | 8082 | gi\|606423 | T09B9.1 [Caenorhabditis elegans] | 50 | 30 |

**Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins**

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 223 | 22 | 19257 | 19799 | gi\|1256141 | YbbL [Bacillus subtilis] | 50 | 29 |
| 233 | 4 | 3102 | 2320 | gi\|887826 | GUG start [Escherichia coli] | 50 | 32 |
| 238 | 6 | 5102 | 3906 | gi\|1161219 | homolgous to D-amino acid dehydrogenase enzyme [Pseudomonas aeruginosa] | 50 | 29 |
| 239 | 3 | 4449 | 5159 | gi\|41519 | P30 protein (AA 1-240) [Escherichia coli] | 50 | 31 |
| 242 | 2 | 147 | 2210 | gi\|160299 | glutamic acid-rich protein [Plasmodium falciparum] pir\|A54514\|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum | 50 | 30 |
| 248 | 2 | 263 | 712 | gi\|143725 | putative [Bacillus subtilis] | 50 | 32 |
| 256 | 8 | 8531 | 7395 | gnl\|PID\|e250452 | C44H9.4 [Caenorhabditis elegans] | 50 | 38 |
| 265 | 3 | 1150 | 893 | gi\|1402527 | ORF6 [Enterococcus faecalis] | 50 | 39 |
| 276 | 24 | 14203 | 14000 | gi\|1591019 | M. jannaschii predicted coding region MJ0297 [Methanococcus jannaschii] | 50 | 33 |
| 276 | 32 | 20601 | 19924 | gi\|1334905 | BXLF2 late reading frame, encodes gp85; homologous to RF 37 VZV and glycoprotein H of HSV (gpIII of VZV) [Human herpesvirus 4] | 50 | 29 |
| 286 | 1 | 1 | 747 | gnl\|PID\|e257895 | homology with truncated ORF2 of pepF2 [Lactococcus lactis] | 50 | 32 |
| 301 | 17 | 11706 | 13313 | gi\|562039 | NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii] pir\|S53835\|S53835 NADH dehydrogenase chain 2 - Acanthamoeba astellanii mitochondrion (SGC6) | 50 | 26 |
| 338 | 5 | 2206 | 3729 | gi\|829194 | bacterial cell wall hydrolase [Enterococcus faecalis] pir\|A38109\|A38109 autolysin - Enterococcus faecalis sp\|P37710\|ALYS_ENTFA AUTOLYSIN (EC 3.5.1.28) N-ACETYLMURAMOYL-L-ALANINE AMIDASE). | 50 | 34 |
| 345 | 12 | 11781 | 13379 | gnl\|PID\|e235181 | unknown [Mycobacterium tuberculosis] | 50 | 32 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 360 | 2 | 2879 | 408 | gi\|40782 | bps2 gene product [Desulfurolobus ambivalens] | 50 | 25 |
| 372 | 1 | 6 | 440 | gi\|1552733 | similar to voltage-gated chloride channel protein [Escherichia coli] | 50 | 31 |
| 372 | 2 | 391 | 738 | gi\|1591749 | TRK system potassium uptake protein A [Methanococcus jannaschii] | 50 | 23 |
| 377 | 3 | 2262 | 1846 | gi\|52797 | kinesin heavy chain [Mus musculus] | 50 | 22 |
| 392 | 1 | 433 | 2 | gi\|147213 | phnP protein [Escherichia coli] | 50 | 33 |
| 399 | 31 | 29803 | 30186 | gi\|146288 | PTS enzyme III glucitol [Escherichia coli] | 50 | 30 |
| 518 | 4 | 2885 | 2040 | gi\|475107 | regulatory protein [Pediococcus pentosaceus] | 50 | 29 |
| 528 | 1 | 3 | 665 | gi\|215098 | excisionase [Bacteriophage 154a] | 50 | 38 |
| 562 | 1 | 631 | 107 | gi\|1592205 | M. jannaschii predicted coding region MJ1595 [Methanococcus jannaschii] | 50 | 28 |
| 596 | 1 | 227 | 1153 | gi\|963039 | orf gene product [Enterococcus hirae] | 50 | 26 |
| 680 | 1 | 2 | 1090 | gi\|1050297 | product p150Glued [Neurospora crassa] | 50 | 27 |
| 755 | 1 | 2 | 430 | gi\|1736469 | Tetracenomycin C resistance and export protein. [Escherichia coli] | 50 | 33 |
| 838 | 1 | 428 | 3 | gi\|530424 | 50S ribosomal protein [Mycoplasma capricolum] | 50 | 30 |
| 14 | 2 | 3453 | 538 | gi\|47049 | asa1 gene product (AA 1-1296) [Enterococcus faecalis] ir\|S10223\|HMS01F aggregation protein asa1 - Enterococcus faecalis asmid pAD1 | 49 | 25 |
| 56 | 7 | 5367 | 4822 | gi\|924754 | glycine reductase complex selenoprotein B [Clostridium litorale] | 49 | 31 |
| 68 | 9 | 4741 | 7389 | gi\|1591494 | M. jannaschii predicted coding region MJ0797 [Methanococcus jannaschii] | 49 | 21 |
| 94 | 10 | 9425 | 6633 | gi\|1146243 | 22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis] | 49 | 30 |
| 98 | 12 | 12306 | 11701 | gi\|1303784 | YqeD [Bacillus subtilis] | 49 | 26 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 117 | 7 | 4789 | 6228 | gi\|435493 | orf4 gene product [Lactococcus lactis] | 49 | 26 |
| 123 | 21 | 18576 | 19745 | gi\|298032 | EF [Streptococcus suis] | 49 | 29 |
| 125 | 4 | 2358 | 1594 | gnl\|PID\|e237295 | unknown [Saccharomyces cerevisiae] | 49 | 27 |
| 125 | 6 | 4235 | 3453 | gi\|1573885 | glycosyl transferase (lgtD) [Haemophilus influenzae] | 49 | 32 |
| 144 | 5 | 3715 | 4062 | gi\|507130 | emm64 gene product [Streptococcus pyogenes] | 49 | 30 |
| 162 | 8 | 10472 | 9120 | gi\|47045 | NADH oxidase [Enterococcus faecalis] | 49 | 34 |
| 179 | 18 | 18426 | 17848 | gi\|40060 | DNA polymerase III (AA 1-1437) [Bacillus subtilis] p\|P13267\|DP3A_BACSU DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7). | 49 | 27 |
| 180 | 19 | 18727 | 19917 | gi\|143000 | proton glutamate symport protein [Bacillus stearothermophilus] pir\|S26247\|S26247 glutamate/aspartate transport protein - Bacillus tearothermophilus | 49 | 31 |
| 224 | 1 | 145 | 1371 | gi\|1103862 | TolA [Pseudomonas aeruginosa] | 49 | 32 |
| 236 | 8 | 10955 | 9249 | gi\|431272 | lysis protein [Bacillus subtilis] | 49 | 28 |
| 278 | 1 | 757 | 2 | gi\|467478 | unknown [Bacillus subtilis] | 49 | 29 |
| 290 | 8 | 6860 | 7366 | gi\|466875 | nifU; B1496_C1_157 [Mycobacterium leprae] | 49 | 35 |
| 318 | 5 | 4065 | 3190 | gi\|144859 | ORF B [Clostridium perfringens] | 49 | 25 |
| 318 | 8 | 6052 | 5033 | gi\|1439528 | EIIC-man [Lactobacillus curvatus] | 49 | 30 |
| 335 | 1 | 534 | 40 | gi\|216861 | 24K membrane protein [Pseudomonas aeruginosa] | 49 | 24 |
| 338 | 4 | 2861 | 2169 | gnl\|PID\|e288536 | F37H8.a [Caenorhabditis elegans] | 49 | 30 |
| 346 | 4 | 1257 | 2273 | gi\|536970 | ORF_f543 [Escherichia coli] | 49 | 25 |
| 355 | 20 | 12902 | 15262 | gi\|292836 | trichohyalin [Homo sapiens] | 49 | 20 |
| 366 | 1 | 1 | 1437 | gi\|405857 | yehU [Escherichia coli] | 49 | 26 |
| 375 | 8 | 7663 | 6470 | gi\|1573546 | H. influenzae predicted coding region HI0561 [Haemophilus influenzae] | 49 | 30 |
| 377 | 2 | 1624 | 392 | gi\|532553 | ORF20 [Enterococcus faecalis] | 49 | 27 |
| 399 | 5 | 3960 | 3142 | gi\|1742362 | nta operon transcriptional regulator. | 49 | 29 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Escherichia coli] | | |
| 456 | 1 | 1070 | 342 | gi\|290533 | similar to E. coli ORF adjacent to suc operon; similar to gntR class f regulatory proteins [Escherichia coli] | 49 | 27 |
| 619 | 1 | 2 | 232 | gi\|665956 | ribosomal protein S20 homolog [Aeromonas sobria] sp\|P45786\|RS20_AERHY 30S RIBOSOMAL PROTEIN S20 (FRAGMENT). sp\|P45788\|RS20_AERSO 30S RIBOSOMAL PROTEIN S20 (FRAGMENT). | 49 | 41 |
| 621 | 1 | 319 | 942 | gi\|149456 | nisin-resistance protein [Lactococcus lactis] | 49 | 29 |
| 630 | 1 | 3 | 1190 | gi\|537145 | ORF_f437 [Escherichia coli] | 49 | 34 |
| 736 | 1 | 859 | 2 | gi\|1592020 | hypothetical protein (SP:P37555) [Methanococcus jannaschii] | 49 | 27 |
| 849 | 1 | 232 | 11 | gi\|145514 | cyclopropane fatty acid synthase [Escherichia coli] | 49 | 35 |
| 47 | 11 | 14140 | 13307 | gi\|1045937 | M. genitalium predicted coding region MG246 [Mycoplasma genitalium] | 48 | 34 |
| 103 | 4 | 2492 | 1605 | gi\|1591514 | membrane protein [Methanococcus jannaschii] | 48 | 19 |
| 127 | 7 | 6836 | 5736 | gi\|1573128 | hypothetical [Haemophilus influenzae] | 48 | 24 |
| 138 | 22 | 14742 | 15590 | gi\|580884 | ipa-89d gene product [Bacillus subtilis] | 48 | 33 |
| 160 | 6 | 3048 | 3665 | gi\|1652295 | serine esterase [Synechocystis sp.] | 48 | 28 |
| 162 | 3 | 3048 | 2491 | gi\|143830 | xpaC [Bacillus subtilis] | 48 | 13 |
| 193 | 2 | 1257 | 310 | gi\|1591153 | hypothetical protein (SP:P46348) [Methanococcus jannaschii] | 48 | 24 |
| 219 | 1 | 61 | 573 | gnl\|PID\|e257628 | ORF [Lactococcus lactis] | 48 | 32 |
| 221 | 11 | 5952 | 6428 | gi\|1303733 | YqaN [Bacillus subtilis] | 48 | 31 |
| 232 | 4 | 2776 | 1712 | gi\|142707 | comG2 gene product [Bacillus subtilis] | 48 | 24 |
| 236 | 6 | 8618 | 7689 | gi\|550075 | cephalosporin-C deacetylase [Bacillus subtilis] | 48 | 26 |
| 238 | 28 | 25896 | 26825 | gi\|47906 | rha regulatory protein [Salmonella | 48 | 31 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
|  |  |  |  |  | typhimurium] |  |  |
| 251 | 2 | 1935 | 640 | gi\|1143026 | ORF10 [Spiroplasma virus] | 48 | 30 |
| 252 | 1 | 2036 | 3 | gnl\|PID\|e228699 | homologous to yqbO of the skin element [Bacillus subtilis] | 48 | 37 |
| 269 | 1 | 481 | 2 | gi\|1045975 | sensory rhodopsin II transducer [Mycoplasma genitalium] | 48 | 28 |
| 315 | 5 | 4604 | 2649 | gi\|396400 | similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp\|P32703\|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549). | 48 | 30 |
| 327 | 1 | 128 | 916 | gi\|216314 | esterase [Bacillus stearothermophilus] | 48 | 30 |
| 330 | 6 | 4486 | 5337 | gi\|43942 | first subunit of EII-Sor [Klebsiella pneumoniae] | 48 | 21 |
| 330 | 7 | 5325 | 6230 | gi\|147404 | mannose permease subunit II-M-Man [Escherichia coli] | 48 | 33 |
| 345 | 10 | 9571 | 10521 | gi\|1736789 | Collagenase precursor (EC 3.4.-.-). [Escherichia coli] | 48 | 26 |
| 509 | 1 | 1 | 444 | gi\|606376 | ORF_o162 [Escherichia coli] | 48 | 33 |
| 531 | 1 | 624 | 109 | sp\|P50848\|YPWA_BACSU | HYPOTHETICAL 58.2 KD PROTEIN IN KDGT-XPT INTERGENIC REGION. | 48 | 33 |
| 549 | 3 | 962 | 369 | gi\|1001212 | molybdenum cofactor biosynthesis protein C [Synechocystis sp.] | 48 | 32 |
| 725 | 1 | 3 | 500 | gi\|1151158 | repeat organellar protein [Plasmodium chabaudi] | 48 | 25 |
| 789 | 1 | 133 | 717 | gi\|42724 | rhaS (AA 1-278) [Escherichia coli] | 48 | 39 |
| 936 | 1 | 32 | 316 | gi\|532549 | ORF16 [Enterococcus faecalis] | 48 | 45 |
| 2 | 2 | 2662 | 449 | gi\|929878 | J1027 gene product [Saccharomyces cerevisiae] | 47 | 20 |
| 4 | 2 | 1002 | 2192 | gi\|763052 | integrase [Bacteriophage T270] | 47 | 29 |
| 21 | 8 | 6350 | 5355 | gi\|1066343 | mu-crystallin [Homo sapiens] | 47 | 29 |
| 25 | 3 | 915 | 2048 | gi\|1064813 | homologous to sp:PHOR_BACSU [Bacillus subtilis] | 47 | 21 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 59 | 2 | 953 | 1378 | gi\|872306 | integral membrane protein [Streptomyces pristinaespiralis] pir\|S57509\|S57509 integral membrane protein - Streptomyces ristinaespiralis | 47 | 26 |
| 81 | 7 | 4970 | 4206 | gi\|1591754 | hypothetical protein (SP:P39364) [Methanococcus jannaschii] | 47 | 22 |
| 82 | 3 | 1534 | 866 | gi\|397526 | clumping factor [Staphylococcus aureus] | 47 | 21 |
| 110 | 5 | 2313 | 3767 | gi\|151928 | 48 kDa protein [Rhodobacter sphaeroides] | 47 | 26 |
| 150 | 11 | 7839 | 9107 | gnl\|PID\|e275490 | C30H6.k [Caenorhabditis elegans] | 47 | 16 |
| 161 | 2 | 116 | 1450 | gnl\|PID\|e283830 | aminotransferase [Sulfolobus solfataricus] | 47 | 23 |
| 165 | 8 | 8081 | 6129 | gi\|924925 | heparinase III protein [Cytophaga heparina] | 47 | 29 |
| 180 | 31 | 31515 | 31054 | gi\|1591753 | N-acetylglucosamine-1-phosphate transferase [Methanococcus jannaschii] | 47 | 29 |
| 194 | 11 | 8247 | 9236 | gi\|1480429 | putative transcriptional regulator [Bacillus stearothermophilus] | 47 | 26 |
| 225 | 2 | 1039 | 701 | gi\|1212992 | Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo sapiens] | 47 | 33 |
| 232 | 1 | 196 | 969 | gi\|293033 | integrase [Bacteriophage phi-LC3] | 47 | 30 |
| 232 | 6 | 3687 | 3340 | gi\|142706 | comG1 gene product [Bacillus subtilis] | 47 | 28 |
| 233 | 10 | 8424 | 6739 | gi\|887816 | possible start 13 codons upstream, for o765 [Escherichia coli] | 47 | 35 |
| 346 | 2 | 706 | 1083 | gi\|536970 | ORF_f543 [Escherichia coli] | 47 | 27 |
| 352 | 1 | 112 | 843 | gi\|1591857 | H+-transporting ATPase [Methanococcus jannaschii] | 47 | 28 |
| 410 | 1 | 3 | 980 | gi\|1652869 | NADH dehydrogenase [Synechocystis sp.] | 47 | 30 |
| 465 | 2 | 1976 | 1749 | gi\|211659 | p68 protein; c-rel proto-oncogene [Gallus gallus] | 47 | 30 |
| 491 | 3 | 3752 | 2466 | gi\|881434 | ORFP [Bacillus subtilis] | 47 | 24 |
| 501 | 1 | 48 | 809 | gi\|467429 | unknown [Bacillus subtilis] | 47 | 33 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 532 | 1 | 3 | 287 | gi\|755724 | alpha-toxin [Clostridium novyi] | 47 | 32 |
| 578 | 1 | 707 | 81 | gi\|532547 | ORF14 [Enterococcus faecalis] | 47 | 30 |
| 605 | 4 | 2051 | 2470 | gi\|1783233 | hypothetical [Bacillus subtilis] | 47 | 22 |
| 626 | 3 | 2459 | 2169 | gi\|1573573 | 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus influenzae] | 47 | 44 |
| 650 | 1 | 1042 | 341 | gi\|404802 | integrase [Saccharopolyspora erythraea] | 47 | 26 |
| 665 | 1 | 714 | 1175 | gi\|143655 | sporulation protein [Bacillus subtilis] | 47 | 22 |
| 754 | 2 | 1086 | 736 | gi\|143835 | PBSX repressor [Bacillus subtilis] | 47 | 27 |
| 845 | 1 | 2 | 241 | gi\|1303952 | YqjA [Bacillus subtilis] | 47 | 26 |
| 911 | 1 | 1 | 456 | gi\|1019640 | ORFX (a homolog to the prgX gene of the pheromone response plasmid pCF10); putative [Plasmid pHKK701] | 47 | 26 |
| 933 | 1 | 16 | 303 | gi\|331002 | first methionine codon in the ECLF1 ORF [Saimiriine herpesvirus 2] gi\|60394 ORF 73; ECLF1 [Saimiriine herpesvirus 2] | 47 | 29 |
| 17 | 17 | 13073 | 13675 | gi\|1304597 | abortive phage resistance protein [Lactococcus lactis] | 46 | 27 |
| 19 | 11 | 5515 | 6393 | gi\|1353529 | ORF12 [Bacteriophage r1t] | 46 | 28 |
| 42 | 3 | 2460 | 3011 | gi\|1064814 | homologous to sp:PHOP_BACSUB [Bacillus subtilis] | 46 | 33 |
| 49 | 9 | 4042 | 5793 | gnl\|PID\|e59644 | predicted 86.4kd protein; 52Kd observed [Mycobacteriophage 15] | 46 | 22 |
| 74 | 6 | 4039 | 3434 | gi\|143542 | RNA polymerase sigma-30 factor [Bacillus licheniformis] pir\|B28625\|SZBSSL transcription initiation factor sigma H - acillus licheniformis | 46 | 27 |
| 89 | 14 | 14259 | 12967 | gi\|1499089 | M. jannaschii predicted coding region MJ0305 [Methanococcus jannaschii] | 46 | 32 |
| 89 | 15 | 15737 | 14427 | gi\|1653339 | hypothetical protein [Synechocystis sp.] | 46 | 22 |
| 94 | 13 | 12634 | 11132 | gi\|1402515 | membrane-spanning transporter protein [Clostridium perfringens] | 46 | 23 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 100 | 18 | 13493 | 11958 | gi\|15470 | portal protein [Bacteriophage SPP1] | 46 | 31 |
| 144 | 2 | 2364 | 1126 | gnl\|PID\|e183450 | hypothetical EcsB protein [Bacillus subtilis] | 46 | 25 |
| 144 | 9 | 8977 | 6236 | gi\|710421 | unknown [Staphylococcus aureus] | 46 | 24 |
| 152 | 7 | 3397 | 4557 | gnl\|PID\|e254991 | hypothetical protein [Bacillus subtilis] | 46 | 25 |
| 158 | 7 | 7144 | 5993 | gi\|1045800 | ribose transport system permease protein [Mycoplasma genitalium] | 46 | 28 |
| 180 | 11 | 10882 | 10055 | gi\|303953 | esterase [Acinetobacter calcoaceticus] | 46 | 23 |
| 181 | 3 | 1173 | 976 | gi\|1591638 | M. jannaschii predicted coding region MJ0975 [Methanococcus jannaschii] | 46 | 36 |
| 240 | 1 | 715 | 221 | gi\|1766062 | Ats1 [Schizosaccharomyces pombe] | 46 | 28 |
| 254 | 2 | 499 | 2 | gi\|153661 | translational initiation factor IF2 [Enterococcus faecium] sp\|P18311\|IF2_ENTFC INITIATION FACTOR IF-2. | 46 | 32 |
| 262 | 4 | 5276 | 4431 | pir\|A45605\|A45605 | mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum | 46 | 20 |
| 309 | 1 | 2 | 673 | gi\|1651714 | type 4 prepilin peptidase [Synechocystis sp.] | 46 | 40 |
| 312 | 1 | 18 | 872 | gi\|580884 | ipa-89d gene product [Bacillus subtilis] | 46 | 32 |
| 324 | 6 | 4450 | 4836 | gi\|1061418 | ArsC [Plasmid R46] | 46 | 28 |
| 345 | 1 | 2241 | 1333 | gi\|144859 | ORF B [Clostridium perfringens] | 46 | 24 |
| 386 | 4 | 1438 | 2421 | gi\|405894 | 1-phosphofructokinase [Escherichia coli] | 46 | 31 |
| 395 | 8 | 3584 | 3853 | gnl\|PID\|e120267 | sucrose-phosphate synthase [Beta vulgaris] | 46 | 25 |
| 491 | 2 | 2527 | 1169 | gnl\|PID\|e267595 | Unknown, similar to peptidases [Bacillus subtilis] | 46 | 29 |
| 495 | 3 | 612 | 869 | gi\|406286 | triose phosphate/phosphate translocator [Flaveria pringlei] pir\|S37553\|S37553 triose phosphate/3-phosphoglycerate/phosphate ranslocator - Flaveria pringlei | 46 | 27 |
| 513 | 1 | 2 | 946 | gi\|143024 | glucose-resistance amylase regulator | 46 | 26 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Bacillus subtilis] pir\|S15318\|S15318 ccpA protein - Bacillus subtilis sp\|P25144\|CCPA_BACSU GLUCOSE-RESISTANCE AMYLASE REGULATOR CATABOLITE CONTROL PROTEIN). | | |
| 520 | 3 | 914 | 2674 | gi\|1163086 | microfilarial sheath protein SHP3 [Brugia malayi] | 46 | 27 |
| 554 | 1 | 3 | 788 | gi\|413972 | ipa-48r gene product [Bacillus subtilis] | 46 | 27 |
| 568 | 1 | 1574 | 3 | gi\|532549 | ORF16 [Enterococcus faecalis] | 46 | 28 |
| 809 | 1 | 506 | 135 | gi\|49021 | surface exclusion protein (SEA1) [Enterococcus faecalis] ir\|S22452\|S22452 surface exclusion protein seal precursor - terococcus faecalis plasmid pAD1 | 46 | 28 |
| 813 | 1 | 2 | 1090 | gi\|150556 | surface protein [Plasmid pCF10] | 46 | 34 |
| 78 | 2 | 4915 | 2516 | gi\|577295 | The ha1225 gene product is related to human alpha-glucosidase. [Homo apiens] | 45 | 20 |
| 81 | 9 | 6123 | 5386 | gi\|147200 | phnF protein [Escherichia coli] | 45 | 28 |
| 85 | 1 | 120 | 761 | gi\|457514 | gltC [Bacillus subtilis] | 45 | 19 |
| 94 | 11 | 10681 | 9668 | gi\|289753 | homology with nucleolin protein; putative [Caenorhabditis elegans] pir\|S44897\|S44897 ZK1236.2 protein - Caenorhabditis elegans sp\|P34618\|YO82_CAEEL HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN HROMOSOME III. | 45 | 23 |
| 108 | 3 | 2427 | 1789 | gnl\|PID\|e263931 | OrfD [Streptococcus pneumoniae] | 45 | 27 |
| 108 | 4 | 3338 | 2352 | gi\|606150 | ORF_f309 [Escherichia coli] | 45 | 25 |
| 131 | 6 | 3981 | 5309 | gi\|1590845 | hypothetical protein (PIR:S51413) [Methanococcus jannaschii] | 45 | 36 |
| 144 | 11 | 10215 | 8944 | gi\|1001554 | hypothetical protein [Synechocystis sp.] | 45 | 30 |
| 164 | 11 | 8247 | 6736 | gi\|409925 | VirR positive regulator [Streptococcus pyogenes] | 45 | 22 |
| 192 | 1 | 1598 | 591 | gi\|1736826 | Lysozyme M1 precursor (EC 3.2.1.17) (1,4-b-N-acetylmuramidase M1). [Escherichia | 45 | 27 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | coli] | | |
| 223 | 16 | 14409 | 15212 | gi\|1651958 | hypothetical protein [Synechocystis sp.] | 45 | 32 |
| 279 | 7 | 5236 | 5772 | gi\|1736514 | Isochorismatase (EC 3.3.2.1) (2,3 dihydro-2,3 dihydroxybenzoate synthase). [Escherichia coli] | 45 | 29 |
| 364 | 3 | 2419 | 4098 | gi\|309662 | pheromone binding protein [Plasmid pCF10] | 45 | 26 |
| 459 | 1 | 2 | 307 | gi\|1679640 | ORFA [Mycoplasma mycoides mycoides SC] | 45 | 27 |
| 491 | 1 | 1022 | 135 | sp\|P27434\|YFGA_ECOLI | HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCPE INTERGENIC REGION. | 45 | 20 |
| 496 | 1 | 847 | 2 | gi\|1208489 | serum resistance locus BrkB [Synechocystis sp.] | 45 | 19 |
| 542 | 2 | 1169 | 804 | gi\|1064811 | function unknown [Bacillus subtilis] | 45 | 28 |
| 63 | 3 | 1047 | 1919 | gi\|39848 | U3 [Bacillus subtilis] | 44 | 26 |
| 93 | 3 | 1108 | 1374 | sp\|Q04747\|SRF2_BACSU | SURFACTIN SYNTHETASE SUBUNIT 2. | 44 | 27 |
| 155 | 10 | 8354 | 7620 | sp\|P35136\|SERA_BACSU | D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH). | 44 | 29 |
| 215 | 2 | 2192 | 1134 | gi\|468760 | ORF334 [Rhizobium meliloti] | 44 | 31 |
| 303 | 1 | 466 | 2 | gi\|431950 | similar to a B.subtilis gene (GB: BACHEMEHY_5) [Clostridium asteurianum] | 44 | 22 |
| 310 | 1 | 284 | 39 | pir\|S01294\|S01294 | intermediate filament protein B - Roman snail | 44 | 26 |
| 311 | 1 | 122 | 2668 | gi\|532549 | ORF16 [Enterococcus faecalis] | 44 | 27 |
| 320 | 1 | 709 | 2 | gi\|290801 | member of super-family of ABC proteins [Francisella tularensis (var. ovicida)] | 44 | 23 |
| 341 | 14 | 13882 | 12998 | gi\|142863 | replication initiation protein [Bacillus subtilis] | 44 | 16 |
| 345 | 15 | 16445 | 18001 | gi\|151282 | DL-hydantoinase [Pseudomonas sp.] | 44 | 34 |
| 386 | 3 | 1340 | 570 | sp\|P46117\|YARA_PROST | HYPOTHETICAL 31.5 KD PROTEIN IN AARA 3'REGION. | 44 | 19 |
| 862 | 1 | 483 | 4 | gi\|929796 | precursor of the major merozoite surface | 44 | 26 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | antigens [Plasmodium alciparum] | | |
| 19 | 3 | 1695 | 1372 | gi\|603263 | Yel055p [Saccharomyces cerevisiae] | 43 | 31 |
| 45 | 17 | 14045 | 14995 | gnl\|PID\|e233895 | hypothetical protein [Bacillus subtilis] | 43 | 32 |
| 57 | 1 | 667 | 317 | gi\|664840 | TagB [Dictyostelium discoideum] | 43 | 22 |
| 71 | 2 | 1537 | 2568 | gi\|1303981 | YqkD [Bacillus subtilis] | 43 | 26 |
| 72 | 18 | 20511 | 20164 | gi\|349045 | merozoite surface antigen 2 [Plasmodium falciparum] | 43 | 36 |
| 94 | 9 | 6581 | 6039 | gi\|1146245 | putative [Bacillus subtilis] | 43 | 28 |
| 180 | 17 | 16391 | 17656 | gi\|290540 | f445 [Escherichia coli] | 43 | 24 |
| 252 | 2 | 2407 | 1829 | gi\|154381 | chemoreceptor [Salmonella typhimurium] | 43 | 19 |
| 276 | 30 | 19091 | 18480 | gi\|15470 | portal protein [Bacteriophage SPP1] | 43 | 23 |
| 311 | 2 | 2666 | 4639 | gi\|160299 | glutamic acid-rich protein [Plasmodium falciparum] pir\|A54514\|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum | 43 | 28 |
| 631 | 2 | 1126 | 2328 | gi\|1519696 | coded for by C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans] | 43 | 27 |
| 11 | 3 | 1509 | 2342 | gi\|143150 | levR [Bacillus subtilis] | 42 | 21 |
| 45 | 14 | 10730 | 12028 | gi\|666069 | orf2 gene product [Lactobacillus leichmannii] | 42 | 23 |
| 72 | 19 | 21070 | 21981 | gnl\|PID\|e236595 | orf7 gene product [Enterococcus faecalis] | 42 | 23 |
| 123 | 35 | 32205 | 32768 | gi\|1772652 | 2-keto-3-deoxygluconate kinase [Haloferax alicantei] | 42 | 27 |
| 136 | 5 | 2737 | 2375 | gi\|153858 | wall-associated protein [Streptococcus mutans] | 42 | 27 |
| 167 | 4 | 2701 | 6540 | gi\|1519696 | coded for by C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 | 42 | 27 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| | | | | | [Caenorhabditis elegans] | | |
| 195 | 31 | 12430 | 13155 | pir\|S33124\|S33124 | tpr protein - human | 42 | 24 |
| 211 | 1 | 187 | 2 | gi\|1653346 | GDP-mannose pyrophosphorylase [Synechocystis sp.] | 42 | 33 |
| 242 | 13 | 8089 | 12447 | gi\|951460 | FIM-C.1 gene product [Xenopus laevis] | 42 | 31 |
| 305 | 5 | 4354 | 5340 | gi\|1408485 | yxdM gene product [Bacillus subtilis] | 42 | 25 |
| 355 | 18 | 9964 | 12549 | gi\|532549 | ORF16 [Enterococcus faecalis] | 42 | 30 |
| 446 | 4 | 4428 | 5261 | gi\|47528 | glucosyltransferase S [Streptococcus salivarius] | 42 | 25 |
| 656 | 3 | 2866 | 3456 | gi\|142857 | MreD protein [Bacillus subtilis] | 42 | 25 |
| 686 | 11 | 3646 | 3921 | pir\|A44805\|A44805 | eggshell protein - fluke (Schistosoma haematobium) (subclone SH.E 2-1) | 42 | 42 |
| 920 | 1 | 41 | 316 | gi\|532549 | ORF16 [Enterococcus faecalis] | 42 | 40 |
| 23 | 3 | 729 | 487 | gi\|414525 | meiotin-1 [Lilium longiflorum] | 41 | 41 |
| 56 | 5 | 3511 | 2324 | gi\|1591610 | probable ATP-dependent helicase [Methanococcus jannaschii] | 41 | 21 |
| 98 | 17 | 16843 | 16274 | gi\|1742129 | Immunity repressor protein. [Escherichia coli] | 41 | 23 |
| 167 | 6 | 6734 | 9811 | gnl\|PID\|e249616 | F56H9.1 [Caenorhabditis elegans] | 41 | 37 |
| 171 | 13 | 10879 | 11871 | gi\|331002 | first methionine codon in the ECLF1 ORF [Saimiriine herpesvirus 2] gi\|60394 ORF 73; ECLF1 [Saimiriine herpesvirus 2] | 41 | 23 |
| 181 | 2 | 1012 | 500 | gi\|455315 | ORF 4 [Plasmid pIP404] | 41 | 24 |
| 230 | 4 | 3664 | 3224 | gi\|498251 | glutamate/aspartate transporter II [Homo sapiens] | 41 | 22 |
| 718 | 1 | 2 | 613 | gi\|984656 | ORF3 [Salmonella typhimurium] | 41 | 22 |
| 19 | 30 | 16391 | 17770 | gi\|806704 | Upf2p [Saccharomyces cerevisiae] | 40 | 21 |
| 164 | 16 | 16440 | 17951 | gi\|348056 | trans-acting positive regulator [Bacillus anthracis] | 40 | 22 |
| 200 | 12 | 5956 | 4841 | gi\|1574243 | H. influenzae predicted coding region HI1405 [Haemophilus influenzae] | 40 | 24 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 216 | 10 | 6799 | 7194 | gi\|146279 | glucitol-specific enzyme III (gutB) [Escherichia coli] | 40 | 27 |
| 292 | 13 | 8633 | 10741 | gi\|1008233 | ORF YJL076w [Saccharomyces cerevisiae] | 40 | 18 |
| 345 | 13 | 14050 | 15333 | gi\|581051 | cytosine permease [Escherichia coli] | 40 | 25 |
| 521 | 1 | 177 | 1466 | gi\|289614 | homology with glucose induced repressor, GRR1; putative Caenorhabditis elegans] | 40 | 18 |
| 64 | 3 | 2646 | 1855 | gi\|154924 | spectinomycin adenyltransferase [Transposon Tn554] | 39 | 27 |
| 100 | 17 | 12037 | 10565 | gi\|1052806 | product required for head morphogenesis [Bacteriophage SPP1] | 39 | 24 |
| 529 | 1 | 326 | 4939 | gi\|295671 | selected as a weak suppressor of a mutant of the subunit AC40 of DNA ependant RNA polymerase I and III [Saccharomyces cerevisiae] | 39 | 19 |
| 49 | 2 | 518 | 931 | gi\|166162 | Bacteriophage phi-11 int gene activator [Staphylococcus acteriophage phi 11] | 38 | 19 |
| 54 | 19 | 11264 | 10854 | gi\|160186 | circumsporozoite protein [Plasmodium vivax] | 38 | 31 |
| 164 | 21 | 22793 | 23587 | gi\|603857 | secreted acid phosphatase 2 (SAP2) [Leishmania mexicana] | 38 | 18 |
| 167 | 3 | 2322 | 2756 | gi\|435039 | proline-rich cell wall protein [Gossypium hirsutum] | 38 | 36 |
| 204 | 2 | 133 | 798 | gi\|396401 | No definition line found [Escherichia coli] | 38 | 25 |
| 475 | 2 | 761 | 1792 | gi\|1574532 | H. influenzae predicted coding region HI1680 [Haemophilus influenzae] | 38 | 27 |
| 164 | 19 | 20738 | 21385 | gi\|165704 | [Rabbit smooth muscle myosin light chain kinase mRNA, complete DS.], gene product [Oryctolagus cuniculus] | 37 | 20 |
| 394 | 6 | 5649 | 6395 | gi\|603857 | secreted acid phosphatase 2 (SAP2) [Leishmania mexicana] | 36 | 16 |
| 958 | 1 | 1 | 459 | gi\|951460 | FIM-C.1 gene product [Xenopus laevis] | 36 | 28 |

Table 2: *E. faecalis* - Putative coding regions of novel proteins similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) | Match accession | Match gene name | % Sim | % Ident |
|---|---|---|---|---|---|---|---|
| 399 | 21 | 16383 | 21359 | gi\|1707247 | partial CDS [Caenorhabditis elegans] | 34 | 13 |
| 150 | 12 | 9056 | 11740 | gi\|1015903 | ORF YJR151c [Saccharomyces cerevisiae] | 33 | 19 |
| 195 | 34 | 13017 | 15512 | gi\|632549 | NF-180 [Petromyzon marinus] | 33 | 18 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 2 | 1 | 458 | 3 |
| 2 | 3 | 2208 | 2624 |
| 5 | 3 | 928 | 1440 |
| 8 | 6 | 4792 | 5877 |
| 8 | 7 | 5480 | 5262 |
| 12 | 1 | 2 | 832 |
| 12 | 2 | 771 | 4622 |
| 13 | 1 | 2 | 1684 |
| 14 | 1 | 531 | 130 |
| 15 | 2 | 862 | 1197 |
| 16 | 1 | 51 | 200 |
| 17 | 4 | 3309 | 3665 |
| 17 | 13 | 10079 | 10261 |
| 17 | 18 | 14431 | 13682 |
| 17 | 22 | 21525 | 21956 |
| 17 | 27 | 27055 | 27567 |
| 18 | 4 | 2172 | 1591 |
| 18 | 5 | 2524 | 2249 |
| 18 | 7 | 3467 | 3715 |
| 18 | 8 | 4082 | 3555 |
| 18 | 9 | 4333 | 4055 |
| 18 | 10 | 4395 | 4204 |
| 18 | 11 | 4498 | 4677 |
| 18 | 12 | 4656 | 5393 |
| 18 | 13 | 5878 | 5492 |
| 18 | 15 | 6296 | 6931 |
| 19 | 1 | 1047 | 676 |
| 19 | 2 | 1068 | 1247 |
| 19 | 4 | 1747 | 2031 |
| 19 | 5 | 2244 | 2612 |
| 19 | 7 | 2797 | 2943 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 19 | 9 | 3873 | 4730 |
| 19 | 13 | 6884 | 7420 |
| 19 | 14 | 7428 | 8042 |
| 19 | 16 | 9246 | 8425 |
| 19 | 17 | 9412 | 9615 |
| 19 | 19 | 9733 | 9918 |
| 19 | 20 | 10032 | 10334 |
| 19 | 21 | 10422 | 11009 |
| 19 | 22 | 11516 | 11944 |
| 19 | 24 | 12423 | 12881 |
| 19 | 26 | 14606 | 15427 |
| 19 | 27 | 15414 | 15848 |
| 19 | 28 | 15802 | 16134 |
| 19 | 29 | 16064 | 16393 |
| 19 | 32 | 17846 | 18052 |
| 19 | 33 | 18021 | 18356 |
| 19 | 34 | 18334 | 18684 |
| 19 | 35 | 18659 | 19036 |
| 19 | 36 | 18991 | 19677 |
| 19 | 37 | 19671 | 20132 |
| 19 | 39 | 22603 | 23337 |
| 19 | 40 | 23319 | 25580 |
| 21 | 2 | 762 | 262 |
| 21 | 5 | 3440 | 2925 |
| 21 | 10 | 7684 | 7241 |
| 23 | 5 | 2098 | 2652 |
| 23 | 8 | 4912 | 4709 |
| 23 | 9 | 4911 | 5246 |
| 23 | 10 | 5087 | 5353 |
| 23 | 22 | 14318 | 14926 |
| 23 | 23 | 14924 | 15565 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 23 | 24 | 15559 | 16083 |
| 23 | 29 | 17567 | 18022 |
| 25 | 2 | 553 | 1005 |
| 25 | 5 | 3363 | 2653 |
| 26 | 2 | 1220 | 1654 |
| 27 | 1 | 297 | 4 |
| 28 | 1 | 239 | 2833 |
| 29 | 5 | 3244 | 2822 |
| 29 | 6 | 4014 | 3301 |
| 29 | 7 | 4168 | 4557 |
| 29 | 8 | 5620 | 4595 |
| 32 | 3 | 2646 | 1375 |
| 32 | 4 | 2573 | 3010 |
| 39 | 9 | 4636 | 4986 |
| 40 | 2 | 1346 | 981 |
| 43 | 1 | 120 | 620 |
| 43 | 4 | 1972 | 2280 |
| 45 | 3 | 1557 | 1961 |
| 45 | 4 | 2012 | 2230 |
| 45 | 5 | 2218 | 2553 |
| 45 | 11 | 7226 | 5670 |
| 45 | 12 | 7270 | 10113 |
| 45 | 13 | 10013 | 10732 |
| 46 | 1 | 42 | 872 |
| 46 | 2 | 886 | 1125 |
| 46 | 4 | 2807 | 3100 |
| 47 | 4 | 5101 | 5625 |
| 47 | 10 | 13239 | 12847 |
| 49 | 1 | 106 | 504 |
| 49 | 8 | 2858 | 4132 |
| 49 | 10 | 5777 | 6193 |

Table 3: E. *faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 49 | 11 | 6166 | 6720 |
| 52 | 5 | 3505 | 3110 |
| 52 | 7 | 5160 | 5603 |
| 52 | 8 | 5662 | 5459 |
| 54 | 2 | 400 | 729 |
| 54 | 4 | 1326 | 1610 |
| 54 | 5 | 2354 | 1335 |
| 54 | 6 | 1676 | 2080 |
| 54 | 7 | 2151 | 2576 |
| 54 | 12 | 4181 | 3954 |
| 54 | 13 | 5975 | 6289 |
| 54 | 14 | 6869 | 7144 |
| 54 | 15 | 7433 | 7107 |
| 54 | 18 | 9764 | 11086 |
| 55 | 2 | 252 | 440 |
| 56 | 2 | 1344 | 658 |
| 57 | 9 | 12450 | 12605 |
| 58 | 7 | 7066 | 6425 |
| 59 | 3 | 1350 | 952 |
| 59 | 4 | 1225 | 1515 |
| 59 | 7 | 2958 | 3200 |
| 62 | 6 | 4116 | 3007 |
| 63 | 1 | 77 | 364 |
| 63 | 2 | 455 | 1060 |
| 63 | 7 | 5422 | 5910 |
| 63 | 8 | 5870 | 6751 |
| 63 | 9 | 6688 | 7296 |
| 64 | 2 | 1849 | 1523 |
| 64 | 4 | 3183 | 2644 |
| 64 | 5 | 3422 | 3213 |
| 65 | 5 | 3787 | 3389 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 65 | 7 | 5043 | 4300 |
| 65 | 8 | 5354 | 4959 |
| 65 | 9 | 7005 | 6328 |
| 67 | 6 | 3719 | 4060 |
| 68 | 2 | 569 | 348 |
| 68 | 5 | 3234 | 2821 |
| 68 | 6 | 3808 | 3221 |
| 68 | 10 | 7495 | 8106 |
| 70 | 2 | 2102 | 1614 |
| 70 | 3 | 2019 | 2231 |
| 71 | 3 | 3362 | 3787 |
| 72 | 21 | 22464 | 22709 |
| 72 | 22 | 22690 | 23019 |
| 72 | 23 | 23013 | 23834 |
| 73 | 1 | 154 | 2 |
| 74 | 1 | 61 | 486 |
| 74 | 3 | 1334 | 1981 |
| 75 | 4 | 3227 | 2136 |
| 75 | 5 | 3994 | 3251 |
| 75 | 6 | 3348 | 3632 |
| 75 | 7 | 4519 | 4043 |
| 75 | 8 | 4296 | 4529 |
| 75 | 10 | 6518 | 5769 |
| 76 | 2 | 1079 | 1897 |
| 76 | 4 | 2113 | 2436 |
| 76 | 6 | 4737 | 4105 |
| 77 | 3 | 1874 | 2704 |
| 77 | 4 | 2665 | 2459 |
| 78 | 3 | 5814 | 5398 |
| 79 | 3 | 848 | 1645 |
| 79 | 4 | 2121 | 1642 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 81 | 8 | 5392 | 4961 |
| 81 | 13 | 8428 | 8874 |
| 81 | 21 | 15746 | 14802 |
| 82 | 1 | 858 | 4 |
| 82 | 2 | 198 | 383 |
| 83 | 3 | 2194 | 2604 |
| 83 | 4 | 2728 | 2405 |
| 83 | 6 | 2855 | 3172 |
| 83 | 10 | 7188 | 6184 |
| 83 | 11 | 7415 | 7065 |
| 83 | 17 | 12259 | 12561 |
| 83 | 21 | 15890 | 16456 |
| 83 | 23 | 16946 | 17251 |
| 84 | 5 | 7071 | 7949 |
| 85 | 7 | 6518 | 6174 |
| 89 | 2 | 1012 | 599 |
| 89 | 3 | 1382 | 939 |
| 89 | 4 | 2350 | 1370 |
| 89 | 5 | 2523 | 2314 |
| 89 | 9 | 7505 | 7182 |
| 89 | 16 | 15846 | 15673 |
| 89 | 19 | 20070 | 19045 |
| 90 | 1 | 3 | 689 |
| 91 | 7 | 3834 | 4127 |
| 91 | 8 | 4288 | 5268 |
| 91 | 9 | 7259 | 5748 |
| 91 | 12 | 9737 | 8973 |
| 91 | 13 | 10162 | 9731 |
| 92 | 3 | 1458 | 958 |
| 92 | 4 | 1934 | 1287 |
| 93 | 2 | 479 | 949 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 93 | 4 | 1344 | 1727 |
| 94 | 1 | 770 | 45 |
| 94 | 3 | 1460 | 1618 |
| 94 | 5 | 2279 | 1734 |
| 94 | 12 | 11000 | 10641 |
| 95 | 11 | 7674 | 7907 |
| 95 | 12 | 8604 | 8056 |
| 95 | 13 | 8725 | 8546 |
| 96 | 1 | 758 | 1018 |
| 96 | 2 | 1038 | 1469 |
| 98 | 5 | 6809 | 5994 |
| 98 | 10 | 10338 | 10652 |
| 98 | 11 | 10650 | 11558 |
| 99 | 2 | 232 | 513 |
| 100 | 4 | 3728 | 4048 |
| 100 | 6 | 5866 | 5378 |
| 100 | 7 | 6574 | 5921 |
| 100 | 8 | 6923 | 6534 |
| 100 | 9 | 7355 | 6921 |
| 100 | 10 | 7698 | 7339 |
| 100 | 11 | 8226 | 7744 |
| 100 | 13 | 9395 | 8514 |
| 100 | 15 | 10368 | 10102 |
| 100 | 19 | 14770 | 13505 |
| 100 | 20 | 15300 | 14758 |
| 100 | 21 | 15783 | 15298 |
| 100 | 23 | 17699 | 17292 |
| 100 | 25 | 20933 | 20625 |
| 100 | 26 | 21200 | 20946 |
| 100 | 28 | 23713 | 23156 |
| 100 | 29 | 23948 | 23691 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 100 | 30 | 24312 | 23965 |
| 100 | 31 | 24550 | 24287 |
| 100 | 32 | 24912 | 24565 |
| 100 | 33 | 25173 | 24910 |
| 100 | 34 | 26339 | 25158 |
| 100 | 36 | 27251 | 26994 |
| 100 | 37 | 27945 | 27232 |
| 100 | 39 | 28442 | 28227 |
| 100 | 40 | 28657 | 28403 |
| 100 | 46 | 30439 | 31146 |
| 100 | 47 | 31158 | 31712 |
| 101 | 2 | 850 | 464 |
| 101 | 3 | 2453 | 1899 |
| 102 | 6 | 5023 | 5616 |
| 102 | 9 | 6704 | 7111 |
| 103 | 7 | 5454 | 5296 |
| 105 | 2 | 1244 | 1828 |
| 106 | 4 | 5114 | 3294 |
| 106 | 6 | 7622 | 6168 |
| 106 | 7 | 6577 | 6867 |
| 108 | 6 | 5192 | 4158 |
| 110 | 1 | 2 | 454 |
| 110 | 6 | 3689 | 4207 |
| 110 | 9 | 9374 | 8553 |
| 110 | 10 | 9903 | 9361 |
| 110 | 11 | 10175 | 9843 |
| 111 | 6 | 3118 | 3267 |
| 112 | 4 | 2170 | 1043 |
| 114 | 2 | 1347 | 1135 |
| 116 | 8 | 4782 | 5147 |
| 117 | 4 | 2437 | 2670 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 117 | 6 | 3876 | 4640 |
| 117 | 8 | 5643 | 5927 |
| 117 | 9 | 6195 | 6488 |
| 117 | 12 | 9655 | 9837 |
| 119 | 1 | 3 | 500 |
| 119 | 2 | 670 | 1158 |
| 119 | 4 | 2730 | 2284 |
| 121 | 3 | 2276 | 3670 |
| 123 | 14 | 14304 | 14555 |
| 123 | 16 | 15305 | 15147 |
| 123 | 24 | 21896 | 22663 |
| 123 | 34 | 31458 | 32207 |
| 125 | 3 | 1581 | 1300 |
| 125 | 7 | 4516 | 4346 |
| 126 | 2 | 85 | 312 |
| 127 | 2 | 1047 | 787 |
| 127 | 3 | 2006 | 1299 |
| 127 | 4 | 3432 | 1924 |
| 128 | 4 | 3094 | 2747 |
| 128 | 5 | 3466 | 3305 |
| 128 | 6 | 4625 | 3507 |
| 128 | 7 | 4726 | 4550 |
| 128 | 13 | 8947 | 8522 |
| 128 | 15 | 9325 | 9582 |
| 128 | 17 | 10126 | 10380 |
| 128 | 24 | 17649 | 18038 |
| 129 | 1 | 276 | 1769 |
| 130 | 7 | 6478 | 6702 |
| 130 | 11 | 9386 | 9769 |
| 133 | 7 | 6622 | 7380 |
| 135 | 2 | 2289 | 1153 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 135 | 3 | 3380 | 2271 |
| 135 | 5 | 3778 | 3930 |
| 135 | 6 | 5835 | 5137 |
| 135 | 7 | 6649 | 5852 |
| 135 | 8 | 7021 | 6647 |
| 135 | 9 | 7420 | 7034 |
| 136 | 2 | 963 | 379 |
| 136 | 3 | 2009 | 939 |
| 136 | 4 | 2344 | 1973 |
| 138 | 4 | 5051 | 3636 |
| 138 | 11 | 8499 | 8753 |
| 138 | 12 | 8682 | 8536 |
| 138 | 13 | 8923 | 9270 |
| 138 | 14 | 9333 | 9887 |
| 138 | 15 | 9628 | 10308 |
| 138 | 16 | 10422 | 10216 |
| 138 | 23 | 15980 | 15678 |
| 138 | 24 | 16437 | 16063 |
| 138 | 30 | 19388 | 19828 |
| 139 | 3 | 1068 | 1466 |
| 139 | 4 | 3338 | 1983 |
| 139 | 5 | 3769 | 3317 |
| 139 | 6 | 4114 | 3818 |
| 139 | 7 | 4838 | 4236 |
| 139 | 10 | 5639 | 5175 |
| 142 | 1 | 369 | 106 |
| 142 | 2 | 1005 | 367 |
| 142 | 3 | 2140 | 980 |
| 142 | 4 | 2504 | 2127 |
| 142 | 5 | 2821 | 2474 |
| 142 | 6 | 3294 | 2806 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 142 | 7 | 4000 | 3635 |
| 143 | 1 | 650 | 3 |
| 143 | 3 | 1090 | 173 |
| 143 | 4 | 1044 | 433 |
| 144 | 10 | 7570 | 8403 |
| 144 | 12 | 10727 | 10335 |
| 145 | 1 | 188 | 30 |
| 145 | 2 | 775 | 978 |
| 150 | 9 | 6876 | 7166 |
| 150 | 13 | 11538 | 11242 |
| 152 | 1 | 35 | 445 |
| 152 | 2 | 405 | 914 |
| 152 | 3 | 912 | 1430 |
| 152 | 4 | 1349 | 2212 |
| 152 | 5 | 2210 | 2896 |
| 152 | 6 | 2739 | 3368 |
| 152 | 8 | 4479 | 4694 |
| 152 | 11 | 6647 | 7321 |
| 154 | 7 | 4557 | 4195 |
| 155 | 3 | 1227 | 2180 |
| 155 | 12 | 8726 | 9022 |
| 156 | 3 | 3179 | 2664 |
| 158 | 11 | 10876 | 11220 |
| 160 | 1 | 545 | 3 |
| 162 | 1 | 228 | 1349 |
| 162 | 2 | 2513 | 1653 |
| 162 | 7 | 9163 | 7664 |
| 162 | 9 | 10619 | 10990 |
| 162 | 11 | 11891 | 11427 |
| 163 | 3 | 1043 | 1234 |
| 163 | 5 | 3217 | 2021 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 163 | 6 | 3455 | 3198 |
| 163 | 8 | 5611 | 4931 |
| 163 | 9 | 5969 | 5580 |
| 163 | 10 | 6144 | 5926 |
| 164 | 2 | 1100 | 1687 |
| 164 | 9 | 5729 | 5259 |
| 164 | 10 | 6778 | 5639 |
| 164 | 12 | 8277 | 8450 |
| 164 | 17 | 18224 | 18526 |
| 164 | 24 | 24751 | 24536 |
| 164 | 27 | 25764 | 26369 |
| 165 | 1 | 17 | 481 |
| 165 | 2 | 2213 | 1389 |
| 165 | 12 | 9871 | 9689 |
| 165 | 14 | 11416 | 10367 |
| 166 | 3 | 1250 | 1669 |
| 167 | 5 | 3774 | 3439 |
| 167 | 7 | 10479 | 14498 |
| 167 | 10 | 17476 | 18768 |
| 168 | 2 | 665 | 393 |
| 172 | 9 | 7018 | 6701 |
| 172 | 10 | 7097 | 7930 |
| 173 | 1 | 2 | 412 |
| 173 | 3 | 2341 | 2024 |
| 173 | 6 | 4234 | 5055 |
| 173 | 9 | 7882 | 7295 |
| 173 | 10 | 7413 | 7571 |
| 173 | 14 | 12308 | 11748 |
| 174 | 4 | 2350 | 3021 |
| 174 | 5 | 3082 | 3498 |
| 178 | 3 | 866 | 1105 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 179 | 8 | 8115 | 7816 |
| 179 | 17 | 17407 | 17135 |
| 180 | 4 | 3524 | 4537 |
| 180 | 5 | 4686 | 5687 |
| 180 | 6 | 5897 | 6949 |
| 180 | 9 | 9721 | 9299 |
| 180 | 10 | 9996 | 9715 |
| 180 | 20 | 19805 | 19954 |
| 180 | 23 | 21808 | 21509 |
| 180 | 25 | 24127 | 26460 |
| 180 | 27 | 27977 | 27474 |
| 181 | 1 | 381 | 82 |
| 183 | 1 | 190 | 2 |
| 183 | 4 | 1849 | 2211 |
| 183 | 5 | 2350 | 2568 |
| 183 | 7 | 3592 | 2978 |
| 183 | 8 | 4176 | 3571 |
| 185 | 2 | 1260 | 1424 |
| 185 | 3 | 2722 | 1301 |
| 185 | 4 | 3612 | 2671 |
| 187 | 2 | 727 | 1302 |
| 187 | 3 | 1293 | 1745 |
| 187 | 5 | 2592 | 2173 |
| 189 | 1 | 18 | 2180 |
| 190 | 1 | 466 | 68 |
| 190 | 2 | 896 | 411 |
| 190 | 4 | 1878 | 2165 |
| 190 | 5 | 2740 | 2384 |
| 190 | 10 | 10281 | 8875 |
| 191 | 2 | 861 | 658 |
| 191 | 3 | 1096 | 827 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 192 | 2 | 1881 | 1564 |
| 193 | 1 | 316 | 2 |
| 193 | 7 | 4667 | 3813 |
| 194 | 1 | 30 | 641 |
| 194 | 2 | 608 | 1582 |
| 195 | 1 | 2 | 433 |
| 195 | 2 | 431 | 943 |
| 195 | 3 | 1055 | 465 |
| 195 | 4 | 972 | 1487 |
| 195 | 5 | 1507 | 1995 |
| 195 | 6 | 3314 | 1851 |
| 195 | 9 | 3089 | 3529 |
| 195 | 10 | 3521 | 3312 |
| 195 | 12 | 6604 | 6837 |
| 195 | 13 | 7049 | 6786 |
| 195 | 14 | 6825 | 7700 |
| 195 | 15 | 7682 | 7047 |
| 195 | 16 | 7202 | 7417 |
| 195 | 18 | 8278 | 9036 |
| 195 | 20 | 8583 | 8837 |
| 195 | 21 | 8871 | 9602 |
| 195 | 22 | 9251 | 9403 |
| 195 | 23 | 9600 | 10022 |
| 195 | 25 | 10020 | 10226 |
| 195 | 26 | 11229 | 10024 |
| 195 | 27 | 10659 | 10946 |
| 195 | 28 | 10944 | 11318 |
| 195 | 30 | 12449 | 12246 |
| 195 | 32 | 13212 | 12505 |
| 195 | 33 | 12558 | 12773 |
| 195 | 35 | 13673 | 14011 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 195 | 36 | 14811 | 14143 |
| 195 | 38 | 16061 | 16363 |
| 195 | 39 | 16320 | 16799 |
| 195 | 40 | 16515 | 16333 |
| 196 | 1 | 608 | 1411 |
| 197 | 9 | 9269 | 9553 |
| 200 | 2 | 1103 | 249 |
| 200 | 3 | 1335 | 1033 |
| 200 | 4 | 1769 | 1284 |
| 200 | 5 | 2124 | 1747 |
| 200 | 6 | 2792 | 2106 |
| 200 | 7 | 3073 | 2708 |
| 200 | 8 | 3510 | 3061 |
| 200 | 9 | 4126 | 3467 |
| 200 | 10 | 4350 | 4042 |
| 200 | 11 | 4847 | 4368 |
| 200 | 14 | 6487 | 6182 |
| 200 | 15 | 6681 | 6499 |
| 200 | 18 | 10749 | 9307 |
| 200 | 20 | 11787 | 11464 |
| 200 | 22 | 12859 | 12410 |
| 201 | 1 | 509 | 105 |
| 201 | 3 | 3704 | 3237 |
| 202 | 7 | 5296 | 4817 |
| 205 | 2 | 117 | 323 |
| 205 | 5 | 1669 | 2148 |
| 206 | 2 | 546 | 196 |
| 206 | 3 | 841 | 632 |
| 206 | 4 | 1622 | 777 |
| 206 | 9 | 5466 | 5035 |
| 209 | 1 | 472 | 86 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 209 | 3 | 1510 | 1280 |
| 210 | 3 | 3175 | 2363 |
| 210 | 6 | 5281 | 4868 |
| 210 | 8 | 5619 | 6002 |
| 211 | 4 | 1708 | 3756 |
| 212 | 1 | 919 | 2 |
| 213 | 2 | 1107 | 1826 |
| 214 | 2 | 2106 | 1237 |
| 214 | 4 | 3677 | 3132 |
| 217 | 6 | 3548 | 3162 |
| 218 | 1 | 1 | 1218 |
| 218 | 3 | 2731 | 3378 |
| 218 | 5 | 4188 | 4667 |
| 219 | 3 | 1386 | 910 |
| 219 | 4 | 1595 | 1344 |
| 220 | 2 | 794 | 1144 |
| 221 | 1 | 110 | 295 |
| 221 | 2 | 326 | 880 |
| 221 | 4 | 1496 | 1825 |
| 221 | 5 | 1907 | 2200 |
| 221 | 6 | 2169 | 2555 |
| 221 | 8 | 3425 | 4246 |
| 221 | 9 | 4233 | 5111 |
| 221 | 12 | 6419 | 6757 |
| 221 | 13 | 6751 | 6987 |
| 221 | 14 | 6911 | 7120 |
| 221 | 16 | 7400 | 7909 |
| 221 | 17 | 7963 | 8199 |
| 221 | 19 | 8597 | 9079 |
| 222 | 17 | 11376 | 11597 |
| 223 | 6 | 5328 | 5008 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 223 | 12 | 12189 | 13307 |
| 223 | 13 | 13291 | 13716 |
| 223 | 14 | 13601 | 13434 |
| 223 | 17 | 15331 | 15068 |
| 223 | 19 | 15940 | 17160 |
| 223 | 21 | 17710 | 19089 |
| 223 | 23 | 19800 | 20708 |
| 223 | 25 | 22857 | 22027 |
| 223 | 26 | 22757 | 23365 |
| 225 | 1 | 756 | 394 |
| 225 | 5 | 3793 | 2945 |
| 226 | 1 | 141 | 536 |
| 226 | 2 | 521 | 871 |
| 228 | 8 | 5473 | 4835 |
| 229 | 7 | 6749 | 6057 |
| 232 | 2 | 1461 | 910 |
| 233 | 5 | 3359 | 3063 |
| 233 | 11 | 7226 | 7456 |
| 236 | 1 | 3 | 482 |
| 237 | 1 | 1 | 219 |
| 237 | 3 | 1197 | 991 |
| 237 | 5 | 2009 | 2329 |
| 237 | 6 | 2319 | 3056 |
| 237 | 8 | 3261 | 3701 |
| 237 | 10 | 3900 | 4763 |
| 237 | 11 | 4730 | 4963 |
| 238 | 11 | 9966 | 9238 |
| 238 | 19 | 16613 | 17728 |
| 238 | 29 | 26812 | 27663 |
| 239 | 2 | 1576 | 4245 |
| 239 | 5 | 6393 | 6956 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 239 | 6 | 6902 | 7237 |
| 240 | 5 | 1537 | 1809 |
| 241 | 1 | 228 | 1040 |
| 242 | 9 | 6581 | 7015 |
| 242 | 10 | 6988 | 7368 |
| 242 | 12 | 7488 | 7928 |
| 245 | 2 | 1670 | 1251 |
| 247 | 2 | 1558 | 1812 |
| 250 | 4 | 3210 | 2998 |
| 251 | 1 | 622 | 2 |
| 252 | 3 | 2598 | 2383 |
| 252 | 4 | 2911 | 2564 |
| 253 | 1 | 1 | 345 |
| 253 | 2 | 359 | 898 |
| 254 | 1 | 2 | 307 |
| 254 | 3 | 318 | 4 |
| 256 | 5 | 3768 | 4040 |
| 256 | 7 | 7292 | 6639 |
| 256 | 9 | 9589 | 8465 |
| 257 | 2 | 992 | 294 |
| 257 | 4 | 4528 | 3596 |
| 257 | 7 | 6894 | 6718 |
| 257 | 8 | 7252 | 6884 |
| 257 | 9 | 7986 | 7231 |
| 258 | 2 | 544 | 804 |
| 258 | 3 | 1224 | 2921 |
| 258 | 4 | 2964 | 2728 |
| 258 | 5 | 2919 | 3752 |
| 258 | 6 | 4120 | 5298 |
| 261 | 1 | 3 | 362 |
| 264 | 1 | 582 | 361 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 264 | 2 | 881 | 561 |
| 264 | 3 | 1367 | 879 |
| 264 | 4 | 1966 | 1361 |
| 264 | 5 | 2316 | 1945 |
| 264 | 6 | 2636 | 2295 |
| 264 | 7 | 3194 | 2634 |
| 264 | 8 | 3531 | 3055 |
| 265 | 2 | 398 | 817 |
| 265 | 4 | 1583 | 1071 |
| 265 | 6 | 3293 | 3009 |
| 265 | 7 | 3186 | 3046 |
| 266 | 1 | 451 | 2 |
| 266 | 4 | 1983 | 2225 |
| 266 | 7 | 2540 | 2325 |
| 268 | 1 | 798 | 1223 |
| 268 | 2 | 1912 | 1265 |
| 270 | 4 | 3977 | 4186 |
| 270 | 6 | 4397 | 4573 |
| 271 | 5 | 2719 | 3066 |
| 271 | 6 | 3041 | 3352 |
| 271 | 9 | 6278 | 5862 |
| 271 | 10 | 6550 | 5993 |
| 271 | 14 | 10291 | 10004 |
| 272 | 3 | 1870 | 1199 |
| 272 | 4 | 3378 | 1831 |
| 276 | 5 | 2350 | 1994 |
| 276 | 8 | 3702 | 3103 |
| 276 | 9 | 4441 | 3692 |
| 276 | 10 | 4595 | 4416 |
| 276 | 12 | 8173 | 7382 |
| 276 | 14 | 10001 | 9762 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 276 | 15 | 11065 | 9890 |
| 276 | 17 | 11642 | 11250 |
| 276 | 19 | 12892 | 12503 |
| 276 | 21 | 13302 | 13099 |
| 276 | 22 | 13663 | 13271 |
| 276 | 23 | 13995 | 13642 |
| 276 | 25 | 15065 | 14211 |
| 276 | 27 | 16293 | 15955 |
| 276 | 29 | 18482 | 16563 |
| 276 | 31 | 19951 | 19016 |
| 279 | 3 | 1469 | 1675 |
| 279 | 4 | 1600 | 1923 |
| 279 | 5 | 2269 | 2105 |
| 279 | 10 | 7698 | 7279 |
| 280 | 3 | 3138 | 2968 |
| 281 | 4 | 2055 | 2552 |
| 282 | 1 | 316 | 2 |
| 282 | 2 | 456 | 1232 |
| 282 | 3 | 1957 | 1346 |
| 283 | 1 | 1 | 450 |
| 283 | 3 | 1098 | 1556 |
| 283 | 5 | 2062 | 2238 |
| 283 | 7 | 3127 | 3312 |
| 286 | 3 | 2883 | 2698 |
| 287 | 4 | 2359 | 2180 |
| 290 | 10 | 8820 | 9074 |
| 290 | 11 | 9008 | 9172 |
| 291 | 2 | 1103 | 855 |
| 291 | 3 | 2622 | 1123 |
| 292 | 1 | 2 | 283 |
| 292 | 2 | 701 | 330 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 292 | 5 | 2459 | 2866 |
| 292 | 7 | 4252 | 4995 |
| 292 | 9 | 6704 | 7096 |
| 292 | 10 | 7066 | 7827 |
| 292 | 12 | 8377 | 8622 |
| 292 | 15 | 11502 | 12674 |
| 292 | 17 | 13326 | 13727 |
| 292 | 18 | 13738 | 14778 |
| 294 | 1 | 117 | 623 |
| 294 | 2 | 905 | 723 |
| 294 | 6 | 2496 | 2272 |
| 295 | 7 | 4274 | 4510 |
| 300 | 4 | 3525 | 3337 |
| 301 | 6 | 6714 | 4852 |
| 301 | 13 | 10150 | 9914 |
| 301 | 16 | 11316 | 11657 |
| 301 | 18 | 13199 | 14398 |
| 301 | 19 | 15724 | 14657 |
| 306 | 3 | 1135 | 2727 |
| 306 | 4 | 2742 | 4025 |
| 306 | 5 | 4004 | 4552 |
| 306 | 6 | 4527 | 5117 |
| 306 | 7 | 5131 | 5466 |
| 306 | 9 | 5642 | 5968 |
| 306 | 11 | 7000 | 8013 |
| 306 | 12 | 7926 | 8138 |
| 306 | 13 | 8180 | 8908 |
| 306 | 14 | 8899 | 9120 |
| 306 | 15 | 9118 | 9510 |
| 306 | 16 | 9508 | 9963 |
| 306 | 17 | 9964 | 11313 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 306 | 18 | 11319 | 11570 |
| 306 | 19 | 11540 | 11707 |
| 306 | 20 | 11626 | 11856 |
| 310 | 2 | 1126 | 176 |
| 310 | 5 | 4215 | 3556 |
| 311 | 4 | 5671 | 6006 |
| 311 | 5 | 6173 | 6778 |
| 311 | 6 | 6833 | 7225 |
| 311 | 7 | 7236 | 7520 |
| 311 | 8 | 7492 | 7926 |
| 312 | 2 | 859 | 1506 |
| 312 | 3 | 1449 | 1808 |
| 312 | 4 | 2043 | 2306 |
| 313 | 4 | 3568 | 3122 |
| 319 | 1 | 3 | 881 |
| 319 | 2 | 832 | 1185 |
| 321 | 1 | 638 | 898 |
| 321 | 4 | 1862 | 2131 |
| 321 | 5 | 2168 | 2548 |
| 321 | 6 | 2470 | 3159 |
| 321 | 7 | 3069 | 3395 |
| 321 | 8 | 3461 | 3733 |
| 324 | 1 | 3 | 692 |
| 324 | 2 | 867 | 1592 |
| 324 | 4 | 2392 | 3021 |
| 327 | 6 | 5052 | 5213 |
| 330 | 5 | 3745 | 3464 |
| 333 | 2 | 998 | 717 |
| 333 | 3 | 947 | 1534 |
| 335 | 2 | 1024 | 521 |
| 338 | 11 | 8869 | 8591 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 340 | 5 | 3931 | 3608 |
| 341 | 6 | 3484 | 3155 |
| 341 | 7 | 4348 | 3482 |
| 341 | 8 | 6419 | 4332 |
| 341 | 10 | 9264 | 7672 |
| 341 | 11 | 10777 | 9245 |
| 341 | 12 | 12026 | 10779 |
| 343 | 1 | 459 | 262 |
| 343 | 4 | 3905 | 2661 |
| 345 | 4 | 3467 | 3201 |
| 345 | 14 | 15320 | 16447 |
| 345 | 16 | 18409 | 18927 |
| 345 | 18 | 19974 | 20465 |
| 347 | 1 | 763 | 1155 |
| 350 | 5 | 3273 | 2980 |
| 351 | 1 | 693 | 280 |
| 351 | 2 | 1268 | 654 |
| 351 | 3 | 1716 | 1222 |
| 353 | 4 | 2749 | 2546 |
| 354 | 1 | 2 | 298 |
| 355 | 16 | 8911 | 9399 |
| 355 | 19 | 12476 | 12904 |
| 355 | 22 | 15766 | 15608 |
| 355 | 23 | 17165 | 17461 |
| 355 | 25 | 18313 | 19104 |
| 355 | 26 | 19092 | 19598 |
| 355 | 27 | 19692 | 19495 |
| 355 | 28 | 19734 | 20198 |
| 355 | 29 | 20196 | 20471 |
| 356 | 2 | 2204 | 1536 |
| 356 | 4 | 2887 | 2537 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 356 | 5 | 3167 | 2859 |
| 357 | 1 | 381 | 4 |
| 360 | 3 | 3167 | 2877 |
| 361 | 1 | 7 | 909 |
| 363 | 1 | 1405 | 167 |
| 363 | 6 | 7178 | 8404 |
| 364 | 1 | 41 | 331 |
| 366 | 2 | 1386 | 1598 |
| 367 | 19 | 8690 | 8941 |
| 368 | 4 | 1786 | 1947 |
| 369 | 4 | 1652 | 1428 |
| 372 | 6 | 5262 | 4534 |
| 376 | 2 | 625 | 293 |
| 377 | 1 | 331 | 2 |
| 379 | 4 | 2975 | 3142 |
| 382 | 3 | 2951 | 3277 |
| 382 | 4 | 4183 | 3320 |
| 383 | 6 | 6158 | 5637 |
| 386 | 9 | 5725 | 6027 |
| 387 | 2 | 486 | 980 |
| 390 | 2 | 1668 | 2057 |
| 390 | 3 | 3499 | 2867 |
| 391 | 1 | 2 | 154 |
| 392 | 5 | 5163 | 5387 |
| 394 | 1 | 1 | 375 |
| 394 | 8 | 6437 | 7585 |
| 394 | 9 | 7542 | 7967 |
| 394 | 11 | 10354 | 10713 |
| 395 | 5 | 1957 | 2229 |
| 395 | 9 | 3869 | 4216 |
| 395 | 11 | 4571 | 4960 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 398 | 1 | 395 | 1180 |
| 399 | 7 | 5691 | 6134 |
| 399 | 10 | 7662 | 7820 |
| 399 | 14 | 10111 | 9845 |
| 399 | 22 | 16699 | 16481 |
| 399 | 29 | 28519 | 28244 |
| 401 | 1 | 189 | 4 |
| 401 | 2 | 178 | 1044 |
| 401 | 3 | 1038 | 2141 |
| 401 | 5 | 3517 | 3939 |
| 402 | 3 | 919 | 1269 |
| 404 | 1 | 578 | 12 |
| 405 | 1 | 293 | 643 |
| 405 | 3 | 1926 | 1501 |
| 407 | 1 | 80 | 406 |
| 407 | 4 | 3188 | 3670 |
| 408 | 5 | 3037 | 2681 |
| 408 | 6 | 3786 | 3475 |
| 410 | 2 | 811 | 1092 |
| 413 | 2 | 742 | 1314 |
| 413 | 3 | 1275 | 1532 |
| 414 | 2 | 908 | 678 |
| 414 | 3 | 1137 | 1889 |
| 414 | 4 | 2738 | 1959 |
| 416 | 3 | 1945 | 1709 |
| 418 | 1 | 3 | 350 |
| 418 | 2 | 331 | 930 |
| 419 | 2 | 619 | 296 |
| 419 | 4 | 937 | 773 |
| 419 | 5 | 1305 | 910 |
| 419 | 6 | 1183 | 1521 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 419 | 7 | 1859 | 1299 |
| 419 | 8 | 2170 | 1850 |
| 419 | 9 | 2483 | 2160 |
| 419 | 10 | 3399 | 2470 |
| 419 | 11 | 3708 | 3397 |
| 420 | 3 | 1649 | 1452 |
| 421 | 6 | 3983 | 3510 |
| 424 | 1 | 797 | 3 |
| 424 | 2 | 513 | 851 |
| 424 | 3 | 1029 | 733 |
| 424 | 6 | 1859 | 1551 |
| 424 | 7 | 3076 | 2780 |
| 425 | 1 | 52 | 384 |
| 425 | 2 | 1031 | 777 |
| 425 | 3 | 1127 | 1936 |
| 427 | 2 | 1488 | 1114 |
| 427 | 3 | 2114 | 1464 |
| 430 | 2 | 1334 | 1489 |
| 431 | 1 | 420 | 196 |
| 431 | 2 | 634 | 269 |
| 432 | 2 | 1133 | 1372 |
| 432 | 3 | 2014 | 1439 |
| 432 | 6 | 3869 | 3378 |
| 433 | 1 | 292 | 2007 |
| 435 | 1 | 706 | 131 |
| 435 | 2 | 1730 | 1047 |
| 439 | 1 | 1 | 627 |
| 441 | 1 | 1 | 513 |
| 441 | 7 | 10592 | 7974 |
| 443 | 1 | 31 | 744 |
| 447 | 2 | 744 | 322 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 449 | 1 | 3 | 212 |
| 449 | 2 | 471 | 286 |
| 449 | 3 | 551 | 393 |
| 451 | 1 | 823 | 314 |
| 452 | 2 | 322 | 714 |
| 452 | 6 | 2806 | 3342 |
| 452 | 7 | 3358 | 3792 |
| 454 | 1 | 1033 | 2 |
| 455 | 3 | 3214 | 3837 |
| 455 | 5 | 4078 | 4488 |
| 455 | 6 | 4965 | 4117 |
| 455 | 8 | 5123 | 5473 |
| 457 | 1 | 940 | 35 |
| 461 | 2 | 476 | 691 |
| 461 | 4 | 1548 | 1991 |
| 461 | 5 | 2322 | 1948 |
| 461 | 6 | 2664 | 2449 |
| 462 | 5 | 2810 | 2064 |
| 464 | 2 | 2162 | 1530 |
| 465 | 1 | 1762 | 38 |
| 465 | 3 | 2373 | 2050 |
| 467 | 2 | 652 | 1260 |
| 467 | 3 | 1149 | 1442 |
| 469 | 2 | 922 | 1101 |
| 470 | 2 | 971 | 1768 |
| 473 | 2 | 450 | 220 |
| 475 | 1 | 1 | 969 |
| 477 | 2 | 1064 | 843 |
| 482 | 1 | 1 | 534 |
| 484 | 1 | 130 | 543 |
| 484 | 2 | 1320 | 1159 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 487 | 2 | 1258 | 1929 |
| 488 | 2 | 509 | 162 |
| 488 | 4 | 2247 | 1945 |
| 489 | 1 | 1 | 396 |
| 489 | 2 | 560 | 255 |
| 490 | 2 | 1096 | 458 |
| 491 | 5 | 5167 | 4433 |
| 491 | 6 | 5975 | 5247 |
| 491 | 7 | 6811 | 6041 |
| 494 | 1 | 650 | 3 |
| 497 | 5 | 3351 | 3536 |
| 497 | 8 | 4757 | 4308 |
| 497 | 10 | 5229 | 5086 |
| 497 | 11 | 5967 | 5671 |
| 499 | 1 | 663 | 247 |
| 502 | 2 | 1324 | 851 |
| 504 | 1 | 3 | 650 |
| 507 | 2 | 727 | 906 |
| 507 | 3 | 840 | 1010 |
| 510 | 3 | 2056 | 2574 |
| 512 | 2 | 854 | 300 |
| 514 | 2 | 1067 | 669 |
| 518 | 5 | 3119 | 2970 |
| 520 | 1 | 3 | 467 |
| 520 | 2 | 452 | 231 |
| 520 | 4 | 2218 | 1859 |
| 521 | 2 | 988 | 821 |
| 522 | 1 | 409 | 885 |
| 524 | 1 | 579 | 4 |
| 525 | 1 | 1 | 144 |
| 525 | 2 | 86 | 352 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 529 | 2 | 5731 | 6147 |
| 533 | 1 | 1044 | 157 |
| 536 | 3 | 587 | 1462 |
| 539 | 7 | 6180 | 6662 |
| 540 | 1 | 198 | 476 |
| 543 | 3 | 2179 | 1835 |
| 543 | 4 | 2404 | 2177 |
| 543 | 7 | 3924 | 3700 |
| 544 | 2 | 1004 | 870 |
| 546 | 2 | 497 | 324 |
| 547 | 3 | 717 | 965 |
| 549 | 2 | 371 | 135 |
| 550 | 1 | 527 | 3 |
| 550 | 2 | 864 | 709 |
| 550 | 3 | 1540 | 1277 |
| 550 | 4 | 2039 | 1509 |
| 552 | 5 | 4681 | 5073 |
| 552 | 8 | 8390 | 8223 |
| 555 | 1 | 470 | 267 |
| 560 | 1 | 635 | 210 |
| 560 | 2 | 834 | 514 |
| 563 | 2 | 1215 | 1469 |
| 564 | 1 | 8 | 511 |
| 564 | 2 | 1019 | 555 |
| 564 | 3 | 577 | 744 |
| 565 | 1 | 321 | 4 |
| 565 | 5 | 1266 | 1619 |
| 567 | 2 | 1055 | 531 |
| 571 | 3 | 1149 | 886 |
| 573 | 1 | 208 | 666 |
| 573 | 2 | 651 | 1148 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 573 | 5 | 2558 | 2809 |
| 575 | 1 | 262 | 2 |
| 584 | 1 | 268 | 110 |
| 584 | 4 | 1310 | 795 |
| 584 | 5 | 1329 | 1574 |
| 586 | 1 | 771 | 4 |
| 588 | 1 | 346 | 56 |
| 588 | 2 | 1078 | 434 |
| 589 | 1 | 1 | 555 |
| 591 | 1 | 217 | 2 |
| 592 | 2 | 674 | 868 |
| 593 | 1 | 190 | 2 |
| 593 | 3 | 1035 | 1268 |
| 601 | 1 | 77 | 274 |
| 601 | 2 | 172 | 576 |
| 602 | 2 | 759 | 415 |
| 604 | 6 | 2868 | 2416 |
| 606 | 1 | 271 | 798 |
| 607 | 2 | 633 | 797 |
| 613 | 1 | 420 | 82 |
| 616 | 2 | 593 | 435 |
| 616 | 4 | 975 | 730 |
| 619 | 3 | 641 | 817 |
| 620 | 1 | 863 | 3 |
| 621 | 2 | 1493 | 2014 |
| 627 | 1 | 113 | 763 |
| 628 | 1 | 2 | 163 |
| 631 | 1 | 1 | 516 |
| 631 | 3 | 1715 | 1521 |
| 633 | 1 | 280 | 2 |
| 634 | 3 | 1139 | 1387 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 637 | 2 | 1613 | 738 |
| 637 | 3 | 1597 | 2208 |
| 637 | 4 | 2242 | 2694 |
| 637 | 7 | 3550 | 4545 |
| 637 | 9 | 4767 | 5171 |
| 639 | 1 | 175 | 2 |
| 640 | 2 | 468 | 689 |
| 643 | 1 | 496 | 320 |
| 645 | 1 | 1 | 537 |
| 645 | 2 | 539 | 1024 |
| 647 | 1 | 64 | 855 |
| 647 | 2 | 1419 | 895 |
| 649 | 1 | 2 | 364 |
| 651 | 1 | 539 | 3 |
| 653 | 2 | 738 | 550 |
| 656 | 8 | 7784 | 8587 |
| 657 | 2 | 1356 | 967 |
| 657 | 3 | 1708 | 1376 |
| 661 | 1 | 2 | 244 |
| 664 | 3 | 1149 | 820 |
| 672 | 1 | 546 | 10 |
| 673 | 2 | 1207 | 1827 |
| 676 | 1 | 443 | 790 |
| 679 | 1 | 998 | 219 |
| 682 | 3 | 749 | 1171 |
| 685 | 1 | 176 | 511 |
| 685 | 2 | 498 | 199 |
| 685 | 3 | 480 | 947 |
| 685 | 4 | 1000 | 1443 |
| 686 | 4 | 1567 | 2001 |
| 686 | 5 | 3238 | 1712 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 686 | 7 | 2965 | 3435 |
| 686 | 8 | 3441 | 3067 |
| 686 | 9 | 3752 | 3339 |
| 686 | 10 | 3530 | 3826 |
| 688 | 2 | 628 | 894 |
| 689 | 2 | 582 | 331 |
| 690 | 1 | 275 | 90 |
| 690 | 2 | 487 | 248 |
| 696 | 1 | 239 | 9 |
| 696 | 2 | 1237 | 233 |
| 696 | 3 | 1424 | 1200 |
| 697 | 1 | 20 | 520 |
| 698 | 1 | 29 | 313 |
| 698 | 2 | 217 | 483 |
| 701 | 5 | 1061 | 1534 |
| 707 | 2 | 855 | 538 |
| 709 | 1 | 1 | 675 |
| 710 | 1 | 3 | 416 |
| 712 | 1 | 674 | 96 |
| 713 | 1 | 933 | 139 |
| 713 | 2 | 1125 | 1436 |
| 716 | 2 | 1226 | 765 |
| 721 | 1 | 3 | 371 |
| 726 | 1 | 543 | 94 |
| 729 | 1 | 19 | 210 |
| 731 | 1 | 532 | 2 |
| 736 | 2 | 309 | 644 |
| 738 | 1 | 561 | 4 |
| 740 | 1 | 488 | 3 |
| 749 | 2 | 20 | 475 |
| 751 | 1 | 1 | 456 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 751 | 2 | 454 | 774 |
| 753 | 1 | 76 | 729 |
| 754 | 1 | 761 | 21 |
| 755 | 2 | 345 | 539 |
| 756 | 1 | 1 | 375 |
| 764 | 2 | 528 | 1088 |
| 772 | 1 | 1 | 558 |
| 772 | 2 | 432 | 866 |
| 775 | 1 | 706 | 2 |
| 778 | 2 | 992 | 834 |
| 780 | 1 | 52 | 351 |
| 782 | 1 | 3 | 557 |
| 783 | 1 | 28 | 609 |
| 791 | 1 | 1 | 582 |
| 791 | 2 | 859 | 641 |
| 791 | 3 | 1235 | 711 |
| 797 | 1 | 2 | 289 |
| 797 | 2 | 287 | 3 |
| 801 | 2 | 598 | 191 |
| 805 | 1 | 1 | 414 |
| 806 | 1 | 392 | 3 |
| 810 | 1 | 3 | 317 |
| 810 | 2 | 407 | 3 |
| 815 | 2 | 443 | 282 |
| 819 | 1 | 39 | 668 |
| 830 | 1 | 291 | 4 |
| 830 | 2 | 476 | 162 |
| 834 | 1 | 561 | 46 |
| 834 | 2 | 953 | 453 |
| 837 | 1 | 3 | 317 |
| 837 | 2 | 320 | 589 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 839 | 1 | 1 | 753 |
| 841 | 1 | 1 | 489 |
| 855 | 1 | 308 | 3 |
| 861 | 1 | 1 | 330 |
| 863 | 1 | 451 | 221 |
| 870 | 1 | 21 | 503 |
| 890 | 2 | 1548 | 1255 |
| 895 | 1 | 3 | 140 |
| 896 | 1 | 2 | 400 |
| 897 | 2 | 244 | 498 |
| 902 | 1 | 1 | 300 |
| 904 | 1 | 294 | 4 |
| 910 | 1 | 143 | 3 |
| 917 | 1 | 36 | 518 |
| 918 | 1 | 3 | 167 |
| 918 | 2 | 116 | 373 |
| 920 | 2 | 243 | 515 |
| 922 | 1 | 669 | 259 |
| 926 | 1 | 2 | 394 |
| 927 | 1 | 119 | 556 |
| 928 | 1 | 493 | 179 |
| 930 | 1 | 526 | 344 |
| 933 | 2 | 257 | 418 |
| 936 | 2 | 243 | 683 |
| 937 | 1 | 341 | 3 |
| 942 | 1 | 58 | 228 |
| 945 | 1 | 318 | 4 |
| 953 | 1 | 254 | 48 |
| 959 | 1 | 1198 | 164 |
| 959 | 2 | 1740 | 1123 |
| 963 | 2 | 462 | 232 |

Table 3: *E. faecalis* - Putative coding regions of novel proteins not similar to known proteins

| Contig ID | ORF ID | Start (nt) | Stop (nt) |
|---|---|---|---|
| 965 | 1 | 403 | 2 |
| 969 | 1 | 360 | 4 |
| 970 | 3 | 673 | 314 |
| 972 | 1 | 3 | 470 |
| 973 | 1 | 2 | 700 |
| 974 | 1 | 2 | 235 |
| 974 | 3 | 270 | 467 |
| 981 | 2 | 154 | 405 |
| 984 | 3 | 164 | 337 |

# SEQUENCE LISTING PLACE INDICATOR

PAGES 280 TO 2076, WHICH ARE THE COMPLETE SEQUENCE LISTINGS FOR THIS APPLICATION ARE LOCATED AFTER THE DESCRIPTION, CLAIMS, ABSTRACT & DRAWINGS.

(1) GENERAL INFORMATION:

(i) APPLICANT: Charles Kunsch
Patrick J. Dillon
Steven C. Barash

(ii) TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

(iii) NUMBER OF SEQUENCES: 982

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

(B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

(D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: A. Anders Brookes

(B) REGISTRATION NUMBER: 36,373

(C) REFERENCE/DOCKET NUMBER: PB369PCT

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAGTCAATCA CTTGCAAGTC GTTTTCTGTC ATATGGCCGA CTAGCTCAGT GACACCAGGA 60

ATATAGCCAC CAGGGAAAAT ATAACGATTA ATCCAAGCAT TTTTAGCCCC ACCTTGTTGG 120

CGACTGATCC CATGAATCAA CGCCGTACCT TTAGGCGCTA AATTCCGCTG AACGACATCA 180

AAATATTCAT GTAGATTTTC CGCACCGACA TGTTCAAACA TCCCAACACT CGTAATATGG 240

TCAAAAGACT CTCCTTTTAA ATCACGATAA TCCATCAATT TGACAGTCAT TCGATCTTGT 300

AGATCTTCTT TTTCTATAAT ATGGCGAATA TGATGAAATT GCTCTTCACT TAATGTAATC 360

CCAGTTGCTT TGGCTCCATA TTCTTTCACC GCAGTTAAAA TTAACGTGCC CCAGCCGCAG 420

CCAATATCCA GTAAAGTGTC GCCCTCTTTG ATAAACAATT TATCTAAAAT ATGATGAACT 480

TTATTCACTT GCGCTTGTTC TAATGTATCT TCAGGCGTTT TAAAATAAGC ACATGAATAC 540

GTCATTGTTT GGTCAAGCCA TTTTTTGTAA AAATCATTTC CTAGATCGTA ATGGCTGTGA 600

ATATCCTCTT GCGAACGTTT TTTTGAATGA CTTTCTTTAG GAAGCCATTT AATAAATTTA 660

GCATTGTGTA AAAAGCTATC CTTTTGGTTA TACACATCAT AAATCAGsGC TTGGATATCG 720

CCTTCGATTT CAATTTTGCG ATCCATGTAG GCTTCCCCTA AAGTTAACGA AGCGTTATTC 780

AGTAAATCCT TCACAGGAAT TTTTTCATTG AATACAATTT TAAAAACCGG ATCCCCCGAC 840

CCTTGCCCAT ACTCTTTGAC GGTACCATCC CAGTATGTGA CTTGTGTCTT TTTTGAAAAA 900

GACCATTTAA ACAGTTGACT GTACGTTTCT TTTTCTAACA TTGCATTCCC TCCATTAAAT 960

ACCATTTGAA GCCAAAACAA AAAGAAGTCG CTTTCCGGTA GTTCGTCAAA ACAAACACCA 1020

CAGTCCGTTC TAAACTGAAG CACAGAAAAG TTATCACCCC TTCTATGTTC CGCTTCTTTT 1080

TTTGCAATTA CAGTTCTATT CTACTCCTCT TTTAAAAATT TGAACATTCT TTTAACGTAA 1140

TACCTACTAT TGTTATTCTT TATCACAAAA AAACTAGAGC CAGTCCTTGA CAGACTCCTC 1200

TAGTTCTAAA TATTATGCTT TCTTACGCAT CCGTTGTTCC GCATGAGTGT AAGCGCCATG 1260

```
CCATACGTGC CCCACATAAG GATTAACTTG AATACCGTGT TTAATCGCCG CTGCTACAAA    1320
TTTTTTTGCT AAAGTTACTG CTTCTAACAC CGAATAACCT TTCGCCAAGC CAGCTGTGAT    1380
TGCCGCTGAA AAAGTACAAC CTGCACCATG ATTATAATCA GTAGGATATA ATTCATTTTC    1440
CAAAAGATGC GCGGTGTGAC CATCGTAAAA CAAGTCCAGT GCTTTTTCAC CAGCTAAGCG    1500
ATGTCCCCCT TTAACCACGA CATGCTTGGC TCCCATTTGT ACAATTCGTT TTGCCGCTTC    1560
TTCCATCTCC GCCACGGAAG AAATTTCGCC TAAACCAGAT AAGATGCCCG CTTCAATTAA    1620
ATTAGGCGTG GCCACTAATG CTAATGGCAG TAAATCGTTT TTTAGGCCTT CCACACTTTT    1680
GGGTTGCAGA ATTTGTGCCG TTCCCTTACA AGCAATGACT GGGTCAATCA CGACTTTTTG    1740
AATTTTCTCT TGTTTAATGT ACTTACTAGC CATTTTAATA TTTTGTTCAT TACCCATCAT    1800
CCCTGTTTTC AAAGCCGCTA CTGGACCGCC TGCAAAAACC GAAATCAATT GTTTTTCTAA    1860
GAGCGTTTCT GGCAATTCAG TTACTTCATG TGACCAACCT GTCGTAGGAT CCATCGTCAC    1920
AATCGAGGTT AAACTTGAAA ATCCAAAAAC TCCATACTCT TCAAATGTTT TTAAATCTGC    1980
TTGAATCCCT GCCCCTCCAG TTGAATCGGA GCCTGCAATC GTCAATACTT TTTCCATTAA    2040
ATCACCTAAC CTTTTTCTCC AAGTATACTG AAGAAACAAG TCTGCTAAAA CAGCCAATTG    2100
GCTTATTTTT TAGCCAGCCA ATTTCTAAAC AAAAAAAAGA CCAGAGAATA AATTCTCTGG    2160
TCTTACGTCC GAATACCCCA GTTTTTTACG CTGGTTAAAA CTATAGTTAA AAAGTTAATT    2220
ATTTAACGAT TTCAGTAACA ACGCCTGAAC CTACAGTACG TCCGCCTTCA CGAATAGAGA    2280
AACGAGTTCC GTCTTCGATA GCGATTGGGT GAATTAATTC AACGTCCATA GCAACGTTAT    2340
CACCAGGCAT TACCATTTCA GTACCTTCTG GCAATTCTAC AACACCAGTA ACGTCTGTTG    2400
TACGGAAGTA GAATTGAGGA CGGTAGTTAG TGAAGAATGG AGTGTGACGT CCGCCTTCTT    2460
CTTTTGATAA TACGTATACT TCAGCTTkGA ATTTgGTGTG TGGAGTGATT GTAGCTGGTT    2520
TAGCTAATAC TyGyCCACGT TCGATATCTT CACGTGCTAC ACCACGTAtA AAGCACCGAT    2580
GTTGTCGCCT GCTTCAGCGT AGTCTAATAA TTTACGGAAC ATTTCAACAC CTGTAACAGT    2640
TGTTTTAGAT GTTTCGTCTT TAATACCAAC GATTTCAACT TCGTCACCAA CGCGAACTTC    2700
ACCACGTTCA ACACGGCCTG TAGCAACAGT ACCACGTCCA GTGATTGAGA ATACgTCTTC    2760
GACTGGCATC ATGAATGGTT TGTCAGTATC ACGTTCTGGA GTTGGGATAT ATTCGTCAAC    2820
TGCAGCCATT AATTCTAAGA TTTTTTCTTC ATAAGACTCG TCGCCTTCTA AAGCTTTCAA    2880
AGCAGAACCT GCGATAACTG GAACATCATC GCCTGGGAAA TCGTATTCTG ATAATAAGTC    2940
ACGAACTTCC ATTTCTACTA ATTCTAATAA TTCTTCGTCA TCAACCATAT CCATTTTGTT    3000
TAAGAATACA ACGATGTATG GTACACCAAC GTTACGTGAT AATAAGATAT GTTCACGTGT    3060
TTGAGGCATA GGACCATCAG CAGCAGAAAC TACTAAGATA GCTCCGTCCA TTTGAGCAGC    3120
ACCAGTGATC ATGTTTTTAA CGTAGTCCGC ATGTCCTGGG CAGTCaACGT GTGCaTAGTG    3180
ACGAGTTwCA GTTTCATATT CGATATGAGA AGTGTTGATT GTGATTCCAC GTTCTTTTTC    3240
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TTCTGGAGCG TTATCGATAG AATCGTAGCT TTGTGCTTCC CCGCCACCGT GTTTTGATAA 3300

TACAGTAGCA ATTGCAGCTG TTAATGTAGT TTTACCATGG TCAACGTGTC CGATAGTACC 3360

AATGTTAACA TGGGATTTAG AACGGTCAAA TTTTTCTTTT GCCATTTTGA ATGTTCCTCC 3420

TAAAAATATA AATTTTATTG TTTGTTTTAT ATGTGATAGA CGTTACTAAA AATCGTCTGA 3480

TCATCATAAG CTATTTTACA CGAAATCTTG AAAAAAGGAT AGTTCTAAAA ACAAACCTTT 3540

TATTCTCAAG GAAAATTATG CGTtGCCGCC GTTTTTCTTG ATGATTTCTT CTTGAACAGA 3600

CTTAGGTACG TCTTCATAGT GGTCAAATAC CATCATAAAT GTACCACGTC CTTGTGTTGC 3660

TGAACGTAAT GTTGTAGCAT AACCAAACAT TTCAGCTAAA GGTACCATCG CATTAACGAT 3720

TTGAGAGTTA CCGTGTGCTT CCATACCTTC AACACGTCCA CGACGACTTG TTACGTGTCC 3780

CATGATATCA CCTAAGTAAT CTTCAGGAAC AGTAATTGTA ACTTTCATCA TTGGTTCTAA 3840

AATAACTGGG TTTGCATTTT TAGCCGCAGC TTTCAATGCC ATAGAAGCAG CTACACGGAA 3900

GGCCGTTTCA TTTGAATCGA CATCGTGGTA TGAACCATCG TAAAGTTTTG CTTTGATATC 3960

AACTAATGGA TAACCAGCAA GAACACCGTT GTTCATAGAG TCTTCTAACC CTTTTTCAAC 4020

TGCTGGGaTG TATTCACGAG GAACCACACC ACCGACAATT GCGTTTTCAA ACTCGAAGCC 4080

TTTACCTTCT TCATTTGGTG TAAATTCAAC CCaTAcGTGA CCGTATTGTC CTTTACCACC 4140

AGACTGACGA ACGAATTTAC CTTCTGCTTT AGTCGCAGCA CGGAATGTTT CGCGGTAAGA 4200

TACTTGAGGA GCACCTACGT TAGCTTCAAC TTTGAATTCA CGTTTCATAC GGTCTACTAA 4260

AACGTCTAAG TGCAATTCAC CCATaCCAGA GATAACTGTT TCACCAGTTT CAACC 4315

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTGTGCCAT AGATTTGACC ATCTGCTGCT GTTGTAGTTT CCCAGTTTGT AATTTGGTAA 60

TGTTGTAAGA nCTTAGTTGG GACATTAATG GCAAAAGTTT TTTGGCGATA GGTATTAAAA 120

TTGGTTTTAC CCACCCAACC TTCATAGGCT TCAAATTCAG CTCCACCTAA CAAAGGGTTG 180

TCGGAAATAA TCCAAGTGTC TTTTTGATGA TTCCGAATAA AACGAACGAT TGTACTGTTA 240

AAGCCTTTCG TTGTTGTACC GCCGTAATCT TTTTCTGCAG ACCAATGGTT CCAAACCGAG 300

TCATACTCTA AAGCATTCGG AAATTCATTG GTTGTAAACC AACCGAGTGA ATTAATTTCT 360

TTACTTAGTT GACGACTTGC CCAACCTGAT TCGCCTTGGT TGCCCCAAAC ATCAACATAA 420

ATATAATCTA GATTCGGTGc TTTTtGTTTT AATcnTTAAA GCGCTCATAG CGACGACCAC 480

TCAATGTAtC GGGtCTTkGT TTAATAAAAT AAGACGGATC TAACCAATCC CAGCCACGCT 540

TCGTTGGATC AACTAATTCC TCATTAAATC CTTTTGCTTC TGGGTAAGAC TCGGTGTCAT 600

TAATATGCAC ACCGAAAACG GCATTTAATT TATGTCCTTC ATCAATTAAT TGATTCAACG 660

CTTGTTCCCC ACCAGGTCGC TGACCAATAG CACCGTAATC TGGATGCGCA GAATCATGTC 720

CTTCATTTTG ATACCCTTTT AGTAAATTCA TTTGTCCTAA TCCATCTGTT AAATTGTAAA 780

TACGTTTTGA TTCGTCTAAC GTCACTAAGA ATGGGTTTGT CGCCTGACTA GCAAAGTTAA 840

AAGGAATCCG TTGGTTGACT AATTCAGGGA CTTTTTCCGC ACCCATTGGG TTATTCATAA 900

TTGAACGGAA CCCAATTGCC GCATCTTGCC AATCCACCCG ATTGTCGTCG TTGCTATCTT 960

TTGAGAATTT AACTTTCACT TCTGGCGTTT CTCCAGTTGT GTAATCTTCC GGTGCATCAA 1020

ATGGTCGATA GGTCCATGCC CCACTTGACA AGGTTGTTAC AAAACCAGTC GCCGCTTCTT 1080

TTGTTTGTTT ATGGATTCGA TTGTTGTCAC TACCATCGAC AGAGCCGTCT CCATAGGCGT 1140

TCGTCCAAAA ACTTGCAGCA TAATTCGCCG TATTTAAGAA ACCATACATA TATTTTTTCG 1200

TTTCTTCTTG GCTTGTTGTA GTTAAATCTT GGATAGTATC ACCATTTTTA TTTCCGTTAT 1260

TTGCATTTGT CCCAGTATTC ATCACAACGC CAGCAAAAGT CGCCCCTTCA TCTGTACTAT 1320

TGACAGAAAT CAAGCCTTGA TTTGGAATTG AAATTGTGTG TATTTTGGTT CCTTCTTCAC 1380

GAATATCTGA GAGTTTCATA GCTAATTCTT GGCCTTCGGA AACAGTCAAT GTCGTTGTGA 1440

AACGCAAACC AATTTCTGGG ACAGCTACGT TATAAACGGC TTGaTTTGCT TCaCTCTTCT 1500

GTTTTTcAGC AGTTGCTTTA tATGCTTTGC CAyCAAyCAT TACTTGGTCa ATTTTCTCgT 1560

GTTGGCCATT AAAAATCACT TGATTACTCT GAGGGTCTTC GTAGCGAATA ATTCGTGGAA 1620

ATTGTGGATC AACCACGGCT GTTAAATCTG CGGAAGAGAT TTTGTCGCCT TTTTCAGCTT 1680

CATTGTCTTT AGCAACAACA ATGCTGGCTT TTGCTTTGAT GTTTGTATTT TCCAAAGTAC 1740

CGTCGACTTC AAAAGTTCCT GGTTCTTTAT ATGCATCAGG ATCGATTTCA TTCCAACGGA 1800

CTGCTTCATT GGCTTCTTTA CCAGTATTAT AGGTCACTTT TACTTGTTTC GGtAATTTTG 1860

GTGCGACACC AATTTTTGTA AAAACTTTGA CTGGCGCAAT TTGTGTCACT TCTGGCACAA 1920

TTTCTGGAAT GCTATCTACG GGGCCATTTT TAAAATAGTC ATAATTGACA ATTTTTTTGT 1980

CGTACCACAA ACGGACACCC ACATGTCCGG CTTCTGTTGG AATTTTGTCT CCATTGGCCA 2040

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CATAACGTAC TTTCAACAAA TAATTCGTAT CTTCATTTAA CGTTGGCCCA GAAATTGAAT 2160

CATTCCACGA ATTAGGGCTT TCAACTAACC ATTTGCCATT CGCGTTATAG CCTACAAAAA 2220

CCCAGCTATC TTTGGTATTA CCACGTATAA TCACACCCGT TCGACCGCTT CCAGCAGTGT 2280

ATTTAAACTT TGTTTCTACT TCACCATCAG CTAATTTAGG GGAATCTAAA TTTAAAGATA 2340

CGGCATTATT ACCTGCTGCT GCATCTCGTG AAATCGCCAA TGACTCTCCT GCTAATTCTC 2400

GATTTGTTTT ACCAATCACA TCTTGCCACT CACCAGTTTT CCCTCCTGGA AAATCAGATT 2460

GCCACAATTT TTCTTCTGTT GCGGTAGGTT CCACCATTGA TGAGCTTGTT TCAGTGCTGC 2520

TGTTTGTTGT TTCTTCTGCA GACGTACTTA ATGGTACTAA AATCGTTGCG CTTGCCAATA 2580

GTGTCAATGT ACTAAATCGT TTTATTTTTC CATGTTTCAT CTGaTAAATC AGCCCCCTGA 2640

ACATTTTTGG AACACGCTTT CATTTATTTA ACAATTAAAG GGGGGTTnCC AAAAATTAAA 2700

TTGTnTTCAT TTTTGG 2716

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGAAATTGC TAGCGTTTTC CGCCATTGGC TATGTTTAGT CGCAACGGAG GGACCsCtGA 60

CTTTTTAGCG AAGCATcgTT GCCTGTTAAG aAAGTGACGA AAATTTCTAA TCCTGAAGGG 120

GAAACCGTGC TGGATGTCAT TCGCAATGGG AATGCGCAAG TGGTAATCaG TACCATGGAT 180

AAAAATCGTT CCAGTGcCAA CCAAGATGGA TTTTCAATCC GTCGGGAAGC AGTCGAACAT 240

GGGATTCCAT TGTTTACCTC ACTTGACACA GCAAATGCGA TTTTAAAAGT TTTAGAATCA 300

AGAGCCTTTA CGACAGAAGC CATTTAAGCA AAAATCTGGA ACAATCGTCT GAGGAGGACT 360

GTTCCAGATT CTTTTACGAA GAAATAGAAA ATCATTTATA GGGGAATCAG AGAATAAAGG 420

AGTGAAGGAT ACTGATGCAG AGAAAGCAAG AAATGATGAC CATTGTAGCT CAAAAACAGT 480

TAGCGCCACG GATTTATCAG TTAGACTTAC AAGGCGAGTT AGTGAAAGAG ATGACACGAC 540

CTGGACAGTT TGTGCATATC AAGGTTCCGC GTGCAGATTT ACTTTTGCGG CGACCGATTA 600

GCATCAACCA AATTGATCAT TCGAACGAAA CCTGTCGTTT GATTTATCGA GTCGAAGGCG 660

CTGGAACGGA AGTGTTTGCC ACCATGAAGG CTGGTGAACA ATTAGATATT TTAGGTCCTT 720

TAGGAAACGG CTTTGATATA ACTACCGTAG CAGCTGGTCA AACTGCTTTT ATCGTTGGCG 780

GAGGAATCGG GATTCCCCCA TTGTATGAAT TATCAAAACA ACTCAATGAA AAAGGCGTGA 840

AAGTGATTCA TTTTCTTGGT TATGCATCAA AAGAGGTTGC TTATTACCAA CAAGAATTTA 900

TGGCATTAGG AGAAACACAT TTTGCCACAG ATGACGGCTC GTTTGGCGCT CATGGCAACG 960

TGGGCCGTTT ATTGTCAGAA GCGTTAGCAA AAGGACGGAT CCCTGATGCA GTGTATGCTT 1020

GTGGTGCGAA TGGTATGTTA AAAGCAATTG ATTCTTTATT TCCAACACAT CCACACGTTT 1080

ACCTTTCTTT AGAAGAACGG ATGGCCTGTG GAATTGGGGC TTGCTATGCC TGCGTTTGCC 1140

ATAAAAAAGG AGACACTACT GGAGCAAAAA GTGTCAAGGT CTGTGATGAA GGTCCGATTT 1200

TTAAAGCAAG TGAGGTTATC TTATGATGAA AAAyCCTTTA GCCGTTTCAA TTCCAGGTTT 1260

AACATTAAAA AATCCAATTA TTCCCGCCAG TGGTTGCTTT GGGTTCGGGG A 1311

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCCTCTGATG AACCGATTGA AAGAATTAAG GAAAGAAnAA AATATTACTT TAGTTGAGTT 60

AAGTGAGGAG TTAGGTATTC CACGTTCCAC TCTTAATAGG TATGAAAACG AAGATAGCGA 120

ACCAAAACAA GAAaCTTGGG AAAAATTAGC TGATTATTAT GGTGTTTCTA CGGCTTATTT 180

AATGGGGATA TCCAACCAAA AGGTTAGCGA AGAAAAAGCT TTGACGGCCG CAAAGAAAGT 240

TTATCAAGTC TATCTTTCCG ACGACGATTT AGGAAAAGAA ATTCGAAAAG CTCTAATGTA 300

TTTTAATAAA AATGATTTAG ATAGTGTCTT AAAACAAGCA ATGCAGCAGT ATTTTACTAT 360

CCCAGCCGTT GAATGGAATA CAGAATTTCA ATCTTTAAAA AATACTGGTT TTCTATACAG 420

TTGGTTAGAA GGATATTTGG TAGACAGGTA TCGAAAAGAA GTGAAAACTA ATCATAATTT 480

AATTACAAAT ACGTATTATA GTATCCCTTC TATTGATGAT GTGAATGAGT ATGGAATTTT 540

CTCTGATGAA ATTCAAATAC CGTTGACTGA AGATTTTAAA CAAATTTTCA AAGTTGAGGA 600

TCTATCCACG AAAACACATG AAGAAATAAA AAAACTTTTT AAATCCGATT CTACGCTCAT 660

TGcTTACAGC TATGAAAGCT CCGTAGACGA TAAATTAAAA GATGATATTA ATATGATTTT 720

AGATAATGCT CGTTCCGAAA TTCTTAATCT AAAAGAAAAA TATCCTGATA AACCTAGTAG 780

AATAGaACAA ACAACCGTAC TCATATCTAA AGACGAAGAT ACTTCCTTTT GGTCAAGGAA 840

TGGCTCAAAT GATTATATAG ATGAATTGAA CTTATCTGAG GAAACTAAGA AATTATTTGT 900

TCATTTAGGT TCAGTATTTA TTGAGGAAAA AAAACGTAAA TCAAAAGCTA AAGAATGAGT 960

TTTTTTCTTT GTATAATCCA GTTATAGAAA CATCTCTCCC CTAACATCTA CATACTATTG 1020

GCGTGGTGGT AGATAGGAGA AAAACAATGA CACAAATTAA CAAGTATACA AAAAAAGACG 1080

GTACAACCGC CTATATGTTT AATGCTTATG TAGGACGTCA TCCCAAAACT GGTAAAAACG 1140

TTTATCGTAA GCGGCAAGGA TTTAAAACAA AAAAACAAGC ACAAATTGCA CTTGCTGAAA 1200

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AAATAACCGT TATACAGTGT CAGGACTTAG TTAATAAATG GTTTAATCAA GGACACAAGC 1440

AATACTCGTT CTATAGAAAA CTCACTGCTC AGATTATGCG ATATGGCGAA TCTATGGAAC 1500

TAATGAATAC TAACCCAATG AGAAAAACAA TCCTTCCTAA GTGGAAAGAG GAAGAAACAA 1560

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AGACCGTAGC ACAAGACGAA TTCTATAATA TACTCACTCA AACGCCCAAA ACAGCTTCTA 1800

GCACACGTTC TATCAGCTTA GACAATGAAA CACTTCAAAT TATGGCTAAA TGGCGTACAA 1860

TCCAACGTAG TGAcTATTTC CAAATGGGCT TTAATACATC TAGTGAAGAA CAATATATTT 1920

TCACGAACAA CCATAATAAA CTGCTCTCAC CAAATGTAGT TAATATATGG CTCAATTGCT 1980

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GCACTGCTAT TACTGATCGT ATCTATTCTC ATGTTATGCC TGAAGAAAAA GAAAAAACAG 2160

CAGATAAGTT CGCTCAATTC GTCGGTTTTT AATAAATGCA CAGACAAAAG CACAGATCTT 2220

TACTATTTTT ATGTAAAAAA AAGAGCTAGA ATCCTTATAA ATAAAGGTTT CTAACTGGCA 2280

TTAGTAACGC TATTAATGAA ACAACGTGTT TAATCATATA ATAAACCAAC AAATAAGTAA 2340

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ATAACTCCTG CATTGTTAAA AAGAACATCA ATTCGTCCAT ATTTTTCCAT TGTAAGCTTG 2940

ATTACACGCT GAACTTCCTC TTCTTTCGTT ACATCTGCTT GTTGCACGAG AATCGTTGCT 3000

TCAGGAAGTT CTTTTTTTAT AGCAATTAAA CGTTCTTGTC GACGTGCTGC AATGACTAAC 3060

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GCCGTTTCAT TGGCAGTTCC GGATGATTGA CACTTAAGAG ATTAACGCGC GGACCAATTA 3420

AAACATTGTC TTCAATTATA ATGCCCCCTA AATCAACAAA CATAGCTGCC CGATTAATAA 3480

AAATATTTTT ACCAAAATGT ATATTGCGTC CAAAATCTGT ATAAAAAGGT AATAAAATCG 3540

TAACGGTTTC GTCAATTTTG TCTTGGATAA TCGTGGCAAG AAGATTCCTT ACTTCATTAT 3600

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GAATAAGTTG AAATAGTGGT TCATCTTTAT CAATGCTACC TGTTGCAATT AGTTCTTGGA 3720

GATTTTTTGT AAGCATTCCT AATCGCCTCC TTTTGCTAAA TTTATCGTAA TACGTGACAA 3780

CTCCTCTGTC TAATACTTAT AATAAATAGA TAAGTATGCG TTTTAGTTAT AGGAGGGAAA 3840

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GAGGAAGAAT TAGGCGTGAC ATTATTTATA CGAGGAAATC GACAAATACA ATTAACACCT 4020

GAAGGAGAAT ATTTAGCTAA ACAAGGGCAA GATATTTTAA GCTTAGCGAA TAAAACAGTC 4080

ACCAACTTGT CGCAAAATGA ATTCATTAAT GGCGAAATCA CGATTGGTGG CGGCGAAACA 4140

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GCTTTAACAG CCAAAATTAG TTTAATTTGG CGCAAAAATA CGGTTCTTTC CACAGCTGCT 4680

GCATTATTTT TAGAACAAAT AAAAAAAAGT ATTCAACGCC CTGAATAATA GGTCGTTGAA 4740

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TCGTTACGGT CATTTCCTTG GCTGTTTTCT TTTGACCTAA GAACCAAATA CCTGTCAACG 4860

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TAATGATTTG CGCACAGGCC CAACCGACAC CAGATAAAAT TGAAAAGAAT AAATCCATGC 5460

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AACCGCTTTC ACTTTAAAAG CAGGCACAAT ACCACTTCGT CCATTGACGT CATAAAAGGC 6300

GCCTTTACTA CCTACTGTAA TAATTACTGC TTCAAyCCCT AATTGATGAA GTGCTTCTGC 6360

GGCTTTACGC ATACTCGCTT CaTCTGTGAT TTTAATGCCT GTTAAAATTT CGGTTTCTGT 6420

TTCATTTGGT ACAATCATAT CTGTCACGTT TAGTAATTCT TCAGGAACTT GTTCTAACGC 6480

AGGTGCGGGA TTTAAAATCG TTTTGACGCC TGCTTTTTTA GCAATTTTAA ACGCTGCAAT 6540

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AACTGCTTGG TTTGCTCCTT TACCACCACC TGCTGTAAAA TGTTCAATGG CGTGAATTGT 6900

TTCGCCTGGT TTTGGCATTT CTTTGACTCT TAATGTTGTG TCTAAATT 6948

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AATTTGTTGA ACCAGCGATT GCGCnGCnAA TACTGGTTTT TCCAGTGCCA GGCGGCCCAT 60

AAAGAATCAT CGATGAAAGC ATTTTGGCTT CGACCATCCG ACGAATAATT TTACCAGGGC 120

CGACTAAATG TTGTTGACCA ACTACTTCGT CTAAGTGACG AGGTCGCATT CGATAGGCTA 180

AAGGTTGTTG CATAGAAGGA CCTCCTTTTT CATAATCATC TTATTATAAC ATAAAGAACG 240

TACATyCGCT TTTTGGTGGk TTTTTGGGkT TTAGATGGAT ATAGCGGAAG GTTcGTGtAT 300

GATAGGGAGT GGTGAAAGAA ATGAAAGAAA CGATAAATAT CTTTAACACA AAAACAACTG 360

AAGAAGTGGC ACAATACTTG TTAGGGATGT ATTTAGmGCA CGAAACAGCA ACAGGCGTTT 420

TAGGTGGGTA CATTGTGGAT GCAGAAGCTT ATTTAGGTCC TGATGATGAG GCGGCCCATA 480

GCTTTGGCTT GAGAAAAACG CCACGCTTAC AAGCCATGTA TGACAAACCA GGTACGATTT 540

ATTTATATAC TATGCACACG CATTTAATTT TAAATATGGT GACACAAGAA CAAGGCAAAC 600

CACAAGGGGT GATGATCCGC GCGATTGAAC CTGTTGAAGG TGTCGACAAA ATGATTGAAA 660

ATCGCCAAGG ACGTCAAGGC GTGGAATTGA CCAATGGACC AGGTAAATTA GTTGCAGCCT 720

TAGGAATTGA TAAGCAATTA TATGGGCAGT CGATTTTTTC TAGTTCGTTA CGGCTCGTGC 780

CAGAAAAACG AAAATTTCCG AAAAAAATTG AGGCACTACC ACGAATTGGG ATTCCCAATA 840

AAGGTCGTTG GACAGAGTTG CCTTTAAGAT ACGTCGTGGC TGGCAATCCA TATATTTCTA 900

AACAAAAAAG AACAGCAGTA GACCAAATAG ATTTTGGCTG GAAGGATGAA GAAAATgAAA 960

AAAGCAACAA TGCTCACATA CTTAGAGGAA CAACTTGAAA AACACTTAGG AGATTACGAA 1020

gTAGGCCTTG ATTGGGATCG CAAAAACCAT ACCATCGAAG TCATTGTTcG TTTATATGCA 1080

GAAAaCAATG AGCmAGTGGC GATTGATGAT GTTGATGGTA CGCTTTCAGA AGwAGAATTC 1140

ATTGAATTTG AAGATGGTTT GTTATTTTAC AATCCGCAAA AGTCTGTCGT TGATGACGAA 1200

GAGTATTTAG TCACAATTCC TTATGAAGGG AAAAAAGGgC TACGCAAAGC AGTTTTAGAC 1260

GGATTCATTC ACTATTTAAA AGTGGTTTTA GATGAAGGGC AAAGTGATTT GTTAGACTTT 1320

TTATCAGATG AAACAGCGGA AGTTTTTGAA TTGCATTGGG AGCCAGCAGA TTTTGAAGCG 1380

ATGATTAAAA AAGTGGCAGA AACAGAAAAA GAACAATGGA TTGCGTATCC AAGTTATTAA 1440

TTTAGAGGTG AGAACATGAA GTGGACAGAA GTAAAAGTCG AAACGGCTAG CGAAgCAGTT 1500

GAAGCAATTT CAAACATTAT GATGGnArCT GGCGCAAGTG GCGTGGCCAT TGAAGATGCG 1560

TTGGACATTG AAAATTTTGA AAGTGATCTG TATGGGGAAA TTTTAGATAA AGAGCAATTC 1620

ACCCACATTA AAGAAGGGGC GATTGTGATG GCTTATTTTC CTGAAACAAC CTTCTTACCA 1680

GAAATTTTAC CATTTATGAA AGAAAATATT TTACGCTTGC CTGAGTACGG CTTATCCATT 1740

GGTAAAAACG AAATGACAAT TAGTGAAGTA GCAGAAAGCG ACTGGGCAAC TGCTTGGAAA 1800

AAATATTATC ATCCTGTCCG TGTCACACGA TTCTTAACGA TTGTGCCAAG TTGGGAAGCC 1860

TATCACGCAC AAGATGAAGC AGAAAAAATT ATCACATTGG ATCCGGGCAT GGCTTTCGGT 1920

ACAGGCACGC ATCCAACGAC TCGTTTAACC TTGCAAGCTT TAGAAaCTGT TTTACGTGGT 1980

GGCGAAACAG TTCTAGATGT AGGAACGGGT TCTGGTGTTT tGAGTATTGC AAGTCGCTAT 2040

TTAGGGGCTA AAGACGTCTA CGCATATGAT TTAGATGAAG TAGCAGTTGC AGCGGCAAAA 2100

GAAAaTATGG ATTTAAATCC CATTGCGGCC GATGTTCATG TGTCAGCCAA TGATTTACTA 2160

AAAGGGATTG ACCATTCTGC TGATGTAATC GTCGCAAATA TTTTGGCAGA TATTATTGTG 2220

TTAATGATTG AAGATGCTTG GCGTTTGCTA AAACAAGACG GTACCyTCmt TAtTTCTGGA 2280

ATTATTGAAG wTAmAAAAGC aATGGTTTTA GAAGCACTAA CGAAAGTCGG TTTTGTGGTG 2340

GACCAACTCT TTAATCAAGG CGATTGGTAT GCGATTaTCT TGAAGAAACC aGAGGAAGAG 2400

TAAAaTGCAA CGGTATTTCA TGAAAGAaGA TTATCCAgAA AAgATTTGTA TAAgTCGCAG 2460

ATGAAAACTA TCATCATATT GTGCGAGTTA TGCGAATGAC GCCGAATGAT CGTTGTTATT 2520

TAGTATTTCA AAATAAAACT GCCATTTTAG CTGAGATTGT GGAAATTGAT TCAACATCTG 2580

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TTGCGTGTGG GTTACCAAAA GGGGACAAGT TAGAATGGAT TGTTCAAAAA GGCACGGAGC 2700

TAGGTGGCAA TCAGTTTATC GGCTTTCCTG CGAAAAtTCC GTTGTCAAAT GGGACCACAA 2760

AAAAAGAGCA GCCAAAGAAA AAAGATTACA AAAAATTGCC ACAGAAGCGG CGGAGCAATC 2820

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ATTTGACTCA TATGACACAG TCTTGGTTGC GTATGAAGAA TCAGCAAAAC AAGGAGAAAA 2940

AAGTCAATTA GCACAAGTAT TATCCACTTG CCAGCCAGGC GCACGTTTGT GTGTGCTCTT 3000

TGGACCTGAA GGTGGCTTTG CACCGCAAGA AATTGAACAA TTTCTGCAGG CTGGGGCGAA 3060

ACTTTGCGGG TTGGGTCCGA GAATTTTACG AGCAGAAACA GCACCGTTGT ATCTTTTAAG 3120

TGTGGTTAGC TACCAAATGG AACTTTTAAA TTAAACGAAA GCCCGCCTGT AAAATTCTTG 3180

TAGGCATTCT CTTTAAATAA ACAGAGAGTA AAAAAGCGAC AGTGATTGAA ATTTAAGGGA 3240

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TTAAAATAGA TAAAACGTGA ACGAATgnTC TTTATCCAAA GGTCACCTTC ATAGAGGAGT 3360

GAATACCATG CCAAAAGAAG AAATACTGAC AGGCCCAGCG GTCATCAAAA TTGTAAGTAC 3420

CTATATGGGA CCAGAACATG TTGAGTTGGT TCAAAAAGCA TTAACTTATG CTGAAAAAGC 3480

ACACGAAGGT CAAGTCCGAC AATCAGGTGA ACCTTACATC ATCCATCCGA TTCAAGTGGC 3540

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TGTTGTCGAA GATACGGACG TAACACTGGA CGATTTAAAA GAAGAATTTG GCGAAGACAT 3660

CGCAATGTTA GTCGATGGCG TGACGAAACT AGGAAAAATT AAATATAAAT CTCATGAAGA 3720

ACAATTAGCT GAAAATCATC GGAAAATGTT ATTGGCAATG GCGCAAGATT TACGGGTCAT 3780

TATGGTGAAA CTAGCCGATC GTTTGCACAA TATGCGCACA TTAAAACATT TACGTGAAGA 3840

TAAGCAACGA CGGATTGCAC AAGAAACTTT AGAAATTTAT GCGCCTTTAG CACATCGCTT 3900

AGGGATTAGT CGAATTAAAT GGGAATTAGA AGATACTGCC TTACGTTATA TTAACCCCAA 3960

CCAATACTAT CGAATTGTTA ATTTGATGCA AAGCAAACGC GATGAACGTG AAGCTTATGT 4020

GGCAGAAGCA GTCGAAGATA TTCGTTTAGC yACGGAAGAT TTAGAAATTT ACGCrGAAAT 4080

ATATGGTCGA CCAAAACATA TTTATTCAAT CTATCGTAAA ATGAAGGACC AAAAGAAACA 4140

GTTTAATGAA ATCTATGACT TATTAGCCAT nCGTGTTATt GTCGATTCCA TTAAAsaTTG 4200

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TGCGATAGAA GAGCAGATAG TGGGACAAAT CAAACAAGGC TTCATGGTGC TGGTGGGGAT 5700

TCATCAAGAA GACACGCCAG AAGATGTGGC TTATGTTGTT GGCAAAATCA GTAAATTGCG 5760

TGTTTTTGAA GATGACGAAG GAAAAATGAA TCGCAGTATT CAAGAGATTG AAGGATCAAT 5820

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AAATGGCGCA CACATTTTTG TGGAATGATA GAAGGAGAGA AAGACAATGA GTTATCAAAA 6420

ACCAAAAGGA ACAAACGATA TTTTGCCAGG AACTTCTGAA AAATGGCAAT TTGTGGAAGA 6480

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CGCATGAAAT ATCGTTATTT AGATTTACGT CGTCCATCAA TGACAAACAA CATTAAATTA 8160

CGTCACCAAG TAACGAAAAC AATCCGTCAC TATTTAGATA ATCATGACTT TTTAGACATT 8220

GAAACTCCTT ATTTAGGCAA ATCAACACCA GAAGGCGCTC GCGATTATTT GGTTCCTTCT 8280

CGTGTCCATG CCGGTCATTT TTATGCTTTA CCACAATCAC CACAACTCTT TAAACAATTA 8340

TTAATGGGGG CAGGCTTCGA TCGCTATTAC CAAATCGTTC GTTGTTTCCG TGATGAAGAT 8400

TTACGAGGCG ACCGTCAGCC AGAATTTACA CAAATCGATA TTGAAACGAC CTTTTTAACA 8460

CCAGAAGAAA TTCAAACATA TACAGA 8486

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 789 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AATGTCAAAA TTATTAGTTG TTAAAGCACA TCCATTAACA AAAGAAGAAT CACGCTCAGT 60

TCGTGCGTTA GAAACATTTT TAGCTTCATA CCGTGAAACA AATCCATCAG ACGAAATCGA 120

AATTTTAGAT GTTTATGCCC CAGAAACAAA CATGCCGGAA ATCGATGAAG AATTATTATC 180

TGCTTGGGGT GCACTTCGCG CTGGCGCAgc ATTTGAAACA TTAAGCGAAA ACCAACAACA 240

AAAAGTGGCT CGTTTTAATG AATTAACTGA TCAATTTTTA TCTGCAGACA AAGTAGTAAT 300

TGCTAATCCA ATGTGGAACT TAAACGTACC GACACGCTTA AAAGCTTGGG TAGATACAAT 360

CAACGTTGCT GGAAAAACAT TCCAATATAC TGCAGAAGGA CCAAAACCTC TAACAAGTGG 420

TAAAAAAGCC TTACACATCC AATCAAATGG CGGCTTCTAC GAAGGAAAAG ATTTTGCTTC 480

TCAATACATT AAAGCGATTC TAAACTTTAT TGGCGTTGAT CAAGTTGACG GATTATTCAT 540

CGAAGGAATC GATCATTTCC CTGATCGCGC GGAAGAACTT TTAAATACTG CCATGACCAA 600

AGCAACTGAA TACGGTAAAA CATTCTAAAT TTTCCGAGTG ATTTACATCA AAAaGAGACA 660

AGCAGTTCGT TCACTGCTTG TCTCTTTTGT TACGTAGATT CTTGTTGaTC TGGcTTATCt 720

TCATcATACA AACCGGaAAC GaTTTGGtAC CACTCaAAAA TGTGTGTAAT ATCACnTTAG 780

CTGCGGCAT 789

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGTCGTTTAT TACGTCGTGA CGGTAATGCA CGGGAAAAAA ATTAGGCATT AATGAAGCCT 60

TTTTATACAA ATTAGTGCCT GTTGTTGGCG AAATCATGGT AAGCTACTAT CCAGAAGTAT 120

TACAACAAAA AGACTTCATC GAAAAAGTGG TTCGGACAGA GGAAGAAnGT TTCCATGAAA 180

CCATCAATGA AGGTTTAAGC ATGTTAAATG AGGTTATTAA AGAAGTTAAA GATGCAAAAG 240

GCGATACATT AGATGGAAAA ATTATCTTCA AACTTTATGA TACTTTTGGc TtCCCCGTAG 300

AATTAACGGA AGAAGTTGCA GAAGATGAAG GCTtGAAAGT CGACCAtGCT GGGTTTGAAA 360

CAGAAATGGA AGCACAGCgT GAACGTGCTC GTTCTGCCCG CAGTAAAGAA ACTTCAATGG 420

GTGTTCAATC TGCTTTATTA ACAGATATTA AAGTAGAAAG TAAATTTGTT GGCTATACAG 480

AATTAACACA TGATAGTGAA TTATTTGTTA TTATTCAAGG TGACGCACTA GTAAATGAAG 540

CATCTGCAGG AACAGCCGAA TTAATTTTTG CTGAAACACC ATTTTATGCT GAAATGGGTG 600

GACAAATTGC TGACCGCGGC TATGTAAAAA ATACCGCAGG GgAAGTCGTT GCCAACGTGG 660

TGGATGTGAA AAAAGCACCA AACGGTCAAT TTTTACACAA AGTAGAAGTT TTGGCGCCAT 720

TAGCAGAAGG TCAAATTTAT CAATTGCAAG TGGACGAACG GATGCGGACA CGTaTTTTGA 780

AAAATCATAC GGCAACCCAT TTATTGCATC GTGCTTTAAA AGATGTGTTA GGGGaGCATG 840

CCAACCAAGC AGGCTCATTA GTTGCACCAG GACATCTACG TTTTGACTTT ACTCATTTTG 900

GGCAAGTTAC ATCAGAAGAA CTAGCGCGGA TGGAAGCCAT CGTTAACGAA AAAATCTGGG 960

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TTTTTAAAGA TGTCAAAGAC ATCAATGGTG TTCGTTATAT TGCCGCTCAA GTCAATGTTA 1440

AAGACATGAA TCAATTACGC CAATTGGCTG ACCAATGGAA ACAAAAAGAA TTGTCTGATG 1500

TACTAGTTCT AGCAACTGCA CAAGATGAAA AAGTAAGCTT GTTAGCGGCT ATGACAAAAG 1560

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GCGGTGGCGG CGGTGGTCGT CCTGATATGG CTCAAGCTGG TGGGAAAAAT CCAGCAGGGA 1680

TTGCGGATGC CTTAGCAGAA GTTGAAAACT GGTTGGCAAA TGCCTAATTA AAAATGTTTT 1740

CCCTATTATT AATATAAGGA GAATGCTCTT TATAGCaATA ATGACAGCCC TCTTCAAAGT 1800

TATGAAATTG ATTTTGAAGG GGGTTCTTTT TTTtAAATGA TTAAGGAGAG GAAACAGTAG 1860

ATTGCACGAA TGTGTAAGTT TTCATCTTCA ATTGACAATG GTATAATAAG CAACGGAGGA 1920

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TCTGCCAAAA CCCAAGTCAG TAAATCCAAT TTGACGGATA AAATTATCGT ACGTTTAGCG 2160

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AAGGAACGCC TTGTTTTACA ACCGAaTATT GGTGAACCAA CTTTACGCCG CTGGTTAATG 2340

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GGGCCAGTTT TAATTAAAAA ACAAGGACCG GTTTTTACTA AAAAATGGCA ACGAGAATTA 2520

AAACAGCGCA AAACTGTTCT TGCACAACTA GCAAAAGCAA GTGGAGAACA TATTGAAAAG 2580

CAAGCGAAAC TACAGCAAGA CCAACAATTA ATTGAGGAGG TACTGGCCAA TGGCTGTGAA 2640

CGGTAAGACA TTGATTCGAC GCTTCAATGA CTATTGTCCC GAATGGTTAG CAGAAACGGG 2700

AGATCCTGTG GGCTTGCACA TTGGTACATT AGATAAACCA ATTGAAAATG TGATGGTTAC 2760

CTTAGATGTT CGTCCTGAGG TCGTTGCAGA AGCAATTGAG AAGCAGGTTG ATTTAATTAT 2820

TGCGAAACAC CCACCTATTT TCCGCCCAGT TAAGCGATTA ACCACAGATA ATTTTCAAGA 2880

AAAAATGTAC GCTGATTTAT TAAAACACGA TATTGCTGTT TATGCAGCGC ATACTAACAT 2940

GGATATTATT GACAATGGGC TAAATGATTG GTTTTGTGAA TTATTGGGAA TTAAACAGAC 3000

CACCTTTTTA ACTAAAACAC ATACTGTTCC TTATAAAAAA TTAGCCGTTT TTGTGCCAAT 3060

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GCTACGTTAC CTAGTAACGT GGAGAAAGAC GTTCGTTCAA TCGGCTTTAT TGCCCATATG 4020

GATACCGCTG ATTTTAATGC AGTGAATGTT TCTCCGCAAA TTGTTGAGAA CTATGACGGA 4080

GAATCAACGA TTCCTTTAGA TAAAGAAGGC AAATTCACTT TAAACACGAA AGACTTTCCT 4140

AACTTAAAAA ATTATCGTG 4159

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATCGATACAA TTTTTCTTTT GTCACAACAG AAGAAGAATT ATTAGAGATT TTAAAAGATG 60

CCTTAAAAGA TAAAGCCTTA GTTGTCAGTA CATTAGTCAG TAAACAACTA ATCACAGCGG 120

CGAAAGAATT TAGTGAACGA ACAGGGTTGT TATATTTAGA TTTAATGGCG CCATTTTTTG 180

AATTAATTCA AGCGAAAGCC GGAGTAGATC CTATTGAAGA GCCTGGACGA CGCCACCAAC 240

TAGATCGTGC CTATTTTGAT AAAATCTCAG CGATTGAATT TGCTGTAAAA TATGaTGATG 300

GCAAAAATCC TCAAGGGTTT CTTGATTCTG ATATATTGTT GTTAGGCGTT TCGCGGACCT 360

CAAAGACGCC AGTCAGTATG TATTTAGCGA ATCAAGGCTA CCGCGTTTCT AACTTACCAT 420

TAATTCCAGA AGTTCCATTG CCGCCAATTT TGGAAGAAAT GGATCCACAA AAAATGATTG 480

GTTTAGTTTG TTCGCCAGAA ACATTAGGAC AGATTCGTAG CAGTCGGTTG GCTTCCTTAG 540

GTTTAGGTAA TGAGACCAGT TATACCAATG TTGAACGGAT TGAACAAGAA TTAGCTTATG 600

CCGAAGAGAT TTTTGCGAAG TATGGCATCC CAGTGATTGA TGTAACCGCA AAATCTGTCG 660

AAGAAACAGC CTTTTTAATT AAAGAAAAAC TAGATGAAAG AAATTAAAAA GCTTGGCAAC 720

CTCACTAAAT TTCAGTGAAG TTGCCAAGCT TTTTATACTT AATTGAGCTT CTTTTTGTTA 780

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ATAATGAATA TTTTCTGTTT TCATATATTC AAATAAATGA ATAAATAAGA AATCCATACT 1080

TCCAGAAGGG GCTTTTTCTT TATGGTGACG CATCAAGTCG ATGGTACCAA CTTCATTTGT 1140

GTAACTAGGA ATGATATTAG CGAAAGAGAC CATTTCTCCT TCAGCATTTC GGACAACAGC 1200

AATTGGGTTT CTTTGAAGAT ACGCTTCATC GAAAAATCCT AGTGAAAAGC CTTTTTCTTT 1260

TCGATTGTCT AACCAACTAT CCGAAATAGC TTTTAATTCG TGCATTTGTT CGGTACTAAA 1320

AGGAGGTTGG AGTACGTCAA ATGAATAGCC GGCTTTAGTA ATTTTATTAA ACACTGCGCG 1380

GGTACCTTTG AATTTTTTCC CAGACATCGT AAATGTTTCT AGATTAACTA AGGCTTCTTC 1440

GCCCATTTTG ATAAATTCGT AGCCATATTC GTGTAGTAAC ATCACGCTGT CCTCATTGGT 1500

TTCGTAAAAG ACGGGTACAT AGCCGAAACG ATCTGTTTCT TTAAGGAATG CATCAATCGC 1560

CGCAGGAAAA TCTTCTTTGT TCCCAGAAGG GTTGCCCATC ACAACGCATT TATTATTAAT 1620

GGTGTTGAAT TGTAAAAAGA CAGTCGGTTC TTCTTTGGGA TATAAGAAAA CCTGTTTATC 1680

ATGAAGAAAG ACAAGTTCAC TGTCAATATT CCCGCCATAA GTTGTTAAGA TATTATGCAA 1740

GATACTATCT TCTGGAAACT CACCAACTTG GTGTTTTTTC CCTTGGAGGT AGCGAACAAA 1800

TAGAAAGTTA AAACTCATAA CTAAGAGGAT AGCGATAAAT CCTGACAACC AGATCCGTTC 1860

GGAAGGGAAC AAGAAAAATT CCACAAAATG ATGACGATGG TGTGGGAAGT TCGGTAAATT 1920

ATAAACACCA ATTACCAGGT ATAACAAAGT CAACAAGCCA AAGATAAAGC CATCAATCGT 1980

CATCCACTCC CAAGAGTAAA CCAGTTGTTC ACGGTACAAT TCTGATTTTG AAAAAATAAC 2040

GATAAATAAT AAAATAGCTA AATAGAAAAT GGAAAACATA CTAAAGTCAA CAACAAATGA 2100

ATACAAGATA GCACCAATTA ATAAAATAAT CGTTGGATAA TAGGCTCTTT tAaCmCGATC 2160

AGCATCCCcG TCCCATAATT mATAATGCAA AGCCTAAAAC AATACTCGGA ATTTGnATAA 2220

TAATATGTGA ACGGAAGGGG TTAATATCTC TTAACCAATG CACTTGAGTG AAGGCTTCTG 2280

GAATAGTGGC TAGGAGCACC ATCATAATTC CTGAAAAATA AAGTAAAACC ACTTCTAGCT 2340

TGTGGGCAAT TTCCAAAGTA ATTTGTTTTA GCAGTTGACG ATAATGAGTA TCCAACTTTT 2400

GGCTTAAGTG TTTTGTAAAG AACAAACAGC CAATTAAGAA CGGAATAATA TAATAGAATA 2460

AACGATAGAG CAATAACCAC AAAACAATAA TTTCACGATC GACACCTAAG TTGCTCAGTC 2520

CTAAAATCAT CATGACATCA AAACTACCTA AAGCCCCTGG AATCATCGAA GCAATCCCAA 2580

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AACCGATAAC CATCATCAAT AACAATTTCC ATAGCGGAAT CTCATCAAAA ATCTGTTTTA 3180

ACTGTTCAAA TGAGATCGTT TTACCAATTG ATAAAAGTTG GGCAACAACA ATAATTGAGA 3240

CCGCAATAAC AAACAGTGTT TTTAGTAATC CTGTATGCGT TTTGATCCAA TGAATAATTT 3300

GTTTCATTTA GACACCTTCA TTTCCTTTAA GAATTTTTCG ATTGTTTTAT TAAAAATATC 3360

TGGTGAGTTT TTGGCAAATA AATGACCCTG TTTATTTACC AAGACCAATT TGCCGGCAGG 3420

AATGGcATCA GCAATCGCCC GTGAATGGGA AAGCGCAATT AAATCTCGAC TGCCAGTAAT 3480

AACAAGAGTA GGACAGGGGA TGTGTTCTAA ATCTTGTTTT GTCAGTCCAG TATCTTCAAA 3540

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GTAATTTGTT kCTTTGCCAA AAATTTGAyA AAAAATTTGA CTGCCATCTA TTGTTTGAAA 4020

ATATTTTTCT ATTGCCATTC TCCGTCACCT ATCTCATCTA TAATCAATCG AGTCCTCTCT 4080

CATTATAGAG TCTTTTGTCT TTTTTTTGTA ATAAAAAACA GAAAATTTTC CGAACAGTTT 4140

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AGGAGGGAAA GTTGATGTCT TTAATCGTTT TAATTGGTGC CCAAGCTGTC GGGAAAATGA 4260

CCGTTGGCAA GGCTTTAGAA AAGCAGTTAG ATGCTAAATT ACTATTTAAT CATCAAACCA 4320

TTGACTTATT TGCAAACTAT CTTGGGTATA CGGAACGTGc ATTTCAATTG TCTGATTCCG 4380

TTAGAAAGGA ACTTTTTCAT GCCTTTGTCG AAAATCCAGC CACAAATACA ACAAAAAACA 4440

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AAGCCAGCAC TTGGTTCATC TAAAATATAC ATAATATCAT TTAAGGCGCT GTTTACATAC 7860

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ACTCTACTTC CTAAACAATC AGGACATCTT TTTACGGTAA CAAAGTGATT AAGGTATTTT 8160

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TCATACAAAG CTGTATGAGG CCACTCTTTG GGTGGATTAG CTAGTTTTTG TTGTGGAGCa 8280

TATAArmrTA ATGCTAACTC TTCAGGAGmw TAGTCCTTGA TTTTwkTATC CAAATCAAAT 8340

AGACCACTAT GGGCATAACG CTTCCACCGC CAGTTGC 8377

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GTTTTTAAAC ACGAACGTTA AACGGCCGAA TGTTCGGTTT TTACGTTATT TTTGTAAATA 60

ACTAGGAGGC AGTAAGTATG AAAGTTTTTG ATTATGAAGA TGTCCAATTA ATTCCCAATA 120

AATGTATCGT GAATAGTCGT TCTGAATGTG ATACTACAGT AACTTTAGGA AAACATTCGT 180

TtAAAATGCC TGTCkTcCmG CGAACmTGCm AACatTATgr TGrAACgATT GCGGAAcCCT 240

TGCTGAAAtG GTTATTTTTA TATCATGCAT CGGTTTGGAT GAAGAGGCGC GAGTGCCaTT 300

TATTAAAAAA ATGcAACAAA AGGGCTTGAT CACGTCAATT AGTGTGGGTG TGAAAGAAGG 360

GGAATACGCT TTTGTTGAAA CGTTAGCCCG AGAAGGTTTA GTTCCTGACT ATGTGACAAT 420

TGATATCGCC CATGGTCATT CAAATGCGGT GATTAATATG ATTCAACACT TGAAAAAATC 480

TTTACCAGAA ACGTTCGTTA TTGCTGGCAA TGTTGGAACA CCAGAAGCCG TTCGCGAATT 540

AGAAAACGCT GGAGCCGATG CCACCAAAGT GGGGATTGGA CCAGGAAAAG TTTGTATTAC 600

TAAGATTAAG ACTGGCTTTG GGACAGGTGG CTGGCAGTTA GCGGCTTTAC GTTGGTGTGC 660

CAAAGCTGCT CGGAAACCAA TTATTGCAGA TGGTGGAATT CGGACCCATG GAGACATTGC 720

AAAATCTGTG CGTTTTGGGG CaACTATGGT CATGATTGGT TCaTTATTTG CTGGACATGA 780

AGAATCACCa GgTGrAACaA AAGTGGaAGA TGGTGTTGTT TACAAAGAAT ACTTTGGTAG 840

CGCCTCTGAA TTCCAAAAAG GCGAAAAGAn AAACGTTGAA GGCAAAAAAA TCTGGTTACG 900

CCATAAAGGG AAGTTGGCAG ATACTTTAGT CGAAATGCAA CAAGATTTAC AATCTTCCAT 960

TTCATACGCG GGAGGTCGCG ATTTAGAAGC GATTCGTAAA GTTGATTATG TGATTGTAAA 1020

AnATTCTATT TTTAATGGTG ATACCATTTA ACATTCAACT ATAGACTGAA AAGAAGACCG 1080

CACGTAGnAA GGAAATTAAA AT 1102

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1009 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nAAGAATACG GTCTGTCTTT AACAACTTCA ATTGATGATA TTTTAGAAGA TAAAGAGATT 60

CAAATCGTTG TGGAATTAAT GGGAACCATT GAACCAGCCA AAACGTATAT CATGAAAGCT 120

TTAGAAAAGG GCAAACATAT TGTGACTGCC AATAAAGATT TACTGGCGCA ACATGGGAGT 180

GAATTAGTAG CGTTAcCCAA AAACATCATT GTGATTTATA TTACGAAGCA AGTGTTGCTG 240

GCGGGATTCC AATTTTAAGA ACAATTGCTA ATAGCTTAGC GGCAGACAAT ATTCAACAAG 300

TTTTAGGGAT TGTGAACGGT ACGACGAATT ATATGCTTAC GCAAATGGTT TCTGCTGATA 360

AAAGTTATGA AGAAGCTTTA GCAGAAGCGC AAgcGTTGGG GTTTGCTGAA GCGGATCCGA 420

CAAATGATGT CGATGGAATT GACGCAGCCT ATAAAATGGT TATTTTAAGT CAATTTGCTT 480

TTGGGATGAA TGTTTCATTA CCACAAGTTG ATATTCGTGG AATTCGCGGA TTGTCTTTAG 540

ATGATGTCGC TATGGCTAAA CAACTGGGGT ATGAAATCAA ATTGATTGGC TCTGCTGAAC 600

AAAATGAGAA TAGTATCTCG GTGGAAGTGG CGCCTATGCT AGTCAATCAA AAGCACCCTA 660

TTGCATCTGT TCGGAATGAG TACAATGCAG TATTTATTAA AAGTGCAGGC GTGGGGGAAT 720

CAATGTATTA CGGTCCAGGA GCTGGAGCTA AACCGACAGC AACCAGTGTG GTCAGTGATT 780

TAATTACGAT TGCTAAAAAC ATTCGCTTGG CAACGACTGG CCATATGTTC AATTCGTATC 840

AACATAAAAC ACAATTGACG AGTTCCGAAA ATGTATTTGG GCAGTACTAT TTTyCATTAG 900

aTGTTCCAGA TACACCAGGA CaATTTTTGC AGTTGACGCA ATTAATGACT AAAGCAGAAG 960

TCAGCTTTGA TCAtTAGTTC AACAGaAATC AGATGGACAG CGAGCAAGA 1009

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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nCGGnTAAAA TTTTTTCAGC ATCCTTATAT TACCAGTTTG GTCTTTCAAg AcTACTTGcG      60
ATcAGCaCtT TgTAcAgTTA aTTGTGCGCA ATATGCCAaC AaTCCAGaGC TTTtAACTaG     120
TCAaTTATTT GGACATCTTA AAGgCGCTTT TACGGGAGCA GaTTCCGATA AAATTGGGsC     180
CTTTCAAAGT GCAGAAGGGG GCGTTTTATT TTTAGATGAA GTTCATCGTT TGAGTCCTGA     240
AGGGCAGGAA AAATTGTTTA CATTTTTAGA TCAGGGTATT ATTTATCGAA TGGGTGAAAC     300
CAATCGGCCC ATTCCTGTTA CGTGTCGGTT GTGCTTTGCC ACAACTGAAG AAATTTCTAG     360
CACCTTTTTA ACGACATTTT TAAGACGAAT TCCTATTCAA ATTAAAATCC CaAGTCTTGC     420
TGAACGCACT CAAGCGGAAA GAAAACAATT AATTATGCGA GCATTTTATG AGGAACAGCA     480
AGCTATTCAA AAAGCAGTTA CTATCACGCC ACAAGTTATC CAACTTTTAG AAAACCACCA     540
TTATGTAGGC AATGTAGGTG AATTAAGAAA TAATATAAAA ATTATTACTG CACGCAGCTT     600
TGCCGCCAAT CTTGATAAAT GTGTTATTCC AATCACTTTG CACGATCTAC CGAAAGAATT     660
TCTGGATCAA TCAATCAAAC TAGTTCCTGA TGAAAATGAA TTGCCTATTC GTTTAGATGA     720
GCAAACAAAT CTGGTTAGTT TGTTAGAGGA AACAGAGCTT GCGCAArGAA GAATTATCCA     780
GAGTTATGAA CGAATCCTTC GTCTTTATGT CTCTCACCAT CATCATCTTT CCACTGCTAA     840
TAACGATATC TCGAAAGAAA TTGAACGCTT ATTCGATGAT TTATTATTTG AAAAGAAGCG     900
AGAGAAAAAT CACGAAATGC TATTGTTTAT TACGCAAAAT ATCCGTCAAT TATTGGAAAC     960
GATTGAATCG TCTTATCAAA TTCGGTTTAA TGGCAGTTTA GTCTATGCAT TAAGCACCTA    1020
TCTGTTTCAA CGAAGATGCA TTGATTGGTT TCCAGAACAA GAACCTACAA CAGTCATTGA    1080
CGAACTTTTA ACAGAAGTTC AAACCAAATT AGCAACTAGT TATGGtACGC TGAACAACTG    1140
TTAACTTTAG TGAAACGTTC ATTAGATATT GAACTATCCC AGATGGAwCG AATTATTGTC    1200
ACCATTTATC TTCACTATTC GGGTTCAGTA AAGAAAAGTC ACTATCCGAA AGCGGTGATT    1260
GTTGCCCACG GATATGCCAC AGCAAGTAGT ATTGCGAATG TTGCAAATCG GCTGTTAAAT    1320
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CACTTAATTC ACTATATGGA ACGTCAAGAA ACGAGGAATG GTTTAGTAAT TCTTTTTGAT    1440
ATGGGTTCAT TGAAAGAwAT TTATCAGTAT TTtCCGGCAG AAGrAGAAGG kCCtTTTTTA    1500
tTAATGraTa ATGtGACmAC mAGcTTGGCT CTGkCTaTwG GAGrAGCCmT TwAAGmCGAA    1560
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CAGCCGTTAA AATTAGAGAT TTACTTGAAA AAAGTTTACC TGCGGAAGCA CAATTAAAGA    1740
TTATTCCTTG TGAATATAAT CAATTACGTA ATGCAGAGTC GATCAAAGAA AGTTTTCCAG    1800
AATATGAGAT TGTCGGCATC ATCGGTACAA ACAACCCGTC TTCAAATGAC CTCCCGTATA    1860
TCTCTTTAGA AGAGTTGATT GCAGGAAAAG GAATTACGAC CCTTTTAGAA TGGACAAAGA    1920
GAGAATTAAC TAAAGATATG CTGTCCTATG TAAATCATGA GTTGATTCGT AaCTTTTCAT    1980
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TAGATCGGGT CATTCAATCA GTGACGATTT TAGATACAGA AAAAATTATT CGACAAGTAG 2040

AGGTCTTTTT AATTCAATTA GAAGAGCGGT GGCAACAAAC AATTCAAAAT GATCGTAAAT 2100

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AAAATTATAA TGGCGCTGAA CAACTAAAGC AGTGTCAAAG AACGGTCTTG CAAGAGTTAA 2220

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CAGCCTTAGT CTTAGGCTTG CCAATCGCAA CGTTAACGTT GaTTCTTAAA AATATTTATT 3660

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TCATTGTAAC TATTTCATTT GCCGTGGGCA GCAACACCAT TAAAGGCTTA CTTGATCTGA 3840

TCCCTGAATT TATTCAACAT GGATTGTCTG TTGCAACGGG GATTATTCCA GCGCTAGGAT 3900

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TCmATAATTG GCyTGATrGt GGkArGTGCy ATGaCCGCCT CCATGATTGA TTTAACTATC 4740

CCgATTACAA TCAGCgGAAG TGGGaAAAAT GCaGTCACGG TyCAAAATAT CyTTGACGAT 4800

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ATTGGTCTAT TTTAGGAGGC AAAATATGAA AACGATGCTG GATTATrTAA ATGAGGAGCA 4980

aGCAGCTCTA rCTCAGaTTC TTAACCAATT TCAaTTAACT GATACAGACG TTTCAAAGGT 5040

CACGCACTGt CTAATTTTAG CAACTGGCTC GTCACATAAC GyTTkTCAGG CGGCTAAArT 5100

TTACCTTGAA GAAGTGGCGC CTATTTATGT GGAAATCCAA GAGCCGTTCA ATTTTGCTCA 5160

TTATGGCAAA GTGGATGATC GGTTTGATCT GGTCGTAGCG GTTTCGCAAA GTGGTAAAAG 5220

TGCTTCAACA ATTGGATGCC ATTGCAAAAA TTAAAAACCA AACGTCTGTA AAAACAGTGG 5280

CCTTGgACAA GTGaTGTCAC CAGCCCGATT ACGGaGGTTG TGGaTGaAGT CCTGGaTTTa 5340

AAAATAGGGc TTGAAACAGT TGGtTTTGTC ACAAAAGGGt ATACGGcAAC ACTTTTaAAT 5400

TTAtTTCtAt TTGGtTTgAA ACTGGGCTAT CAAAAGCATC AATTAACAAA AGTAGAGGTT 5460

GAAGAAGAAT TAGCAAAACT TnACCAAAGC AATTCAGGAA ATCGATTCGG TGATTTATAA 5520

AACCGAACAA TTTTGGGCAA AAAACGGAAA AAAGGAAn 5558

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AnATnTGAAT CGTATAGCGA AGCAATTCTC TGATCAGAAT nATTTAACTT CGTTTGGGAA 60

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AAATTTCTGG CGCAAAACGT ATAACGGAAA ATCACCCACT CAGGAACTAC TGAAGGTTGC    120
AACGGAGGAT TTAGTACAAC ATAAAATGAT TAAACAGCTG GCAACGGAGT TAGAAATAGC    180
CCACTCACAA ACATTTGGGc AAGAAAAAAA AGAATGGCAA GACCAAAAGA GCAGTTTAAC    240
GCTCTGGCAA TTTTTAGATG CAAAAGATCA ACAATTACAG GACCAAATAA AAGAGAAATT    300
AATGGAGAAA GAAAAGCCAA CGCAAAAAGA ATTGCGGcAG GCCTTTGAGC AATTGGATGA    360
TAAATwTAAA AAGACCGATT ACTTTGTTGA AGCAATTGAA ATTCCAAATT TTTCAGGTAA    420
GCAAGCAGAA TTAGAAAAAA TAGCCGAAGC AATCTCTCCG AATCTATCTT ATGAGGAGAC    480
GTTATTGGAG TGGCAAAATA AATTACCTAA TCTTGTTATT GAATCGTATC AATTGAAGAG    540
TGCAGAAATC CAAAAAGAGG ATATTTATTC GTTGTCTGTT GGGGAGATTC TTAGTGAAAA    600
AGCTGTTGGT ACCGTGGTGA AAGGATACCA CGAAAACCAA TACTTTTATA TTTTTAATAA    660
GGAAGGAGGG CAACTTTTAC AGTTTGAAGA AGCACCACAA TTTGGCAAAA ATGCCTATAT    720
CAACACACGC TACAAAGAGA AaTTAGCTAC GTATCmACmA GCAACCAAAG TAGACTTGTT    780
GGAGAAAGAC AGAGAAAAGT TTTTTCAAAA TTATCAAAAT AAAAACAGTT AAGGAGCAGA    840
AAATGAGAAA AAAAGCGTAT TTTAAAAGTG TAACCATCTT CCTTTCTATT TTGCTTGTTT    900
TTTCCCAGCT TCAATTATTT AGTCTTCCTG CTTATGGGGA AACAGTGAGT GATCAACCGT    960
TACTTTTTCG TTCAGTAGGT GTCGCTCAAA GTGGGACGAC CTACTATGTG GATGGGGAAG   1020
GAGGAAATAA TGCCAATGAT GGGCAGTCGC CAGCCAGTGC TTGGCGTGAT TTTGAAAAAG   1080
TGAATCAGAC GGAGTTTCAG CCAGGCGACC ATGTTCTGCT GAATGCGCAA AGTACCTGGA   1140
ATAACCAATT GTTGCATCCA AAAGGGAATG GGACAGCGGC ACAAAAGATT GTCATTGATT   1200
TTTATGATAC GAATGACAAA GGAGAAACCA TTTTTGAAAC AACACGGCGT CCGATTATTA   1260
ACGGTGGTGG CACCTACAGC ACAGGGACTT TCAAACGTGC AATCTCAGGG GCCGTGCAGT   1320
TAGTGAACCA AGAATATTGG GATATTTCAA ATTTAGAAGT GACAAATACA CCAGAGCTAG   1380
ATAATCTCGA AGGCTATAAG AAACCAGGAG ATGCTCAAAG AGCGGGGATA TTAGTACTAG   1440
GATATGAACA AAATCGAACG TTCAATAGTG TCACGATAAG GAATAACTAT GTTCATGATG   1500
TTCAAACAGA ATATTATTTA AATCTAAGTG GGAATACTGC AACCAAACGA TTAAAAGCGG   1560
TAGGTGGAAT TATTGTTTTA GGAAGTTGGT TTGATGAGAA TGGCAATGTA GTAACGGCAG   1620
CTAATGATCA TCGAACAACG ACTGGATTTA ATGATATTTT GATTGAAAAT AATGTGATTC   1680
AACGAGTGGG ACTTGAAGGA ATTCGAACAA AAGCTGATTC AGATACCtCA AGAGGCAACA   1740
CTTTCTACAA AACGTTTTCT AATATTACGA TTCGTAATAA CTATTTAGAA GATATTGCTG   1800
GCGACGGGAT TGTCTTGTCA GAAGCCAAAA GTGGCGGTGT CGTCGAAGGA AATGTTGCTG   1860
TCCGAATGTG CAATGCCGAT TATGGTACAC AAAATTACGC GGGCGTTTGG GCAATGTCTG   1920
TAGATGACGG ACTGTTCCAA TATAACGAAg TATACGGAAT CAAATATGGA TTTAACGATG   1980
CTGAAGCTTA TGATGTGGAC ATGCAGTCAA ACAATGTTAT TTATCAATAT AACTATTCAC   2040
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ACAATATCTC AGCTAATGAC GGCGGTGGTA ACCGAGGAAC AGGTAAAGAC AATCCAGGCG 2160
GAGCTGGTGG CTACAATTAT AAAGAACAAA GCATTTTCCA TTATTGGGTG AAAAATGATG 2220
GAGCGGCAAT GCCAACTATC CACAATAATA CGATTTATGT TGGCGACGGT ATTTCAACAT 2280
CATTATTTGG TGAAGGAAaT AGTTCTGACA ACAGTGGTAC AGTAGCCAAT TTTTACAATA 2340
ATATTTTATA CAAAGAAGGT ACCGGACAAT TAAAATTCTT ATCTAATTAT CCAACAAATG 2400
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CAAGTGGAAA CATTTTTGAA AAACCACAAT TAGAAATCAC AGATAACCCT GAAAAAGTGA 2580
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ATGTGATGCG TTATGATGCG TGGAATGGTG CTGGAAATAC AAATGATGAA CGTTTGAAAA 3420
ATACGCAGTT CCAAGTAGAT GTTTATGGAa CAGATACTAA TTGGATGAGT AACACCATTA 3480
CTTGGAACAA TGGTCCAAAT AATTTAAATG TACCAAATGA AGAATTTATT GCTCGACAAT 3540
CTTTTACAAA TAGCTCAATT ATGAATAATC AAAATACAAT CTCTATTGAT ATTAGTAACT 3600
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CGATTACAGA CAGTCGTTTG CCTGGTTATG ATTCTGATAA TGCTGGGTTT GATGCTTTTT 3720
CAAAAGAAGG CGCACAAAAG GCCTATCAAG ACTTTTTAAC AGGCAAATTG ACCTTGCCAA 3780
CTGGTCAACA GCTAGCAGAG GATAGTTTAG CTCCTAAAAT TGTTTTATCG AATGTTTTCG 3840
AAGTCAAACA TGAGTCGATT GAGGTCACGA CAGAAGCGGG TCAAGCCCCT AAACTACCAG 3900
AAAAAACAAC TATTTTTTAT TCGGATGGTT CACAACGAGA AGTGACTGTC AATTGGTCAG 3960
AAGTTCCAGC ATCTTCTTAT CAAAAAGAAG GAATATTCAC TGTTGTAGGA CGAGCAGCAG 4020
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AACTGAATAA GAAAATGTCA TCACTAAGGC AAATAAACTA ATAATAGGCG CTGGAAAGAT 9000

TAATTGGCAA AACAGCACAA TCATTGTTTG AACATTATCT ACATCGT 9047

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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ATTGCTCTTG tTAGGTATCT TTTTATTTGT GaCTTTGCCa AGTAAAAATC TTTCaACCGT 180

GTTATGGATT AATCTGATTG GCGCAGTGAT TGCTAGTGGG GTGTTATTAA GTACACGCTT 240

AGCTAGTAAA GTCGAAGTTC CTGGTATCCA AAAGGGCCGC AAAGAAGTAG GGAAGAATAC 300

CAACAAAACG GCTAACAAAG ACTGGTCTGG CAAGATTTTG GGTGTTGCCG TTTTGGCAAT 360

GATTTTGTTG ACTATTGTCA GTAGTATTAC CAGAATCTCT TCTATTGATG AAATTTATCA 420

AACGATTCCT TTAAAAACGG AAGAAAAAGC TGAAGTTTTA ACTTCGGCGA AAGAAACACC 480

CaTTGCGATT GCACCACAAA CGGCGAAACG AAAAATGTTA CAGAAATTTT CTGtCATTCC 540

CAATTcCAAT ATGTTTACTT TGGaTGGtAT AACGGCACAA GTTGTCAATG GCGAGTATGT 600

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TGGCTATTTC ATCATTAGTG CGACAGATAT CAACGCACAG CCAGAATTTG TAGAAAAACC 720

AATTGTTTAT ACTCCTTCAG CTTACTTTGG CAAAGATGCC GCACGAAAAA TTTACTCCGC 780

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ATTTAAAACG GCAGTATTGA ATGCTACAAC AGGAGAAGTT AACGTTTATG ACAGTCAAAA 960

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CTTTGGTCGT TACAGTCAAG GCTGGTGGAA CCAGACaATG TTTGGTGCCA AAAAAGATGT 1080

CAAAATTCCA ACTGAAAATG GTATTTATGC ATCAGGACAA ATTACGCCGA TGATGAACAA 1140

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ACTAGAAGAT GAAAAAaCCA TTTTTAGCGT AACGaCTAaT AACAGTcCcT GGCGCTATTC 1680

TTAAAaGAGG GCGaCCAAGT GACaTTTAAA GCCGTAGtGA CTGAAAATGC TAAAGCAGCG 1740

AATGTTGAAG A 1751

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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TCCATCAATT TTCTTGAGAT GGCCGTTATC TATTTTAAAC ATAGATGGCA CATGTAAAAC 240

TTTATTTTCT CGGATAAATG TTGACCATTC CTTCATGGTC TCtTTGTTGG TTAATTCTAC 300

ATAGTAAACC TGTTTAGGTG CTTGTAATAG TTTCTCGAAA TCCTGACAAT CTGAACAGTT 360

TtTCTTTTTT AAAACAACAT AAAATGTTTC GCCAGAGTGT TTTTTTTCTT GATACTCATT 420

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ATTTTTTCTT TTTTTATTTT TTGTTATGCC AAAGCTAATA GCCACTATAA GGACAATTAA      600
ACCTGCGATC ATGTAAAGTG GATTTACTGT TGTATTAGTC ATTGGTAAAT GAATTCCTTT      660
ACTTGCTGaT TTTCCAAAAT TGaCTGGGTT CGTTGGTGCT TGATGATTTG TAGGCGTCAA      720
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TGCAGGCGGT GTTACGGTTG GCTTGTTGGA ATGCAACACG TCACCTTCGT TGCCAAAGTT      840
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GGTTTCGTTG CCAAAGGCTG TTTTGACATG CCAATCGAAA CTATCTTCAC GATTGGTTAA     2100
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GACTTCGTAG TGAATCGTGA TGTTTCCTAC GTAACCTTCT GTACTAGTTG CTGAAATGGT     2340
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ATCTTCTGGT GTGCTAGACC CTTGTTGCAA CTCTTGTTTT ACAAAAGGAC CCACTTCTGT 2580

TTTATATTTA TCAAAGTATG AATTCACTGA ACTTAAAGAT TCAACACTTT CCCAATACGC 2640

ATTAATCATT TCATAGCCTT GGTTAGTAAT TTCTTGGTTT AACGCTAAAA CTTCTGCTGC 2700

TGCACCTTGG TAGTCATTAC TATATTCCAC TGAGACTTGA AGAGGATGTC TTGGATCTGG 2760

ATATTCATTG ATTGAATCAT TGGTATTGGT CTTATGCAAG TAACCATCTA AACGTGTATT 2820

AGCGACCCCA TCTGTCACTA ATAGGAAATA CGTTTTTCGA TTCGTTAAAT CTCCGTGTGT 2880

TTGATTGTAC GTATCTAAAG CGAGTTTCAA TCCTGGGGCG GTTGGCGTAC CACCATACGT 2940

CCGAACGTCT CCAAAACCAG AGACAAATTG GCTTTTATCA TAAGTCAATT GCGTATTGAC 3000

GCGCACATTC ATATCATAAT CAGCTGAATT AATTTTTGTC TTTCCATCAG GAAACATAAA 3060

TTGTTTTCCG CCGCGATATG AAGCCAGCAT CACGCGGTCT TGATCAGATA AGCCTTGAAC 3120

CACTTCATCA ATCGCTTGTC TTACATGTGG AAAATTATCT GAAAAACTAC CACTAGCATC 3180

TTCAACAACT ACTAAATCGA CTGGTTCCGT TTCACCCGCT TGAACTGGGA AAGTAGCTTG 3240

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CATTCCTTCT GTATCTCCTG CTTTAACCGC TTCTTCAGCT AAAGCCAATG TGGGACTGAA 3360

ATTTCCCACA ACTGTTCCAG CGACAATCAC CATTGTCGAT AATAATTTCG TTGCTTTCTT 3420

AAACATTTTA ATCCTCCCTA TTTTCTTTCG CTAGTGTTTG GGACACTTGC TTCTCTTTAC 3480

TTCAACTACA GCTCCTTAAA TCTTTCATCA AGTCGATGTG TCTCCTTGTT TTTGTGACAC 3540

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TGGTTTTCAC TTACTTTTTG CTACTTGATT CCTTTTAAGA CTCTTTTTTT ACACAAAAAA 3720

AGTAAAAGAA CCTTTACAGT CCTTTTACTT AATTGTTAGA TGCTATTCAT AATTTTCTTA 3780

GTTTTGTTCT ATAAGCTGAA TAGTTTAGCC TGTTTATTTC AACAATATTT GACGTTAGTC 3840

AGCCGTTTCG TTATAGTTAA AGAAAAGGCT TTTTGGTAGG AGTGAATACG ATGAATGAGT 3900

GGCCCCATCA GTTAATGACG CTTTTAAC 3928

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGTTAGGTAC ATTGCTGGTT AATGGAACAA GTGAACAGTT ATATGAAACA AaCGAmaCCA 60

TTCACTTGGC TTTTCCAGCT GAGAAATTAG TTATTTTAGA AAAATAAAAA CCATTTTGGA 120

GGAAGATTTA AAAATGAAAA AACGCGTAAT TTTAGGGACA TTAGTCGCTG CAACGTTATT 180

AATGACTGCT TGTGGAAACA GCGAAgcAAC TACGAAAAGC GAGAGCAAAG GTGGAAGTAA 240

TGCTTTAGTC GTTTCAACTT TCGGATTAAG TGAAGATATT GTCAAAAAAG ACATTATCGC 300

TCCATTTGAA AAAGAGAATG AAGCGAAAGT TACCTTAGAA GTAGGCAATA GCGCAGACCG 360

CTTTACGAAA TTAAAAAATA ATCCCAATGC GGGAATTGAT GTCATTGAAT TAGCACAAGC 420

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TAATTTAAGT CAGTTAACGC CGGGAGCAAA AGAGGTTTTT GAAAGTGGTG CTGGCGTACC 540

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AAAAGATAAC GGGAAGGCCG CTTTTGAAGC GATGAAAGAA TTAAAACCAA ACGTTGTTAA 780

AACGTATTCA AAATCGTCAG ACTTAGCyAA TATGTTCCAA TCTGGTGAAA TTGAAGCAGC 840

TGTGGTTGCT GATTTTGCGG TTGATATTAT TCAAGGCGCA CAGAAAACGT GACGTATATC 900

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AACAAAGAAA CCGCCTTTAA ATTTGTTAAC GCACGGATTA GTGAAGAATC ACAAAAGGCC 1020

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GCGAAAAATA AAACATATGG TGCCATTGCC GAACGTGCCA AAACAGTCGA TTTTAATTTT 1140

ATTAATAGTC AACTAGCGGA TTGGATTGAT CAATGGAATC GGACGATGAA TCAATAGTTT 1200

TAGAAAAGAG GGACAAAATG AACGTCGATG TATTACTAAA AAATGTGTGG CTGTATCAAA 1260

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ATAAATCAAT CACTCCTGAA AATATTCAGG TGATAGTAGA CAATGACTTC TACAATTATG 1980

CAAGTATTAT CACGGATGAC GTGATGGCTG ATGATTTGCT AAAAGGTCAT CTAAATGAAA 2040

ATGTCAAAAA AGCTGTTCAT GCAGGGTTGC CTATCGAAAA AGCCATTTAT ATGGCAACTT 2100

ATACGCCAGC CAAACGAATG GGTCTCCATG ATCGCGGCGA AATTGCACCT GGTAAAAAAG 2160

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GAAAGGTCGT TTTTGAAAAA GGCGAGCCCT TCCATTATCC AGAAAAAATC GAAGAGTTTC 2280

CAGCCACTTA TCAACAAACC ATCCAATGTA AAAAGTTAAC AGAAGAAGAT TTACTTTTAA 2340

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TATCTGGCAA CGATGGGGGG CGCTAAAACG TTAGGCTTGG CGGAGCAAGT CGGCTCATTG 4020

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ATTTTTGATG CCTATTCAGC GTTGGTTTAT TCAGCAAATG CTAGCAATGT TGAAGCCGTT 4140

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GGTTAGTCGC TTTGAAAAGA ATGGTCAAGT CCCAACTTTA AAAATATTGA TCCaACTATG 4620

TAATCGTTTA GAGCTACCTT TGGGGGAACT CTTCCCGCGC GTAGGGATTA AACAACCTGA 4680

AATTCTTGAA AAAATGGAAG AAGCAGAATT CTTCTTGATT ACCAGCGAAC ATGACCAATT 4740

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TTTAGAAACA AGTGATGCTT TGTTAGAGTA TGCGATTTCC ATCTGTTCTG ATAATCACGT 5160

CACGTATTAC TTGGCAAGAG CAGCTTTCCA ACTTGCGAAA AATGCCTTAG CTGAAGAAAA 5220

GCCGCAAGAG CAAATTTTAG AACTACTACA AGATGCCCG 5259

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AGGCCGTnTG AAGTGGaCCc TnGAgGAaTT wGtTCaAAAr GCmAAgGnTT TAATTGGaGA 60

AGGCcAmCGT GGAACnTGCG CaACmATTcA TTGrAGAACA TAAAGaTGAA TTAGGCGAAC 120

ACTATCATAA AATTACAGCG ATGTTAGCTG ATACAACgAC CgATGgTTTG TTTGATAAAA 180

TTAAAGGATT GTTTCAATAG TTGAAAAAAA TCTGAGATAA AAGTGTTTAG CTCCAAAAAC 240

CAAGTAGGTA CGATGATTTC ATTTGTTCAT GCTTCACGGT GAAACATTGC AACTCTCGCC 300

GTTTAACAGT TTTTGAGCGT GGAGCAAAAA TCCAAAGTGA TTTTTGTCCC ACGCTCTTCT 360

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AATCCGCTCC CCGTTTCACC ACAGGCATAT TCGTAATAGC TAAAATGAAG AGGGCTAAGA 480

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CACTTTCCAA CAGAATAATT AAGGGCATAT GCAAGAGATA AGGGTAGAGG GTATCTTTTC 600

CGAGGGCGCT TAAAGGTAAC TTTCGTTTCG GCAATAATGC AAACCAAGAA AGAGACACCA 660

ATGCTGCAGC AACGTAAAAG AACAGCTGAA TGAAACTACT GTATTCAAAG GCCGGACTAA 720

TTyCAGCGTA GGAAGCCCAA CCAGTTAAGA aGCCCCAAAA TTTCGTTGCC AATGACCATT 780

GACTATTTAC AAATAAAAAG GAGCTTAAAA TTACGCCTAT CGCTGCCCAT TTGACTTTGC 840

GATGATCTAA AAAGGTTTGT AGCTTTTGAA TATCCATTAA GTAGCCACAA TAAAAGAAAG 900

GGAAGAAGCC CAGAGTCCGT CCTAAAGACA AGAAACCTTC CACAGGTAAA TAGCCTGAGG 960

CGCAgCcGAT AACAATGATG ATTGGCAACA TGATTTTCGG CTGAACGCGC TGAAGAAAGA 1020

TGGTAATTAA GTAGAAACTT GCTAAGGAAA GTAAGTACCA AGGAACGCCT GTTTCGTTCA 1080

GTAAATCAAA ATTCATTTTA TTTGCAAAGG CGAAATTAGC AAGCGTAATC AACAACTTCG 1140

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AATTTAACAA TCCAACAAGG CGAATTTTTT GTATTAGTAG GGCCGAGTGG TAGTGGAAAA 1740

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AATGAACAAG CGGTAACCAA TTATCCTTTA CGTGAATTAC GACTAAAAAT TGGCTATGTT 1860

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GAACCTTTTA GCGCGCTAGA TCCGATTTCA AGACATCATC TTCAACGTTT GGTGAAAGAA 2160

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GCACTGATTG AAACTTTTTT CGCTCGAAAA GAAGAATATC TGCAAGCGTT AATCGAGCAT 2640

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TTGCTTCCCC CAAATGAATA GTGGGACGTA CATAATCGGT TTCTTCAAAC GTTAAGGTGA 7620

CACAATCGCC AGCTTGGACT GGAAAATGAA AAGCAGCTGT TTCTCCGTTG ATTTTGACAT 7680

TTTT 7684

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AAAAGTTGAT AAAGAATCAG GTGCTATTGT ACCAGGAACG GTTTTCCATT TAGACTTTGG 180

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AAATACGCGG GAAAAAGGTC AAATCATTCT GGATAAAACC GGGATTGAAA CAGGAAGTGA 420

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GGCCCTTGTG ACCAGCAATA TCAAAGGGCA AAACCAAGAA ATTACTGGGG AAACAACTCT 720

GATAAAAGAA GACAAGGATA CTGGAGATAA AACACAAGGC AGGGCAGTCT TTGAGGGGAC 780

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AATTAAAGGT TCTTCACCAA TAAAGGCTAA ATAGCTGACT GTCACGACCC AGCCACGAGG 28620

ATCTCGATCT GGGCGACTAA AGCTGTGTAA TTGTTCAATA TTTTCTTGAG AAATCACCAC 28680

ACCAGTTTCC TCTTTTGTTT CTCTTAAAAC ACTATCTTCA GTAGATTCGT TGCGATTAAC 28740

AAAACCGCCA GGAAGCGCCC ATGAGTTTCT AAAGGGGTGA CCTTTACGTT GAATCAGTAA 28800

GACTTTTAAT TGATCAGCTT CCTTGTTGTA ACAAAGAAGA ACCATATCAA CGGTTAAAGA 28860

GGGTTTTTCA TATTCAGGTA ATTCTTGTTG ATGATACCAA GTTAAAAACT CTGCTAAGCT 28920

AGCTTGGCGT TCATAATAAT TTTTTTCTTC GGCTTTAGAA GCAAATTGTG GCACAATTGC 28980

TCCTCCTTTC AAAAAGAAAC ATGGTTTTCT TTTATTGTAT CATTAAGTGG CTGAAATACA 29040

ATATTCAAGC GTAAAAAGAA AAGCAAGCCT GGGACAAAAA TCACTTTGGA TTTTTGTCCC 29100

AGGCTTGTAC TATAAGAAGT TTGTTCTAGA CGTTATTTAT TGTGTTAATT CTAATAATTT 29160

ATTTTTCAAA TCTTCTTCCA TATGGCCAAG TTCGATTTCG GCAGCTTGGC GTTTTTCTTT 29220

TCCTTCTTGT TGAATACGTA ATGTTTCTTG GATAGTTTCA ATTAAATCAT TTTGTGTTTT 29280

TTGtAATGTT TCAATATCGA CTAGGCCACG TTCGTTTTCT TTTGCTGTTT CAATTGCAGA 29340

AATTTTTAGC ATTTCTGAAT TTTTCTTCAG TAAGTCATTG GTGGTTTCAG AGACTTGACG 29400

TTGAGCAGTC ACAGCATCTT TTTGGCGGAG TAAGGTTAAG GCGATGACTA CTTGGTTTTT 29460

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ATCCATTTGA TCTCCAGATT CTTCCGCTTT TTTCATGGCT TCAGGGATAA TTTGCGTCCG 29700

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AATTTCGTAA ACGGATTGTT TGACTTTACC TAACATTTTT TGAATAAAGT TGCCTTCGCC 29940

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ACCAACAGGA CCAATGTCTT GTGCTTGAAC GTGGTTTAAC ATCGCTTGCG AAAATTCGCC 30060

GAGTTTGATT TGGGCATTTG AACCATAGGT AATTACTGCT TGTGAATCTT GGACATCAAT 30120

TTTTGAAGCT AATTCTTTTG CTTGGGCTTG ACGTTCTTGT GGTAATTTAT CAATTAAACG 30180

AGGAGCTGCT TGCTGTTCTT TTAACTCAGA TAGTTCATTT TGTTGCGTTG GTGTTAGTTC 30240

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CAGcAATGaT TAAGGCTCCT AAAAGAATAT AGCCAATCAG TAATTTTGTA TTTAATTTGT 31020

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GTTATTTTAG CATACTCTGT GAGAGAAAAG ACATACAGCG GAAGATGTAT TTTATGATTT 31140

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CAGGCGCAGT AGCTATGATT CCGTTAACCG CAGAAGGAAA AATCGTCTTA GTTAAACAAT 31620

TTAGAAAACC CTTGGAACAA GTAATTTTAG AAATTCCGGC GGGAAAAATT GATCCTGGAG 31680

AAGAAAATCA ACTGGAAACG ACGGCTATGC GGGAATTAGA AGAAGAAACT GGGTATCGTG 31740

CAGGTCAGCT TACCTACATA AATTCAATGT ATCTGTCACC AGGATTTGCT AATGAAAAAT 31800

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ATGAAATCTT GGAACTTTAC GAGCTAACAA TAGCTGAAGC CAAAGCAGAG GTGGCAAAAG 31920

GCACGATTTG TGATGCCAAA ACACTTTTTG CTATACAATA CTGGGAATTG TATTTACTGC 31980

AGAGACAGTT TAAGGAGGAC ACGCAATGAG CAAAGGTCCG TTAGTCACTC GGACAGAGCT 32040

TCGCAAACGC AGAGAAGCAG AAGAAAAAGA AGCGGAACGT CGTCAGCAAG AAGAGCAGAA 32100

GCTGGCGGAA AAAGCGTATA AGCGAAAAGA AAAAGAAATT TCGACGTTTT ATCGTAAAGA 32160

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AGGAATTGGT AAAGTGGCCT CAGCTGTGAC CACGACTTTA TTGATTCATC AATATGGCGT 32520

AAATATGGTG ATTAATACAG GTTCTGCTGG TGGTATCGGT GAAGGACTAA AAGTTGGCGA 32580

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CTATGGACAA TTGCCTGGTG GTGTGCCTTT GTATTTTGAA ACAAGTGAAT ACTTGCGGAT 32700

GGAAATTGCG AAAGCCGCTG AAAAAACTGG TTTAGCTATT CGTAAAGGAT TGATTGTTAC 32760

TGGAGATA 32768

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAGTAGAACG TAAATGGTAC GTAGTAGATG CAACAGATGT TCCTTTAGGA CGTCTATCAG 60

CAGTTGTTGC TTCTGTACTA CGTGGTAAAA ATAAACCAAC ATTCACACCA CATGTGGATA 120

CTGGAGATTT CGTAATCGTA ATTAACGCTG ATAAAGTAAA ATTAACAGGT AAAAAAGCTA 180

CAGACAAAAT TTACTACCGT CACTCAATGT ATCCTGGAGG ATTAAAATCA GTGACTGCTG 240

GTGAATTACG CGACAAAAAC TCTCGCCGTC TTATCGAAAC TTCTGTAAAA GGTATGCTAC 300

CTAAAAACAC TTTAGGACGT AAACAATTTA CTAAATTGAA CGTATACGGT GGAGCTGAGC 360

ATCCACATGC TGCACAACAA CCAGAAGTAT TAGATATCAC GAACTTAATT TAAGGAGGGA 420

AATTCATTGG CACAAGTACA ATATAGCGGC ACAGGCCGTC GTAAAAATGC AGTTGCCCGC 480

GTACGCTTAG TACCAGGTAC TGGTAAAATT ACTGTAAACA AAAAAGACGT AGAAGAATAT 540

ATTCCACATG CTGACTTGCG TGAAGTTATC AACCAACCAT TTGGCGTAAC TGAAACAAAA 600

GGCGCTTACG ATGTAATCGT AAACGTAAAC GGTGGTGGCT ATGCTGGACA ATCAGGAGCT 660

ATCCGTCACG GAATCGCTCG TGCATTGTTA CAAGTAGATC CTGACTTCCG TTCTGCTTTA 720

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TCAAGACACT TTCCAAATTT TGGAGGGTGT CTTTTTTTGT GTTTTTAGGT ACGACAATGG 900

GTACGAGTTT TTTAAACCAG CTATTCATTT TATATTTTTT GCTTCTGCTA ATCGTTGTTC 960

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TTTTGTATCA GAATGGGTGA GCGCTCTAGA AATTTGTTCC ATGGTTGCGC CACCTTCATA 1080

TGCTAGCGTA CTAAAAGTAT GTCTTAACTT ATGAGAAGAA GTATTTATTA AGTGTTTGTG 1140

TCGACGTTTA ACTGAGTTGA TGCGGTAGTT AAGATAGTCT ATGTGTACCG GGACATTCAC 1200

ATTTCCCTTT CTATCAATAT AAGTGAAAAG AAATTGCTCT GCATTTTGnT tAATTCCAAG 1260

TTGTAAAAGT TCTTGTGCTT GTTCTTTTTT CCATTTCATT AACAACTCTA TAAGGGAGGA 1320

AGGCAATTGG aATTTAGTGT TTTTTCTTCC TTTGGTAGGA GTTAAATTTC CTAGCTTGwC 1380

TTTGCTTTGG ACAAGTAGTA TTGTTCCATT CTGTAAATCG ACATGTTTCC ATTGCAGAGC 1440

ATAACTTTCA CTTTTACGAT CGCCTAAATT TAATGTTAAG GTAAAAAGGA CAAAATCTTG 1500

AAAGGTTAGA TGTTTGTTAT TGTAGTCTTG TTGAATGGCT TGAATCCACT CAAGAAGTTG 1560

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GACCTGTTCA TAAAATTCTT TGAAAGAAAT ATTTGCTTTT AATTCAAAAG CTCGTTCATG 1980

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CCAACTTATC ATAAAGTACT ATTCCGTTAA TACTGATTCG TGGAAGTCCA ACTGTAATTA 2340

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GAACACATTC ATACGTCCAG CCCAACGTTC GCCGTCTTTT TGCCAAAGGG AGACTTGGAC 4320

TACTTGGTAT TCATTTTCAA GCTTTTCTTT AGGTAAAGTT AAATCGTTAA TTTTTACTGC 4380

CATTTCATAT CCTCACTTTC TTTTAGTACA TTTTTTAGTA CAAACATATT CTAATGGAGC 4440

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CATATAAATA TGATGAAGCG GTTGATTTAT ATAGAATAGC TCAACTACCA GAAACTTTAT 5340

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AATACAGAAG ATAGTAGAAA ATATAGGGAA ATATGATAAA AAAGAGTTTT TGCAAAGACT 6480

TGCTGCACTA AGAATTCCCT TTGAAAATAG AGATAAGGCT GTATTATTGG ATGCAACAAC 6540

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TAACCTTATG GTTTCTACCG ATGTTTGTAA AAATGTCAGA TTCCAAACGA ATTnCCATCA 6900

TTCACTCGCG AAATATnTAT nCCTAATAAA 6930

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTACTTTCG TCCAATATTT ATTTCTTCTT CAAGCTGATA AATAGACACA TCTCTATCTT 60

TTGCTAGTTT TTTTATACGT TCCAAAAGGT TCATATGAAA ACATTCTCCT TCTAGTTACg 120

mGTTATTTmC AAAAAAAGTT AGTAAAAATG TTTGACATTT ACAATATTTG TTAGTAATGT 180

AATCACGTAA GCTAATTTAT TAGCTAATAA GTTCTCAAAT AAAACCTATA AACAAAACTT 240

GAAAATCGTT GGGGAACGGT AAAAGTATTG TTTTAGAAGG CTTTTAAAGT CTTATTTAGC 300

TATGGGTTCA TTTTACAATA TGTGTTAGAA AGTGTCAACG AATTTTATTA AATTAGCTAA 360

TTTTTTAGCT TACAAATTAA AAAGAAGGAA TGGAAGAAAT GAAAATTGAC GAaGCTGTTT 420

CAAAAGCAAT GAAAAAAGGa AAATATATTT ACAGGGAGTC TGAAAATGAC TGTTCAGCTC 480

ATGTAAAATAT ACTTCCTACA AATACCTATG ATTGTTGTCT ATTACTACAA GAAAATAGTA 540

ATTCTGTTGG CAAACGGTGG AACCCTACAG CAAATGATTT AATGGCGAGT GACTGGGAAA 600

TACGTTAGTC AAGGCCCAGT GTTTTTGTAA TAACTTTAGC TGCGATTTCA CTCATTATGT 660

CAATTGAGAC ACTTGcTAGT TTGGATGATA TTnTTTTTGA TTCCTTCCAA tTTTCGGATC 720

TCGAATATTG TCCAAATATT TATGACCATC GAATGTAAGG GAAGAGATAC ATGTCATATA 780

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TTTGGAGACG GCATAATTAA TTTCCTCTGA ACTATATTTT TTTAGTAGAT CTGATTTAAA 900

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CCACTTGCTG ATAAGGAAAT TATATCAAAA AAAGAAAGTG AGGTAATTAA ATGTCACAAG 1080

ATTTAGCTAT TGAAGTAAGG GCAGCGCTAA TTCGTGCAAA GAAAACTCAA TCTTGGTTAG 1140

CGAAACAATT AGGGATTTCA AGTCCGTACT TATCTGATAT TCTTCATGGT CGTAGACGTT 1200

CAGAAGAGCA AGTTCGGAAT ATCAmAAAAA TATTAGATAT TAGATAGGAG GTGTAGGTAA 1260

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GAAATCAAAT CCGGATTTTT CAATAAACTC ATCAATATTA GAGAATTTAG TATTTTCAAT 1560

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GCCATTTTTA GCAAATTGAT TTAGCTCATG TTGTAATTCG TCAAATCCAT TTAATTCGAA 1680

TTTCATAATA TTTCACCTCG CTTTCAAATT CATTTTACCA AGAGGTGAAT TGTAAAACAA 1740

TCAGTATAGG AGGTGATAGC AATGGAAGTG ATTTTAACTC CAGAAAATGA AGCTTCTCTA 1800

AGAGATTTTG TACACGGAAT TATTGTTGAT GAAATAGAAA AAGCaCGaAG aGaTACCGcA 1860

GTTGaTAAgC gaGtCtTAAA tCaAACaGaG rTTGcaAAAT AtTTcaATGt TTCCACAACA 1920

ACAATAAGGG AATGGGAGAA GCTAGGTCTT CCACATGGAT CAGTAAGTAA ACAAGGGAAG 1980

TTCTACGACA AAGAAGGGTG TCGGAGATGG CTTCTATCAC AAAAAAGATA AATCTTGGGC 2040

AAGCGAAATC AAGGGAGGAA ATAAATATGA AAAAAATATA TCACTTAAGA CGTATGGCGG 2100

CACTGTTGGT TGTATTCGGA CTAGGTCTAT TGGTAGGTGG CAATATTGGC CCATTAATCC 2160

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ATCGAGAAGA AAAAAAACAA AAATAAAGAC CCACTTCGAC GGCCATCAAA GTAGGTCAGT 2280

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TTGAAACAGG CCAAGGAAGT ACTGCGTTTT GTGGTTCAGT TATCGGTTTA GCTATACTCT 2460

TGCAAAAACT TGTAGGTGAT CTAAAAGAGC AATTAAGTAT AAGCGAATCT TGTGATTGTC 2520

CAGAATGTGT AGCAGAAAAA GCCGAAGATG CTGCAAATGA AAAATCTATG GATGAACTAC 2580

TAACTGCATT TTTACGAGGT GAACTGCAAT GATTGAAGTA AGAGGTTTAA GTGATGATGT 2640

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GGTTGAAAAA TTCTCTGGAA AAAATCAAGT TGGTTTCCAA ATTTACAACT TGTTAGATGG    17700
CCAATTAGTT TACTCACCAT TCGAGCCGGC TGTTTATCGT TATGAAATTA CAAAACCAGT    17760
AGGTGGTTAA TGTGAATAAC GAaGCTGAAA CATTATCTTT AGAAGAAAAA TTCAAAGCAC    17820
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GTATgCTTAT GAaTATCGTG TTTCAGAAGA TGAATTAGAT AAGGCGTTGA ATGCGATCAC    18000
GCCATTTATC ATCCAAGGAG TGATTCAACA TGCCGAAGAG GCAGACGAAT AGGTTTCGAT    18060
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CTATCACAGA AAAGTTTAGC GCTGTTAGAA TCGATTCTGT GACCTATAAA ATCACTCGTA    18300
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TCGTCTAAAG TGCATAGACG AATGCCCTAC TATCAAATCT CTTTTTATAC AACAGGTACT    18540
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GACATCTTAA TTGCCATGAT GACCACAAAA GATGCAGTAG GTACAGAACC AGCATTTGGC    19140
GAGGTTGTTC GTTTGCCAAT AGCCACAAAA TTGGGAATTA AAGGAAATGG AACAGCTTTA    19200
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CAGCTTACGG ATGGGTTCAA TGGGACGGTT CAGCATATCC ATTGGTAGGC GCACCAACTT 25380

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GACAAGTAAG TCCATTAACa GTTGATGaAT TTaAAnnTCT ACGGTCTTTG GTTGGTAACG 25560

TTACTTCTGT TTTTTCAGAA 25580

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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ATACGTTTAT TACTGGTAAA TTAGCCAGTG CAGGTGTCTC AGGTTTTGAA CCTTTGGATG 120

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GGAACTTAAC TGCCCAACAT AGAACTGCTT CTTGGGATTA CTATATTACT AAAAATGGCT 240

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AACAAGAAGT TCCTAATAAA GTTGTTAAAC AAACAATTAA TATTCCGACA GACCGCAAAG 360

GTTATCATGT CATTTACGCT GTCTGGGGCA TTGGTGATAC GGTGAACGCC TTTTACCAAG 420

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ATTATGATTA CATTGcCCCA CAATTATATA ACCAAGGCGG CGACGGtGTC TGGGttGATG 1200

AAGTTATGAC TTGGGTTGCT CAAAGCAACG ATGCTCTAAA ATACGAGTTC CTCTATnATA 1260

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GGTCCAGCGA CATGATTTGG GTTATAACTA TTACTTTTTA TTTTCTCTAC TGGAACCATT 240

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AAGTACCTTT AAATGGTCTG ATACAGTCAT AAACACGATC TATCTCCTCC CAAATAAAAC 4620

AAAAAAAGGC TGTAATCGCA TTTTGATTAC AGTCTTTTTT TGTAAATGTA TTAATTAAAG 4680

CTTTACTTCC GGTCTTTTTA TTTAATGACT TTAGTCAGTT GAAATCTCTA AAGAGATTTC 4740

GACAAAAAAA CCACGCGTAA TGCGCGTGGA GGTCAGAGCT TTAGCGATAA AAGTTTAGCA 4800

CATACTCGTT GGAATTGTAA GTATCATCTT GTGTTTACAC CAAAATATAG AAGAAAAGTA 4860

ATCTATGGTC AATTGAGGCG AGATATAGGG AAAATACTAA GAAAATTGTG TGAGATGAAA 4920

GAAGTCGAAA TCATTGAAGC GCATGCAATG CCCGACCATA TCCATATGTT GGTAAGAATT 4980

CCACCGAAGT TGAGTGTATC AGGTTTTATG GGTTTCTTAA AAGGAAGAAG TGCAGTAATC 5040

ATTCATGAAC GTCATGCGAA TTTAAAATAC AATTATGGAA ATCGATCCTT TTGGTCAAAA 5100

GGTTATTATG TGAGCACTGT AGGACTGAAC CAAAAAACGA TAGCAAAGTA TATACGAGAA 5160

CAAGAAGCAG AAGATCGAGT AAGGGATAGT ATAAACAAAA GAGAGTATAA AGATCCATTT 5220

AGGAAGTAAC AGCTAGATAA GAATAGAAAG GTAGCGGTTG GCGGTCTCTA AAAAAGCTCC 5280

CTTAAAGGGA GCAGCAGGTA GCGAGCCCTT CTAGGGCTAT TaAAAAGCCA CCCGCTATGC 5340

GGGTGGATAT TTACTTAATA AATCAATTTT CCCAAATTAT TTTCTTTAGC TTTCTTAACG 5400

ATTTCTGTTG CAACTACCAC ATCTAATACA GCCGAACCAA CTGTTTTGAA GATCGTGATT 5460

TGTTCTCCAC TTGTCCGACC GACCAATTCT TCATTGATCA GTTGGCCTAG TTCTCCATGA 5520

TAGCTGTCTC TTTGAATATA TCCATCTTGC AGCGGTGAAA TGaAGTCCCC AGCTTCTTTT 5580

AGAACACCGT CCATGGTATC AAAAATAACA ACATCTGCGG CTTTAATTAT TTCTCGTGGa 5640

ATTTCACACA TTTCCGGTGT GTAAGCACCG ACTCCATTGA TGTGCGCACC TTTTTTGACC 5700

CACTCAGCAG AGAATGTCGC ACGTTTTGAA GTGGTCACAC TTGTGATGAT GTCTGCTCCT 5760

TCAACGCATT CTTGACTGGT TTTTGTTGGG CGCATCGTTA CAGAAAATTG TTGCATCATT 5820

TCTTCAGCAA ATTGGTTGGC ACGCTCAAAA TCAATATCAA AAATCCGAAC TTCTTCTAAT 5880

TTACGAACGG TCAACATTGC TTCTAATTGT GACTGTGCTT GTCCACCGGT TCCAATCAGC 5940

GCGCCGATTT TAGCATCTTT TTTTGCAAGA AGTTCTGTTG CTGCTCCTTG AACAGCGCCT 6000

GTTCTTAATT GTGTCAAATA AGTACCATCT AAACAAGCGG ATACCATACC CGTTTCTGGA 6060

TCCAATACGA TCATCGTTGC TGGTACACTT GGTAAGTTTT TCTTGATGTT TTTAGGATAC 6120

ACGGAAACGA TTTTGACACC TAGTGCTCCT TCGCCACCTT CTACATAAGC TGGCATATAT 6180

AAGCTTTGTC CGTTACTTTT TGGCACATCG ATATTGGTGC GAAGAGGCAC AATTGCCTTT 6240

CCTGCTGAAT ACAATGACAA TGCTTTTTTG TCTGCATCGA TGGCTTCTCT CATTGAAAAA 6300

TTTTTGATAA TATCTTCTTT TTTAAGAAAT AGCATTTGAA TCGCTCCTTA ATTAGCTGCT 6360

GTAGCTTTTT TTAATTGACT GCTCAACATC GTATATGCAC TGTATAGTAA GACCAAAATC 6420

ACGATCCATT TCAGAATATA GGTATCTAAA GATTTGACTA GGAATACAGC GACCAATACC 6480

CCTAATACAC CGAAGGTTGA AGTGAAAAGT GTGATTTTTC TGCTGTATTC ATCAAATTTA 6540

ATGAATTGAA CACTGCCGAT CGGTACTGAG AATGTACAAG CCCCCATCAT AATAGGAAAG 6600

GCTGCAACTG GATTCAAGCC TAGCAAGTAG ACAGTTACCA TTGTTAACGC ATAAGAACCA 6660

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CCGCCATACA ATTCACTGGC TGTTCCGTTT GAGgGAAkCC AATTCATTTG TCCCATAAAA 6780

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AACTTCACGA CAAATCTTGG TCCTAAATAT GCACCGATAA TTTGGCAGAT AATACAAACA 6900

GCTAATGTCT TGATCCCTAC GTTGATAGCA GTGATATAAG ACAATGCCAT GACGGCTACC 6960

GGTACTACAC ATTGGGTATT CAACGTTCCG GGTAGTTTTT TCATGCTGAC CCATTTCAAC 7020

TTTGGATAAA GGACGGTTCC GATAGCAAAG TCGGAAACGC CAAATGTTGA AAGAAAGAAG 7080

GTGATAAATG ACGTGAAGGG CAACAGACGC ATATCCCCAG GTTCTTCTTT GAAATTTTGT 7140

TTGTTTTTGA AAAGGTCTCT TAGAAAGTAA ATAATAAAAT ATAGATTGAT TGCGACAATT 7200

AGTGCCAGCA AAATATTCCG AATCATAAAA ATTCCTCCTA CTAGTAAATC TTTCTGATTC 7260

CCTCAAAGTT CTCACCATAT TTTGCTTTAA GTTCTTCAGA AGATTCTGCA ATCACTTTTA 7320

GTGTATATGC ATCATGTTTG ACATATTCTT TAGCTAGATT GACCATGGCG TGGTTTTTTG 7380

TCCAAGTGAC ATCGGTTGAT TGCAGTTCTT CATTAATGGT GCCAAACACG ACTTCTTGCT 7440

CATCGGCGAC GATGTTGATC CATCTTGCCC CAAAGTCATC AAGTTTGTCT GTTTCAAAAC 7500

CATGAATGTA ATACTTTTCT AAGGGAAGAT CATATTCATG GGTAGAACTG AATAAAATCA 7560

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GGTTCTCATG CCAAACTTGG ATGAGCAAAC TTTCTTTTGC ATTTTtCACC AAATGCTCTG 7680

CTTaTCCaGA ACATACTcGA TGCCATCAAC TTTnCCACAG CATGTCTTCT TCATCTTTTT 7740

CCTTAATCAT TcCTAGATTC TTTGTAAGAa AAGaAAGATC aTTTTTAACA CTTTTTTCTA 7800

ATTTCTCTAA AAACTCaTTT GCCGAGATGG CATGATAAAG TTTAGGTTCT GATTTATTGA 7860

CGACAATCAA ATTCTTTTTT AATAGTTTTT CCAAAATGTT ATATACTTTC GAGCGTGGCA 7920

CcCTGAGATT TTACTTACTT CATATCCTGT AAGATTACCT TTTTCTAATA GGGTGGTATA 7980

CACTCTTGTT TCCATCTCTG AAAAATCATA TTTTTTCATG ATTTGAATCA TCGTTTCCAT 8040

TGATTAATCC TCACTTCATT TTTAGTAGCT ACTACGGTAA CAACTATAAT TTTTTTTTGA 8100

TCATCTGTCA AGAGTTAGTT CAATAAAACA CATATAAGAA TTAGCTTAAA AACAAGCTTT 8160

tTATTAAAaA TaAATaATAT AATAGGGA 8188

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3467 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TGATGAGCAT AAGGAGGACA GGCATGAACA AAAAGAATAA TGGCATGAAA AATGGTTTAT 60

ACTACGTCTT AGTAGTACTT GCCATGGTCA GnGTTGTCTA TTTCATTTTT GGAAATAACA 120

ACCAACAATC GCCAGACATC GATTACTCAA CCTTCCAACA ACAATTGGAA GACGGAAAAG 180

TCAAAGACAT GACCATTCAA CCAACTAATG GGGTTTACCG GATTGAAGGT CAGTATAAAG 240

AAAAACAAGA AGTGAAAGAC ACAGGTGGTC TGTCATTGTG GGGCTCAACG CAAGCGTCGT 300

CAAAAGGCTT CACAACAACC GTTTTACCTA GTGATACAAC CTTAGCTGGC ATTCAAGATG 360

CGGCACAAAA TAACAAGGTG AAGCTAGTTG TCAAAGAACA ATCAACAAGT GGTGCTTGGT 420

TGTCACTGTT GTTTAGTTTC TTACCATTAG TGATTATTTT CTTCTTCTTC TACATGATGA 480

TGAGCCAACA AGGCGGTGGC GGTGGCGGCG GTGGCCGTGT GATGAACTTC GGTAAATCAA 540

AAGCCAAAGA AGCCGATAAA AAAGCTAACC GTGTCCGCTT CTCAGATGTA GCTGGTGCGG 600

AAGAAGAAAA ACAAGAATTA GTTGAAGTAG TGGAATTCTT AAAAGATCCA CGTCGTTTCG 660

CTGAATTAGG CGCACGGATT CCTGCGGGCG TACTATTAGA GGGACCTCCA GGGACTGGTA 720

AAACGTTACT TGCTAAAGCC GTAGCAGGTG AAGCAGGTGT GCCATTTTAC TCAATCTCAG 780

GTTCAGATTT CGTTGAAATG TTTGTCGGGG TCGGTGCTAG CCGTGTCCGG GATTTATTTG 840

AAACAGCGAA GAAAAACGCG CCTGCAATTA TCTTTATCGA TGAAATCGAT GCAGTTGGTC 900

GTCAACGTGG TGCTGGTATG GGTGGCGGAC ACGACGAACG TGAACAAACC CTTAACCAAT 960

TATTAGTTGA GATGGATGGT TTTGATGGCA ATGAAGGAGT TATCGTAATT GCTGCAACGA 1020

ACCGTTCAGA CGTGTTAGAC CCAGCGTTGT TACGTCCAGG TCGTTTTGAC CGCCAAATCT 1080

TGGTAGGACG TCCAGATGTC AAAGGTCGTG AAGsgATTTT aCGTGTTCAT GCGAAAAACA 1140

AACCGTTAGC TGATGACGTT GATTTGAAAG TTGTTGCACA ACAAACACCA GGTTTTGCTG 1200

GTGCTGATTT AGAAAATGTC TTAAACGAAG CAGCCTTAGT TGCCGCTCGT CGTAACAAGA 1260

AAAAAATTGA TGCTTCTGAT GTGGATGAAG CCGAAGACCG CGTAATTGCT GGTCCAGCTA 1320

AAAAAgATCG CGTGaTTAAT AAAAAAGAAC GCGAAATGGT GGCTTACCAT GaAGCAGGAC 1380

ACACAATTGT TGGTTTAGTC TTAAGCCGTG CTCGTGTTGT CCaCAAAGTA ACAATTATCC 1440

CTCGTGGTCG CGCAGGCGGT TATATGATTG CTTTACCAAA AGAaGATCAA TTCTTAATGA 1500

CTAAAGAAGA TATGTTTGAA CAAATCGTTG GCTTACTTGG TGGACGTACA GCAGAAGAAA 1560

TTATCTTTGG CGTTCAATCA ACAGGGGCTT CAAATGACTT TGAACAAGCA ACAGGGATTG 1620

CTCGTAGCAT GGTAACTGAA TATGGAATGA GCGACAAATT AGGACCTGTT CAATATGAAG 1680

GAAACCATCA AGTCTTTGTC GGTCGTGATT ATGGTCAAAC AAAAGCTTAC TCAGAACAAG 1740

TGGCGTTTGA AATCGATCAG GAAGTTCGTC GTATCTTAAT GGATGCTCAT ACGAAAGCGC 1800

ATGAAATTAT CGAAGCGCAC CGTGAACAAC ATAAACTAAT CGCTGAAAAA CTATTAGAAT 1860

ATGAAACATT AGATGCAAAA GCAATCAAAT CATTATTTGA AACAGGTAAA ATGCCTGAAG 1920

GTGCTGACAG CGACTATCCT AGTGAAAAAG AAGCGCAAAC ATTCGAAGAA GCAAAACGTG 1980

CTTTAGAAGA AAAAGAAGCG CAAAAACAAG TTGAAGAAAA ACAAGACTTT GAAGAAGCGA 2040

AAAAAGAATT ACATGATGAA GCAGAAGAAG TCAAAGTAGA AAGCGAACAA ACAGAAAAAG 2100

AAGTCCAATC TGAAGAGAaA AAAGATTCAG ATTCCAATTC TGAATATGAT CGCAATAACT 2160

ACGAAGATCG TTATAAATAA CCAATTAGTA GAAGGTGCAG TATTTGTCGA GTTGACGAAT 2220

ACTGCACCTT CTATAATATT AAGATATTCT ATAGAAGGAA GATTATTTGG TTGAAAAAAC 2280

ACCTGATTCC TAGTATTATC yGACTAATGG aCmAAAAAGC ACCAAGAGAG nGAGGAAAAA 2340

GAATGGAAGA TTATTTAGTA AAAGCCCTTT GTTATAAAGG TTCAATACGA GCATATGCCA 2400

TCAGTGCCAC TGAAACTGTT AGCGAAcGCa aAGAAGACAT GATACATGGA GTTCTTCTAC 2460

TGCAGCGTTA GGACGCACAT TGATTGGAGC CCTTTTACTA GGAGCGACTT TAAAAGGTGA 2520

CGATAAATTA ACTGTAAAAG TACAAGGAAA TGGCCCAGCT GGCGCTATTA TTGTCGATAG 2580

TAATGGCCGC GGAGAAACAA AAGGCTACAT TAAAAATCCA CATGTCAGCT TAAAGTTGAA 2640

TGCAACAGGT AAAATTGATG TACGTGGTGC TGTCGGTAAC GAAGGAATTT TCACAGTCAT 2700

TAAAGATTTA GGATTAAAAG AAACCTTTTC TGGACAAACA CCTATTGTTT CTGGTGAAAT 2760

CGGTGAAGAC TTTACATATT TTATGGCGGT CTCTGAACAA GTTCCTTCAG CTATCGGTTT 2820

AGGTGTATTG GTGGACACGG ATGAATCTGT GAAAGCAGCC GGTGGTTTTA TGATTCAAGT 2880

AATGCCAGGT GCCGATGAAA GTACCATTGA TTTTATTGAA CAGCGTCTAG CGGAAGTGCC 2940

ACCAATTTCA CAATTACTAG AAAATGGAGA AACACCTGAA CAAGTCTTGT ATCGCTTATT 3000

GGGAGAAGAC GAAGTAGAAA TTTTAGAAAA AATGCCTGTA CAATTTAAAT GTGACTGTTC 3060

CAAAGAAAAA TTTGCGACCG CTTTGATTGC TGTTGGGATC GATGAATTAA ATGCGATGAT 3120

TGATGAAGAT CATGGAGCAG AAGCAGTTTG TCAATTCTGT AACAATAAAT ATCACTATAG 3180

TGAAGAAGAA TTAATTGAAc TTCGCGATGA AGCGATTCGC AATACGAAAC AAAAGTAGGA 3240

GGAAAGACTA TGTGGAAAAT TGGAGACGTT GAAATCCCCA ACCGTGTTGT CGTAGCTCCG 3300

ATGGCGGGTA TTAGTAACGC CGCTTTTCGT GTGACTGTAA AAGAATTTGG CGCaGGATTA 3360

GTCGTTTgTG AAATGATTAG TGACAAAGGa ATTAAATTAA GAAACAAAAA AACCTTAGAA 3420

tGCTATATAT TGATGAGCGG GAATAnCCTT TAAGTGTACA ATTTTGG 3467

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTTGAnACAA TTGGGGCAAA AAATGTTTTG GCAAATGAAA AAGGCTGGTT ACCAGTGACA 60

GAAGAAGCGG CCATTGCTGC AAAACCAGAG GTCATTTTAA CCAATGTTAA CTATATGAAA 120

GATCCCGCCA AAGAAATTTT AGCTCGTAAA AACTGGGAAA GCGTTCCAGC AGTTCAAAAC 180

AAAGAAGTTT TCGAAATCGA TAACATGTCT AGCTCTTTAC CAAATAACCA CATTACCAAA 240

GCATTAAAAC AAATGGCAAA AGCTGTTTAT CCAGAGGAAT ACAAGGATTT AAAAGATGAG 300

TAAAAAAACG TGTCTCATAC TGATGCTCTT GATTAGTATG AGCATGCTCT TTTTGGGTAT 360

TAAAATTGGA AGTGTTCAGA TTTCGTTAAC GGATTTGCTT CAAATTTTAG TGAAAAAGAC 420

GGTTTCAGAA GATGGGATTT TAGAAGGAAT CATCTGGAAT GTTCGGTTAC CGCGTGTCGT 480

GATGGCCTAT CTCGTGGGCG CAGGCTTAGC AGTAAGTGGC ACGGTGATGC AATCGCTCTT 540

AGGTAATCCT TTAGCTTCTT CGTATACTTT GGGCGTATCA GCGGGAGCAT CCTTAGGTGC 600

TGCGTTAATC ATGGTAACTG GAGTAACTGC TTCGATCTTA GGGGCATTTT TATtGCCTTT 660

AACTGGTTTT ATCTTTGGCT TAGCAACGGT CTTTTTAGTT TTGTTATTTA CGCAAACAAT 720

GGATAGTCAA ATGTCCAATC AAACAGTTGT TTTAGTAGGA ATGATTATGA CCTTGTTTGT 780

CGGTGCTATT TTGACGTTGA TTACAGCACT TTTCCAAGAT TATTTGAAAC AATTAGTCTT 840

TTGGCAAATG GGTAGTTTTT CTGGCAGTAA TTGGCAAAAA ATTGCTATTT ATTGTCCAAT 900

CTTGCTTGTC AGCAGTCTGT TTCTTTGGTT TGATGCCAAC GCATTGGATG TTCTCGGTTT 960

AGGAGAAGAA CATGCGATGT TAGCGGGAGT AGAAGTCAAA ACAGCAAAAC TACGCATTAT 1020

TCTTTTGGCT AGTTTATTGG CAGGAAGTGC GGTTTCATTT GTCGGTGTGA TTGGTTTTGT 1080

TGATTTAATA GCACCACATA TTGTCCGTCG CTATTTAGGG GCGACTCATC GCTGGCTGAT 1140

TCCCGGTTCA GCAATCTTAG GTGGGACCAT CATGGTACTA GGGGACACGA TTGCCCGCAC 1200

GATTTTATCA CCAAGAGAAA TTCCCATCGG GGCCGTAACA GCCTTGATTG GAGCGCCATT 1260

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GATTATACGG TTTACGAAAC AGTTTTGATG GGGGCGTATC GACAACAAGC ACAACGTTTT 1620

TTACCTATTG TTTCtAAmCA rGAAAArGAA CGAGTCCTTw ATwATTtAGA ACGCACGGGT 1680

TTATTGCCTT TAAAAGATAA mGTTGTCAAT CAGCTTTCAG GAGGACAACA ACAACGAGTA 1740

TTTTTGGCTA AATTATTTGT ACAAGATCCA GAAATTATTT TATTGGATGA ACCCmATAAT 1800

CATTTGGaTA TTCGGTATCA ACAAGAATTG ATTCAGCAGT TAAATGAGTG GAGTGCGCAA 1860

GAAGGGAAAA CGTTAATCGG GGTGTTTCAT GATATCCGTT TAGCGTTAAC GCTAAGTGAA 1920

AAAATTGTGT TTATGAAGCA AGGGAAAGTG GCCGCGCAAG GTGATTTTCA AACGTTGGCT 1980

TCCAAAGAAT TTTTACAAAC GATTTTTGAA ACAGATATTG TCTCCTATTT TCAGAAACAA 2040

CATAAAGTTT GGGAAACTAT TCAATAATTT TGACAAGTTT TTTGGAAACA GGTAAGATAA 2100

AGGCAAAGAA TCAGAAACAC AATGGCGTGT TTTAACAAAT CGGCAAAGGA GCCCAAGACT 2160

AAGTACGTGA TGGTACTTGC TTTGGGCTCC TTTTTTATGG AGGTAACGAT GAAACGAATC 2220

ATTTTAATGG GAGCTATCGG TTGTGGCAAA ACCACGTTAT GTCAAGCTCT GCAAGGCAAA 2280

GAATTAATTT ATGATAAAAC ACAGGCGGTG GAATTTCATA CAGAAATGAT TGATACACCA 2340

GGCGAGTTTA TTTTGCATCG ACAATATTAT AATGCATTAA ACGTCACAGC GGCAGAAGCA 2400

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GAAGCAGAAT GAAAATTTAT ACAAAAACTG GCGATAAGGG AATGACGAAA TTAGTCGGCA 2700

GCTCAACCGT CGCTAAGGAT TCTGATCGAG TTGAAAGTTA TGGAACGATT GaTGAATTGA 2760

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AACTAGAAGC TTTACAACAT TTACTTTTTG ATGCGGGAAC AGATTTGTCA ACACCGATTG 2880

AAGCACAACG ACCATTTAAA TTACAAAAGG CAAGTGTGCA TTGGCTAGAA CAGCGGATTG 2940

ATTTCTACAC TGCACAATCA CCAGATATTG ATCGTTTTAT TTTACCTGGC GGAACCCCAG 3000

CAGCCAGTAT GGTTCATGTG GCTCGGACGA TTGCACGGCG CGCAGAACGC ATCATTGTTC 3060

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ATGAACGAAG CGAAATGGTT TTCCATAAAA TTAAAGAAGA TGGATTGTAA ACAGTTGCTT 3240

TTCTAAAAAA CTTATGGTAA ATTTCAGATA GaTTAAaCGA ATATTTTATG AaAAATATGA 3300

ATGGAAGCCA GTGAGAATCT GGCACGGTCC CGCCACTGTG AAGAAGCAAG GTTGCTTTTA 3360

AGTCAGGTCT TTTCATTTTT TCATTATTGG GCATGCTGTT TCGAGGCAAA ACAGGATGTT 3420

TCTTAACAAC GCTTGTGTTG AAAATCCAGC CCAAGATATT TGTATTAATC CAATTAATGG 3480

CACGAGGAAG TGCTTTTGGG AATTTTGGGC TGGTCTTTCA ATGTTGAAGG AGATTTCAGG 3540

TACAATGACG TACTGCTATA TTCCCTTTTT TTATTGACAA TTAATTAAAG GCGTTGTACT 3600

CTATGGATAA GGTTTCGTGT ACAATGGCGT ATACATAAGG AAGCAAAGAC GCTTCAGACA 3660

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AAACAATTCA TTTCCCTACC GAACTATGGG TAGGAGAAGG CGCATTAGCC AATTTGGAAA 3780

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CCGATCCACC AATTGATAAG ATTGCTGCGG GAATTAAGCA TTTAGCGACA TTTCAAGGAG 3960

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TGAGTGTCCC ACCAAAAATC ACAGCGGATA CAGGAATGGA CGTCTTAACG CATGTTATTG 4260

AAGCGTATGT TTCAACAGAA GCAAATCCGA TTTCAGATGC GTTGTGCGAA AAAGTCGTTC 4320

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TGAATCACGG TATTGCTCAT GCGGCCGGTG CACGTTTACA TGTGCCACAT GGACGAATGA 4500

ATGCAATGCT CTTACCTGAA GTCATTGCAT ATAACAGTGG CTTAGCGAAT GGCAAAGTCA 4560

CCAACGAACC AACAGCTAAA CGTTATGCGC AGTTAGCAAA TTGTCTAAAT GATACACAGA 4620

CAACCAATGC ACGGATTGGT GTTCAACAAT TTATTCGACA AATCAAGCAA CTCCGTCAAA 4680

AATTAAACAT GCCTGCCACT TTTAGTGACT ATGGTTTACC AAAAGAAGAA GTCCAGGCTG 4740

CAATCCCAAA AATAGCTGAA GGCGCATTGA TGGATGGCTG CACCAAAACA AATCCTGTCC 4800

AACCAACAGC AGCAGAAGTG ACAAAAATTT TAAATTCTAT CTTATAAGCG ATTGACAGGA 4860

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GCGTACGTTA AGTATGAACA AACGCGCACG TATGAGTGAA ATTGCAGAaT TGATTGTAAT 5940

GGATGATGAA TAAATGAAAC GATTAGAGCA ATTATGTCAC CAATATACCA ATCTTTCAGA 6000

ATCAGACATT AAAGAATTAC AACGTACAGC ACGTTATCTT TCTTCGACGA CACTCTATCa 6060

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TGAACATCGA ACGATTGGTG TCATTATTGT CGAGATTGCG GCAGATGAAG AGATTCAAGC 6360

GGACTTACAA AAAGAGGAGC TAAATAACTG CCAGTTAGCA AAAGTAGCGA AATCAACTAG 6420

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ATGCAC 21126

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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ATACTCACGT AACGATTAAT AGTCGTGGCG AAGTTATTCA GTTAATTGGC GAATCATCAG 300

AGGTAGAGTT AGTCGCTTCC GTGTTAAGAG CGCTACAAAC ATTAATTCAA CGAGGCATCA 360

AAGTGCATAC GCCAGATGTC GTTTCTGCTT TAAAAATGGC CAAAGCTGGA AATTTAGAGG 420

CGTTTATTGC CATGTATGAA GAAGAAATTA TGAAGGACCA TCATGGTCGG GCCATCCGAA 480

TTAAGAATGT TGGTCAAAAA AAATATATCG ATGCAGTTAA AACTCATGAC GTCATTTTCG 540

GGGTGGGACC TGCGGGGACA GGAAAAACCT TTTTAGCCGT GGTGATGGCA GTAGCAGCTT 600

TAAAAAAAGG CGAAGTACAA AAAATTATTT TAACTCGTCC AGCGGTGGAA GCTGGCGAAA 660

GCTTGGGCTT TTTACCAGGT GACTTAAAAG AAAAAGTCGA TCCTTATTTA CGTCCAGTTT 720

ACGATGCCTT GTATCAAATT TTTGGTATGG ATCATACAAA TCGTTTAATG GAACGCGGCG 780

TTATTGAAAT TGCCCCGCTT GCTTATATGC GTGGTCGTAC ATTGGATGAT GCTTTTGTCA 840

TTCTAGATGA AGCACAAAAT ACCACGGTTG CCCAAATGAA AATGTTTTTA ACTCGTTTAG 900

GGTTTAGTTC AAAAATGATT GTTAATGGAG ATACTAGTCA GATTGACTTG CCACGTGGTG 960

TAACAAGTGG TTTAGTTAAC GCCGAGCGTA CGTTAAAAGA CATTGAAAAA ATTGCCTTTG 1020

TAAATTTTGA AGCCAGTGAC GTTGTGCGTC ATCCTGTTGT AGCACAAATT ATTCAAGCCT 1080

ATGAAAAAGA ACAACAAAAG CATTCCTAAG CAGTTAGGGA AGGAGTGAAA GTACCTTTTG 1140

AAAAAAGTAC TTACAAAGTT AGGGGATCGT TTAGGTAAAG CCTATTTACC TATTTTATTA 1200

GCCGTTTTTT CTCTTCTTTT ATTTATGATT ATGTTTGGCA GCGTCCATCA GAAAAGAGTA 1260

GAAATTAAAG AAGGTCAACT GGCCGAGAAA ACCAttCGTG CAAATAAAAA TATCGAGAAT 1320

ACCTACGAAA CAGAACAAAG AAAAAAATTG GCAGCAGAAG CTGTCACACC CGAATATATT 1380

TATCAAGAAG ATACGGCATC TGTCCAACAT AATCGTATTG ATAAATTATT TAAATTGATT 1440

GATTCTGCGA ATGAAAAAGT AGACAAAGAG TACAGCAACA AGCAAGCGAA GGCCAAAAAG 1500

GAAGAAACGA TTCCTGCGCC GACCGTGGAA GAACGAGTAG CTAGCTTAAA ATCaTTGTTT 1560

GAATCTTTAC CGCAAGATGA AGTTACGTTT TATCaAAGTT TTCCTAATGT TTTTTATCaA 1620

ACAATCTTTA CATTAACCTC TGAGCAATTG GATAAGGTTC GTTCAGAAAG TTTGATGTTG 1680

GTGGATGACG CGATGCAAAA TCACGTTCGA GAATCTGATT TGGATAAAAT TCGCCAAGAA 1740

GCTAACGGTA AAATTCAATA CTTAGATATT ACGAGTACCA TGCAACAAGT CATTCGTTAC 1800

ATTGTTAACC AAGGGATTGT GGTAAACGAT ATTGCCAATG AAAAACGAAC AGAAGAgctA 1860

CGCCAAAAAG CGATGAATGC TGTTCAACCC GCAATGATTT ATCAAGGCGA AATTATTGTT 1920

CGTGAAGGTA CTCAAATTGA TGCAAAAGCG GTCGAAAAAC TTGAGCTACT AGGAATGACT 1980

AGTCAAAATA CCTCTATTTT TCCGATGGTG GCATTAGCAT TAGCTATTTT ACTTCAAGTT 2040

GAAGTGTTAA TTTTCTTTAC AAAACAAGTG ACTGAGCCTT CGCGACAACG CTCGTTTATT 2100

ATCTTTTACA CGGGTGCTAT GCTAATCAGT GTTATTTTAA TGAAATTCTT CCAGATTTTC 2160

CAAACAGAGC AGTTGATGTA TATTCCCTTG TTCTATCCGG CAGCCTTTGC GCCGCTGATT 2220

CTAAATCATT TTGTAAATCG TCGTTCAGGG ATAATCGCTG CTATTTTCCA AGTCGTTTTT 2280

GCGTTATTTA TCTTTTATAA TTCTATCGGC ACAAACTCGT TGACGGTTAT TCTGATTATG 2340

TACTTATTCT CAGGATTTCT AGCAACAGTT GTTAAACGGA AACGGATGAG TGAGCAAGTT 2400

TTCCCAGCTT TAATGTGGGT AGTGGTCTTT CCTGTTTTCA TGGCGGTTGT CTTAATGATT 2460

TATCAAGGGA TGAGTTTAAC AGATGGTAAA ACGTGGACAG CTTTAATTTG TGCAAGTGCA 2520

GGAACGGTAC TTTCATTTTT AGCAACAATG GGCTTGCATC CATATATCGA ATTATTAGTG 2580

ACCGATGATA GTATGATTGT CTTGAATGAA TTAAGTAATC CGAACCATCC GTTGTTAAAA 2640

CAACTGTTAG AAGAAGCGCC AGGTACCTAT CATCATAGCA TGATGGTGGC TAGTTTGAgC 2700

GCTAACGCTG TTGCTGAGAT TGGCGGGCGG TCGCTATTAA CACGAGTTGC TTGTTATTAC 2760

CATGACATTG GTAAAATTAA ACACGCCAAT TTCTTTGTGG AAAACTTACC TGCTGGTGCA 2820

GAAAATCCAC ATAACTTTTT ATTACCAGAA GATAGTAAAC AAATTATTTT TGGCCACGTA 2880

ATTGATGGCG CCAAAATTTT AGAAGAGTAC AATATGCCGC AAATGGTGAT TGACATTTGT 2940

CGTCAACATC ATGGCACAAC ATTGATGAAA TTTTTCTATG TGAAAGCAAA AGAACGCAAT 3000

CCTGaAATTA AAGAATCCGA CTTCCGTTAT CCTGGaCCAC GTCCACAAAC aCGAGaAGCa 3060

GGGATTGTGa GTATTGcTGA TACTTGTGAG GCTGCTGTGC GGGCGATGGA TCATCCCACC 3120

AACGAAAAAA TTnCAAGCCT TTGTGCATAA TGTGATTCAA GACAGnATTT CAGATGGCCA 3180

ATTAGATGAA TGTGGGTTAA CGATGAAAGA GATTCGCATC AT 3222

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGACATGATT ACGTTAGACT TAAACTTACC TAGTATGGAT GGGATGGCTG TTTGTCGTGA 60

AATTCGCAAA GTTTCAGCCA ATGTTCCCAT TATTATGTTG ACCGCTCGTG aTTCTGAAAG 120

TGACCAAGTA ATTGGCCTTG AAATGGGTGC GGATGATTAT GTGACAAAAC CATTTAGTCC 180

ATTAACTTTG ATTGCACGGA TGAAAGCTCT ACATCGTCGT GCCGAGGTGG CAGAGGCTGC 240

GCATGATACG TCTGAGAATA CAGATGAAAC ATTTGACGTG ATTACGGATC ATTTTAAAAT 300

GAATACGAAA ACACGAGAAA CATATTTAGA TAATCAATTA ATTGAAGGCT TAACACCTAA 360

AGAATTTGAT TTGCTATACA CTTTAGcAAA AAAACCACGC CAAGTCTTTT CACGcGAACA 420

ACTACTAGAA TTGGTTTGGG ACTATCAATA CTTTGGCGAT GAACGGACAG TTGATGCCCA 480

TATCAAAAAA TTACGACAAA AAATTGAAAA AGTGGGTCCT CAAGTCATCC AAACGGTTTG 540

GGGCGTAGGG TATAAATTCG ACGATTCAGG TGTTGCTTAA TGAAGTATTT GTATCAACAA 600

TTACTTGCTT TTATAGGTGT GATCGCTCTG ATTATTCTCA TTGTCGGAAC GTCTTTCACA 660

CAATTGACCA AGCGCACAAT GCAAGAAAAT AACTATGAAC AGCTGTATGG TTATGCAGAA 720

TCGGCTTTAG AAACACGTGA CTTTTTTATT AATGTCGCAG GCGTTTCAGA TCGAGATGTT 780

TTATCCTATT CATTtCAGTT GACTGAGCGC GTACTCCAGA AGCAAGATGT GCAATTTGTG 840

TTTATTAACA AGGACCGCGA AGTGCAGTAC CCACCAGTTG ATAGCACAAA AAAATTAGAC 900

TTTTCCTTAA TCGATAAAAA TTGGGATCAA ATCATGAAAG GCAATCGTGT TaTGCAACAG 960

AAAACATTGA TATTTACGGG GCCCGAAATA CTTCGTCCTA TGTAATGTTA CCGGTGTATG 1020

CATCAAATCA GTCTTCTGAT AAAAAAGTGA TTATTGGTTC ACTAGTTATT ACACAACCTG 1080

CCAAAAACGT TGACCGAAGT GTTCAGTCCG TGACACAAAA CTTGATTAAA GGCTTTATTT 1140

TTTCTGGTGT GATTGCCTTG TTACTAAGCT ATCTATTTGC GACTTTCCAA GTGAAACGAA 1200

TAAATCGGAT GCGTAAAGCC ACCAAAGAAA TTACTAGTGG AAATTTTGAT ATTCAATTAC 1260

CGGTTCATGA CAAAGATGAA TTTGATGACC TAGCAGAAGA TTTTAATAAA ATGGCCGCGT 1320

CTTTAAAAGA ATCACAAGAA GAAATCAATC GGCAAGAAGA GCGCCGTCGT CAATTTATGG 1380

CGGATGCCTC TCATGAAATG CGGACGCCTT TAACAACTAT TAATGGCTTG TTAGAGGGAT 1440

TGCAGTATAA TGCTATTCCT GAAAATCAAA AAGAGAATGC GATTAAACTG ATGCAAAATG 1500

AGACCGCTCG CTTGATTCGC TTAGTCAATG AAAATCTTGA TTATGAAAAA ATTCGGACCA 1560

ACCAGATTCA AATTGTTGTG AAGAAGTTCA ACGGAACAGA AGCTTTAGAA AATATTGTGA 1620

CTCAACTAAC GGCCAAAGCT GAAGCCGCCG GTAATCAATT GTATTTAGAC ACCACCGAAC 1680

CAATTGATGT GTATGCCGAT TATGATCGTT TCGTTCAAGT GGTTGTCAAT ATTGTTCAAA 1740

ATGCGATCCA ATTTACTGAA AATGGCGAAA TTCATATTGC TTTAGAAAAA GGCTATTTAG 1800

AAACCATTGT CCGTATTTCT GATACAGGAA TCGGCATGAC GGAAGAGCAA ATTCTGAATA 1860

TCTGGGATCG TTATTACAAA GTAGATCCAT CCCGTAAAAA TACGAAATAT GGAGAATCAG 1920

GATTAGGCTT ACCAATCGTT CAACAATTGG TCCGTTTGCA TAAAGGAAAA ATTAATGTTG 1980

AGAGTGAACT TGGTAAAGGC ACCACGTTTA TTATTTCATT TCCTGATGTT GAAATTACTG 2040

AAAACTAAAG AAAACGTCTG GTCACAATCA GTGCCAGACG TTTTCTTTAG TTTAATAACG 2100

CATGTAGAGA CAGGGGGTGC ACATAGGGAC TATCAATAAT TTGTGGATCT TTTGTCAGAA 2160

ATAGCAAGCG CTTGTTTCTT TTTTGAACTG CTATTTTTAA TTGAGGTAAA ATTTCTTGAC 2220

GTTGTCCAAT CGTTAATGAA GAAAAGATGT CATCAATCAC TAACGTACTT GTTTTTGAAA 2280

GCAAAAGTTG TATTATGCGC ATTTTAATTT TTTCAAAAGT CGTAAAAGAA GTAAAGGAAC 2340

GACCAAGTAA GGCAGGTTCT AATTGGAACA CCTGGAAAGC TTCGGCTAGA ACTACTTTTC 2400

GATCCCGTTC TTTGATCGTA CTAGCGATAA ATAAATTTTC TTCTAATGGC AAGTAGGGCA 2460

AAAAGGTTTC ACTAGAAGAA AGCCTAGTAA TGGTTAATTG GTTTGTTTGG AAAAAATCGG 2520

CCAATGCGAG TTCTTGTTCT GGAGCAGAAT AAATGATTCC ATAAACTTCT CGCAAAGctA 2580

ACGCGTCGAA TGAGGATTTT TTTTCGGTTA TTTTTTTGAA TGATGGTGTG ACATTCATAG 2640

AAAATCCCTC CCTTATTTCT TATGTGTACG TAAATAAATC AACGTGAAAG GAGTCCCGCA 2700

AACAAGAGGA ATGCCAAGCA AGATTAAGCA GTTAACAAAG CAATTACGGA TTGTATAAAG 2760

TGACTGCATA CTTTTAAAAT CAAAAGAAAA CGCTTGGATC GTTTGAATCC CTAAATGCTG 2820

GATATTTGTA ATCGTGACAT CCTGGTCGGT ACTTTTAGCT AAAAATGCTG GAGTTTCCAA 2880

ATGAGACCAC TGTAAAATAG CATCACGAGC AGCCCAAAGA ACAGTATTAT ACGTTTCTTG 2940

AAACATTAAA GTGAAAAGTA AAAAACTGAA AATTCCTAAT AGAGCCGGTA AACATAACTC 3000

TAGTAAGAGC TGTTTGGTGA CATACATATT TGAAAAGTGC ATGTGATACC ATGTATGTAT 3060

TTCTTCCTTT TTTATGCGTA ATGTCACATA CATCAACAGA AGAAAAGTAA CACCAAAGAA 3120

AATGACACTA CCTAGATAGA GGTGCCAATA GTATTGGATC AGTTGGTAAT GGTAACTAGT 3180

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CGTGATTTTT TTATGATAAA AACTACTAGC TGTAGCGTAA CGGACACTTC TCATCAACTT 3360

TCACCTCTCT AAACTATCTT TAGTATAGTG aAATAATATG AATTAwTTAk GAaAAAGtAG 3420

CAAAAaGCTT GAGCAAATkG CTCAAGCTTT TTGAAGATTt ATTtACCCGT TTTTtGATAG 3480

CCTtGATAAC TGTCAGtGTG ATATtCATCA ACGGTtGATT TATtATkGTT TTTACTGTAA 3540

ACACTCGTTG ATTTTnCACC nTTTcTTTTT CAATTGCTTC CAGTTGTTGC AATTGGTTCT 3600

TGTAATCATA GTCTTCTGGG TTAACTGGTT TTAAGCCGCT ATTGGTATAG AAACGAAGCA 3660

AGTCACCGTT AGTAATTTGG TCAGACGTTT CTAATTGTTT CGTCGCTTTG GCTTTTAAAT 3720

CAGCGACTTC TTTCTTAACT TCTTCGGTTG GCTCTGTAAT TAAAGTGCCT GTTTTAGTAT 3780

CGTAAATGCT AGAACCTAAA ATAGTATATT TAGGTGTTAC AACATTGCCG TTGCGGAAAG 3840

CAACGATTTG ATTGTGTTGT TTAGAGAATA AATCTTGGCC TAACTGAATG TAGTTTTTCG 3900

TATCGACACC AAGCAAGTGT AGAAGGGTTG GTAAGGCATC AACTTGGCCG CCATACGTAT 3960

GGTTCACACC GCCATTTTCT TGACCAGGAA CGTGAATCAT ATAaGGAACA CGTTGCATAT 4020

TGGCGTTGTC AAAATCGTTC CAATCTGCTT TGGTTTTACC TACTAACTCT GCTAAGTTTT 4080

GGTTTCTTGA ATTAGAAACC CCATAGTGAT CGCCATAAAG AACAATGACT GAGTTTTCAT 4140

AGAGACCTGA AGATTTCAAG TAGTTAAAGA ATTCTTCGAC CGCTTTATCT AAATAATTCG 4200

CTGTTGCAAA GTAACCATTA ATTGTTTCGT CAGAGGTTTT TGCAATTGGG AATCCTGCTT 4260

CATCGTTTGT AAATTGAGAA TAAGGATAAT GATTGGACAC AGCAATAAAT TTAGAATAGA 4320

ACGGTTGTTG TAAATGTTCT AAATATTGAA CGGATTGATT AAAGAATGGT TTATCGTGTA 4380

ACCCATATTG GAATGAGTTA TCTGAATTAA CATCATAATA ACTAGCATCA AAGAAATAGT 4440

CATAGCCTAA ACGTTTATAG GTTTCATTTC GATTCCAGAA GTTACCGGCA TTTCCGTGGA 4500

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ATAGATTGAA TAAGAAAAAG ACAACAGAAA GGAGTGTGAC AGAGACTGCT ACACGTGCGC 5100

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GATAATACAC GACATTTGAG AAGAGCAGTA AACTCATCAA GAAGTAAATA ATCATCATTG 5340

TAATATAAGA AGCTTTTTTA CGGCGAACAT ACAAAGCGAT GGCTAATAAA AAGACCGTTG 5400

TGGCAATTGG ATTAATTAAG AGTATGAAGT ACTCGTTAAT ATTTTCCAAA CGTAAATGGA 5460

AATCAACGGC GTACGCAAAG AGGTTTTTTA GCCACAGTAA GATGGCGATT AGCGAGAATA 5520

ACCCCAGTCG CGTGTTCAAA ATATTTGTTT TAAATAATTT TTTCAAAATA AACGTCCTTT 5580

CTAAACGATG ATTCTATAAA AGTAAAATTA GGTAAATTTC GTATTTTACA ATATCGCTTT 5640

AATTTTACTC TTTCACAAAT TTTATGTCAA TTCTTACCGA AGTGAGGAAT GGTGATGTTA 5700

AAGAAAACTT ACTATTTCCT TAAACTTTTT AGTTCGTTAA ATGACGTGAA GCTTGAATCC 5760

TTTAAAGACA GATGGGCCTT TTTTTGCTAT ACTAGATAGG ACTTTGAAAA GTAGGTGTAC 5820

AGAATGAAAC TTCAAGTAAC TAAAAAAGCA GAACATAAAT TTAAAAAAGG ATATCCTTTA 5880

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CGCACAGTTT ACCCTGACAT TATTGGTGCC TACGAAAAGA TTCGCTTTTC CACAAAAGAT 6300

TTACCAGAAT CACAGTTTTT GTATGGCGAA CAAGCACCCG AGCCATTACT TGTCACTGAA 6360

AATGGCGTTC AATTTGCTAC CTATTTAAAC GAAGGATTAA TGACAGGCAT CTTTTTAGAT 6420

CAAAAAGAAG TTCGTGGTCG ATTAGTAGAT GGTTTTGCAG TAGGTAAAAC AGTCTTAAAT 6480

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CATTTAAATC TTGCCCCGCA AAAGrTTATT GTTATGGATG TTTTgACTAC TTTAAATATc 6660

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CAAAAAGAAA GTTTTTTCCG TTGCTAAAAA TTATGGGGAG CTAGTGAAAG ATTCTATTGA 6780

TATTTTAACG GATAAGGGAA CGCTTATTGC CTCAACCAaT GCGGCAAATT TATCCTTAGC 6840

CAAATATCAA AAAATGGTGA TTACTGCCTT GCAAGAGAAA AATGTCCGTT ACAAGATTAC 6900

GGACACGTAT CAATTACCGG CAGACTTTCA AGTGAATCCT AATTTTCCAG AAGGTAATTA 6960

CTTAAAAGTC CTGTTTATCG AAATTGAAAA ATAATTTTTT ACACCAAGCA AAAGTCCCAG 7020

CGCCGCTAAT CGGTATTGGG ACTTTTGCTT GGTnTTTATT TTATAGTAAC TTTTGGGCTT 7080

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CAAAATACGG GCGGCTACTT GGTCTGATTT GCTGCCAGCA CCAGAGGGCA CAGAGAAACC 7200

CAATTCTGCA GATTCTTTGT CTAACTCTTC TAAAAAAGCA GCGCGGCTAA TAATAGAGGC 7260

GGCAGCAACG GCAACATGAT ACTGCTCTCC TTTAGTGACG AAGAACAATT TTTCAGTGAC 7320

TTGATTTTTT TCATTACGAA CATATTTCCG ATAATTATTT TCAGGGGTGA ACTGATCAAT 7380

TAAAATCCCT TCTGGCTTTG TGGGAGCCAA TTCTTGTAGC AACAGATAAA TCGCTTGGTT 7440

ATGCAAAGCG ACTTTCATGT GTACAGCATT GTAGTTTGGT TGGATCTCAT TGTATTTTTT 7500

GGGTTCAACG ATTAATAACT TGTAAGGAAT CAGTTCTTTA ATGACATGTG ACAATTGAAT 7560

AATTTGTGGG TCGGTTAATT CTTTGGAATC ACGAACACCT AATGATTTTA GTTTGCTAAT 7620

CATGnTTTTG TCAACATAGG CAGCACAGAC AGTTACTGGA CCAAAATaGC TACCATTaCC 7680

GACTTCATCG GAACCtATCA CAGgACCcAT TTGCCCAAAA TCCAGCAGGG CAGTTGGTAG 7740

TTAGTCTGGG GGAAGAAACT TTTTnTCTTC TTGGGTGTTG GTTACCTTCG GTTTCCCTTT 7800

CCCCCAAAAC CG 7812

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1769 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTCAGCGACA GGGATGTTAT TGATGATTAA ACGTTATCAA TCGCAATTCG TGTTTTGGCT 60

ACTAGGAAAT ATTTTTTCAA TTTTGTTATG GTTCCGAGCA GGGACGCACG CTGGTGGTGA 120

TTATGCGATA TTTGTTATGT ATTGTATGTA TACTTTTAAC TCAATTTTTG GTATGTTTAA 180

TTGGTTGAAG ATAAAAAATA AAATGGAAAA AAATAGGTAG GGAGTTCGAT GGCAGTGaTT 240

GTTTTAGCAG GTACGATTGG CGCTGGTAAA TCTAGTTTAA CAGCTTTAAT TGCAAACCGT 300

TTAGGTTCAG AAGCCTTTTA CGAATCAGTT GATGATAATG AGGTATTACC TTTATTTTAT 360

GCGGAACCGG AAAAGTACGC ATTTTTATTA CAAATTTATT TTTTAAATAA ACGTTTTGAT 420

AGTATTAAAC AAGCATTAaC GCATGAAAAT AATGTATTGG ATCGCTCGAT TTATGAAGAT 480

TCATTACTTT TTCATTTAAA TGCAGATTTA GGTCGTGCCA ACGAAACAGA GGTCAAAGTG 540

TACGATGACT TATTACAAAA CATGCTCCAA GAATTGCCTT ATGCTGCGCA TAAAAAAAGA 600

CCTGATTTGT TAGTTCACAT TCGTATTTCA TTTCCCAAAA TGTTGGAACG CATCAAAAAA 660

CGTGGCCGTC CTTATGAACA AATTGAGACA GATCCAACGT TGTATGATTA CTATCAAATG 720

TTGAACGAGC GTTATGATCA ATGGTATGAA GACTATGATG AAAGTCCTAA AATTCAAATT 780

GATGGCGATA AATATGATTT TGTCGAAGAT CCTGAAGCGT GTCAATATGT CTTGGCGTTA 840

ATTGAGAAGA AAATTGAAGA ATTAGAAAGA TAAATAAAAA GAAGCAAGTC CGGACTTGCT 900

TCTTTTTGAC TTAAAATGTG GATAGATAGG CTAAAGTTGC TACTAAATAA AGGAGTGTAG 960

TGCTAAATTA TAGAATCGGA TTTTAACCTT CCCCTAAGTT AAAATCGGAT AATCTATCTA 1020

TCGACAGTTT AAGTTTGTAT AAAATAGCGG TAGCTATTAT CAACGAAGTC ATTCATCGGT 1080

TGACCTGACT TCTCTAGAAG TATACCATCG AAAATAACCG ACAGTTGTTC AAAATTTGGA 1140

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TCACCCGCGA TTGAATGAAA ATCAATGGTT TATTCTTCGA AAACAACGCC TAATGCAAAA 1500

GGTTCATGCT TTTCGCAAGC GACATATGAC TCAGAAAGAG TATCGTTATT TTAAATGTCC 1560

AAAATGTCAG CAGTCATTAC GTGCGCCGAA AGGACGAGGA ACAATCAAAG TCACTTGTTC 1620

AAACTGTCAA AATCAATTTA TCAAAAAAGT CTGATCTTCT GTGTTTTTTG GTCTAGGCAA 1680

CTTTCGGACT TGTGGTATAC TTGAGAAAAG AAACCATTGG ATATTCTAAA AGGGGAATAT 1740

CTTGkTAAAA AAGGAGACAA AAAACAATG 1769

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CnGTCGTTGA CGCATCAACG CCTCnCTCGA GTATATGnGT TCACCTTCAC CGCGTTTAAT 60

AGcAAAcGcT GTTaCCGTTA AATTTTCATT GGCATTAGCT AATCGATTTG TTACTTCTGC 120

AATCGTTGCT TCGACATTTT CCTTTTCTTT GGCAACAATA AGACTGACAG AAGACTTATA 180

GGTAATCACC GCAAAAATGG TAAAAACTAC AAATATAAAG AAAGAACTTG CGAAAGCCCA 240

CTTTATAGTT AAAGATGGGC CTTCCAGTTC TTTTTTAATC GTTCTTTTCA TTAATTAGTT 300

CTCACGAACG CATAACGTAG CCAGTTCCAC GGACAGTTTG GATGTAGCTT TCTTCTCCAG 360

GTACGTCAAT TTTATTTAAT AAGTAGCGGA TATACACATC CACAACGTTT GTTTCTACTT 420

CTGTTTCATA GCCCCAAACT TTATTTaGTA ACACATCACG TGCCAAGACA ACGTTCACGT 480

TTTCCATTAG CGTTAATAGT AATcGTAtTC GCGkTTkGTt AATTCAATCA TTTCAGAATT 540

ACGACGAACG ACACGATTTT CTTTTTCAAT TGTTAAGTCA CGATATGTAA TCGTTGTTTG 600

TTTTGCAACG TTTTTATCGC CCTCAATATC AATACGACGA AgTAACGCAC GTAAACGAGC 660

TAACAATTCT TCAATTGCAA ATGGTTTAAC AATATAATCA TCCGCTCCAT GGTCTAAGCC 720

AGAAACACGG TCAATTACTG AATCACGCGC AGTCATCATA ATAATTGGTG TATTTTTCAC 780

TTGGCGAACA CGGCGACATA CTTCTAATCC ATTTAATTCT GGTAACATCA AATCAAGAAG 840

GATAGCATCC CATTCGTTGT TAAGAGCGGC TTCCAATCCT GTACGACCAT TGTAGTGTAC 900

TTCTGTCGTA TACCCCTCAT GTTTTAATTC AAGCTCAACG AATCTCGCTA AGTTCTTTTC 960

ATCTTCAATA ATTAAAATGT TGCTCATTTG ATTAATTGTC CTTTCTCTTT AAAAGCTATA 1020

CTCAAGCTCA ACCTTTTTAT TCCTTACTAC TTATTAGAGA ATTACTACTC AATCTATCTG 1080

GTTCTTTTTT AAGCCACAGT AAAACCATGA GCATGGTGAG CCACACTCAT GGTCTCCAGC 1140

GTGTTTATTC TTCGTTGTAC CAGCTGTAAT GGTAGATTCC TTCTTTGTCT GTGCGTTCGT 1200

ACGTATGAGC ACCGAAGTAA TCACGTTGTG CTTGAATTAA ATTCGCTGGT AAGCGATCTG 1260

AACGATAAGA ATCGTAATAA GCAATTGCAG ATGAGAATGT TGGTACAGGA ACACCTGCTT 1320

GAACAGCaAT CGCaACAACT TCACGAACGG CTTGTTGATA TTTTyTCGTA ATTTCTACGA 1380

AGTATTCATC TAACAACAAG TTTTCAAGTG CTGGATTTTT TTCATATGCA TCGGTAATTT 1440

TTTGTAAGAA TTGTGCACGG ATAATACAAC CTGCTCGCCA GATTTTTGCA ATTTCACCAA 1500

ATGGTAAATC CCATCCGTAT TCTTCAGAAG CTGCACGGAG TTGTGCAAAA CCTTGCGCAT 1560

AACTCATTAA TTTACTAAAG TATAAaTgTT CGCGAATTTT TTCAATCAAT TCTTTTTTAT 1620

CGCCTGCAAA GTTAAAGGCT GCAGGTTTTG ATAAAATGCC ACTTGCTTTT ACGCGTTCTT 1680

CTTTGTAAGC CGAAATAAAA CGTGCAAATA CTGATTCTGT AATTAATGGT AATGGTACGC 1740

CAAGATCTAA CGCACTTTGG CTTGTCCATT TACCTGTTCC TTTGTTGCCT GCTGCATCAA 1800

GAATAACATC AACGATTGGT TGGTCGGTTC CTTCATCATC TTTACGTGTC AAAATGTCAG 1860

CCGTGATCTC GATAAGGTAA CTGTCTAATT CGCtTCGTTC CATTCTTT 1908

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCTTCTATkG TTAAtTGCaw CTTGTCCAAC TCCTTGyCTT CTTCTACATT ATAACTAAGT 60

TAGGTGACTT TTTCACTAAT AACCAATTGA AACTTTTTCT TGAAAACTTT TTGCATTTTT 120

CATAATTTTG CGTTATTAGC GGATACATTA ATGAACTTAT GGTAAACTAA CATTCTGGAT 180

GGTTCATTCC AGCCAGCCAA TTAAAAACTA TTTTTAGAGC GTTCAACACG CTTATTCATG 240

ATTTTTTTAT AAAGGTGGAC TTATTTTGAT GAAAAACAAA TCGAAGCTTT TATGGTTAGG 300

AAGTTTTTTC TTGCCGTTTT TACTTCTGTT GCTTGTATGG ATGACATTAC AACTTGCGCC 360

TTTTGGTGAC AACAACTTAT TAGTTAGTGA TTTAGGCACA CAATACATGC CTTTCTTGAG 420

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TGCCTTGATG GGCACTACGA TGTTTAGCTA TTTAAAATAC ACCTATCAAA AAGTTGATGG 660

CACCACGTTA CTTTTTTCAA CGTCCTATAG TTTCTGTGGC TTTGTCACCG TCTATAGCCA 720

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GAATTACTAT ATGGGTTATA TGATTTGTCT CTTTGCTGTT TTGTACAGTA TCTATTGGTT 900

CTTTAAAAAG AATACCAAAG CCCATGCTAT TCGGCAATTT TTTAAACAAA GTCCGTTATT 960

CATCCTCGTT TCTTTTTTAA CAGGAACCGC AACTAGCTTT TTATTATTAC CTGCAGCAGA 1020

AGGGATGCTC TATACAAAAA AAGCAGACTT TGATGTCTCG ACGTTCTTTT TAACGCCTAA 1080

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GTTCAACACT TCATTCTTCT CGCAATTAGG CTTAGGTTCT ATTAATTATG AGTTGCGTCT    1140
AGACCATTTA CCAACCGTTT TTGCTGGATT ATTTGTGACA CTCCTCTGTG TTGCCTATTT    1200
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TTTTTTAAGC TTTTGGTTAG AAGCCTTTAA TACTGTCTGG CACATGTTTC AAAGCCCAGC    1320
TGGTTTCCCT TACCGAAATG TCTTTATTTT TAGCTTTTTA TTGATTGTCT TTGCCTATGA    1380
AGTTTGGCTT AAAAAAGTGA CCATTCCTTG GACCGCACCT ATTATTTTTA GTCTGCTGTT    1440
AGTCATTGGC TACGGATCTT TGTATTATGG TCCACAAAAG AATCTCTTAA TTTCGATCAA    1500
TTATTTATGG CTAAGTTTAC TTTTTATTTG GTTGATTTTC TTTTGCTTGC GTTTAGCGCA    1560
CAAAAAGGCC TTAAGAAACT ATGTAGTCGT GGCTTTATTC TTACTGGTCA GCACAGAATT    1620
AACAACGAAT TTCTGGATTT CTTTTAAACA CATGCCCTTT GGTAGCCAAG CAACATTTGC    1680
CCAAGATTAC CGAAAACACA GCCAATTAAT CGATGAAAAA ATGGCCTCAG CACCAGAACT    1740
TTATCGCATG AAACAAGTCA TTCCTTCCAA AGAAACAGGG TTCCGTGAAA TCAATAACGG    1800
CTACAATAAT CCTTTACTTT ATGGCTATGC TGGCGTTTCT AGCTATACTT CGACTTTAAC    1860
TGCCACTACC CAAGACACAT TAAGTGCGCT AGGTTTATAT CGAAAAAATG ATCGCCGGAT    1920
TGCTTATGTG GATAATTCAC AACTAACTAA TTTACTTTTA AATGTGAAAT ATGACTTTTT    1980
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GGaAAACGAT GAAGCGATCG GTATGGGCTT TTTGGCGCCA ACCGCATTAA CCAAGTTAAA    2100
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AATTGAAGCA ACCTTTAAAG TGAATAGCAC TGGTGACTTG CATCTTTATA TTCCGAATTT    2280
AAAATGGAAA AAAGTTACAC AATTGAAGGT AAACCAACAA GTTATCTCGA CGCCGATTTA    2340
TATTGCAACC AATCAACTGT TCAATTTAGG GCATTTTGAA AAAGGAACTA CCGTGACCCT    2400
GTCACTAACT GCTGAACAAG TGGTTGATTT AACCAATTGG CAACTTCAAA CTTTAGACCA    2460
AACAGCCTTT AATCGTGCGG TTGACAAATT ACGCCAACAA GCTCTTCACG TGAATGCAAC    2520
TAAAAAAGGC CATTTAAATG GCGCACTGAA TGTACCTGGA AATGACACTC AGTTACTGTA    2580
TACGTCCATT CCTTATGACC AAGATTGGCA AGTCAAATCG TCGCTACAAA AAGAACCCTT    2640
AAAAACACAA CGCATTCTAG GTGGCTTTTT AGCTGTTGAA GTCCCAGCTG GCAAACAGCA    2700
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TTTACTGGGA ACGGCTGGTT ATCTTGGGTT TAAAAAATAC CGTCGAAAAC GTCAGGAGGC    2820
CACTCATGAC TAATCAGAAA AAATTTTTAA ATGGACTCAT TCGGTGGTTA CCCCTAGTTG    2880
GACTGGTGCT TTTCTTCGGC TTAATTCTAT GGGGATATTC CAGAGGAATT TTTCATTCTG    2940
TTGCTTCCTT GCAAGCTTTT ATTAAACAGT TTGGTAACTA TGCGGTTCTG TGTTTCATTC    3000
TTTTACAAAT CGTCCAAGTG ATTATCCCTA TTCTACCTGG AGGAATCTCT TCTGTTGCAG    3060
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GAATGTTGAT GTTTGGCAAT TTGCAAGGAC TTTTGTATAG CTATCTTGGA TTGATTAkTG 3120

GTGAGTTTAT TGGCTTTTTA CTGGTTCGTT ACTATGGACG TAGCTTTGTA AAAATAATCC 3180

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TGATCCAATG TGTACACCAA GATGCTCCGT GTTGTTTGTT TAGCTGCTTC ATTGTCTCCG 4140

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TTCTAATACG TGCCCTTTTC TTGTAACATT CATTCTGAAA TCCTCCTTTT CCACTTTCAA 7020

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CAAATTCTCG TTGCGTCTAA AATTATTTTT TAATAATGCC TTGCCTAAAT TGCCACAACC 7440

AATCAGAGCA ATTCTTTTTT CTTCTTGCGT ATTTAAAATA TTACTGAATA CCTCAATTAA 7500

ATACgGCACA TCGTn 7515

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATATGGCCTT CACTTTAGTG AAGAGATTTA ATTGTCTTTA CAGATAAACG CTTAATTTTA 60

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TGGCTTCTCG CATAAAAAAT TCTTTTTCTT CTTGTGTTAA CGTTGTTTCT TTTTTTCCCA 1020

ATTAATTTCC ACCTTTCGGC TTTTTCCCAC TAAACTTCTG TCTTGCTTCA TGGTACAATA 1080

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GCAAAATTAC CTGCCGAAGG GACCTTTCGT ATGTTGCAAA TTCAAACGAA TGTCACAAAA 1380

GAATTACAAG CTGAATGGCA ATTTAATTTA ACAAAGATGT TTCCAGATAC AGTTGATTGT 1440

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ATCTTTTGTT ATTTGTTATT AAGAAAGTAG TACGTCCATT TTTTACTCGT ATGTTTTTTA 1980

TTCCCAATTA GAAAGTAGGC GTTCCAATGA AAATTACCGC ATATGTCGCT AGTGCATTTA 2040

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GAACCCAAAA AATGGCCATC GCCAAAGAAC TAGGATTTGC AGAAACTGCT TTTATTTCAG 2160

ACTCAAAGAT TGCTGATTTC CGCCTTGAAT ATTTTACACC AAAAGAAGAA GTCGACTTAT 2220

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CAGCATATAC AATCGAAACG AACAGCGGTT TGCTCGCAAT CACGGCTAAC GGTGAACAAC 2340

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GTTTGACTGC CTTTTTAATT TCTTTGATAT TTTCTTCCAT GGAAGGTGCC GCTTGCGTCT    5040
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CAATCACTTT TTCAGAGAAA TACCAGATTT TTTCTCCTGA AAATTCATAT CTTTTCTCTA 5100

GTAATTCAAA CGCTAATGTA TCTAAGTCAA CCGTAATCCC TTCATCTGGT TTTTGTGATT 5160

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TCAGCAATCA ACTGTAAATC AATCGCATTA CTCATATGAT GCAACCCAGT GATGACTAAT 6240

GGTGCGTACA TAAAGCCAAA GACGGCGCCA AATAACCAAT TAAATGTTGA CGTTAATCCT 6300

GCATTTACGA TATCAGAAAC CCAACTACCA ATCGTCCAAC CGATTGGTCC TAAAATGACA 6360

TGTGCAGCCA ATACTGTTGG TACTAAAGCA AACAATGGGA CAAAAATCAT TGAAATTGCT 6420

TGAGGAATCA CTTTTCTAAA GAAAATTTCA AGATAGGCAA GCAAGAAGCC GGCTAACATG 6480

GCTGGGATAA CTTGCGCTTG ATAACCAATC ATGTTAACTT GAGCAAACCC AAAATCCCAG 6540

AAAGGAATTT CTGCTGCTTT AGTCGTCGCA ACTGAATAAG CATTCAGAAG TTGTGGTGAG 6600

ACTAATGTAA TCCCTAGGAC AATCCCCAAG ATTTGTGTGG TTCCCATTTT CTTCGTAATA 6660

CTCCACGTAA TCCCAACTGG CAAGAAGTGG AAAATTGTTC GCCGATTAAC CATAAGAATG 6720

AATTGACTCC ATTCCAAAAT TGAGAAACTT CCACGATTGT TTGACCATCA AGAAAGCCAA 6780

ATGGAACCCC TTCCAAAATA TTGCGGAACC CTAAAATCAA TCCCCCGATA ACAAGTGCAG 6840

GAATCAATGG TGTAAAAATC TCAGCTAAAA CAGAAACAAC TCGTTGAACA GGACTCAAAT 6900

TACTTTTGGC AGCTGCTTTC CCTTCTTCTT TTGAAACCCC TTCTAAACCG GAAATTGCAG 6960

AAAAATCATT ATAAAATTGT GGGACTTCAT TCCCAATAAT TACTTGAAAC TGTCCAGCAT 7020

TTGTAAAGGT TCCTTTTACA GAAGGAATAT CTTCAATCAC AGGTACATCC GCTTTTTTTG 7080

GATCTTTTAA TACAAAACGC ATTCGAGTTG CACAATGAGA AACAGCTGAA ATATTTTCTT 7140

TGCCTCCTAC TGCTTT 7156

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTCGTTGTA ATTCCAACTG GAATTCCTAA TACGAACTTA GAAACGTCGT ATCCATTTCT 60

TGCTTTAATG TCAGTTGTTT TTGGACCAGT AGCTGGAGGG CTAATTGGTT TGATCgGTCA 120

CACgTTAAAA GATTTTACCA CGTATGGTAG CGCTTGGTGG AGCTGGATTA TTTGTTCAGG 180

AATTATTGGT ATTATTTTTG GCTTCGCTGG TCGTAAAATG GATCTTCAAC ATGGTGAATT 240

CACAACAAAT GACATGGTGC GTTTCAATAT TTTCCAAGCC TTTGGCAATA TCGTCGTTTG 300

GGGCTTAATC GCGCCTAGCT TGGATATTTT GATTTATAGT GAACCCGCAA GTAAAGTGTT 360

TACACAAGGC GTATTCGCGA CTGTTTCAAA TATTGTCGCT GTGGGGATTA TTGGAACATT 420

GTTGATGAAA GCTTATGCAT CAACAAGAAC AAAGAAAGGC AGTTTATCAA AAGATTAAGA 480

AACTGTCGAA ATAATTTAAA TGGTTAAGGG TCTGCCCTAG TAATTACTTT GCTAATGCTC 540

AGACCCTTTC TTTTATGGAG AAACTGAGGT GAGGCCGAAT GAAAAAACCA ATCATTACTT 600

TTAATAATTT TTCCTTTCAA TATCATAGCC AATCTGAACC AACATTAAAG GGGATTCAAT 660

TAACCATCTA TGAAGGAGAA AAGGTTTTAA TCGTTGGGCC TAGTGGTAGT GGTAAATCAA 720

CATTGGCGCA ATGTATCAAC GGGTTAATTC CCAATATTTA TGAAGGTGAG ATTCAAGGAA 780

CAGCTACGGT TGCTGGTAAA AATATCCAAG AAACAAGTCT ATTTGATTTG TCTTTTGATG 840

TAGGAACTGT TTTACAAGAT ACCGATGGGC AGTTTATCGG TTTAACGGTT GCTGAGGATA 900

TTGCTTTTGC TTTAGAAAAC GATGCAGTTG AACAAGCAGA AATGAAAAAA GCGGTTCAGA 960

AATGGTCCGA GATTGTTGAG CTGAATCAGT TATTGCAACA CCGTCCACAA GATTTGTCAG 1020

GTGGTCAAAA ACAACGTGTA TCTATGGCGG GCGTTCTAAT TAACCAATCA AAAATTTTAC 1080

TTTTTGATGA ACCTTTGGCT AATCTTGACC CACGAGCGGG ACAAGAAACA ATGACTTTGA 1140

TTGACACCAT TCAACAAGAA ACAAAAGCGA CTGTTTTAAT AATAGrACaT CGCTTAGAGG 1200

ACGTtCTTTG CGAATCAGTT GATCGAATTA TTGTCATGAA TGAgGGCACa ATTATTcTGA 1260

TACAACGCCA GATGAATTGT TA 1282

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5840 base pairs
(B) TYPE: nucleic acid

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

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

TAAGGATTGT TACTGCTTTG CAGGCAAAAC CAGAGTCTTC CATTAACACA ATCAGTGGAG 60

GGATTCTGGG CTTTTTTTAT AAAAAAGTGA GGTTGCATTC ATCATGAGGA TTGAAAAAGT 120

TTTAAATAAT AATGTCGTGC TTTCAAGAAA TGAGCAAGGC GAAGAAATTG TTTATATGGG 180

ACGCGGCTTA GyCTTTCAAA AGAAGATTGG AGACACGATC AATCCAGATT ATGTTGAAAA 240

GGAATTCGTG TTAAAGGACT CCGCTATGGC AGGGCAATTC CAGCAGCTGT TTGAAGACGT 300

CCCCACCAAA GAAGTAGAAG TCGTCAAACA AATCGTTGAT TTAGCAGAAA CAACGCTAGC 360

GATTGAGCTT TCATCAAATA TTTATTTAAC TTTAACGGAT CATATTCACT ATGCGTTACT 420

TCGAGCCAAA GAAGGAATTG ATATTCCGAA TCCTCTTGTA TTCGAAACAC GCAAATTTTA 480

TCCTAAAGAA TTTGAAATCG CAAAGCAAGC ATTAGCGATT ATTGCTGAAA AGCTAGGGGT 540

TCAATTTTCA GAAAATGAAG CGGGCTTCAT TGCTTTTCAT ATTGTGAATG CTGAACAAGG 600

AAATGGCAAT ATGGAAGTTA CCATGGAAGC AACCAAGATG GTTCGTGATA TTTTAACGAT 660

TATTAGTCGC TACTTTGGAC AGGTGTTTGA TGAAGATTCA TTGAACTATC AACGAATTGT 720

TACACATCTT CaATATTTTG CGCAACGTTA TTTAAAACAA GAAGCGCATG aTGAGGAGGA 780

CGAATTTCTT TTtGCATtGG TCCAAGGAAA GTATCCTAAG GCGTTTCAAG CGGTCCAACG 840

TATTAATGAG TATTTATTAA AAAGCTATGA TCGACCAATT GATCAAGCGG AAATGATTTA 900

TTTAACCATT CATATCCAAA GAGTGGTCAA TGATAAAAAA GCATAACAAC CAATAATCGC 960

GGATTGTTAC TGATAATGCA GGCAAAACCT AGATTGAAAA AACCGATAAC GATTTTCGCA 1020

GACTGCGCAC TGTGAAGAGA AGGATCTGGC TCTTTTTCAA TGTAGGTTTT TTTGATATTA 1080

AAAATTAATG GAAATGAGGt CTAGAGATGA GTAAAAATCA AGAAATTGCA GCACGTGTGT 1140

TAAAAGCTGT TGGGGGCGAA GsCAmCGTTA ATAGkGTTGk TCACTGTGCy ACACGCTTAC 1200

GtTTTAAATT AAAaGrTGAA AATAAAGCAG ATACAGCTGC ATTGAATGCT GACCCAGATG 1260

TTATTCAGGT AGTTCAAAGT GCAGGACAAT ATCAAGTGGT TATTGGCAGT CACGTTAGTa 1320

TGTCTATAAG GATTTGATGG CCAACAGTGG ACTAGGTAAT GATTCTGATA ATAGAGAAAA 1380

AGAAAGTGGC GGAAATATCT TTAACCGTTT AATTGATATT ATTTCTTCTA TTTTTACACC 1440

GTTTTTAGGT GCAATGGCCG GCGCTGGGGT TCTAAAAGGC TTCTTAACAT TGGCTGTAAC 1500

TATGGGCTGG TTAGCTGACA CTTCAGGCGT ATATCTTGTT CTCTTTTCGA TTGCAGATGG 1560

TTTATTTACT TTCTTACCAA TTATGTTAGC GTTTACGGCT GCTAAAAAAT TCAATACTAA 1620

TCCCTTTTTA GCGGTTGCTT TGGCGATGGC CTTGGTTCAT CCCAGCATTA CTGCTTTAGC 1680

AGGCAAAACA ATTAGCTTTG CTGGTCTTCC AGTGATTATT GGGCCAAGTG GCTATACTTC 1740

TTCGGTTTTA CCAATTATTT nGGCTGtTTT TGCACAAAGT TATGTAGAAC GTTTCTTCAA 1800

AAAAGTAATT CCGAGTTTTC TACAAATTAT CTGCGTTCCG TTAGCTGTTT TCCTTATTAT 1860

GGCACCTGTT ACCTTCTTAG CTATTGGTCC TATCGGGACG GTCATCGGCG ATTGGTTGGG 1920

ACAAGGATAC AACGCAATTT ACGCTTTTAG TCCAATTATC GCAGGGTTAT TAATGGGTTC 1980

GTTGTGGCAA GTCTTGGTAA TGTTTGGTAT GCATTGGGGC TTTGTACCAA TTATGATGTT 2040

AAACTTAACA CAAGGTGGCG ATACGATGGT ACCGATGTTA TTACCAGCCG TTATTGCACA 2100

AGGCGGGGCT GCTTTAGCTG TCTTTTTCCT AACAAAAAAT GTGAAACTAA AAGGTTTGGC 2160

TTTGTCTTCA AGTATTACGA CTATTTTTGG AATTACTGAA CCAACTGTAT ATGGCGTGAC 2220

TTTACCATTG AAAAAACCAT TTATTGCAGC TTGTATTGGT GGCGGTATCG GTGGTGCATT 2280

TGTGGCTATG AATCACGTGA AAAACTTTAC GTTTGGCTTG GTTAGTATGT TGAGCTTGCC 2340

TGGCTTTATT CCTGCAGAGA CAAAAGATAC TGCACCGATG ATTACTGGTG CAATTGGTGC 2400

CGGAATTGCC TTTATCATTG CGTTTGTCTT AACGTTTGTC TTACGTTTTG AAGATCAACC 2460

TAATCCAGAA ACAGCAACTG AAAAAACAGA AACTGATAAG ATGGTGGCAC CTGTAAAAAC 2520

GAATCAAGAA GACAAAATTA TTTTAGCAAG TCCACTTCAA GGTGAAATTT TACCGCTAGA 2580

AAAAGTACAA GACCCTGTTT TTGCTTCAGG TGCTTTAGGA AAAGGTGTTG CAATTGAGCC 2640

GACTGAAGGC AAACTGTATG CACCCGCAGA TGGTGAAATC ACCACATTAT TTCCGACAGG 2700

ACATGCTGTT GGCTTGACGA CAACAGAGGG CGTTGAATTA TTAATGCATA TTGGCATGGA 2760

TACGGTCGAA TTAGATGGTA AAGGCTTTGA ATTATCAGTG AAACAAGGTG ATTCTGTTAA 2820

AAAAGGAGAT TTGCTAGTTA CTTTTGATAT TGCTGCCATT AAAGAAGCTG GTTATCCGGT 2880

AGTTACACCG ATTGTGGTAA CGAATACGAA TGATTATTTA GATGTTTTGG ATATGAACCA 2940

AACAGACGTG TTACATGGTG AAGACTTTTT AGCCATTATT AAATAAAAGA CAATTGGAGG 3000

AGGAACAAGT ATGACAACAA CGACAAAATT TCCAAAAGGA TTTTTATGGG GCGGTGCGAC 3060

CGCAGCCAAT CAATTAGAAG GGGCTTACTT AGCCGATGGT AAAGGGTTAT CTGTGGCAGA 3120

TGCGATGCCG GGAGGAAAAC AACGTTTCGC TATTTTAGGA GATGAAGCGT TTGATTGGAC 3180

GATTGmCGAA ACGAAATATC GCTACCCTAA TCATACAGGA ATTGATCACT ATGATCGCTT 3240

TAAAGAGGAC ATTGCGTTGT TTGCTAAAAT GGGCTTCAAA TGTTATCGCT TTTCAATTGC 3300

GTGGTCGCGT ATTTTTCCAC AAGGAGATGA AACACAACCG AATGAAGCCG GCTTGAAATT 3360

TTATGATGCG GTTATCGATG AATGTTTAAG CTATAACATT GAACCAGTAA TTACGATTTC 3420

TCATTATGAA ATGCCACTGC ATTTAGCGAA AGAATACGGC GGGTGGAAAA ATCGTCAATT 3480

AGTTGACTTT TATGAACGTT TTGCGGAAAC TGTTTTAACA CGTTACCACC AAAAAGTTAA 3540

CTATTGGATG ACATTCAATG AAATTAATTC AGCTTTTCAT TTCCCAGCGC TTAGTCAAGG 3600

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ATTTGTTGCA AGTAGTAAAG CTGTAAAAAT TGGCCATGAA TTAAATCCAG AATTACAAAT 3720

TGGATGTATG ATTATTTATG CCACAACGTA TGGCATTGAT TCGAATCCAG TCAATCAAGT 3780

TGCTACAATG ATTGAAAACC AAGAGTTTAA TTATTATTGT ACAGATGTTC AAGTTCGTGG 3840

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TGAAGAAGGA GATTTAGAAT TATTAAAAGA ATACCCAGTG GATTACATTG GCTTTAGTTA 3960

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TTTAGGCGGC GTTAAAAATC CCTTCTTAGA AGCAAGTGAA TGGGGTTGGC AAATTGATCC 4080

CGAAGGCTTA CGAATCGCCC TAAATGAATT ATATAATCGT TATCAAAAAC CTTTATTTAT 4140

TGTGGAAAAC GGCTTAGGTG CAATTGATAA AGTAGACGAA AATTTCTATG TGGCAGACGA 4200

CTATCGGATT GATTATTTAC GTCGTCATAT TGAAGCAATG GCAGAAGCAG TTGCAGACGG 4260

CGTCGATTTA ATGGGCTATA CGCCGTGGGG CTGTATCGAT TTAGTCAGTG CTTCCACAGG 4320

TGAAATGAGT AAACGGTATG GGTTTATTTA CGTTGATTTA GACGATGAAG GAAATGGTAC 4380

TAAAAACCGT TATGAAAAAA AATCGTTTAA TTGGTACAAA CAAGTTATTG AAACTAATGG 4440

ACAAAACTTA GACTAGTTAT TGTAATTAAA CAAAACAAGA TAAGCGTAGT AGGTTGTTGC 4500

TTCTGTTTCC GCTGTTTATT AATTTTTAAG CTTGGACCAA AAATCTAAAG TGATTTTTGG 4560

CCCAAGCTCT TTTTTGTCAA TTTTTCAAAA TAGTGCACAA TACGTTATAA TAGAAACAAC 4620

TGAGAGGAGC GTTTCTAATG ATTAAGCAAT TACAACATCC ATTTTTTGTT ATTATGGGTC 4680

CGAGTGGTTC TGGCAAGACC GCAATTACAA GTAAGGTTTT TCCGAAAAAC TATAAAGTTA 4740

TCTCGCATAC TACGAGGAAA AAACGATTGG ATGAAGTGGA TGGCGTGGAT TACTATTTTG 4800

AAACAAAAGC AAGTTTTCAA GCCTTGATTG AAACCAATCA GTTAGTGGAG TATGATTTTT 4860

ACCATGGAAA CTATTACGGT GTCGGTGTAG CTGCCATCGT TGAAACAACG AAAGAGCATC 4920

CAGCCTATAA TGCGTTAACT TTTCCAGGCT TTCAAGCGGT CTTTGAGCGT TTCGGCGAGT 4980

CCGTCATTCC AGTTTTTTTT GACGTTTCAA AAGAAAATAT TTATCAACGT TTAAAACAAC 5040

GAGAATCTGA TCCTAAAATT ATTGAAGAAC GTTTAAACCT TTATGATCAA GAAATTCTTA 5100

TCAAAAACCA ATTGGAACAA TATCCTAATT ATCAACGAAT AGATGCCAAT GGACCTATAA 5160

AAGAGGTCGC TGGCTTGTTA CAAGAATGCA TCAAACACTA TTATTAATCA AGCAACTGGT 5220

GAGACAGAAT CTAACATCAA TTTTGTCTTG CTAGGTGCTT GATTTTTTTT GTAAAAAACT 5280

TGCATTCTGA ATAGAGAGTG CTATAATGAC ATGGTGTCAT ATGACAATGT GTCATAAAAG 5340

GGAGGAACAC AAATATGCCT ACGAATACGT TTTTTCATTT GCCAGAAGAA AAGCAACAAC 5400

GCTTATTAGA TGCTGCGCAA ATTGAATTTT CGCGCCATTC TTTACAAGAA GCGTCAATTG 5460

CAAATATTGT TAAATTAGCG GGAATTCCGC GCGGTAGCTT TTATCAATAT TTTGAGAACA 5520

AAGAAGATTT GTATTTTTAT TACTTTGCGA CATTAAGAAA AAATAGTGAA CGAGATTTAG 5580

AGAAACAAAT TATTGCGGAA AATGGTGATT TAATCGAAGC CATGGATGTC TATTTCTCCA 5640

AAATGATTGT CGAAGTGCTA ACTGGaGAGA ATGCTTCTTT CTATCGGAAT TTATTTGTCA 5700

ACATGGACTA TCGTGCtTCA cGTCGGGTGA CGGGATnAAT TTTAGCCGAC TGGGGGAAGA 5760

GGGAAAAAAA ATAGGGAAAC CAGCCACTGT CCATnAAGCC TAGAnGGGAG GAAAAAGGnC 5820

CATGCCTGCC CCATGGCGGA 5840

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGATCTTTTT GACGACGTTC AATTTTACGT TTTTTCTTAT TGCTGTCTTC AATTGCCCAA 60

TTAATTTTTT TCTTGTATCC TGGTTTAATT TTTTTCTTTT TCTTTTTCAC TAAACCAATT 120

AACGTTGGGT CTAATTCTTC TCGAGATTTT TCTCGTTTTG TTCGACGATT ACGATCATAC 180

GTCTCTACAA TCTCACCATT TTTAATTTCT TTTGGTTTGA AAGAAACACC TAACTGCTCA 240

ATCTGAGTAA tCGCTTCATC ATCTgCTGGT GAATATAATG TTATGGCAGT CCCATTcAAT 300

CCATTACGTC CTGTGCGGCC AACCCGATGG ATAAAGAAGT CCAATTCATG TGGAACTTCT 360

GCATTGATGA CATGTGAAAC CCCTTCAATA TCAATCCCAC GTGCGGCTAA ATCAGTAGCT 420

ACTACATATT GGTAGTCAAG ATTTTGAACT TGACGCATCA CACGTTTTCT TTCGCGTGGT 480

GTAATGTCTC CATGAATTTT GGCAACTTTT AGGCCCTGAT CTTTTAAGTA ATCGGTGATT 540

TCATCAACTC TTTGTTTAGT ATTTGCAAAA ACAATCGCTA AATAAGGATG CCCGATAGTC 600

AATAATTGAT AAATTATTTT ATTGCTGTTT TTTCCTTTGG TGGAAATCAA CCAATTGTCA 660

ATTGTTTCTG AAATAACTGC TTTTGGTTTG ATATGTTCAA TCACTGGATT TTCTAAATAT 720

TTTTTTAAAA ATGGTCGTAA TTTTTCTGGA ATGGTTGCAG AAAAAACGAG CATTTGTAAT 780

TTTTCTGGCA AACGACCCGC AATTTGATCG ACTTCTGCTA AAAAGCCCAT ATCTAATGTC 840

ATGTCTGCTT CATCGACAAC AAAGGCAAAA GCCGTATGCA CTTTCAAGGC TTGTTCATTC 900

ATCATATCTA AAATACGCCC TGGTGTACCA ATCACCACAT GAGGTTGCTG ATGCTTTAAT 960

TTATTTAATT GACGTTGTTT ATCTGTTCCG CCAACAAAAT TTGACACTCG AATTTCTGkT 1020

TGACTGAAAC GAGCCAGTTG tGCGCTTCTT GATAAATTTG ATTGGCTAAT TCACGACTAG 1080

GCGCAGTAAT CACAATTTGT ACTTCGTCGA TAGTTGGCTT AACTTTATCC ATTAATGGAA 1140

GTAAAAAAGT ATGCGTCTTT CCACTTCCTG TTTGCGATTG TCCAATAACA CTTTTCCCTT 1200

TCTTAATGAT TGGGATTAAT TTTtCTTGGA CTTCTGTTGG TTCTTCAAAC CCTTTTTCTG 1260

CGAGTGCTTC GTTGATAAAA GGTTGAAATT GAAATTGTTT AAATGAAGGC ACTTGCCTCA 1320

CCTCTTCTCG TTAAATTCTT TATGCACTTT GGCATTATAA CACAAAAACA ACTTTTACTC 1380

ACCTGCTGAT TCCTTTGTTT TCGCAACTTC TAATGTACTG ACTGTATAAG TGTGGCTGGC 1440

TTTTTCATAA AACAAACGCC GTTTTTTACG AATCAAGGTT AACAAAACGT TGATCAAAAA 1500

TAGTAAATAT AAAATTAAAC AGAACAAATA CAGAAGCAGT GACACCATTT GCAACATCCT 1560

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ATTAGAAGAA TTCAATAACT CAGTGGCATT GGCTAGATAA ATACTAATTA AACCATACAC    1620

AAAATACAAA TAACCGTAGC GAACAAACAA GGCTTTTAAA CGAATTTTTT CATGTCCTGT    1680

TTCAACCACC CGAATGCGAA CAACTTTTTT CCCTAACGTT TGACCATTTG TCAGTTTCAT    1740

CATGACGATA AAGACCGCAA ACACCATGAT AAAGAACCAC ATCCGATCTG AAAAAATCGG    1800

ATAATTGGTT GCCCAATTTT TATAAGCTGG AATGAAATTT AGTCCAAAAA CGAGCAGGCC    1860

TTGCACAAAG CCAATCACCA ACCAATCAAT TCCCCATGCA AAgAAaCGTC TTAACAGGCT    1920

AACTGTCTGC CCTTTTTCAT AAGAgGTGGC ATCAATTTCT TCTCTTGTTG GCAATAAAAA    1980

GGTAAAGAGC GGCGTCAACC AATAACCAAC TATGCCTCCG ACGGTATTAT TAATTAAATC    2040

ATTGACATCC GCCAAGCGAT ACGAACGTGG ATAAATAAAA TAAAGGCCAG ATAACTGTGT    2100

TAATTCAnAA AATAATGACA ATAAAAAACT CGCAAGAACT GTTTTTAAAA ATGAACATTT    2160

GAAATAATAC CGTAAATACA CACCAAAAGG TAAAACTAAT AAmACATTAA ACAGTGGTTC    2220

TAAAACGGCA TGCTGTTTTA ATGCTGGCAA ATACGTACTA GGATCTTTGA TCGAAAAAAC    2280

AGTTTCGTTT AAAATCCCTG AAATAAAATG AAAAGGCCGC AGTTCCATTG TTGGTCCTGT    2340

GTATTGAGCC ACTTCTGCTC GAGATGGCAA CGGTAAAATT ACCAAGAAAT AGGCACATAA    2400

TAAATAAAAA ACAAATGAAT ACAAAATCAT TGCTCGTGTC CAAACAAATG AACCATATTT    2460

GCGGTATTCA TAGATTAATA ATGCCCCAGA AATAAAAAAT GCTAGAAACG GGAAAATAAT    2520

GATTGCCCAT TTAATTGGTT CGCTATATAC TGCCATAAAA ATCCCTCCAA GATAAACAAT    2580

TTCAAGTATG AATGCCTCAA TAACACTATA CTTGTTTCTA AAAAAATGTA CCAACAATAA    2640

ATTTTATTTT GCAAATCCTC TCCTTTGCAG TATCATTAAG AAAAAGGAGG ACGTTCTCAT    2700

GTTACAGCCA TATTTTGCGT TTGGAGTGCC GCTATTTTTA CTTGTGCTCT ACTTACTCTT    2760

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AACATTTCTC ATGGTTTTTA GTTTCCAAGT ATTGCAAGAA TCATGGACCA TCAACCCTGA    2880

AACGTTAAAA GATGCCGCTT ATTCTCCGCA ATGGTTATGG ATTCCTTTAG GTATCGGGTT    2940

AATCCTCACA CTTTACAACG CTTGGCACGG CCTTCGTACA ATGATAAAAT ACAAGACCGA    3000

TAAACATTAG TAAGAGTCTA GGACGATGGT TGTGTCCTAG ACTCTTACTG TCTCATCATT    3060

CAAATGAAAT TTAATTTTTC TTAACAAACT CTGATTTTAA CTTCATTGGA CCAAAGCCAT    3120

CTACCTTACA ATCGATGTTA TGATCACCTT CCACTAAACG AATGTTTTTC ACTTTTGTGC    3180

CTTGTTTAAT TGCGCCACTG GCACCTTTAA CTTTCAAATC TTTGATTACA GTAACACTGT    3240

CACCATCCGC TAAAAGATTG CCATTTGAAT CCTTAACTAC TAAGCCTTCT TCTGCAACTT    3300

CTTCTGTTGG TGACCATTCA TGACCGCATT CTGGACAAAT AAATAATCCG CGATCTTCAT    3360

AGGCATATGC CGACCCACAT TCAGGGCAGT TTGGTAATTG CTCTGTCATT AACGTTCTCC    3420

TTTGTAAAAA ATAATTCTTT TTCATTTTAC CTTATTTTCT AGTGAATGAA AAGTAGTCCT    3480

AATGATTTAT CAACGTCCGA TAACTACTTT CTAATTACTT ATTTATTTTT GAGCCCACTC    3540
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TTGGCAAGCT GCTTGGATTT CTTGGTAAAT CACTTCAATT TCAGCCGCAT CACGTGCATT 3600

AGCGCCACTT GCCAAAGGAT GGCCGCCGCC ATGATGTTTT TTAGCAATTG TATTAATGAT 3660

TGGTCCTTTG GAACGTAACC GAACGCGATA ATAACCTTCC GGCTGTTCAA CAAAGATTGC 3720

CCATGAGAGA ACATCTTCAA TTTTTCCTGG CATTGAAACA ATGGCTGCCG TTTCAGAATC 3780

GACAATATCA TAACTGTTTA AAATACTTTG TGGTAAAACG ACACGAGCAG CGCCATTTGC 3840

GTCGATTTCT AAATTTTGAT AAATATAACC CGCTAATTTA GCAACCTTTA AAGGCATTTG 3900

GTCTAACTCA CGATTTAAGT CTGCGGCATT AAAGTTAAAC GTACGCAATT GCGCACGACA 3960

GCGAGtGTAT GCGCCGAaGT GGaAGGATAA AGAAAACGTC CTGTATCCCC CACAATCCCA 4020

GCATACAATA AACGAGCTGC ATTATCTGTC ATCGTTAATT CTGCTAAATG CTGTgCCAAA 4080

AATCAACAAT AATTTCACTA CAACTACTTG CATTTGTATT CACCCAAACT AAATCTCCAT 4140

AAGGTTCATC ATTCGGATGA TGATCGATTT TAATTAATTG ATCGCCTAAA GAAAAACGCG 4200

CATCACTAAT TCGTGGAGCA TTTGCAGTAT CTGTTACAAT GACTAATGCA CCTCGATAGA 4260

CATCGTCAGT AATAACGTCC ATTTCAGCTA AAAACTCTAA GCCTTCCACT GGTCCGCCTA 4320

CTTGATAaAT ATTTTTTyCA GGAAAGCTCG CTCTTAAGAG TTCTGCTAAC CCAACCTGTG 4380

AGCCAATTGC ATCTGGATCC GGCCTTTGAT GTCTATGAAT AATAATTGTT TCATATTGTT 4440

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TCTAATTTtTG CAGAGCGACG GCCAATTTCT AAAATCCGTG GACGAATGTC CAATTCACTT 4620

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ATGACTTTAT CCACGGTTAA ATGTTCACTT TTACCAATGA CATCTTTGGC TGTGACAATC 5100

CCCACTAAAC GTAATTTCTT ATTTACTACT GGGAAACGAG AATGATGGGT ACTTTCAGAT 5160

AATGCCTGAT AATCTGCAAT CGTCTGAGTT GTCAATAAAT AATTGGtTTT TTCAAGCGCT 5220

GTATAAATAT CACTGACGAG TAAAATGTCT TTTTTAATCA GCTGATCACT TAAAGCACGG 5280

TTAATCATAG TAGCCACAGT AAATGTATCA TATGTGGTTC TCAAGACAGG CATACCCAGA 5340

CGATCTGCTA AcTGCGCAAT CTCTTCAGAT GTTTCAAATC CACCTGTAAT TAAAACGGCT 5400

GCCCCATTTT CTAAAGCAAG CTTTTGCACA CcTTGGCGGT TACCAACAAT CATTAAGGAT 5460

CCGGGAGTAA TATATCGCGT CATCGCGGTT TCTGTCATCG CACCAATTAC AAATTTATTA 5520

AGGACTTTGT CTAGACCAGA GcTACCGCCT AACACATCCC CTTCAATAAT CCGGACCACT 5580

TCACCAAATG TTAATTTTTC AATATGTTTT TTTAACTTCC GCTCAATTCG TATCGTACCA 5640

ACACGTTGAA TGGTGGAAAC AAGCCCAATA TTTTCTGCAT CTTTGATGGC CCGATACGCT 5700

GTTCCTTCAC TAACACTTAA ACTTTTGGCA ATGCTTCGAA CAGAGATTCG ATCGCCAATT 5760

GGTAAGTCTT CAATATGTTT TAAAATTTGA TCATGTTTCG TCGCCATAAT TTCCTCCTAA 5820

ACTAGGATCG TCTCTCCTGG GTTTAATACT TTCCCGCCAA CTACTTGCTC TACGAATATT 5880

GCTGGATTTT GTTGGATAAC AGGAAAGGTA TTGTAATGAA TTGGAATGGT TATTTCGGGA 5940

TTTAAGTAAG CGATTGCTTC TAGCGCATCC TCTGGTCCCA TCGTATAATT ATCGCCAaTT 6000

GGTAAGAACG CTACATCAAT GGATTTGTCT TTTGCAAAAA GGCGCATATC TGAAAACAAC 6060

GCCGTATCAC CAGCGTGATA AATTTTTTtA TCTTCTGCTT CTAAAATAAT CCCACTTGCT 6120

TCGCCCATGT AGGTCATTAC GCCGTCTATT TCATAACCGG AACTATGCAA AGCTGGCACA 6180

AATTTAACCG AACCAAAAGG AAAGACATAA CGCCCACCTA GATTCATTCC ATGCGCTTTT 6240

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TAATCAGGGT GTAAATCTGC AAGTGAAACG TcCGCTAAAG GGTTGCCATT AATAAAAGGA 6420

TCAAATAAAA GGTTCGTGCC GTCGTTTAGA CGAATTTCAA TACATGAATG TCCATGTCCT 6480

ATCAGTTCCA TTTGTATTCC TCCTACGGTA TTTTCTACAC AATCTTATGA TAATTAATCG 6540

kCAAATTCAT yCTaAAAGTA GkaCaGTTaG TACAGTTACC TTCCTTAATG 6590

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATAAAGAGGT AAATGAAGGA GAAATGCGAT GAAAAAAAGA AAGGCAAGAT ATTTGAAGTT 60

GGTATGTATT GGAATTTTAG GGATTTATGC GGGCGCCAGT TACTACAATT CGGAACCATT 120

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AAGAGCGGAC CAAGCCAATC AAGACCAAGG AACCCTTACT TCTTCAACGC TGAACGAAAC 240

AATAATAAGT TCGTCTGAAC AACAAGAAAG TTCAACACAA AATGACAGCA GTGACCATCA 300

GGAAAATAAT GTGGAACCAT TAGAATCTGA AAATAGTTTA CCGCCACAAG AAAAGACAAT 360

TGCTAGTACT AAACCAACCG AATCGTTACA AAATGAGCAA CCAGTATCTG AAGAGCGTAA 420

AGCGCTCACT GAGAAGTCAC CTCATAATCA GGAACCACAA AATTCTACAT TAACTGAAAA 480

GACCAAAGAG CCGTTGGTAC ATTCAGAGGT AGACAATAGT CAAGAAAAGG AAAAGCAAGC 540

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GGCGCCAAAT TATAATTTGT TTGGCATTAA AGGAGCTTAC CATGGTCAAA GTGTCAGCTT 780

TCCCACACAA GAAGATGATG GTAAAGGGAA GATGACCACC ATTCATGCCG ATTTTCGTCA 840

GTACCCATCC TATAAAGAGT CATTAACAGA CTATAGTAAA TTAATCATCA ATGGGCTGGC 900

GGGTAATCCA ACGTTTTATC ACGGCGTTTT GAAAGCAAAC ACGACGAATT ATCAGCAGGC 960

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GTTGATTGAA ACCTATCAAT TAACTGAATA CGATCAAGAA AAGAAGAAAC CAGTAGTGAC 1080

TAATTTGGCA GAAGAAAAGA AACCTTCGTT TGATAAGGAA GCAGTCAAAG AACAGCTAAA 1140

AAAAGAAGCA GTCGTCTATG AAGTAAGCAA AGGAGATTCT CTCGCCACCA TTAGTCAGAC 1200

GTTTGGTGTG TCAGCAACAG CCATCTTAAA ACAAAATTCA AAGACTCAAG AAATGTTTTA 1260

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AGAGCAATCA AATGGTAAAG CGAATGACTC AAAAACAGCG TCTACTGAGT ATTATGAAGT 1440

AAAAAGAGGA GAGACACTCG CAAAGATTGC TAAAAAAACG GGCTATTCCT TAACCGCCCT 1500

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TCAATTATCT CGAAAATTTA ACGTTCACAG AATCTGATAT TGCATATCTC CGAGAAGTTG 2520

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GCTCTGCTTT AGAAGGGGAT TTGGTTTTTA ATAACGAACC GTTAATTCAA ATTGAAGGTC 2640

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AGCCGAAAAT GTGACAGCTT TCTTCACCAA ATATGGCGAT GGCGGAgcGG ATATTTTACC 4320

GTTATTTCGT TTAAATAAGC GCCAAGGAAA AGCTTTGCTG AAAGAACTTG GGCACCAGA 4380

AGCCtTGTAT CTAAAAATAC CAACAGCTGA TCTAGAAGAT GACAAACCGT TAGTTGCAGA 4440

TGAAgTTGCC TTAkGTGTCA CGTATGATGC CATTGATGAC TATTTGGAAG GCAAAAAAGT 4500

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CTGAAGTCAT TATTGGATAA CTCGCCACAA AAAGCTCATC GCTTGAATGG CGAAAATTTA   5160
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ACGACTATTC ATATTTCACG TAATGGCACA TATTTAGGCC GAATTACTTT TACAGACACT   6060
GTACGCCCAG AAGCAAAAGA GACTATGGAA AAATTACACC AATTACATCT TCAACGAATT   6120
TTAATGCTGA CGGGGGATCA AGAATCCGTT GCAGAAACGA TTGCTGCAGA AGTAGGAATT   6180
ACCGAAGTAC ATGGGGAATG TTTACCACAA GATAAATTAA CTATTCTAAA AGAATTGCCT   6240
AAAGAAAATC ATCCAGTCAT CATGGTAGGA GATGGTGTAA ATGATGCACC TTCGCTTGCT   6300
GCTGCAGACG TAGGTATTGC TATGGGTGCT CATGGAGCTA CTGCGGCTAG TGAAACTGCT   6360
GACGTTGTTA TTTTAAAAGA TGACTTAAGT AAAGTCAGCC AAGCGGTCGA AATTGCCCAA   6420
GATACCATGA AAATTGCCAA ACAATCTGTA TTAATCGGAA TTTTTATCTG CGTTTTACTA   6480
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GTGGACACTG TGTCAATCTT ATCTGCTTTG CGTGCTCGTC GAATTGGCCA GTAAGGTGGA 6600

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TTATAATAAA GATATTTGTG AACATATTGG TAATTGTGTT CGTGGAAATC CAGAAGTCTT 6840

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ATGCAACGCT CAACAGCAGT TCTTGGCGCA ATTTGGATGA TTTTATTATT TGTTTTGGCG 7620

TTCTTATCTT CAAAATAAGT ACGTAATCTT TTAAAAT 7657

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTCAATGAA ATTTTCTTGA CAGCCCTTTC TTATTTCCTG TTTTTCTTTC GTTTTTTTTA 60

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TATTTACTGA ATACGTGTTT TCTGAACATT TCGTACTACT GTCTTCCTTG TAAAAAAAGC 240

TGAGACAAAC TGACGAATCG GTTTGTCCCA GCTTTGCGTC CGAGTACATA TTGCTTAAAA 300

TCAAATGATT GAATTAATTA GACTTAGATA GCTGTTGtTG CTCCGCGGtA AACAATACCA 360

CGACGAGGaT CaACAGTAAT CACTTCGTCA TTATTAATTA ATGAkGTkGC ATCTGCAGCA 420

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GTTTTTGTAA CTAAAATAGC TCCTTCAGTC GCTTTAGCAA CTGCTTCTTC AGCAGTTGCT 600
GCCACAACGG CTTTTGCAAT AATTGCTTCT TCGCCGACAC CTTGACCTTG AACTAATTTA 660
GAACCGATCA TTTGAATTTT CATTAAGTTT GTTGTCCCTT TTTCGCCAAC TGGAACACCA 720
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GCTAAATTAA ACATTtCATC TGTGCTTGAT GGkTTGTCAG CAACTGTTGC GTAAACACCC 840
CATGATAATG ACAAGCTACG TGCTTTTTGT TCTGAGAACG TAATTGCAAC GATATGTGCT 900
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TCTGTTTTGC TATATAATTT CAATGCGAAT GAATCTTGGT TAACTAATGT TTCTTCTGTA 1080
CGAACTGCAA TACGAGCCAT TGTTTGAACA GCTTCTAATG GGTAATCCCC TGCTGCAGTT 1140
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AAGATTTCAT CGATATTATC GATACCTTCT TGGTTTTCGA TTTTAGGAAT GATTTGGATG 1440
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CAGTTACTTC TAAATCGATT AAACCATCAT CTAAAAGAAT GTGTGAACtA CGTTTACATC 1740
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GCGAGCCCCC ACGAACCACG TGTCCTAAAA TTGATACACG CGTATGGAAA TCACCGTATT 2400
CAGAAAGTTT ATCAGCAAAT TCATTTCCGC CCATTACGCC TTCTGCTAAA ATGATTAAGC 2460

AATGTTTTTT CCCGCGGTCG CGGCCTTCTT GAATACGTTT GGCAACGTTT TTCATATCAA 2520

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CGTAAACTTC GATTCCATCA AAAATACTTT TGCGTACGAC TGCACGAATT GCAGCGTTCA 3060

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ATTGGATCTA CATCTGTAAT TGATAGCACA TAGGACACTA AAGAGCCTGC AGCTGAACCT 5580

CGGCCAGCGC CTGTAACAAT TTGATTGTTA TGACAGAAGT CCATCACATC CCAAACGATT 5640

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AAAGGAATGT CAACTCGGCA ATTTTCAGCT AGCTGAATCG TATTCTGGAC CACTTCTGCA 5880

CCAGCTATTT GAAGCATTTG TTCCATCGTC GTCTCTGCTT CACGCAAGTA ATTCAGACCT 5940

TCTATTTCCG GTGTTTGGCT TGTAATATTC AATTGATTAT TTTCTTTGAT GCTCTCAAGA 6000

ACAGTTACGG CAAAGCCTTC TTCCCTTGTT AAATGACGTA CCTCTTGCAA AGCCACGCCA 6060

GGTAATTGTT CTCTTTGGTA AAAAGAAAAG AGCGCTGGAT TACGTTGTTG ATTCATTGAA 6120

AAAGAATGTT CAACAAATAA CGACTGGGGA TCAAAATATG AAGCAAGTTG TTGGAAAGCG 6180

TGAACCGCTT GTTGTTCATC TTCAAAAAAT GTTTGGGCGA CTTCTCCTTT AGCTGACAAA 6240

GTCACGGCAA ATAAATCACT TAATAAGGAT TGATGTTCCG CTAAGTAAAA GGGACCCTCT 6300

GTCGTCATTT TGCTACTAGA TAGTTGCATT AATTGCTGAT ACCCTTTTAA ATTTTTAGCA 6360

AATAAAAGCA ACTCGGAATG CCCTTCTTTT TCTGCTGGGG TATATTCTAA TCTTAAACCG 6420

ATAATTGGTT GAATTCCCGC TTCTTGGCAT GCTTCATAAA ATTCAACCGC CCCATGCAAG 6480

ACATTGATAT CGGTAATCGC TAATGTTTGA TAACCTAACg CTTTCGCTTG TTTTACATAG 6540

GAACGAATCC TAACCGTACT AGATAAAAGC GAATAGGAAG TAACGGTATG CAATTGTGGA 6600

AATGACATTG GACAGCTCCT TTTTGAATCC TTGCTATTTT TTCCTCTTCT CCTATTTTCC 6660

TATCGCGGAT TCTTTACTTT TAAAGAAAAT ATGCTAAACT AAGAGCTAGA AAAGAGGTGC 6720

TCATATGCGT TATCTTGTTG TATTTTTCTG GACCTTCGCA TTAGGCCAAG TCGTTGGATA 6780

TATCGGCGGT GCATTATCTG GTGGTTCATA CGACTTTAAA ATGACAACGA TTCTATCGTT 6840

GGCAACAGCC GTTATTATTT TATTAATTGC aCACTTTGCA GTACCGAAAG AAACCAAACC 6900

TGTTAAATAA GAAAAAACCA GTTACTAAAG TTATTGTAAC TGGTTTTTTT ATCTTTTCAA 6960

CTGTTTAGAG CTTTTTATTT AAAACTTTTC GGAAATTAAA GAAGGACAGC CCAATGTTTC 7020

CTAAAACGAA ACAAGCGGTT ACCAGAAAAA CAGAAGAATA GCCAAAACCA TGGGCAACTG 7080

TCGACCCTAC CATCGGTCCT AAAACTTGAC CGAAATTACT ACACATCTGA TTGTAACTAT 7140

AAACTCTACT TACGCCCTCT GTTGGCGTTA TTTTACTAAT TAACGTATTA ATTGATGGCA 7200

TTAAAGCACC TGTTGAAAAA CCTAAAAGGA ATCGTAAAAC ACCTAACTGA AAAGGTGTTT 7260

GCACAAACGC CATGGGAATG TAACAAATAA AAGAAAGAAT TAATCCGCCT AATAAAACTT 7320

TTTGGTTCCC AATGCGGTCC CCAATTTTTC CCAAAGTTGG AGAAGAAATA ATTnnTGAAA 7380

CGCCGGCAAT CGAAACAATC AAACCACTAA CAAATAATAC ATTCTCTGTA TCGC 7434

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2732 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCGGAACAAG CTTTTAAGTG AAATTGAGAT TTTATATAGT GAAGAATTTG CTATTGCTCA 60

ATGGGCTGTA GAATATTTAA CACAAACCTT AGAGATTCCA TTTAGTTATG ATGAAGCGGG 120

GTATATTGCG ATTCATATCC ATAGTGCTCG CAGCGGGCGT ACTGATAATA GTAAAAGTAT 180

CCGTGAAGTT ACAATCGTTT CTGAAATTAT TCATTTAATC GAGCAGGAAT TGGCTATTGA 240

TATTCATGAT GATAAAAATA GTCTCAGTTA TTCACGTTTG GTGAATCATT TACGTTTGTT 300

TATTCATCGC TTCCAACAAA ATCAATACGC TGTTTTAGAT GAAGAAATTT TGGAAGTCGT 360

AAAGAAAAAG TATGCTGAAA GCTATGAAAT CTCAAAAAAA GTACAAGTAT TATTAATGAG 420

AAATTTTCAT TATCAAGTAC CAAATGAAGA ACTTGGTTAT TTATCGATTC ACATTGAACG 480

ATTAAGAATG ACCAAATAAT AAAAATTAAA TAGTTTATGT GAGGAGTTAC GTATAATGAA 540

AGCGTATATG CAAAGAATGG GACGTTCGTT AATGTTACCA GTTGCTGTAT TACCGGCGGC 600

TTCTTTATTA GTCGGTATTG CTAACTGGAT CGTGGGAACA ATCGGTGCTA GTCCAGCCAC 660

AACTTTTCTA ATGAATGGTG GTTTGGCTAT CTTAAACAAC TTAGCATTAT TATTTGCGGT 720

TGGTTTAGCG TTAGGAATGT CAAAAGATAA AGATGGATCG GCAGCATTAG CTGGTTTAGT 780

CGCTTATTTA GTGCCAAAAA CTGTTTTAGC GCCTGCTTCT ATCCAAGCCA TTAAAGGCTT 840

CAAGGATATT GCTGAAGTAA ACCCAGCCTT CAACAGCATG GACAACAATG TCTTTGTCGG 900

GATTGTCGCT GGTTTAGTTG CCGCGGCAAT GTATAATCGT TTCTCTGGTG TGAAATTGCC 960

AATGGCTTTA TCATTCTTTA GTGGAAAACG TTTAGTTCCT ATTATGTCAG CTATTTCGAT 1020

GTTAGCAATC TCAGCTGTCT TATTCTTCTT CTGGCCAGTT GTTTATAACG GATTAGTTGC 1080

ATTTGGTAAA GGAATCTCTA GCTTAGGTTT CGTAGGAGCT GGCTTGTATG GTTTCTTTAA 1140

CCGACTATTA ATTCCAACAG GATTACACCA TGCCTTGAAT TCTGTTTTCT GGTTTGATGT 1200

TGCTGGTATC AATGATATTG GGAACTTTTT AGCTGGTCAA CAAGCGTTAG ATACTGGTAA 1260

AGCAATTGTA GGACAAACAG GGATGTACCA AGCTGGTTTC TTCCCAGTAA TGATGTTCGG 1320

TTTACCAGCA GGTGCTTTTG CTATTTATCA ATGTGCACGT CCTGAGAAGA AAAAAGTTAC 1380

AGCTTCATTA ATGTTAGCTG CTGGTTTTGC GGCTTTCTTT ACAGGCGTTA CTGAACCTTT 1440

AGAATTCTCA TTTATGTTCG TTGCTTGGCC TTTATATGTT TTACATGCGG TCTTTACAGG 1500

TATTTCTTTA GCATTCGCTG CGTTTATGCA TTGGACAGCT GGCTTTGCCT TTAGTGCAGG 1560

TTTTGTAGAC TTCTTCTTAA GTTTGAAAAA CCCAGTCGCG AATCATCCAA TGATGTTGGT 1620

GGTTCAAGGA CTTGTCTTTG CAGCAATTTA CTACTTCGGT TTCCGTTTTG CAATCACTAA 1680

GTTTAACTTA ATGACACCAG GACGTGAAGA AGGCGATGGC GAAGAAACGC CAGATGTTGC 1740

AGAAGGTGAC AACAAATTTG CTTCTCTAGC TCGTCGTATT TATGATGGTT TAGGCGCTGA 1800

TGCTAATGTA ACTTCTATTG ATAACTGTAC AACTCGTTTA CGCTTAACAG TGAAAGATAC 1860

AGGCAAAGTG GATCAAGCAA AAATTAAAGC AACTGGGGTT CCTGGTGTGA AAGTCATTGA 1920

TGACACCAAT ATCCAAGTGA TCGTTGGTAC GGAAGTACAA TTTGTTGCTG ACGAAATGCA 1980

ACGATTATAT AACCACCAAG CGCCAGCAAC ACCAGTCAAA GAAACACCTG TTTCTCAATC 2040

AGTTGTTGAA GAAAAAGCAC CAGTTTCAAC GAAAGAAACT GAATTATATT CTGTAGCGAA 2100

TGGGAAAGTT ATTCCTATTT CTGAAGTACC AGATGATGTT TTCTCAGCAA AAATGATGGG 2160

TGACGGTTTT GCTGTCGTAC CAACAGACGG CGAAGTTTCA ACACCCGTTG CTGGTAAAAT 2220

TACTAGCATT TTCCCAACAA AACATGCGTT AGGTATCCAA ACAGATTCAG GCATTGAAGT 2280

ATTATTACAC ATGGGTCTAG ATACTGTTGA GTTACAAGGT GGACCATTTA CATTACATGT 2340

TGAAGAAGGC CAAGTTGTAA AACAAGGCGA TAAAATTGCA ACCATTGATT TAGCGGCATT 2400

AGAACAAGCT GGCAAAAAAT CAGATTTAAT TGTTGTTTTC ACAAATCAAG ATATTGTTGC 2460

TCAATACGAT TTACAAAAAG CAGGTCAAAC GACTTCAATG AATGATGTAA TCGGAAATGT 2520

TACCGTAAAA TAAAAGTAAA AAAGGGCTAG CCGTAAGGCA GCCCTTTTTT TGATGAAATT 2580

CGATAAAATT ACTTGTTATT CTATTCTAGG TGAAAACGTT CAATCTTGCG AAGTTACGGT 2640

TTGTTCACAA AAAAGTTACT TTTATTAAAT AAAACTAAAG AAGTAACAAA AACTTCGCnT 2700

TTTTCAGTTA TTTCAAGTAA CATAGAACGT AT 2732

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCAATGGCTG GATGGAACAG AACAAGACGT GGTATCACGA TTACATCCGT GCGACAACTG 60

CACAGTGGAA GGCTACCGTG TAATATCATC GATACTCCAG GACACGTGAC TTCACAAnTG 120

AGTACACGTT CTCTACGCGT ATTAGATGGT GCGGTAACAG TTCTTGACTC TCAATCAGGT 180

GTAGAaCCTC AAACAGAAAC TGTTTGGcGT CAAGCGACTG AATATAAAGT TCCTCGTATT 240

GTATTCTGTA ACAAAATGGA TAAAATCGGT GCGGACTTCT TCTATTCAGT AGAATCATTA 300

CATGATCGTT TACAAGCAAA CGCTCATCCA ATTCAAATTC CAATCGGAGC TGAAGAAGAC 360

TTCACTGGAA TCATTGACTT GATTAAAATG AAAGCTGAAA TCTACACAAA TGATTTGGGA 420

ACAGATATTC AAGAAACTGA TATTCCTGAA GATTATTTAG AAAAAGCGCA AGAATGGCGC 480

GAAAAATTAG TTGAAGCTGT TGCTGAAACT GACGAAGACT TAATGATGAA ATATCTTGAA 540

GGTGAAGAAA TCACTGAAGA AGAATTAGTC GCTGGTATCC GTCAAGCAAC AATCAACGTT 600

GAGTTCTTCC CTGTATTAGC TGGTTCAGCA TTCAAGAATA AAGGGGTTCA ATTAATGTTG 660

GACGCTGTTC TTGATTACTT ACCATCTCCA TTAGATATCG ATGCTATCAA AGGGATCGAT 720

ACTAAAACAG ACGAAGAAAC AACTCGTCCA GCTGATGACG AAGCACCTTT CGCTTCATTA 780

GCATTTAAAG TTATGACTGA CCCATTCGTA GGTCGTTTAA CTTTCTTCCG TGTTTATTCT 840

GGTGTCCTTG AAAGTGGTTC ATACGTATTG AACGCTTCAA AAGGCAAAAA AGAACGTATC 900

GGTCGTATCC TACAAATGCA CGCCAACACT CGTCAAGAAA TTGACAAAGT GTACTCTGGT 960

GATATCGCTG CTGCTGTTGG TCTAAAAGAC ACAACAACTG GTGATACATT ATGTGCATTA 1020

GATGCACCAG TTATTCTTGA ATCtATTGAA TTCCCTGACC CAGTTATCCA AGTCGCTGTT 1080

GAACCTAAAT CAAAAGCTGA CCAAGATAAA ATGGGCGTGG CTCTACAAAA ACTTGCTGAA 1140

GAAGATCCAT 1150

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAGCCTAATA AAGAAGTAAA AGCCTTCTTA GACTATATGG TCACCGATGA TGTTCAAAAA 60

ACAATTGTCA AAGACTTAGG TTATTTAGCC ATCACAGACA TGCAAGTAGA ACGTGATGTA 120

AATGGAAAAG TAACTGAAAA ATAAACAAAA AAACTCAGCC AATAAACAGG ATTGGCTGAG 180

TTTTTTTAGG CTTCTTTTTT TGTTAAAGGC AAGGTGrTTG TAAAAGTGGT CCCTAAGCCT 240

AAGTGACTAT CAATGGCGAT TTTACCGCCT AATAATTCTG TGTAATTTTG GACAATAGCT 300

AGACCTAGAC CGGTGCCACC AGAATGACGG AnACGTGCTT TATCGACACG ATAGAACCGT 360

TCAAAGATCC GTTCTTGGTC TTTTTGACTA ATGCCAATGC CAGTATCTTG AACAGATAAA 420

CGTAATTGCT GATTTTCTAT AGCATAAGAA ATAGTAATCT GACCATTTTC TTGGGAATAC 480

TGAATGGCAT TTTCAATTAG ATTCTTCACG ATTGGATAAA ACAATTCGTA TTTGGTGAAA 540

AACTGGCTCT CTGGCAGACC ATGAACGACT GTTTTCAGCT GTTTTGCTGC CAATTGTTGC 600

TGATAAGAAC CGAGAATTTC TGTAATAAAT TTTTCTAAAG TAATTTCTTG TTCTGCATAA 660

GGAATTGTCG CGCTGCCCCG AGAAAGTTCT AAAATTTCTT GAATTAATTG TTGCAGACGC 720

TGGGCATCTT TTTGCATGAT GTGCAAAAAT TGATTAAGGA CTTCCGGATC TTCTTTGGCA 780

CCGTCTATGA GTGTCTCGGT AAAGCCCAAA AGAGAAGTGA CAGGCGTTTT TAATTCATGa 840

GACACGTTTG ATACAAAATC TTTTTGCATT TTTTCTAGTT GGCGAACGCG CGTTAAAtCA 900

TAGGCAATTC CTAACACTTG ATAAtCATTG GcGCTTTGAT CATCCAAGTA ACGAAGAGAA 960

AGATCTAATC GTAAAGGTGT TGGTCCTTGT GTCACAGTGA TTTCTTGATG TAAACTGTTT 1020

TTTTCAGCGA CGACTTGATG GATTAAATGA ATCAAATCGG CGTCTTGAAT CACTTCGAGA 1080

TAATTGCTTT GCATATTTTT AGCAGAGAGT CCTAACATTT CCTGCATTTT AGGGTTCAAC 1140

AGACGAAGCC GTCCTTGCGT ATCAATGATA AAGACACCAA TCATCAACTC ATCTAAAAGT 1200

TCGTGAAATT GCTCATCCGC AGACGTATAC GCTTTATACG TTTGACTTAC TTGTTGaCTC 1260

AGTAGGTTAA TAGTTTCGTA AAGTTCATTC CATTCAGAAG ATTGCTGGaT AATGGATCGA 1320

TTTTCATCTG GATGTTTAAG CATTCGTTTC AGAATCGGTA AGACAGTCAC TAGCGGTTGA 1380

TTTTTTTGCC GTAACAATAA AAAGATAAAC AAGGTAATTA GTAGGAACAA GATGCCAAAT 1440

GTAAAGATAA TATAGCGACG AAAAGATTGA ATATTTTTAG AAAATAGCGC GGTTTGTTCC 1500

GAAATCCGAA TAATGCCAAC GATTTCTCCT GATTTTAAAA CAGGCGTGGC AACGTACAGA 1560

AGTTCTTTAT TTAACGTTTT ACTCTTTCGT AAAGCTGAAC CATAGGTAGC TCCTGATAGA 1620

ACCGCAGCGA TTTCAGGTCG TTTTTTGTGC GACTCTAGCG GTTCATTTTG GCTGCTGTCA 1680

AAAAAGACGG TACCATTTTT TTGCAACAAA GTTACCCGTT CTTCTGCATC ATCTAACGCA 1740

tGGGTGaCAA GGAGTTGTTG TTGGTTTGTC AGTTGCCCTT TTTCGAAAAC GGAAGGGGGC 1800

AACTGGTCTG TTAAAAGGGT ATTTTTTCTT CTTAAATAGG TTTCTTGCTG AGCAACCATT 1860

TCTTTTTGAA AGAAAAAATT GGTCGCTGCA ATACTCCCGA CAAATAATAA AAGCATGACT 1920

GCCGCAACTA AAAAATATTC AATCCGCAGT CTCTTTTTCA TCGTTTTGGC TCCTGAAAAC 1980

GGTAGCCAAA GCCACGGACA GTTACTAAGT AAACGGGCCG TTTGGGATCG GGCTCGATTT 2040

TATCACGTAA ATGACTAATG TGGACATCGA CGATGCGACT TTGTCCAGCG AAGTCATATT 2100

GCCAAATTCG TTCCAACAAG GTTTCCCGAT TAATGACCCG ATCTTTGCGT TTCATGAAGT 2160

AAACGAGTAA TTCAAATTCT TTCGGTGTTA GCTCAATGGG CTGATTGCGC ACAAAGACTT 2220

CATAATTTTG TTCATCCACA CGAATCTCGC CAATCACAAG CGGAgCTTTA GGTGTGTCCT 2280

CTTGAAGCGT TTCGGTCGTG GTAGGTTTTA AACGACGGAA AATAGCTTTC ATGCGTGCTA 2340

GGACTTCTCT GGGACTAAAA GGTTTTGTTA AATAATCATC TGCCCCAATT TCTAAGCCGA 2400

TGATTTTATC TACTTGTTCA TCTTTGGCAG TTAAAATCAA AATAGGCGTG TCAATTTTTT 2460

CTCGACGAAG TGcTTTGGTA ATTTCTAAGC CATCCATACC AGGAAGCATT ACATCTAAAA 2520

TTATAAAATC ATATTGATTA GACAAAGCTA ATTCGAAGCC GTTTTTACCA TCTTCGGAAG 2580

TAGTCACCTG ATAGCCTTCT TTTTCCAAAT TAAAGGTTAA CAAAGTTAAA ATCGATGGTT 2640

CATCATCGAC GACAAGAACT TTTTTCATTT ACATAACTCC TTCAAGAAAT TTCTGAAAAT 2700

AAGTGTATAT TTCACTATTG TTAGTTTAAC ATATTTTTAG AGGAAGAACG TACTTTAAAG 2760

TAAGCGAGAA TGCTACTTTT GAGAAAAGTC AACTCATGGT ATAATAGAGA AATGAAATGA 2820

GGAGAAGCGA ATGATTGGTA TTAGTAGTTG CTTAGGTGGG ATTTGTTGCC GTTACGATGG 2880

AAAATCTCAA GAACAAGAAG CGTTAAAACA ACTTGTAACT AATGGAAAAG CAATAATGAT 2940

TTGTCCCGAA GTTTTAGGGG AGTTGCCTAT TCCACGTCCG CCAGCAGAAA TCaTTGGCGG 3000

GGATGGCTTT GATGTTTGGG CGAATACTGC TTATGTATAT ACGGATAACG GGGAAGATGT 3060

GACTGAGACA TTTAAAGCAG GGGCACAACG CGCGTATCAA AAATTAAAAG CCCTACAAAT 3120

TACAACCTTG ATTTTGAAAG AAAAAAGTCC CagCTGTGGC AGCCAGCTGA TTTATGATGG 3180

ACAATTTTCT GGCATTAAAA AAGCTGGAGT TGGAGtCGCA ACTGCTTATT tTATTCAACA 3240

AGGAATGACC GTTTATTCTG AAGAAACATG GCAACTTGCG GACATTTCTT TTTAAAAGGT 3300

AAAAACTTAG TAAAAAAAGA TTGACTATTC CCTATGAAAT CGGTAaCCTA TAAGGGATTG 3360

AaGATGGGAG CACGGCTCAT GGAAaTGGmA AAAACAAACC GCATGAATGC GTTATTTGAA 3420

TTTTATTCGA CATTATTAAC GGAAAAGCAG ATGAATTATA TGGAGCTTTA CTATGCTGAT 3480

GACTTTTCTT TAGGAGAAAT TGCGGAAGAA TATGAGGTTA GTCGCCAAGC GGTTTATGAT 3540

AACATTAAAC GAACCGAAAA AATTTTAGAA GAATACGAAA AAAAGTTACA TCTTTATTCA 3600

AACTATGTTG TACGGAAAGA ATTTCTTGAA CAACTACAGC AGTATGTTCA AGAAACTTAT 3660

CCCAAAGATA GTGAAATCAA AAAATATATT GAACAAATTC AAGAAATAGA GGAATGAAAC 3720

TATGGCTTTT GAGAGTTTAA CAAACCGCCT ACAGCAGGCA ATGAGTAAAA TCCGTCGTAA 3780

GGGAAAAGTT TCCGAAGCCG ACGTAAAAGA AATGATGCGA GAAATCCGTT TGGCTTTATT 3840

AGAAGCCGAC GTTAATTTAC AAGTGGTCAA AGATTTCACA AAACGTGTCA GAGAACGGGC 3900

AGTAGGAGTC GAAGTATTAG AAAGCTTATC ACCAGCCCAA CAAATTGTAA AAATTGTTGA 3960

TGAAGAATTA ACGAAAACGT TAGGTTCAGA AACGGTTGAA CTGAATAAAT CTCCAAAAAT 4020

CCCGACAGTG ATTATGATGA CAGGGTTACA AGGGGCTGGT AAAACAACTT TTACTGGTAA 4080

ATTAGCAAAA CACTTAATGA AAACTGAAAA CGCTCGTCCG CTTTTAATCG CTGGTGACGT 4140

TTATCGTCCA GCAGCGATTG ATCAGTTGAA GGTTTTAGGT CAACAATTAG AAGTTCCCGT 4200

TTTTGATATG GGaACAGATG CTAATCCAGT GGAAATTGTT CGTCAAGGGT TAGCATTAGC 4260

AAAAGAAAAG ArAAATGATT ATGTCTTAAT TGATACGGCC GGCCGTTTAC ACATTGACGA 4320

AGCTTTAATG GACGAATTGA AACAAATTAA AGAGTTGGCT GATCCCAATG AAATTCTGTT 4380

AGTTGTTGAT GCGATGACGG GGCAAGATGC TGTCAACGTT GCAGATAGTT TTAATGAACA 4440

GCTTGGAATT ACTGGGGTTG TTATTACCAA AATGGATGGC GATACTCGTG GGGGGGCTGC 4500

GCTGTCAATT CGGGCAGTAA CGGGTGCTCC GATTAAATTT GTCGGTTCTG GTGAAAAATT 4560

AACCGATTTA GAAATTTTCC ATCCCGATCG TATGTCGAGT CGTATCCTAG GTATGGGGGA 4620

CATGTTGACG CTAATTGAAA AAGCGCAACA AGATTACGAT GAGAAAAAAG CAGAAGAACT 4680

TGCTCAAAAA ATGAAAGAAA ACAGTTTTGA CTTTAACGAT TTCaTTGAGC AATTGGATCa 4740

AGTTATGGGC ATGGGACCGA TTGAAGACTT ATTAAAAATG ATCCCTGGAA TGAGTAACAT 4800

GCCTGGTATT GAAAATGTCA AAGTCGATCC AAAAGATGTG GCACGGAAAC GGGCGATGGT 4860

CTTATCAATG ACCCCTGCAG AACGTGAAAA TCCTGATCTA TTAAATCCTA GTCGCCGCCG 4920

CAGAATTGCA GCTGGTTCAG GAAATAGTGT GGTTGAAGTC AATCGTATGA TTAAACAATT 4980

TAAAGAATCC AAAAAAATGA TGCAACAAAT GTCCAAAGGG GATATGAACA TTCCTGGTAT 5040

GGATCaAATG TTAGGTGGCG GCGTTAAAGG CAAGCTAGGT AAAATGGCCA TGAATCGTAT 5100

GATGAAGAAA AACAAAAAGA AGaaAAAGAA AAAAAGATAA ACAGGCTTTA GTTAATTATT 5160

GGAAGAAACa GAAAGTGCGT CATCAGTCTC TTCGACTGAT GGCGCACTTT CTGTTTAAGC 5220

GTAGTTTTGG ATAATTGCGT TTAACGCTTC GGCAAAACCA GCGCCGTGTT GTTCATAATA 5280

TGACGTAAAT CGTTCATCGC CAACATACAT AAGGCCTAAC CCTTTGTGTG CTTCTGGCGA 5340

ATAGCTTGAC CAAGAGTACA TTAACCAATC TTTGTGTAAT TGGAAAATTT CTTGCGCAAG 5400

TTGGCTAGTC AACTTGGGTG ATTTTTGATA CATGGCTAAC TTAGAAAATA AATCTTTTTC 5460

CACGTTCTGC ATTGCTTGCA TGTCTTTTTC CGTCAAGTTT AAATATTTTT TGTTGGCTTG 5520

TTCAAtCGTT TCGTTGCCAT ATTTTTCCCG AATCTCTTTA CCATATTTTT CTtCGTTTTC 5580

TTGAACTTTT TGTTGTTTGA ATGCTTCGAA TTTTTGCTGA TCTGACATGT TTATCTCTCC 5640

TTTGtAATGG TGTAAGGTTT GTTGAACAGA GGCTAAAAGA CGATCAATTT CATTGCGCTT 5700

TTCCAATAGT TTTTGTTGAT GCTCGTATAA AGCCTGTTCA ACATTAAAGT CAGGTTGCTC 5760

CAAAATTTCT TTAATTTCAT CTAGTTTCAG ATCCAATTCA CGGTAAAAAA GAATTTGTTG 5820

CAAACGATTC ACCTCGGCTT GCCCGTAAAT TCGATAACCA GAAGAATTAA TTCTGGCTGG 5880

TTGAAGAAGA CCAATTTCAT CATAATATCG TAACGTCCGT GCACTGACGC CAGATAGTGA 5940

AGCCATTTTT TTAATTGTAT ATTCCATCAT TCATTCCTCC TGACAAAATC TATCATAAAC 6000

CTTTACGTAA CGAGAGGGTC AAGCAAAAAA ATAAAAAAAG TGAGACAACC TGTAAAAAGT 6060

TGCCTCACTT TTTCTCGATT GATTCAATTA GGCAGTTAAG CGATTAAAGA AATCCACGTA 6120

AGCATCTACA ATTGATTGTA AGAAGCCAAC AGTGCCATCA ATAATTTTAC CATCTTCACC 6180

AATTAAGTTC GTAATACCGC CAATATAGGC TTCAGGTTGT TGTAAAGTTG GAACATTTAA 6240

GAAGACTAAT GATTGTCTTA AATGATGGTT CGCACCaAAT CCGCTAATkG CaCCTGGtGa 6300

AACACTCaCC aCAAGTCCtG GTTTTTayCC CCAAACGcTT TCgCCATACG GACGTGAACC 6360

GACATCCCAA TGCATTTTTT AAAACAGCTG GTACTGAACG GTTATATTCT GGTGTTACAA 6420

ACATTACGCC ATCTACTTGT TTAACTTCTT CACGGAATGT TGTCCAAGCT TCGGTGGGGG 6480

TTCCTTCaTC ATCCmAATCT TGATTGTATA ATTCTAAATC ACCTATGTTA ATGAAAACAG 6540

GTTCGAAATC AGCTGGAAAT AAGTCCGCCA TTGTTTTTGC TACCAATTTG TTAAATGAAT 6600

CTTTTCTTAA ACTCCCTACA AAAATACCAA TTTTTTTGTC ATGTAAATCC CTCCATTTTT 6660

CTTTTACTTA CTTTATGATA GTACTTTTTC AAAAAAAGCG CAAACGTTTT ATCCTTGTAC 6720

ATTGTTGAA 6729

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AACtGTTCAC TTGtTCCATT AACCAGCAAT GTACCTAACG CTGTTTCCAC TTCATATTGA 60

TAGCTTTTCC CTAAAAATGT TCGGACAGCG ACAGTACCTG CGACAGTATT AGTAGCAGCT 120

TCTGAAACAA TCTCAATGTC CTCTGGAcGA AtCGTTGCCA CCGTCGTTGT AACATTTGGT 180

TCAGGATTAG TCGTTTTCAC TATTTGATTT GTTTGTGTCC GATAATGACC GGCTTCCATT 240

TTTTCGACAG AGAAAAAGTT TTCAAAACCG ATAAATTCTG CAACAAACTT AGTACGAGGC 300

AAACGATAAA TCGTTTCTGG TGAATCATAT TGTTCAATCA CGCCATTATT CATAATGGCC 360

ACTTTATCTG AAATAGAAAA ACATTCTTCT TGGTCATGTG TGACAAAAAC TGTCGTAATG 420

CCTAATTGTT GTTGAATCCG TTTGATTTCA ATCCGCATTG CCACTCGCAA TTTTGCATCT 480

AAATTACTCA ACGGTTCATC TAGTAGTAAT AGTTTAGGTT CGATAATCAG AGCACGTGcT 540

AGCGCAACCC GCTGTCTTTG ACCACCAGAT AATTGTTTTG GATAACGGTC GCCCAAGCTT 600

TCTAAACCAC ATACTTTTAG CATTTCCGTG ACTTTTTGGT CCATGGTTTG TTTGTTTTCT 660

TTGCGTAATT TCAGCCCAAA AGCGACATTT TCTGCAATCG TTAAATG 707

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4985 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nCTCGGTACT TnCCCCATGG GTGGATGTGC CCGGTTCCAT TCnAGGTGAT TTAGCCAAAC 60

GTTCCTTATG CGTAAGCCTC TGAAGTCAGC CACCTTTACG AACGAAAAAG AGAGCGCAGC 120

AACGATTGCT TATTTAAGGG AATTGATTGA AAAAGTTGGT TTCAmCCCTA AATATTATAC 180

TGCCATTAAT TCAAGCTATG ATTTACCTTA CGATTTTTAT CGTCCAAATA AAGACCGTCA 240

TCGTACACAA ATTGAATTGA TGCAAAAAGA TGGCTCATTA GTGGAATTGG CAACGGTCAG 300

TCCCCTAGTT GCAGCACTTG CTGGTCAGAG TCAAGGAGAT GAACGTTTCT ATTTCCCTAA 360

AGAAATGCTT GACCAAGGAA ATAAAAAACA TTACGATTTA TTTGATGAGA CGTATCGTGA 420

GTTTTCAAGT TACATTCATA ATGGTGCGTT AGTTTTAAAA AAATAGGTTT TCTAGGAGGA 480

TTCTATGTCA ATTAAGTTAG TTGCTATTGA TATCGACGGA ACATTGCTAA ATTCACAACA 540

CAAGATTtAC CCCACGGGTC AAAGAAGCGC TCCAAAAAGC AAATGAGCAA GGTGTTCGTA 600

TTGTTTTATG TACAGGCCGT CCTTTGCCAr gCGTGAAAGA ACAATTGGAT GAATTAGCCT 660

TATATGGTGA AAATGATTtC GTGATtACCT ACAACGGTTC GCTTGTCCAA GCAACCAAAG 720

ATAATACGAT TATTTCACGC TATACCTTGA GTTATGAGGA TTTTTaGAAA TTGAAATGTA 780

TTCTCGTAAA GTCGGCGCTC ACTTGCATAC AATTGATGAT TCCGCTATTT ACACTGCCAA 840

TCGCAATATT GGTAAATATA CGATTCACGA AGCATCTTTA GTGAACATGC CTTTAAAATA 900

TCGTACGGTG GATGAAATGA CACCAGAGAT GAACATTATT AAAATGATGA TGATTGATGA 960

GCCGGAAGTT TTAGATCCTG CCATTGCAAA ATTACCATTA CATTTTACCG AAAAATATAC 1020

GACTGTTAAA AGTACGCCTT TTTACTATGA AATCATGAAT AAAAATGCTA GCAAAGGCAA 1080

TGCTCTAGCA AAATTGGCAG ACCATTTAGG CTTAAATAAA GACGAAGTGA TGGCCATTGG 1140

TGACAATGAA AATGACTTAT CCATGATTGA TTACGCTGGG ATTGGTGTTG CGATGGGCAA 1200

TGCGACAGAA AATGTTAAAA CAATTGCCGA TGTGCATACC ACTAGTAATG ACGAAGATGG 1260

TGTCGCTCAA ATTATTGAAA AAATGGTTTT AATTTAAACA TTCTTTTCAA TAACAATAAC 1320

CCTCAATCTA ATCAACATAG ATTGAGGGTT ATTCGTTATT TTATGATGCT GCCGCTAGCC 1380

ATTTTTCAAC GGCCCAACGG TGGCTTCCTC TTTTTAATAA ACGGACTGCT TCTTCTGGTG 1440

CAACCCAGTG TAAAGTATTG GTCCTTTCTA AGGGTTCGCT AAGTTGCCGC CAAGTATTCG 1500

CTACATAAAA ATATCCAGGA TTATAATAGG CAGTTTGGCG ATGGTTCGAA TAAAAATATT 1560

CATCAGCTTC CCCTAAATAA CAGCCAATTT CTACACTAAT TCCTAATTCT TCTAGCACTT 1620

CTCGGTGGAT CGCTTCTTCT TTCGTTTCGG TGCCTTCAAT TTCGCCTCCT GGTAAAAAAT 1680

AAGCTCCATT TGGCGCTTGT ACCAGAACCA TTGTGTTATT TTCTGGCTTT GAAACAATAA 1740

TGTATGCAGC ATATCTTGTT TGATAGGTCA ATGTCTCTTC TCTTTTTCCA AACGTTGGCG 1800

TTTTCATTGG CGCACCTCTT CTCTTTTCAT CTATTTTACC TGAGAAATTC CTTTAGAACA 1860

AGTCAGAAAC CAAGCGTTTT cTCTACATTT CACGTTTATC TATGCTACTA TTAACGTTGG 1920

AAATATAATT AAGTTTGAAA GGGAGTTTTT AACTATGAAA ATGGCTCATA CATGTGTGCG 1980

TGTAAAAGAT TTAGAGGCAT CATTAGATTT CTATCAAAAA GCCTTCAATT TTGAAGAAAG 2040

TCGCCGTCGT GATTTTCCAG AAAATAAATT TACTTTGGTT TATTTAACTT TACCAGGAGA 2100

CGACTACGAA CTAGAACTAA CTTATAATTA TGATCATGAA GCATACGATT TAGGAAACGG 2160

TTATGGTCAT ATCGCCATCA GTACAGATGA TTTAGAAGGA TTACACGAAA AACATCAAGC 2220

GGCTGGCTTT ACTGTCACTG ACTTAAAAGG CTTACCTGGA ACTGCACCAT CTTATTACTT 2280

TGTTGTCGAC CCAGATGGTT ATAAAATCGA AGTCATTCGT GAACGTTAAA AAGTTTCACT 2340

TGTTCACTTA CTGAGCTTTT TGTGTTTGAG AGCTGTCCGA GACAAAACTT GTCTCGACTT 2400

CTTCTCAAAC ACTTTTTTCA AAAAAAGTGC TACAATAGAA CGTATGAATT TATTGAGGAT 2460

GTGATGTTAT TATGACAAAA AAAATTATTG GAATCGCTGG CAATCAACTT TTGCAGGCAG 2520

CTGAAGTGTT TCACGGTAAC CAAGTGACGT ACACCCCACA AGGTTTTGTC AGCGCTGTTC 2580

AAGCCGCAGt GGCGTTCCTC TCGTTTTGCC AATTGGCCCC AAAGAATTAG CCGCTACGTA 2640

TATACAACAA ATTGATAAAC TACTTTTAGC AGGCGGTCAA GATGTTGCCC CTGAATTTTA 2700

CGGACAAGAA CCCCATATAA AATTAGAAGA AACGAATCGT GATCGTGACG AGTTTGAGTT 2760

AGCCCTAATT GAAGAAGCCT TAAAACAAAA CAAACCTATT TTTGCGGTTT GCCGTGGAAT 2820

GCAATTAGTC AATGTTGCTT TAGGTGGCAC ATTATATCAA GATTTATCGA TGTATCCTCA 2880

ATGGTCAGTT AAGCACGGAC AACAACCCAC TCAACCAATC TTTGCGACGC ATCGTATTGA 2940

TGTTGAACCA GACAGTCAAT TATCAAACAT ATATGGTACA ACTGGTCAAG TCAACTCGTA 3000

CCATCACCAA GCACTACATA CTTTAGGAAA AGATTTACGC GTTACTGCTT GGTCCTCTGA 3060

TGGCCTTGCA GAAGCAGTGG AATCAACAAA TGAACAGCAG CCTTTATTAG CTGTTCAATG 3120

GCATCCTGAA CTAATGTACG CACGTGATGC CAAATCCCAA GCACTCTTTA ACTACTTTGT 3180

TCAAAAATTA TAGTAAAAAC GGmGGGACGT CTTTCGCCCC TCCGTTTTTA CTTGCtATCA 3240

TACTTAAAAA TCAAAATTAT CTGGAtCTGC ACCAAAACGA TGATCCTTAT TTAACTGATT 3300

AATTGCGGTT ATtTCTTCTG GTGTTAATTC AAAATCAAAG ACAGCAAAAT TTTCCTGAAT 3360

TCTTTTTTCG TGAACAGATT TGGGAATCAC GATAATATCA TTTTGTAAGT GCCAACGAAT 3420

AATCACTTGG GCCGCTGATT TACCATATTT TTCACCAATT TTCACTAGTA CTGGTTCAGA 3480

TAATAAATTA CCTTGTCCTA GAGGAGACCA AGCCTCCACG GCAATCTTAT TTTCGGCTAA 3540

ATATTTTCGT AGCGGTTCTT GTGTTAACGT AGGATGTAAT TCAATTTGAT CCACCATTGG 3600

CACAACATTT GCTTCTGTTA ATAAATCTTC CAAATGATGT TGATGAAAAT TGGAAACGCC 3660

AATTGCTTTG GCACGACCAC TTGCGTAAAT TTCTTCTAAT GCTTTCCATG ATTCTTTATA 3720

TTTACCAGCA ACAGGCCAGT GAATTAAATA TAAATCAACA TAGTCTAACC CTAATTTTTC 3780

TAAGCTTTTA TCAAACGCTT TAATCGCATT TTCATAGCCT TGATCTTCAT TCCATAATTT 3840

CGTCGTCACG AAAATTTCTT CGCGGGGAAT ACCCGATTGA CGAATGCCTT CGCCCACCCC 3900

TACTTCGTTT TTATAAACGG CTGCTGTATC AATCAAGCGA TAACCCACTT CTAAAGCCCA 3960

TTTTACTGAA TTTGTTGCTT CTGAGCCATC TTCTACACGC CAAACACCTA AACCTAGGCG 4020

TGGCATTTCA TTGCCGTTTG CTAATTTTTT TGTTTTATCC AAAGTCATGT GTTTCTTCAG 4080

TCCCTTCATT TTCATTACTT TTAGTATACT ACGCATTCTT CTTTCACGAA ACAATCACGA 4140

CTTGTCAGGT CATTTTCTTT ATTTTTAATA AATAACGACG CCAATAAGTC AGCACTCCGA 4200

TTAGTGCCAC AACTACAATT GTTCGAaCCG TAACGCTTCC AATCCACAGT TTAACTGCAA 4260

GTAACCAGAT ACAAAAGAGA TAAACACAGG ACCAATTAAA GGAAACTTTC AATGTACATG 4320

ATTCCGCAAT TTCGATTATC TGACTACTAA AAAAACGACT CCCTAATCGT AAAGCGACTG 4380

GATTATGGAA GATGAATGTT CGTCGCTTGT CAGCCGTCAA GCGAGTAGCA CATCGCTCAT 4440

CAATAAAAAT TGTTACAGGT AATTTAGAAA GTAAATCATT TTTTGCCCAT TCAATTGAAA 4500

CTTTCACGCA GCACTCACAA CCTTTAACAA AATTATAAAA TATATTATTT ATTTACAAAA 4560

TTATAACATT CCTAAAAAAA CATGTTAAGT CTTAAAAAAA AACTTTCTAT TTTCTTCCCC 4620

TTTCGCCGAG AGATTTAGTA TACTAAAAGA AGAAATTTTA GAGAAAGTTG GATTTTTATG 4680

TTGATACTTG GTTTAGCCAG TACTGAAACA GTCGATTCTT CTGCTCCTGA TTTAGCAGAA 4740

GCGACCGTAA AAAAAGTGAG CGCGCTACAA CGCTTTTGGA ACAATATTAA TTGGGATGCC 4800

ATTGTCGCTA CCTTAATTGA AAAAAGTTTA TCAATTTTAT TTTTAATTTT TCTATTTTTT 4860

ATTATTCAGC GAATCGGGAA GTATTTAATT GATCGCACCT ATGCAAATTA TAGTAAAAAG 4920

CAACATTTTA GTGAAAGCCG TTTAAAAACG TTACACACTT TAATCATTAA TGCATTTCAA 4980

TATAC 4985

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGTCTGTCCT TATCTCGCAC AGCTATTTGG AAAGCGATTA ATGAATTGAA AAAAGATGGC 60

TATCAAATTA CTAGCGTGCA AAACAAAGGG TATCGCCTTG AAAAATCAGA TGTCCTTTCT 120

GCAGAAGGCA TTCAGTTGGC ATTATGGCCA CAAACACCGC CTTTAACAAT TACCGTCCTA 180

GAAACATCTG AATCTACCAT GACCGATGCT AAGCGGGCGA TTTTAGACCA GACGCCCGAC 240

AATACTTTGA TTGTTGCTGA CATGCAAGAA ATGCCTCGGG GCAGGTTCGG CCGGCCGTTT 300

TTCGCTACGC CAGGTAAAGG GATTTACATG AGCATGGTGC TTCAACCGAA CCAAAATTTT 360

GAAGAAATCG CTCAATATAC TGTGATTATG GCCGTAGCGG TCGCTCGAGC AATGGATGCT 420

CTGGCAGGCG TTCACACAGA AATTAAATGG GTCAACGATC TTTATTTAAA TGGCaAAAAA 480

GTTTGCGGGa TTTTGTCTGw AGCCATGAGC AATGTGGAAA CAGGGCAGAT TTCTAATGTT 540

ATCATCGGCA TGGGGATTAA TTTTTCAATT ACAGAAACCG AATTCCCTGA GGACATTCGG 600

CAGAAAGTGA CTTCCCTTTT CCCAGATGGT GAACCGACGG CGACGCGAAA TGAATTAGTC 660

GCCAACATTT GGAATCATTT TTACCAAATT TTAGACGAAC GTTCAACGAA AGACTTTTTA 720

GAAGAATACC GGCAACGCTC CTTTGTGATT GGCAAAGACG TCGCTTTTAC CCAAAACGGG 780

CAAGACTTCC GCGGCGTTGC GACAACCATT AATGGAAATG GGGAATTGAT TGTCCAGTTG 840

CCTGATGGCA CGGCCAAAAC ATTGTCTTCT GGAGAAATTA GTTTGGACCA GATTGGTGAA 900

TGGCGTCGAG GATAAGTGGG GAAGTTTAGA AAAAAGCAAG AAAGCACCTG TCTAAATTTA 960

AACAGATGCT TTCTTGCTCT TTAAAAATCA ACTTCTTTTT GTGCTAACAT TTCGCACAAT 1020

TCTTTGGGGA AATTCGTATA GGGATTTTCA TTGATTTTCA TTTCTTCTAA AGGAGACAAC 1080

CAGTTTTTAT TCGTATTCTG AAAAGCAATA GCTACTTTTT CTTCAAGATA CTTACATACT 1140

TCTGCGCCTT TAAAATTTCG ATAACTGTCT TTTAAATGCA GAACTTTCTC TAATCTCCCA 1200

TATAAATtTT CTCTAGTCAT GTATCGATTG ACTTCCTCAA AGTGAAGTAG TAACCAGAGT 1260

TCAAAGCATT CATTTGAAAA AATTGTCTTG ATTTCAGGAC GATGTCGTTG TGCACATCTn 1320

ACCGCGTTTT CAATCGATTC nGTGGT 1346

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCAAAATATk GaTGCAATGG TTtTGkTTyC CTGaCAATAG nTGayCGATC GTCACAAATT 60

CGTATCCTTC ATTTTTTAAC ATAGTGATCA ATCCTGATAC AGCTTTGACT GATTCATGAT 120

GGATATCGTG GATTAAGATG ATTGCGCCAT TAAAGACATT CTGTTTGACA ACATTATTGA 180

TTGCTTCAGG ATTTCTTGTT TTCCAATCTA GCGAATCAAT ATTCCATTGA ATAATTGGCA 240

TGCCAATTGT TTCAGCACTT TTTTTATCAA TAGCGCCATA AGGAGGACGG ATATTGCGAG 300

GCAAGACGCC CGTAGCCTTA AAAATTGCTT TATTAGCTTT ATTCATTTCA CTTTGTAATT 360

CATCTGTCGA AAGTGTATTC AACTGTGGAT GAGAATACGA GTGACATGCT ACCTCATGAC 420

CCTCGTCGTG GACTTGTTTT GCAACATCTG GGTTTTGATC CACCATCTGT CCTAACATGA 480

AAAAAGTAGC CTTCACGTTG TTTGTTTTTA GTATATTCAA CAAATCAAGT GTTGAGCTAT 540

TATTGGGTCC ATCATCAAAA GTAAGAGCGA CATACTTTTT ATTTTCATCT AATGCAGGTA 600

ACGCATCTTT TATACTTTCT TGCGAAACCA GATCTGTATC AATAAAAGGC GCAATGTCTC 660

TGTATTTTAG AATAACTTTA GTAGTTCCAG TTGTGTTCTT TGGTAGGTCG ATGGTCAATT 720

CATCAGGTGT ATAAGTCATT TTACTCTCGT AAGAAATTCT ATCCATCGTT AATACAGCAT 780

CAATTATTTT TTTAGGCTCT TTGGCGTGAT CAAGAATGGA TTGCTGAATC ACCTGTTGAA 840

TACCTAAGAG ACTTCCTTCA TCCGGAATCA AATCCTTATT TGTGATTTCT TTACCAGTTT 900

TTTCGGAAAC ATAAATGGCT TTCTCAGAAA TACTGTCTGG CTTTTTAAAA TTTTCCTTAC 960

TGCGATCCCA GATAAAACTA TCTGCTTCAA TTCTATACTG ACCAATTTTA GAAGATATTG 1020

CTGTTGCTTT TATTCTGGCA ACTGTAAGCA CTTCTTTTTC ACGATGCTTC TTTTGTTGCT 1080

TTTGAGCAAG CTCGTCTAAG AGCTGGTTTG CATTTTTAAA AGGAACAGTA CTTTCATAAA 1140

CTGGACGGTA AATAAGGCAC TTATTTTCTC CGTCATTTAT AGTATCTATT TTCGTTGAAA 1200

TTCCACTTTG GTCTTGCTCT TCTTGGATTG AAGCCATGAG ATTTTTTACA GCAGTTTCAT 1260

ATTTGGCTTG AGCTTCTACT TCTTGCTGTT TTAATGTATA AACAATATAG CCGCCAGTAG 1320

CGACAATTAC TAGAATAAGT GCGGTAAACA ATGCGAATAT ATACTTGCTA TAATTAGATT 1380

TTTTCTTCGG TATTTTTGGT TGTTTGTTTT CGTTTCCGGT TTTGGGCTTT ACAGCTTCAT 1440

TCAATTGATT TGCATTTTCA CAGATATCAG GTTCTTGTTT GTGACGTTGA CTACGACGTG 1500

CATAGATATT TTTATCAGAC ATATGACTTT ATCCTTCCTT TTATCATCAT AAAGTAAAAT 1560

GAAACAGCGC AATTGTAATA AAAAATAATT TATAGATAAt TTTTACAAGA AAGTTTTCTC 1620

TATTATTCtT TTTCtTTTGG CGTAGTAATT ATCGCTAATT CCTCACCATT TTAGATATTG 1680

TGGCTACTTA ATGTTAAACT CAATTTTGAT ATCATTAGAA TCACTAGTTT TGATTTTAGT 1740

TTTTGGAATT GTACCCTTCG ATAGGTTAAT CACTATGGTT GCAGTCTTTG AATCACCAAT 1800

AATGGTCTAG GATTAAAAAT ATAAACTATT ATCCAATCTT GTTCTATTTG ATTAAATATA 1860

CTACTTTAAT ACCTTTAATT TGTGATCAAT TCCAACTTCA CCAAACTCAT TTACAATTAT 1920

AATAATTTCT TCCCTGGGAT GGGGTGAGAC TTGCAAGGC 1959

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTTTATTTG GAGGGATTTA TTGTGTTAAA ACCATTAGGC GATCGCGTCG TAATTAGAGT 60

CGCGAAAGAA GAAGAAAAAA CTGTTGGAGG AATTGTTCTT GCATCCGTTG CAAAAGAAAA 120

ACCACAAACA GGTGAAGTTA TCGCAGTAGG TGAAGGTCGT GTGCTTGAAA ATGGCACAAA 180

AGTTCCGATG GAAGTAAAAA TTGGTGACAC AGTAATGTTT GAAAAATATT CAGGAACAGA 240

AGTGAAATAC GAgGCGTAGA ATACTTAATT GTATCAGCCA AAGACATTAT TGCCACTGTT 300

GAATAATAAA CAACTTTTAC AGAaTAATAT AATAGAAkAA AAAAATTATG AGGTGAAGAA 360

ATCATGGCAA AAGAGnTTAA ATTTGCAGAA GATGCACGTG CAGCAATGCT ACGCGGAGTA 420

GATGTATTAG CAGATACAGT GAAAGTGACA TTAGGCCCTA AAGGTCGTAA CGTTGTTTTA 480

GAAAAATCAT TTGGTTCACC ATTGATTACT AACGATGGAG TAACAATTGC TAAGGAAATT 540

GAATTGGAAG ATCATTTTGA AAACATGGGC GCAAAATTAG TTTCAGAAGT TGCTTCTAAA 600

ACGAATGATA TTGCTGGTGA CGGAACAACA ACAGCGACTG TTTTGACACA AGCCATTGTT 660

CGTGAAGGCT TAAAAAACGT AACTGCTGGA GCCAACCCAT TAGGTATTCG TCGTGGGATT 720

GAATTAGCAA CAAAAACAGC AGTAGAAGAA TTACACAATA TTTCATCTGT AGTTGATTCA 780

AAAGAAGCGA TTGCACAAGT CGCTGCTGTT TCATCAGGTT CTGAAAAAGT CGGCCAATTA 840

ATTGCCGATG CAATGGAAAA AGTTGGTAAC GACGGCGTAA TTACCATTGA AGAATCAAAA 900

GGGATTGAAA CAGAATTAGA TGTGGTTGAA GGAATGCAAT TCGACCGCGG TTATTTATCT 960

CAATACATGG TTACTGACAA CGATAAAATG GAAGCTGTTT TAGAAAATCC ATATATCTTA 1020

ATTACCGACA AAAAAATCTC AAATATTCAA GATATCTTAC CTTTATTAGA ACAAATTCTA 1080

CAACAAAGCC GTCCACTATT GATTATTGCG GATGATGTTG ATGGGGAAGC TCTACCAACA 1140

TTAGTATTGA ACAAAATCCG TGGTACATTT AATGTTGTCG CAGTAAAAGC GCCAGGATTT 1200

GGTGACCGCC GCAAAGCGAT GCTTGAAGAT ATTGCTATTT TAACAGGTGG TACAGTAATC 1260

ACTGACGACT TAGGGTTAGA GTTAAAAGAC ACAACTATTG AAAACTTAGG AAATGCTAGC 1320

AAAGTAGTTG TCGACAAAGA TAACACAACA ATTGTCGAAG GTGCTGGTTC AAAAGAAGCC 1380

ATTGATGCCC GCGTTCATTT AATTAAAAAC CAAATCGGCG AAACAACGTC TGATTTTGAT 1440

CGTGAAAAAT TACAAGAACG TTTAGCTAAA TTAGCTGGTG GGGTTGCTGT CGTTAAAGTC 1500

GGTGCTGCAA CTGAAACAGA ATTAAAAGAA TTAAAATTAC GAATTGAAGA TGCATTAAAC 1560

GCAACACGTG CCGCTGTAGA AGAAGGCATG GTTTCTGGTG GTGGTACCGC ACTGGTCAAT 1620

GTAATTGGTA AAGTCGCTGC GCTAGAAGCT GAAGGCGATG TGGCAACAGG GATCAAGATT 1680

GTCGTTCGTG CATTAGAAGA ACCAATCCGT CAAATCGCTG AAAATGCTGG TTATGAAGGA 1740

TCAGTGATTG TTGACAAACT AAAAAATGTT GACTTAGGTA TCGGATTCAA TGCAGCTAAC 1800

GGTGAATGGG TAAACATGGT TGAAGCCGGT ATTGTTGACC CAACAAAAGT AACTCGTTCT 1860

GCCTTACAAA ATGCAGCTTC TGTGTCAGCT TtATTATTAA CAACTGaAGC AGTTGTTGCA 1920

GACAAACCAG AACCAGCTGC ACCAGCTCCT ATGATGGATC CATCAATGGG CATGGGCGGT 1980

ATGATGTAAA AATAAAAAAG TATTCTAAAA GCTTACGATT GAAAAATCGT AAGCTTTTTT 2040

TTACATAAAG nATAAATAAT CTAAATAATA TCTTTGCTTA TGGTGTTTTC TCAAATATTT 2100

ACTCAATTAA CAAAAAAGAT GATAATTTAA AGGCTTCGTT TTAGCTAGAC AGCCTTGTTT 2160

TTATTCGATA AAATTTAGTA ATAACAATCA TTTTTTGAAA ACTAGTAGTT GGTAATTTTT 2220

ATTTATTAAT AGAATATAAA TAAAAATTAT TATATTTTGA AGGGGAATAT TAGGAAGATT 2280

GAGGTGGAAA AATGGAAAAA TATACAATTG GTGTCGTTCC TTTGACAATT GAAACAAAAG 2340

AATACTGTCA AAATTGGTTT GTTAGTAATC AAGTAGAATG TCAGATCATC CAAGGAACAA 2400

ATATACTTCT TCATTTGCAC CATATTGATG GATTAGTGAT TGAAGTTACT GACCACCAGT 2460

AAGTAAATAC TTGTTGTGAG TTATTAATGA CGATTCGCAA GCAGTCAGAT TTACCGATTT 2520

GGTTATTTTC TCGGACAGAA GTAATTAGTA AAGTCAATCG AATTATTTAT TTACAATTAG 2580

GTGCAGATGG CGTTTTTGAT TATTCTTATG ATCGTCAAGA ATGCATGTTA AGCATGAGTA 2640

ATTTATTGCA ACGTGTAAAA AGACGTTTTT ATCCTAAATT AGCTATTGCA AACGAGGAAC 2700

AAACAGTTAC TAAGAATCTT TCTGAGAGAT TGTATTTAAT TGCGCCAAAT TTGAGTGTTT 2760

GCTTGGGAAG TGGAGAAGAA ATTCTTTTAA CAAAATTGGA ATTTTTCACA ATAGAGTATT 2820

TATACAAACA CGCAGGACAA ACAATTACAT ATGAAGAACT CTACAAAAAT GTCTGGAAAG 2880

ATACTGCGAA TGAACGAAAA TATCGTGTCG CTAATGTGAT TTTCCATTTG CGCAAAAAAA 2940

TTGAACAAGA TGTGAACAAA CCACAATATA TCAAAACAAT TCGTTCAAAA GGCTATATGT 3000

TAACGGTGTA AAAGGTACGA AGGAGGAGAA AAAGATGTGG CAATTTTTGA CTAAAAACAA 3060

TGAAGATGAG GAGTATGAGA AGATGCCAGA TTTTGAAAAT GAACAATCGA TGAAAGCACA 3120

ACCAACGGTA ACAGAAGAAG CAATCTTTGA TGACGAGGTC GTTTATGCAA AAGAGCAATC 3180

CGCAAAAGTA AAACAGGTCC AGCAACAAGT GCCGACTGAA CTGTCAGAAG AGTCATTTTC 3240

TTTTGTTGAA AAACTAGAAG AAGAAAATCA ACTATATCAG CAATCCATTA AAAAGCTAAC 3300

GGAGCAATTA TTAATGCAAA CCAATGAAGT GGAAGCATTA CAAAAACAAG TAGTCGAAAA 3360

AGATGTTCAA CTTAAACATG TTAAAGAAAC ATTAAGTGAT AAAGAAACAA CTATCACTTC 3420

TTTACAGAAA CAATTGTCTG AAGAAAAGAT GCAACAGAGA CAGACCAGTG aAGAGrATTT 3480

AGACACAGCC GTTACGCTTT CTCAAAAAGA AATTGGCGAG TGTTATTAGA AGCCAAACGT 3540

CAAGCAAAAG AAACATTAGT CAGCCAACCA CCAGTTGCAC ATTCATGAGA ATGGACACGT 3600

TGCACTTTAC ACGCTGAGCA GTGGn 3625

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCnCCCCCCT TTTTTTTCCG GTCCCnAATn CCTCCGGCCn TTATTTTAGG TTTCCATTTG 60

GTAAAAATAG TATAGGrGsw AAgCatCaGT TATGTATtAt TAGTGamAGA AGGTTGCcGT 120

GAAGTAAAwA TAAAmAGGAG AGCcAAAGGA TGTTAAmAAA TGTAGAAGTG TTCTGGCAAA 180

ACTTTTTAGA TAAACATGAA TTAGATATGT TGATGCCCGA TGTGTGGATG TTTGGTGATG 240

GCTCTTCTGA GATGGGTAAT CGTTTGGGTC AATTGGTTGT TTCTGGTCGT AAGACAGCGA 300

CATGCTCTTC TTTAGATATT TATAAGATGG AAGAAGAACA ACTCCCTAAA GCTGGTCAAT 360

ACGACATAAT TTTAGATGGT CAGTCTCAAC CGCTGGCTAT TATTCGAACA ACCAAAGTTG 420

AAATTATGCC CATGAACAAG GTCTCAGAAT CTTTTGCGCA AGCGGAAGGT GAAGGAGATT 480

TGACGTTGGA TTATTGGTAT GAAGAGCATG CGCGGTTCTT TAAAGAAGAA CTGGCCCCCT 540

ATCAGTTACA ATTTTATCCC GATATGCTGT TAGTTTGCCA AAGTTTTGAA GTAGTGGATC 600

TTTATACAGA AAAAGAATAG ACAGAGAAGC GGTGACTGAC ACGATTGAAA CGAGCAGTCG 660

CCGCTTTTTT TTTACTGATT TTTTGAAAAA GTTGCGTATG TTTATATAGA CAGGGTGATA 720

GAAAAGAGAT GTGTATTTTA AGTGTCGAGG AAAAGATGGT ACAATAACCT AAGGAGAATA 780

CTAACAAGGA GTGAATGTTA TGAAAGAAGA ATTTTCATAT GAAATTTTAG AAGAAGTCGC 840

TGTGTTATCT GAGAATGCTC GTGGCTGGCG TAAAGAATTG AATTTAATTA GTTGGAATGG 900

TCGTCCACCA AAATTTGATT TGCGTGAGTG GGCCCCTGAT CACGAAAAAA TGGGTAAAGG 960

CATCACCTTA ACTAACGAAG AATTTGCTGA ATTAmGCAAA ACAATTAmaT CCATGTAAAA 1020

GGAGCACCCT GTCAATGAAA AGTATGACTG GATTTGGAAA AAAGACCATT CAAAATGAAA 1080

ATTATCAATT GGATATCGAA GTCAAAAGTG TCAACCAGCG GTTTTTAGAT ATTCAATTGC 1140

GTATGCCCAA GGAACTGAAT GCCTATGAAC TGGTGATTCG GCAAGTAATC AAACGCACGT 1200

TAAAACGTGG GCGTGTGGAA GTCTATGTAA ATCTCCAAAA AATCGGCAAC AATCAAAAAG 1260

AAGTGCGCGT GCAGTGGGAC TTAATTGATC AATTATTAAC TTCGGTAGAT CAACATTTAA 1320

AGGAAAAATA TCCGGAAGCA ACGTTTGATG CAGGGGACAC GGTCAACCAT TTATTAAAGC 1380

AAAATGATTT TGTCGAAATA GTGGAAGCAG AAATTGTTGA TCAGACATTT GAACCATTTC 1440

TTGTTCAAGC ATTTGAAGCA GCCATCGCTA GTCTTGACCA AAGCCGTGTG CAAGAAGGAA 1500

CGCAAATTAA ACAAGTCCTG CTTGACTATG TAGCAGTGTT GACCCAATCA ATTCAAGAAC 1560

TGCAAGCGTT TGTGGGCGTT TTTGAACAAG AATACCGTCA ACGTTTTGAA GCGAAATTAA 1620

ACGAATGGTT AGGTAGCCAA GTGGATGAAA CACGCTTATT AACAGAAATG GCCATTTTAT 1680

TGGAAAAAGG CGATATTCAT GAAGAATTGG ATCGTTTGGA TATCCATATT GATAAGTTGC 1740

ATCAGTTGCT TGACGAAACA GAACCAGTGG GCCGAGAACT AGATTTCTTA ATTCAAGAAA 1800

TGAACCGTGA AGTCAATACG ATTGGTTCGA AATCAAGTCC AATTGAAATA AAAAATAGTG 1860

TCGTTCAAAT GAAAACAACC TTAGAAAAGA TTCGTGAACA AATTCAAAAT GTCGAATAGA 1920

GAAAATGGTT TCGTGTTTTT CCAGAAAACG CTATAATATA GAAGTAACGA ATAAATGACA 1980

GAGGTGAAAG CAATGACTAA ATTTTATGAT GTAACCTTTC AAGAATTAAG TGGTCGTTCT 2040

GTGGTAAAAA CAGAAGTCGC TTCAGACAGA GAACCATTTG ACGTCTGGCA AGATGCTTGT 2100

GCAAGCTATT CTGAAACAGA ATTAAATATC CAAATTAACG AAGACACGTT TGTTACTTTG 2160

AATCGTCACT TTGTTGTTCG CATTGACGTG AAAGAAGTTG ACGGTCCTGT CGACAAACAA 2220

GTTCGTCGTC GCGATGAATT GATGAACGTG GTCAATACGC TTTCTAATAT GGGCTTATAA 2280

AAAATACCAC CAAGCATTTC ACGCTTGGTG GTATTTTTTT TAATTAGAAT AAAAGAAACA 2340

AGCCAACGGC GCATAGGAAA GAAAGAACTG CGGCACTTAA AAAGATTGTC CGCATGGATG 2400

CAGTTTTACT GCTTTCTTTG CCGTGTTTTT TCTGACGTTC TAAACGTTTT TGAAGCTGAC 2460

GGGTAATTAC TGAGAAAATC AGCCCGAAAA GGACTAAAAC ACTTGTGGCA ATCGATTTGG 2520

GAATAAAATG ATTCGGTTCT GCAACGGTGG TATCCCCAGA ATGTTCGTTT GATTCTTCCg 2580

CAGCTTCCGC TGTTGTTTGT TTTGGCTTAA CTTCTTGGTA AGCCACTTTG GGTGCTTGAA 2640

CCGTACTATT TAACAATGTC AAGGGCGTGT CGACTTGCAC TTGCCCTGCT ACTAATTTAA 2700

AAGTAGGCTG ACTGCCtTTG GGAACGACAC CGTATAAATC GTTAGCCAAA GTAACTTTTT 2760

TGTGATCAAT GGTTTGTGGT CCTTTGTCTA AAAGTTTTTT GCGTTCGTAT GTCGTATAGG 2820

CATAGTCCAG CAAAGCATTC CCAGCCACAT GCCGTTCGTA TTCACCATCT TGGTTTTGCC 2880

AATTACCAAC GCCTAAAATG ACTTCAATTA AACGGAAATC TCCTTGTTTG ACAGTCGCAA 2940

TATAGTTAAA GCCGCCTGTT GGACTAGAGC CTGTTTTTAA ACCATCCACG CCTTGGTAGC 3000

CATACTTAGC TCCTGGTAAA GAATAATTGT ACGCTTCAAA CGTTTCCTCG TAAGGCGTGC 3060

CGACCATTGT TTTCACCACT GGTTTATTGG TGATTTCTAA AATTTCTGGA TAATTTTTCA 3120

GAAAATGATA GGTTAGTGAA GCTAAATCTC TAGCTGTAGA GACGTTATCG CCATTTGGGT 3180

CAATTCCTTG CATTTGATAC AGGCCGTTAA AGGCACTTGC TTGCGCTCCA CTGCAGTTGT 3240

AATAGGTAGT ATTTGTCATC CCTAGTTCAG CCGCTTTTTG ATTCATTAAA TGAACAAAGT 3300

CAGTAGGCTG GTTCCCTGAA ATTAAGTTTG CCAACATGAG AGTCGCCACA TTAGAAGAGG 3360

GGACAGCAAT CATTTTTAAC AGTTCACGGA CTGGATAAGC AACACCTAAC GTAATTTTGT 3420

TATTACTAAT GGCATATATT TTAGAAATAT CGACATCTTT TTGCGTAGCA GTCACAGTCG 3480

TATCCATTGT AAATTTTCCT TGCTCCATTG CTTCAAAGGC CAAGTACATG GTCATCACTT 3540

TGGCAATACT GGCAGGATTC CACGCTAAAT CTGGTTGCTG CGACCAGAGA ATTTCTCCAG 3600

AATCAGCATC AACAACGATG GCTGCTTTGG GAATGCCATC CGCTTTCAAA GTCGTCCCCA 3660

TTTTTTTAGC AATCGCGGTA ATATCTTCTT CTGCGTGAGT CACAGTAGGT TGGGCAAAAA 3720

AGGCCCCACa ACTGACAACT AAGCCTAGCA GAAACAAT 3758

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCTTCTAATC CTGATGCATT aGCTGGCGTG GATGCACAAC GTGTAGCAGC TTTCCAAGCG 60

GCTAATGGGA AAGCATTGGT CAATCTACGA AAAGCAACGC AAGCCAACAA AGTAAGTTGG 120

ACTGTTGTAG CTGCTGCTAG TGAAGGCTGG GCAGCTAAAG TCTTTCCAGA ATTAGCAACA 180

AGTGAAGAAC AAGTTGATGC ACTTTGGAAT GAAATTTTCA AAACAACACG AATTTATGAA 240

GAAAACCCAG TCATTGCTTG GGATATCCAT GATAAAAAAT TACAAGAAAA AGCGGCTGAA 300

TTAAACGAAC AACAATTTAC TGCTTTACAC TACACAGCTC CTGGGACAGA TTTAACGATT 360

GGTTTGCCTA AAAACCATTT ATGGGAAGGC GCTGGTAGTT ATAACGCTCG TGGGGAAGAA 420

TTCATGGCTA ATATGCCAAC AGAAGAAGTT TTCACCGCCC CAGATAGTCG CCGCGTTGAT 480

GGTTATGTTT CTAGTACAAA ACCACTAAGT TATGCTGGCA CAATCATTTC GGGAATGAAA 540

TTTACATTTA AAGATGGAAA AGTTGTTGAC TTCTCAGCTG AACAAGGCGA AGAAGCATTG 600

AAAAATCTCT TAGCTATTGA TGAAGGTGCC AAACACTTAG GAGAAGTTGC TTTAGTACCA 660

GACCCTTCAC CAATTTCACA ATCTGGTTTG ATTTTTTATA ATACATTGTT TGATGAAAAT 720

GCCTCTAATC ATTTAGCCTT TGGTTCGGCC TATGCCTTCA ACTTACAAGG TGGCACGGAG 780

ATGAGCGAAG AAGAATTAGC TGAAGCTGGT TTAAATCGTA GCCAAACACA TGTGGACTTT 840

ATGGTAGGAT CTGACAAAAT GAATATTGAC GGCATTAAGG AAGACGGGAC GATTGTTCCA 900

GTTTTTAGAA ATGGCGATTG GGCATAGTCC TACCAAATGT TGAAACCAAA GTTTTTAGCT 960

CCAAGAAATA AGAAGAAACT GCTTTTATTC AGTAGGTTCT TTTAAAATTT AGAAAGTGAG 1020

GCCTAAGTTG CAGCGACTTA GGCCTCACTT TCTTATGCTA AAAAATCAAT TGCATTCGAA 1080

GGACCTTTAA CGTTATAATC AAATTGAAAA CGGATTCTTT TGCACGATAT AAGTTTACTT 1140

TTAAATAAAA GAATTTTTTT CAAAAAAGTA GAATTGGAGA ATTAACATGG GATTATTTGA 1200

TGGATTATTA GGAAATGCAA CACAAAATAA TAATGAAACA GCTGAaAAAG AaTTACGGGA 1260

TGTTTTAATC CCTAACGrAA AAGTAGATAT GGCCTTCACT TTAGTAAGAG ATTTAATTGT 1320

CTTTACAGAT AAACGCTTAA tTTTrGtCGA TAACCAGGA 1359

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTAAnATAn ACCAGGTTTT AGATAGTATT TATTCAAGTT TACCTCnAAG GTATTAATCT 60

GAAACCCkGT TATtTtAtTa GAGAGTTCyT TTTCaAATAT ATGTAAATrG cTAACaACrG 120

GGTTCTGTTT GTTGTTGGAC tATTTTTTTT GATCcCCAmC CGTTCTTGAA AAAAAAcAAA 180

AAAATAAACA GTGyTCGCTT GATTAATCGA ACGTTTGTTC GTATAATGAT TTTGCaAGTG 240

AGGTGATGTT TGTGAAATTT GATTATGAAA AAGAACCTAG TCGCGATATT CTTTGTATTG 300

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ATTGCAAAAG TTTTTACGCT AGTGTAGAAT GCGCAGAACG TGGGTTAGAT CCTTTGAAAA     360
CGATGTTGGT AGTGATGAGT AATGCCGAAA ATGCGGGGGG ATTAGTTTTA TCAGCATCGC     420
CAATGGCAAA AAAAGTTTTA GGTGTTTCAA ATGTTACGCG TAAAAATCAA GTGCCCGCTC     480
ATCCTGATTT ATATGTGGTT CCGCCACGAA TGAATTTGTA CATGAAAAAA AATCAAGAAA     540
TCAATAATTT ATATAAAAAG TTTGTCGCAG ATGAAGATCA CTCTGTGTTT AGTGTAGATG     600
AATCATTTCT TGATGTAACT GCTTCTTTAA GTTATTTTCA TTGTGAAACT GCCTATAAAA     660
TGGCTCGGAT TATCCAAAGA GTCGTTTATA ATCATGTGGG TATTTATGTG ACCGTTGGGA     720
TAGGGGACAA TCCGTTACTG GCTAAATTGG CGTTGGACAA TGGCGCCAAA CATTCGCCAG     780
ATTTTATTGC AGAATGGCGG TATGATCGTG TACCAGATAC TGTCTGGCAG TTGCCTTCTT     840
TGACAGATTT TTGTGGGATT GGTCGCAGAA TGGCTAAACG ACTGAATCGT TTAGGAATTG     900
ATTCTGTATA TGAGTTAGCG CAACGAaTCC GCATCTTTTA CAAGAAACAT TTGGCATGAT     960
GGGGCTTCAA TTGTATGCTC ATTCATGGGG GATTGATCGT ACCTTTTTAG GGAAAAAAGC    1020
ACCACATAAA GCTGAAAAAT CATTTGGGAA TAGTCAGATT TTACCGAGAG ATTATGCGCG    1080
AAGAGATCAG ATTGAACTAG TCTTAAAGGA ACTGACAGAA CAAGTGGCTG CTCGTTTAAG    1140
AAAAGCGCAT TGTCAAACGG AATGTATCAC AGTCTACGTT GGTTATTCCA AAGGTCAAAT    1200
TGACCGTGAA GGACGAACTG GTTGGCGAAA ACAACAAACG ATTCCTGCAA CAAACAATAC    1260
AAAAGTTTTG ATCACCTATG TATTAGCCCT TTTTAGAGAA CATTATCTAG CGGGAACCGA    1320
TGTCCGGCAA TTAGGGCTTT CATATGGGAA ATTAGTTTGG AATGAATCTT TACAATTAGA    1380
TTTATTTTCG GAACCAGAAG AGCAAATTAG TGAAATGGAG TTAAACTATC TGATTGATAA    1440
AATCCGACAA AAATTTGGCT TTCAAGCTTT AATTCACACC TCTTCTTTGT TGGAAGGCGC    1500
GACGGCAATT CATCGTTCAG GATtAGtCGG TGGACATGCT GGAGGAAATG TCGGTTTAGG    1560
AGGATAACAT CATGAAACGA ACAAAAAAAG AmTTTACACC TTATAATGAG TACCATGaTC    1620
GGCCCTTTgA ACTGAAATGG GCGACCGCTT TTGCATTGGG GGAGTTACAA GAAGGAATCG    1680
AAGCTTCTGA CGAATATTCT AAGAGAGCGT TTGAACGCTT ACCGCAACAG ACAACAGAAG    1740
AAATTGAAGA ATACTTAGAG CAGTCTTTAA AAAATAACCA AGTTTTAGAa ATCCAATTGA    1800
ATACATTGGA TGATTTTGGC CGTGTTCAAC CGCCAATTGT TGGTGTTTTT GAAGGGATGA    1860
GTTCAATGGA GTATGTAAAA GTTGGACATA CACATATTTT ATTTGAAGAG ATTCGGCATA    1920
TTAAAAGTCA TGAGTTTACA AAGTGGTCGA GCCTTGATTA AAAAACTATT GTTATACGTG    1980
CGTTTTGTGA AAACATATGA GATAATGTTC ATAGGTAATA GAAATAAAAA TTATGGAGGT    2040
GGCTAGGATG GGACATCATT TAAAAGGACA CCATGGCAAA AAAACAAACG CAAATGGCGG    2100
CTTTTTAACA AAGTTATTGG CAGGTGGCGC CTTAGTGGGC GTAGGAAAAA AGTTATACGA    2160
CAATCGTGAA AAAATTAAAG AGCTGTTAAG TGACGACAAA GAAAAAGGCA ACGACACTGA    2220
AAACAAATAA AGGACTGGAT TGACGGAATG GTAAAAGATG CAGCGTATAT TATTGAAGAG    2280
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ATTACCACGA TTTTAGAAGG AACCTATTTT GTGATAACCA AGAAAGCGAA TAAGCGCCGC 2340

ATGTGTTTAC ATGTTTCAGA TACCGCGAAA GAATTTTTAC GTTGTCGACT GGAGTATGAA 2400

aCATTCTTAG AGCAACAGTT TGATTATGCC aCAATGTTTT TAGAAACATG TACGGAAGAT 2460

GTTTCTGTTG AAATTCAAAC GGGACTACTT GAAGAAACAA ATTATCAAGC ATTAACCGTG 2520

GAAAAATTAC AACAGATAGC CACTAAAATG TAACACAGCT GTTGTGTTAG TTTTGATTCT 2580

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TAACCATGCT TTGTGCAATG TCTTAGTCGT TCGCTAATTG TGAGTAAATA ATCAAGGAAA 3060

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CAAGAATTTC CTGAAATTGA ATTGATTCAT CGGTCGTTTG CGTTAGGATG GTCAGCAAAC 4440

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TACAGATATA TTGAAGTAAC ACCCAATGAT GGAACAATCA TTAAAGAATG GAATACTGTG 5280

ACCATTATAT TTTTCTTGCT GACTGCTTTA ATTTGGTTGG CAAACTTTAC TGTTCGAGCA 5340

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CCCACAGGCA ATCAAAATGT GTTAAACCAT CAAGGGAATA AAGACGGTAG TGCACAATGG 8040

GACGGCCAAA CGAGTTGGAA TGGGGACCCT ACTAATCGCA CAAATTCTTA TATTGAGTAT 8100

GGCGGTACAG GAGACCAAGC CGATTATGCC ATCCGAAAAT ATGCTAGAGA AACAACAACA 8160

CCAGGGCTTT TTGATGTATA TCTTAATGTG CGTGGGAATG TTCAGAAAGA AATCACGCCA 8220

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CAAGAAGTGA CCACCACAAA TCAAGTTATT CCATTGGAAA TTGAAAATAA ATTTTCTTCT    9960
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TGTTCAAGAT CCACAAGGGC AATCGTTAAC GCATATTCAT TTATATCCAA AAAATGAAGA   11280
AAATGCCTAT GACTTACCAC CACTTGAAAA AACGGTACTC GATAAGCAAC AAGGCTTTAA   11340
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TCAGGAATTC CGTTTGTCAG ATAAGGCGGA TACAACGTTG ACACTTTTAC CAGAATCAAT   11460
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TGGATTTACG CTTGATTTTT CAATTAAAGA CTTACAAAAC TTTGCAAATC AAACAATGAC   11580
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CAAGTCTTTT GTCAAAGTTG ATAGTGAAAA TGCGAAAATC ACCTTGCCAG AGGCTGTTTT   11760
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AGGnnTTAAA AGATGGCCAG TACTTCTTGG AAGAAATCTC TGCACCAAAA GGTTATCTTC   11940
TGAATCAAAC AGAAATTCCT TTTACGGTGG GAAAAAATTC TTATGCAACG AACGGACAAC   12000
GAACAGCACC GTTACATGTA ATCAATAAAA AAGTAAAAGA GTCAGGCTTC TTACCAAAAA   12060
CAAATGAAGA ACGTTCTATT TGGTTGACGA TTGCAGGCCT GCTAATCATT GGGATGGTAG   12120
TCATTTGGCT ATTTTATCAA AAACAAAAAA GAGGAGAGAG AAAATGAAGC AATTAAAAAA   12180
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AGTTTGGTAC ACCGTTAGTA CCTTGTTACT AATTTTGCCA CTTTTCACAA GTGTATTAGG 12240

GACAACAACT GCATTTGCAG AAGAAAATGG GGAGAGCGCA CAGCTCGTGA TTCACAAAAA 12300

GAAAATGACG GATTTACCAG ATCCGCTTAT TCAAAATAGC GGGAAAGAAA TGAGCGAGTT 12360

TGATAAATAT CAAGGACTGG CAGATGTGAC GTTTAGTATT TATAACGTGA CGAACGAATT 12420

TTACGAGCAA CGAGCGGCAG GCGCAAGCGT TGATGCAGCT AAACAAGCTG TCCAAAGTTT 12480

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GTTACCTAAA AAACAAAATG GTAAAGATGC AGTGTATACC ATTAAAGAAG AACCAAAAGA 12600

GGGTGTAGTT GCTGCTACGA ATATGGTGGT GGCGTTCCCA GTTTACGAAA TGATCAAGCA 12660

AACAGATGGT TCCTATAAAT ATGGAACAGA AGAATTAGCG GTTGTTCATA TTTATCCTAA 12720

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AGGATTAAAT GGCGCAGAAT TTGTTATTTC TAAAAGCGAA GGCTCACCAG GCACAGTAAA 12840

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GCAAAAAACA ACGAAAAAAC CAGACAAATC CTATTTTGAA AGTCATACGA TTGGTGTTTT 14460

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GGAAAAAGGA AGCTCCTTGT TAGAAGGAAC CTCCTATCCT ACAGGTGGTA CGAATACACA 14580

TGCGGTCATT TCAGGCCATC GTGGTCTCCC TCAAGCCAAA TTATTTACAG ATTTGCCAGA 14640

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AGATCTCGTC ACTTTATTAA CTTGCACACC GTATATGATA AACAGTCATC GGTTATTAGT 14820

TCGAGGACAT CGTATCCCAT ATCAACCAGA AAAAGCAGCA GCGGGGATGA AAAAAGTGGC 14880

ACAACAACAA AATTTACTAT TATGGACATT ACTTTTAATT GCCTGTGCGT TAATTATTAG 14940

CGGCTTCATT ATCTGGTACA AGCGACGGAA AAAGACGACC AGAAAACCAA AGTAGTATGA 15000

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GAGTGTTAAA AATGAAATAT CTGGATATTA TTGCTTTAAT TTTATTGATT GTCGGAGGTT 15600

TAAACTGGTT ATTA 15614

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTCACAAAAA AATGAAAACA CAAATTTAAC TTGGAGGATG TTGAGTAGTG AGCAACGGGA 60

AAAAGATTTT nATTAGTCAT AGTTCAAAGG ATcAAGAATA TGTGGATGCG TTTATCCAAT 120

TATTGAAAAA GTTTGGGTTT CGAACACAGG ATATTTTTTA TAGTTCCACT ATTGAAACAG 180

GTGTACAGCC AGGAGAATTA ATTTTTGACA CGATTAAAAG GGAGCTAACC AATCAACCTG 240

TCATGCTGTA TTTTTTATCT GATCATTATT ATCAGAGTAT TCCATGTTTA AACGAAATGG 300

GTGCTTCTTG GATGCTATCA GATAAACACT ATCCAATTGC GTTAAATAAT TTTTCTATGA 360

AAGATATGAA AGGTGTTATT AGTAGTGAGC GTTTGGCGAT TGCGTTTAAT GATAAGACAA 420

GTACTAATGA AATAAACTGc TTATTAAAAA AGTTATCTCA TGACACAGAT GTACAAGCTG 480

AGCCAGATTT TGAACTAAAC GTTGAGAAAA ATATTCAGCC ATTCCAAAAT AAACTGACAC 540

AACTGATTCG GCAAGCAAGT TATTTAAAAC CTGATGAAAA GGGATATTTT GAAACGrTTC 600

tTAGCACTCA TCGTCCTGTG TATGGCACAG CAAAAGGGGT CTATGACTGT TTTAAATTAC 660

CTAGCTTAAT TGAGCCTAAA AGTTTAGGTT TAGACACGCT ATCAGAGGAT GAAAGCCATT 720

GGCTATTCTT TTTTCTTACG TGGGGAACTT TTCAAGAAGG CGAAAAAGTG CGGTTTAAAt 780

TGAAAAAGGa TAAGGcGTAT AACAATCGGG AATTCAGTGA TATTGGTAAA TGTAAAAATA 840

TTTACGTCTC TTATTTAGAG AAGGTAGAGT AATTGGAGGA GGTAATAAAT GAAAATGAAT 900

TGGcGTCAGT TGGTTGGTAC ATATCGTATT TCTGATAATG GTAAACAATA TCAAAATGAC 960

TGGTTAAATA AGCAAGTTGA TTTAGCCACA GAACTTCGTA AATCTTTTGA TAGTGACTAT 1020

CGTAGAGTAA TTAAAAGTGA TGCATTTaGA CGCTTwnCAa GAkAwAACAC cAAGTTTTyC 1080

CTTTwGrAnC GTAATGaTTT TgGTAAGAAC aCGTTTAACA CATAGCTTAG AAGTGGCAAT 1140

GCATAGCAGG GATATACTTA GATTAGTTAT TTCACAGTTG AACGAACGAA ACATTGAGGT 1200

TATGGAATTA TCAGAATGCT ATCGGTTGTT AGAAACAGCT GCATTAATCC ATGATATCGG 1260

CAATCCCCCT TTTGGACATT TTGGGGAAGA AGCCATTCGT ATTTGGTTTG AAAAAAATGG 1320

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TAAAGCAGGA ATGAAACTAA CAGCCACGAC ATTAGATACA GTTATCAAAT ATACGGCATC 1500

TTCAGATCAA TTAAATAAGC AACAGCTTTT GTCTAAAAAA GTTGGCTATT TTTACTCGGA 1560

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AACAAAAAAA TTTTTAATGT TAGAAAAAGA TAAAACAGAA GAAGCTACCT TACAAGAATT 1800

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TGACTTAATT ATGAGAGGTA TCTATCATAA TGAAATTATC ATTGAAGATT GTGATGAAGT 1920

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AAAAGACTAT TATCGTTTGA AAATGGCGGT GGACTTTGTA TGTAATATGA CGGATGGATA 2220

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TGCCGCCGCT GAAGAAAACT AGTTCATTGC ACAGGCTGAT CGTTTCAGTA AAAATTTTAA 2340

AGATGCTAGT AATTTCACTG AAAATCGGGT ACACTAAAAT TAGCTAGTGT AACTAGCAAA 2400

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AAATACAGCT AGTCACTATT TAAATCAGTT AAACGAAGAA GGAATTCTAG TTAAGATCAA 3000

TACACGACCG GTTTACTTTT TTCATAAAgA AGCGTTTCAG CAACAAAACT ATCTTTTAAA 3060

AAGGAACTGT TTATCCAAGT TTCCAAGAAA TGATCGATGA ACAGCCTGTT TTTGGATCGC 3120

CAAAGnGGAn TTTTnTTCAG TCGGGTCATn GGGTATCGCG GGTAGTTTA 3169

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17087 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GTCTATACAA GTTCACAAGG AGGCGCCAAA CATGACCATT TTAGAATTAA CATTCGCAAC 60

GAACCAACTA ACGACGACTT TTTTTAACCA TAAATTGGAA CCGCTTCACC AAAAAACATT 120

CCCTTTTGAA GCCTTGACTA TCGAAGAAAC GGTTCCTGAA CTGTGCCAAT TGATTTTGGC 180

AGAGGCGGCA CCGATTCTGG GGGGGATTGT GGCTGATTTC CCAGCGGACT TCTTTTCGCC 240

AGAGGAAACG TTGGCGCTGG TTCCGCAAGC GGTGATTCAA GCATTCGCGG AACAGTTGAA 300

CACGCCACTT TTAACGGCAG CCGAACAAGC GGCGGCACCG AATCTGCTAG AAGCATTTGA 360

AGAAAAACGG cAGTATCTGG CTTGGCATTT GGACTATTAT GGCTACGTGC CTGGGAAAAA 420

TGAATATGCG GTGGAGTCCC TGTTAACTGT CGGCAATGGC TTTTTAGGCT TGCGCGGCAC 480

GACACCTGAG ATGACGATTT CTGATGATCA TTATCCAGCG ACCTACATTG CGGGGCTTTA 540

TAATACAGCG GCTTCGGAAG TTGCGGGTCA AGTAGTGGAA AATGAAGATT TCGTCAATGC 600

TCCTGACAAC CAACACATCG CTTTAAAAAT TGGCGATGCC ACTGACTGGT TAACGATTTC 660
TCCAGACACG CTACAACAAT TACATCGTCA ATTGAACTTG AAAACGGGGT TGTTTGTCGC 720
AGAAATGATT TTGAAAGATG CGGACAATCA GCAAATTAAA TTAACGACGA AAAAAATCGC 780
CAATATGGCA CAGCCGAATG ACTATCATCT GCAATATACG TTTGAGCCGT TAAACTTTTC 840
AGCCCCGATT ACTTTGAAAA CCGTCACGGA TGGCAGTGTC TACAACTATA ACGTGGCGCG 900
GTATCGCAAC TTAACAGCGA AACATTTTCA GGTGACAGCA TTAAGCGCGC AGGAAAAACAA 960
AACCGTGATT GAGGTTTGTA CCAATCAATC CAACTTAAGC GTCCGAGAAA CGTCTTTGAT 1020
AACCGGTGAT TTTTTTGAAA AAGAAGCCAT TACGATTCAA GAAGAAGCGG AGAAAATCGC 1080
CCAAGTGGTG ACCGTGATGG CGCACCAAGG AACGCGCTAT ACGCTAGAAA AACAAGTCTT 1140
TGTACAAGCC AGCCACGCCG AACAAAGTTG GCAGGTACCG TTTACGCCGA AGGACTCTTT 1200
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TGCTTGGTTG TATTGGCATA GTACACAGGA TCATGAATTT ATGAAACAAT ATGGCGGCGA 1740
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ACGGTTCTTT ATTGATAAAG TGATGGGACC TGATGAGTTT CACGAGGGCT ATCCAGACCA 1860
AGCGGAAAGC GGCTTGAAAA ACAACGCCTA TACGAATTTG ATGGTGGTTT GGCTATTCGA 1920
AGAATTAACC AACATTTTGG CACTTTTCTC TGAGGAAGAA CAGGCACAAC TTTTTGCCAA 1980
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TGACTGGACA GCGATGAAAG AGAAATACGG CAATATTTAC CGCATGGATC GAATTTTAAA 2160
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GCCTGCGGAT TATTTGGAAA AAAATCTTTT GTATTATCTA AAACGGACGT CTCATGGTTC 2340
GACTTTGTCA CGAATTGTTC ATGCCCAATT GGCAGAAATG GCGCAATTCC ATGAGCTATC 2400
TTGGCAACTT TATCAAGAAG CGTTGTATTC CGATTATCGT GACATTCAAG GTGGCACGAC 2460
CGCTGAAGGG ATTCATACAG GGGTCATGGC TGCGACGATC CACGTTACTT TAGCGACGTA 2520
TGCAGGCGTT GACACGCGCC AGAACGAGTT ATCAATTTGT CCAAACTTAC CTGAACATTG 2580

GCAAGCGCTG GCCTTCCAGT TTATTCATCA AGGCGTGACG TATCAATTTT CATTAACACA 2640

AACCAGTGTC ACGATTACAG CAGATAGAGA CACACAATTA TTGGTTCAGG GCGCGTTGAT 2700

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GAAAATGCGT TTACTCCAGC AGAAAAAGAA GCCTTAGCTC AGCAAAAAAA TGAnCaCTAC 3000

GTTCAATTAT TAGAACAATT AACAACAGAA GATGTTTTAC CTGGTGTCGT GCCATTGCTA 3060

CAGCAAGCCC AAGCACGTCA CATTCCCTGC GCCGTGGCTT CGGCTTCAAA AAACGCGCCC 3120

CTGATTTTGG AAAAATTAGG CGTGCGCGCG TAcTTCGCCA CAATTGTCGA TCCCGACTCG 3180

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GCGGGCATCT ATGCCGTCGG CTTGTCGGCC AGCCAACCCT TAATCGGAGC CGACATGCAA 3360

GTTTCTGAAA TGACTGAACT AAGCGTTGAT GCACTGCTCA ATCGCTAAAG AATGACAAGA 3420

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CGTTCCACAA TCTTTATTAT CGTTAATAAA TCAGCCACGA AAGAGCCAAT CGAAATCTTT 4380

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AAGCCCAGAG GTTTTTCTCC TCTTTAACAG CTTTTAGGAt TTCACGGATT AACGCTAAAT 4560

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CACCACCATG GTCAGGGGAA ACAACAACGA CGTCATCGCC TTGAATGCCG TGTTCGATGA      6300
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GAATTTGGAC CGCATGTAAG TCCAATGTCA ACATTCTTGT TGCACCAGCT TTTTCAATCA      6420
TGTTTGCAAC AAGTTTAGCA GTGATTGGTT CCCGGGCACG TGCTTTACGG TCTTGACGTG      6480
CATACCCATA ATAAGGCATA ACCACGTTAA TTGTTTTAGC ACTCGCACGT TTTAACGCAT      6540
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CGTAAACATG TGCACCACGA ATACTTTCTT CAATATTCAC TTGAATTTCG CCATCACTAA 6660

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(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11764 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AACTCTTTTT GTTTCAATAG GAAGTGCTTA GTGTTTTTTC AGAATTGAAA AATGAATACG 180

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GTTCTAGTGA ACAAGAAGTC GAGGAACGTT GGTCGACTTT GGTGGCTCAG TTTGATCGCT   4620
TGTTAGCTAC CTGTGAGGAG TTGCCAGCTG TAGCGGAAAC AAAGATTGAC AAGGAAGAAG   4680
TTGCCGTGAC TGAATGGCTA CAAGCTGTCA ACGAAACAGT AGCAGTCTTA AGAGAAGATG   4740
GCCCTTTAAA AAAAGTGGTT TTGGCTCGAC AACTTGCTGT GAGCAGTCCT GAAAAAATTC   4800
GAAGTAACCA AGTGCTCGTT AATTTAATGG CACAACAACA AAATACGTAT TTGTTTGCTT   4860
TAGAAGCCAA AGACACAAGT TTCATTGGTG CAACACCAGA ACGACTTCTG TTGGGTACTA   4920
AAGAAACGTT TGCGACCGCT TGTATTGCAG GAACCATTAA AACGGGTCAA ACACCAGAAG   4980
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AAGCACCCAT TATTTTGGAA AATCGAGATG TACAACATCT TTATGTGCCA ATCTCGGGTC      5160
AACGTAAACC GGGAATTTCA TTTTTGGAAA GTGTGATGCA GCTACACCCA ACGCCAGCTT      5220
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CTGTGGCCTT GCGTTCAGGT GTCTTTGCTG GTCAGCAAGG CGTTCTTTAT GCAGGTTGTG      5400
GTATTGTTGC GGATTCCCAA GCAGAGCTAG AAAGAGAAGA AACGAAAATA AAATTTCAAC      5460
CGATGTTACG AGGAATTGGA GGTCAGGTTT AATGAATCAT CAAGAAACAA TGACCGATTA      5520
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GAATTTTCCT TTGCGGGAAC CATTATTACC TGACTTAGAG AGAAAAACAA AGAGTTCTCA      6060
ACAAACGGCT TTATTCGCTG GTCAATCAAT CCTTTCTACA GAACAAGTGC AACAGTTAGC      6120
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AACAATTGTT TTATTAAATA ACAATGGTGG CGGGATTTTC TCTTTTCTAT CTCAACGAAC      6960
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TGTGTACGAA TGTACAAGTT CACTTTATCC TATCATAGAA TGGGTCTTTT TCTACGTCAn 11760

AAAT 11764

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCCAATATAA AGACACAACA GACAAACGaT GAGGAGTGTG AAwTAAtATG TTaACAATTA 60

TTATTGGGTT TATCTTTTGG ACAATGACAC TAATGTTAGG TTATCTAATT GGTGAAAGAG 120

AAGGCCGTAA ACATGAGTAA TTTAACAAAA CGTAAAAAAG ATTTATTTGA AATGAAAAGC 180

GTTGTATTTA AAGATATTTC AAAGCAACAA AGCGAAAAAG CACAAAAAAG AAAACGACTC 240

TTACAACTAA TGAATCAATA TCCCGATTGG GCAAGTCAAA AAAATAAACT TATTATGCAG 300

GAAATTCAAG AATTAGGACA AGCAATCGGT AATTGGTCGA TGGATCAATC AAGACCCATC 360

CAATCCATCA AGGCCGCATC GTTTACAAAA AGCGAGTATC TCTATTTAAT TTGGCTCGGT 420

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CGATTAACAC TTTTAAATGA ATAAAAGTAA AGGAGATTAA CCAATGCGTA CGTCAACATT 540

TAATTATATC AAAGATATTT TAGCAGACTT TTATAAAACA GAAGAGTATA TCCGTCAACG 600

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AGGACTTCAC TCTGTAGTGA CCGAACGAAT GGCGATTACG ATAGCTATGG aTCGTCGTCT 720

GTGGAACTTa GAGAGAAATC GAGACATTAT CAAAAATTGT TTAGCCGAAG CGGaTGAACA 780

AACGCGCGTG ATTATTGAAG AACTATATAT GAAAAAACGG CCCTCTTTAA CATTAATTGG 840

ACTTGCCCAG CAATTATTTA TTAGTAAAAG CCAAGCCTAT AAATTAAGAA ATCATTTCTT 900

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ATGCCACTAG ATGATCCTAA AAATGAATTT ATTGCAGAAA TGCAATGGGT GGAACTGACC 6900

GACAATGAGA ATGAATATAT TGGTTTATAT CGCGTGATGC CAACCACAAT TAAGAAAGAT 6960

GCGAACAATA ATCAAATTCA TTACTCTGCC ACAGAAGCAT TATGTACCTT AGGTGATACT 7020

GTCCTTTTTG GTTGTCACGA AATTAAAAAC AAAACAACGA AAGAGGCCAT TCAATTTTTA 7080

TTGAATAAAC AAAAAACAAA GCATTGGGTC CTAAAAAAAT GTGATTTTTC AAGGAAATTA 7140

ACCTATAAAT GGGAAAATGA AAATGGGTTA GTTGAGCCTT TATTTAGCAT CCCAGCCGAT 7200

TTCGAAGaGG AATATCTTTG GCAATGGAAT ACAGAGGTCT ATCCTTTTGA ACTTTCATTA 7260

GTCAAACCGC CAACAGAACC AGTTGCGCGA ATTCAAGAAG GTTACAACAT GCAAGGATTT 7320

GAAATAGAAC GTAATCCCAA GATGCTAATC AATCGGATTT ATCCATTAGG TTCAGGCGAA 7380

GGTGTTAACA AAGTCAATAT TCGCTCGGTC AATCAAGGGG TTCCGTATTT AGAGAACAAG 7440

GCCGCAATTG ACCGCTATGG TTTATTGGAG TCAATTTGGG TGGAACAGCG TTTTTCTGAT 7500

CCCAAGGCAT TAAAGGAAAA TGCTTTGCGA ATGTTAGAAG AATGGACCAA GCCACAAGTT 7560

TCTTGGGTAG TGACTGCAGC TGATTTAATT AAATTAACAG ATCAACCTTT GGCAATCGAT 7620

CGTTTGCGGT TGGGCACGGT TATCATGATT AATACGAATG AATTTGGGAG TGTCAACCTT 7680

CGTATTAAAA AAGAAAGCAA AAAAGATGTC TTTGGTGCCC CCCAAGACAT TCAGCTAGAG 7740

TTGGGAAACC TGCAAGAAAC AATTCATAGT ACCATGACAG CTTTCAGTCG GAAACAAGAG 7800

ATTAACGAAA CTTACGCACA AGGGGCGACG ACACTTTTAA ATCGTTCAAT ACAAGGAGAA 7860

CTTAGCAAGA CACAGCCAGT GGAGCTGAAT TTATACTTTG ACGAGGACAT TCTTTATATA 7920

AACACCGCAG AATTAACGTT CAAGGCAACT GCTAAAGGAC CTTCGCATTC TGTAACGAAC 7980

ATTGATTTGG TAGTGGATGG CAAAAAATTA CCCCAACTAT CATTGCAACA ACAACGGCTA 8040

AACATTTTGA GTTATTTACG AAAAACAACA GATGAAAAAA TCGAACGCGG CAATCACACG 8100

CTTCAATTTT TCTCTCATCA GCCACTATGG TTGGATGCTT CGGTCATCTG TCGTGTGTAT 8160

ATTCAATCCC AATTGGGTGG CCAGTTTTAA TAAAATAATG AAAACTAGAG GAGTGTGACG 8220

AAATGTCAGT AGAACATATT GAAGAATTAG ATACCCTGAA TCAAGGTCGC CTTAAAATCA 8280

ATGCAATCTT GGATCAGTCG AATGCATCAG CTGAGAAAGT AGATGCTTAC CAAGTCCAGT 8340

TAACGAATGG AATTTCTGAA GCGAAAAACA TAGCAGATGA AGCTGGCAAA GAAGCCGTAC 8400

AAATTGCCAC CGATGCAGGC AATCAAGCmA aTGAAACAGC CAACCAAGCG aTGaACaATG 8460

CCAAAACAGC AaTCATGATT GCAGGaAATG CAGTTTCAAC GGCAAATAAT AATAAACAAG 8520

AATTTGATAC TTTACGAAAT GATTTCGATC AATTAGTAGC AGAAGCGGGT GATAGTAATC 8580

CAGAAATTGT CCAAGCACGT ACAGATACAC AAGGCATCAA ACAAGCTACC TTAGCGAATC 8640

GTCTTCAAAT TGATTTGAAT GACCGTATGA CAAAAGCAGA CGGTATTTCT TTATTGGCTA 8700

AGCCAACTAC TGTCAAAATG AAGTTAGACT TTAACGGTAA AACGGCCGGC AATACAGCCA 8760

CCAATGCAAA CAGTTATTCC ACTGATTTTA CGGCAAAAAT TCTTAAGAAG CCAACAGAAG 8820

TTTGGGAGGA AGTTTCCCAA GCGGACTACA ATAAAATGGC CAGCCGTGAT GATGAGGGCG 8880

TGAAAACAGG TTCCACCCAA AGCGGTGTGA TTCCGCAACA ATTAGCGGCC TTCAATCTCG 8940

TTGAAGCCGC TAAAAAATTA ATTCCACAAA TGTTTGAAAC AGTCACAACT GACGAGGCGG 9000

TGGCATTTAT TCGCCAGAAC GTTCAATTTT TTACGATTAA TCAACGTGTG AAAGCCGCTG 9060

CGCCCAATAA TCAAACGATT AAAATCGCTA CGTATTTACC AACTACGGAT AATTGGGTAA 9120

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ATTTTATCAC AGATGAAGGT TTCATTTATT TAATGAGCTA TACAGATTCA TCGAATGGGG 9240

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CCCAAGCGGT TTTAGCGAAG AGTGGTTTTG TTCAAGCAGA GCAACTCAAT ACCCATATGG 9360

AAAATCAAGA TAACCCGCAC CAAGTAACCG CTGAACAAGT GGGGCTAGGC AATGTAGAAA 9420

ATTATGGnTT CGCATCAGAC AGCGAAGCAG TCGCGGGAAC TTTAACGAGT AAATATATGC 9480

ACCCGAAAAA CGTTGCGGAA GCGATTAAAG GTCAAGCTGT GACACAAACA GGTGATCAAG 9540

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CCTCTAGAAT GGCCATTTAT GAAGCTAnTG GAGTTGGTGA AGyCGAGGCA AAATATCAGg 9660

CGGCCTTTAA TAAGGAtAAT ATGAAATTTG TATTAATTAG GGTAGGAAAT CGTGTCGATG 9720

CATTTGTAAG ATGTAATTTG AGTGATCCaA CGAAATTGAA TAATAATTTG GTTAAAGTGT 9780

TTACTGTTCC AACAGGATAT ACATTaTCGA CGAAGATTAC AAAGGGAATA TGGAATyTGG 9840

CGTTAACTGC TATGCAATAT ACATTCCCTC AACCGAATTG TGCTGGTTTA TATGAGATGG 9900

GAAATCAAGG AATTCTTTTT GGTGCTAACC GTGCTGGAAA TATTTACCTA CAAGGAAGTT 9960

GGTACACGGA CGATCCGTTT CCAACAAAAT AACAAGCTAG TTTAGGAGTC TTTTTATGGA 10020

ACGTTATCTC AACACAATAA CAATGCTTTT AAGCATTTTC GGTGGGATTG TCGTACGTTT 10080

ATTAGGCGGA TTAGATCAAT TGTTGGATGT CTTCCTCTTT TTAATTATTG TCGATTTCAT 10140

CACAGGTTGG ATTAAGGCAA TCGCCACAAA AGAATTGTCC AGTCGGATTG GTATGCTCGG 10200

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GAAGGGAAGT TATTTTGACT TTCCTTTCAT GGCTTTTTTA AGAAAGGAGC ATGCTATGTT 10560

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TGTCGGATCT GGTGGACGAG TGAAaCAATT AGCTCCTGCT GGCCAAATTC AATATGGCGC 10860

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GGCGACATTT AAAAAAGATT ATGCTGCCTA TGTTAATTTG GCCCGTGATT TGGCTCAGAA 10980

CATTGGTGCT GaTTTTTCTC TGGaCGATGG AACAGGTTAT GGCaTAGTCa CTCATGATTG 11040

GaTTACAAAA AATTGGTGGG GAGATCATAC AGATCCTTAT GGtTATTTAG CGCGTgGGGG 11100

ATtAGTAAAG CGCAtTGGcA CmAGATTTaC aAcGGGCGTT TCyGrAACAg GTGaGACTGG 11160

TCATTATTCA GCCAGGTAAA CCTAATGCGC CAAAATATCA AGTAGGACAA GCAATTCGTT 11220

tCACTTCAAT CTATCCAACA CCAGATGCTT TAATCAATGA ACATCTATnA GCAGAGGCAC 11280

TTTGGACACA AGTAGGAACA ATTACAG 11307

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2866 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAAGCACAAA TGCAACAAGT TGTGATAGCT ATTCAAAATA CGGAAGCCTT TCAGTTATTG 60

AATGTAATGA AGGTTATAGG AGATGAGTAA ACATGTATGA AGGTTTGTTA AAACAGTATC 120

AAGCGTATTT GCCCGTAACA GAAAAAACAC CAATGATTTC TTTAGCCGAA GGAAATACGC 180

CACTGATTCC TTTACCTAAT TTATCCAAAG AATTAGGTAT TCAATTATAT GGAAAATACG 240

AAGGCTTAAA TCCCACTGGC TCATTCAAAG ATCGCGGGAT GGTGATGGCT GTAGCAAAAG 300

CGGTAGAAGA AGGTGCCAAA GCGATTGTTT GTGCTTCTAC AGGAAATACT AGTGCCGCCG 360

CTGCTGCGTA TGCCACAAGA GCAGGCATTA AAGCGTATGT AGTGATTCCA GAAGGGAAAA 420

TCGCACTGGG AAAATTGGCG CAAgcTATTA TGTATGGGGC GGACATTATT TCGATTCCAG 480

GTAACTTTGA TGAAGCATTA AAAGCGGTGC GAGAGATTGC GAAAACTGAG GCAGTTGCGC 540

TAGTTAATTC AGTGAATCCT TATCGCTTAG AAGGGCAAAA AACAGCAGCT TTTGAAGTTT 600

GTGAACAATT AGGTCAAGCG CCCGATGTCT TAGCGATTCC AGTTGGAAAT GCCGGCAATA 660

TTTCCGCTTA CTGGAAAGGC TTTAAAGAAT GGCATGAAAA ACAAGGAACA ACTTTACCAA 720

GAATGCATGG TTTTGAAGCA GAAGGTGCCG CAGCGATCGT GAAAGGCCAA GTGATTGAGC 780

AACCTGAAAC CGTGGCAACA GCGATCCGGA TTGGGAATCC TGCTAGTTGG CAATTAGCAG 840

AACAGGCACG GGATGAATCC GGTGGTTTCA TTGATGCCGT GACAGATCAA GAAATTTTAA 900

CGGCTTACCG AAAAATTGCT GCTCAAGATG GGGTTTTCAT TGAACCTGGT TCGGCTGCTT 960

CATTAGCTGG AGTTATTCAA CATGTTAAAA GCGGTAAAAT CAAAGCAGGT GAAACCGTCG 1020

TGGCAGTCTT TACTGGTAAC GGACTGAAAG ATCCTGATAC AGCAATGGAG ACAGAAGTAG 1080

CTATTTCAAA AATGAGTGAC GTGGAAGaAA TGCGTCTGcA CTTACgAAAA GGAGTCGCAA 1140

CACTATGaAA ATAAGAGTAC CTGCCaCtAG TGCCaACTTA GGACCTGGCT TTGATTCATG 1200

TGGCATTGCA TTATCCGCTT ATTTAACAAT CAACGTTTTA GGTGAAAGTG AATTTTGGGA 1260

AATTCAACAT ACTCTGGGAG AAGAGATTTC TACTAATGAA GAGAATTTAT TAATTCAAAC 1320

GGCATTGAAA ATTGCACCAG AATTAACACC AAAAGTTATT CGGATGGTTT CTGACATTCC 1380

CCTTGCAAGA GGACTAGGCA GTAGCTCAAG TGTGATTGTA GCAGGCATTG AATTAGCTAA 1440

CCGACTAGCA CATTTAAATT TGTCCCCTAA AGAAAAAGTC CGTTTGGCCA CAGAGATGGA 1500

AGGACATCCG GATAATGTGG CCCCAGCTAT TTTAGGAGAT TTCGTGGTGG CTAGCCATGT 1560

AGAAAACCAA GTCTACCATG TCAAACATCA CTTTcCAATG tGTGATGtCA TTGcATTTAT 1620

TCCAGAGGAA CCATTATTTA CCGAAAAAAG TCGCGCTGTT TTGCCCGAAA AATTGGCTTA 1680

TAAAGAAGCG GTCGCGGCCA GCTCAATTGC CAATGTTATG ATTGCCGCAA TTTTAAACGG 1740

GGATTTACCT TTAGCAGGCA AAATGATGGA ACAAGATAAA TGGCATGAAA CGTATCGTCG 1800

TTCATTGGTT CCTCACTTAA AAGAAATTCG TCGTTTAACT CAGCAAAAAG GTGCTTATGG 1860

CTCTTTCTTA AGCGGTGCTG GTCCAACTGT GCTAATCTTG TCGCCAGAAG AACGAACCAA 1920

CGAAATTGTT CAAAGCTTGG AGAAATTATC TACCAAAGCG AGCATCCAAA TTTTCAATAT 1980

TGATCAAGAA GGTGTTCAAG TCTTTTAAAA AAAACGAGAA AAAATCACTA GTGATTTTTT 2040

CTCGTTTTTT TTAATCCTCG GATGTTTCCG TGGAATAATA ACTATGATCT TCTAAGTTCA 2100

AAGCATTAAG AATCATTGAG GCAGTTTCTT CAATTGAAAG AGAAGCGACA TCAATAACGA 2160

TACAACCTAA TTTTTGATAA AGATCATTAG CAAAAGCCAG TTCTCGCCGA ATTTTTTCAA 2220

TATCTGAATA AGAAGTATTT TCAGGCAATC CATATGCGCG CATTCGTTCT TTACGAATCC 2280

CGTTTAAAAC ATTGGGATCA TTGGTTAAGC CAACAATTTT TTTAGGGTCC ATTTCGAATA 2340

ATTGTTTCGG TAAATGTGCT TCAGGAATTA GTGGCAAATT AGCAACTTTT AAGTTCTTGT 2400

TGGCTAAAAA GAGACTTAGC GGTGTTTTAG AAGTTCGGGA AACGCCAAGA AGTAACACAT 2460

CCGCTTCTAA AAAGCCTCGT GGGTCCTTGC CATCGTCATA TTTGACAGCA AATTCCATTG 2520

CTTCAATTCG TTTAAAATAA TTTTCATTCA GATGATGTAA GGCACCTGGT TCCCGCATGG 2580

GCGCGACACC TGTTAATCGT TCGATTTCCG CAACTGGTGG TGTCAAAATG TCAAAATGGA 2640

ACAATTGATG CTCATTGAAA AATTGATTAG CAATCGCCAC GAGATGATCA TTAATGATms 2700

tATGCAGTAC CATGGCCTCT GCTTTTTTGG CATCTTCTAA CGCTTGCACC AGTTTATCTT 2760

CGTCTTTAAC GAATGTTCGT CTAATCAAAG TAAAATCAAC AGTGGGGTAC TGGGCCATTG 2820

AAGCAGCCGC CAATTTTGAA GCGGTCTCGC CAGCAGAATC TGAGAT 2866

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GATTTnAAAn nAATTAATTG AAAATACCCG CTGsCAtGaC ACGGGAAGGG aTTACGAAAG 60

AAATTCCAAT GGACGAAATT GTTCCAGGAG ACATTGTAAC TTTAGCTACA GGAGaCATGA 120

TTCCTGCAGA TGCCGTGTTG ATTTGGACCa AAGATTTATT CGTTAATCAA TCgTCGCTAA 180

CAGGCGAATC CATGcCyswC GAAAAATTTG TGGATGCAGG TGTGGATCGT CAACAAACAG 240

AGGTTTCTGC ATTAGATATG CAAGACCTAG TGTTTATGGG CACAGATGTC TTGAGTGGAC 300

AAGGAAAAGC GATTATTTTA AAAACTGGGC AACATACATT TTTTGGTGAT ATTGCTAAAA 360

ATGCTACAAC ACAACGAGGA AAAACTAGTT TTGACTTAGG CTTAGCAAAA GTCAGTAAGT 420

TTTTATTACG AATGGTAATG ATTTTGTTTC CAATCGTTTT CTTGATTAAT GGTTTAACTA 480

AAGGTGCTTG GGGCGAAGCG TTTTTCTTCG CGATTGCCGT TGCAGTTGGT TTGACACCAG 540

AAATGTTGCC AATGATTGTT ACGAGTAACT TAGCCAAGGG TGCATTATCC TTATCGAAAC 600

ATAAAGTCAT TGTTAAAGAA TTAGCGGCTA TCCAAAATTT AGGTGGTATG GATGTGCTCT 660

GTACAGATAA GACTGGAACG ATTACCGAAG ATCGTGTAGT TTTGGTTCAA CATTTGAATC 720

CATTAGGTGA TTTGAGTGAC GAGGTTCTAA ATTTAGCCTA CTTAAATTCT TCTTATCAAA 780

CAGGTTGGAA AAATTTAATG GATATTGCCG TTATTAATTT TtATGAAGAG CATCAATGGA 840

AAACGCCGTT TAAAAATGTC ACTAAAATTG ATGAAATTCC TTTTGATTTT TCTAGACGCC 900

GCTTAACGGT TGTCGTGAAT GCAGATGATC ATCAATTGAT GATTACGAAA GGCGCCGTGG 960

AAGAAATGGA AGAAGTGTGC ACGCATGCGC AAATTAATGG CGAAATTGTA CCATTAAGCA 1020

CTGCTGTACG AGAAGAACTA CGCCGAGTGA ATGTTCAAAT GAACAAACAA GGGATGCGTG 1080

TGTTAGCGGT AGCTGTAAAA AAAGATGTCC ATAAAGAAGC AGTTTATTCA GTTGAAGATG 1140

AAAAAGAGAT GACATTGATT GGGTTTATGG GTTTTCTTGA TCCAGCAAAA GAGTCAGCCG 1200

TCAGCGCTAT CCGCTCCTTA CATGAACATG GTGTCAACGT GAAAGTGCTA ACGGGCGATA 1260

ATGACATTGT CGCCAAAAAA GTCTGTAAAG ATGTAGGCAT TGAAGTTTCC CATGTGTTAT 1320

TAGGTTCTCA AATTGAAGCA ATGACAsnTG AAGAGTTGCG GGCGCAAGTA GAAGAAACTA 1380

ATTTATTTGC CAAATTAAAT CCGATGCAAA ATCTAAAATT ATTGAATTGC TACAAGCAAA 1440

AGGTCATACG GTTGGTTTTA TGGGGGATGG CATTAATGAT GCACCGGCAT TACGAAAAGC 1500

TGATGTGGGC ATTTCAGTAG ATACTGCAGC TGATATTACT AAAGATGCTA GCTCGATTAT 1560

TTTACTGGAA AAAAGTTTAA ATGTACTGGA ATCTGGTGTG ATTGAAGGAC GAAAAGTATT 1620

TAGCAATATG ATGAAATATA TTAAAATTAC CATCAGTTCT AAT 1663

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CTTAATGGnG ATGGnAAGGG GATATTATTG GTTATTTTTT GAGnATATAT GATATCCTTT 60

ATTATGTAGG AATCnTATTA TATGGsAGGm ACGAGCGATG AAAGTTATTG TTTTAGGATC 120

ATCACATGGA GGTTATGAAG CGGTAGAGGA ATTACTAAAT CTTCATCCTG ATGCAGAAAT 180

TCAATGGTAT GAGAAAGGTG ATTTTATCTC ATTCTTGTCT TGTGGCATGC AGTTGTACCT 240

AGAAGGAAAA GTGAAAGATG TTAATTCTGT TCGCTATATG ACTGGCGAAA AAATGGAGAG 300

CCGTGGTGTA AATGTCTTTT CTAATACTGA AATTACAGCG ATTCAACCAA AAGAACATCA 360

AGTGACAGTG AAAGATTTAG TGTCAGGTGA AGAACGTGTT GAAAATTATG ATAAATTAAT 420

CATCAGTCCC GGAGCTGTCC CATTTGAATT AGATATTCCA GGTAAAGATT TGGATAATAT 480

TTACTTGATG CGTGGTCGTC AATGGGCCAT TAAATTAAAA CAAAAAACAG TAGATCCAGA 540

AGTCAATAAT GTGGTTGTGA TTGGTAGTGG TTATATTGGG ATTGAAGCTG CCGAAGCATT 600

TGCAAAAGCC GGCAAAAAGG TTACTGTTAT TGACATTTTA GATCGTCCAT TAGGGGTATA 660

TCTAGATAAA GAATTTACAG ATGTTTTAAC AGAAGAGATG GAAGCTAATA ATATTACCAT 720

TGCAACTGGT GAAACAGTTG AACGTTACGA AGGCGACGGT CGTGTGCAAA AAATCGTTAC 780

AGATAAAAAT GCGTACGATG CTGATTTGGT CGTTGTAGCG GTTGGTGTCC GTCCAAACAC 840

TGCTTGGTTA AAAGGTACCT TGGAATTACA TCCGAATGGC CTAATCAAGA CGGATGAATA 900

CATGCGGACA AGTGAGCCGG ATGTATTTGC AGTAGGGGAT GCTACGTTAA TTAAATACAA 960

TCCTGCAGAC ACAGAAGTAA ATATTGCCTT AGCAACGAAT GCTCGTAAAC AAGGTCGCTT 1020

TGCTGTGAAA AACCTAGAGG AACCAGTTAA ACCTTTCCCT GGTGTTCAAG GATCTTCTGG 1080

CTTGGCCGTC TTTGATTATA AATTTGCTTC AACAGGGATT AACGAAGTCA TGGCTCAAAA 1140

ATTAGGAAAA GAAACAAAAG CGGTGACAGT AGTAGAAGAC TACTTGATGG ACTTTAATCC 1200

AGACAAACAA AAAGCTTGGT TTAAATTAGT GTATGATCCT GAAACAACAC AAATTTTAGG 1260

CGCTCAATTA ATGTCGAAAG CAGATTTAAC TGCAAACATT AATGCTATTT CATTAGCGAT 1320

TCAAGCCAAA ATGACGATTG AAGACTTAGC CTATGCGGAC TTCTTCTTCC AACCAGCGTT 1380

TGACAAACCT TGGAATATTA TTAATACAGC GGCTTTAGAA GCGGTGAAAC aAGAACGTTA 1440

ATAGAAGAGA mAATAAAACC CATGAGTATT TATAGTACTC GTGGGTTTtA TTTTTATTTT 1500

GTATTCAATT GATTTTTCAA CTCTTGTTGG ACACGAGTTA ATTCTTGTTC ATCCACACGT 1560

TGATAGGAAA CACCATCTTG CATAAAACCA GTACCTTGAA GTTGGTCTTG TTTCACTTTA 1620

CCAAAGGCAC TGCGATAATC TAAGGCAATT TTTTTCATGT CATCAAAACT TAAATCTGTC 1680

TTCATATTAT CAGAAACAGC TGTTAAAATT TCTTGaTAGT TGCTTACGCT GTTAAGACTT 1740

AAGACTTTTT GGACGATGCC TTCAATCACT TTTCTTTGAC GTTCTTGGCG GCCGTAGTCA 1800

CCATTAGGGT CTTCGTAACG CATTCTTGAA TAGGAGAGTG CTTGTTCACC ATCCAATGAA 1860

ATTTTACCAA TCGTAAAATC ATATCCGTCT TGAGAAAAAG TCAGATTATT GTTCACTTCG 1920

ATTCCGCCAA CCGCGTTGAC TAATTCTTTT AAACCAGCCA TATTAATTGA AACATAATGA 1980

TTAATAGGTA TGTTTAAATA GTTTTCAACT GTGTCCATTG CTAAAGATGC GCCACCAAAA 2040

GCATAGGCGT GATTCAATTT ATCTTGTTTT CCTTGACCTG GAATATCAAC ATAGGTATCG 2100

CGAGCAAGAC TGACTAAGGT TGTTTGCTTG TCACGAGGAT TAACTGTTGC AACAATTGTT 2160

GTATCCGAAC GACCTTGCTC GACACGCCCA TCATCGCCTG TATCAATCCC TAATAATAAA 2220

ACAGAAAAAG GCTCCTTATT GTTTAAATTG ACCTGACTTT TTTTAGATCG TTCTACTGTT 2280

TCATAGGTTT TATCCATTGA TTTAGAAACA TCCCAATAAA GTTTTGCTCC CATtCCAaCA 2340

ACTGCAaGAA aTAGAmCCAa GATAATTCCA ArGATAATGG CAAAAATTTT CTTCCCTTTT 2400

GACATATTTT yCCTCCAATA ATTTATCACA GGTTGTGATT TTTTTCTTAT AGGTTAATCT 2460

TACTAATTTT TAGTGAAGAA GTATATAATA ATTGTTGAAA GACTATAAAA CTTTAAGGTA 2520

TTTTGCATTA TTTTTGCTTA ATCTTTTGAA ATATCTCAAT TCTATTAAAA TATGCGAATT 2580

AGTATATTAC ACGTTTCCAA TGTGTTTCAT TGTTGATTAA TTAGAATTTT AGTGGTATTT 2640

TTGTATTTGT AATTAGTACA GATTTTAATT GGAGGTATAA CAGTGAGTAA AAAAGGATCA 2700

GATATCATAG TAGAAAGTTT AATCAATCAC GAAGTGCCCT ATATTTTTGG GATTCCCGGT 2760

GCAAAAATTG ATGGGGtTTT TGATGCATTA GTtGACAAGG TCCAGAATTA ATTTTAGCTC 2820

GACATGAmCA AAaCGCTGCC TtTATGGCAC nAGGGaTTGG TCGTTTGACG GGAGAGCCTG 2880

GCTTAGTTAT TGCAACTAGT GGACCTGGTG CCAGCAATTT AGCAACTGGG TTAGTAACTG 2940

CGACTGCAGA AGGGGACCCT GTTTTAGCAT TGGCTGGACA GGTGAAACGG TCCGATTTGT 3000

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GTACAGAAAT TCAAGATCCA GAAACATTAT CTGAAAATAT TGCCAATGCT TACCGTATCG 3120

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GAATGCGGGC CTCTGCACGA AAAGTTACCG CAGCCATTCG TGAATTGGTT GCTATAACTG 3360

GTTTGCCAGT CGTGGAAACG TTCCAAGGAG CAGGCATTAT TTCAAAAGAA TTAGAAGAAC 3420

ATTTCTTTGG GCGTGTTGGT TTATTTCGAA ACCAACCTGG GGACCGTTTG TTAAAAAGAA 3480

GTGATTTAGT GATTGCGATT GGTTATGACC CAATTGAATA TGAGGCACGT AATTGGAACG 3540

CAGAAAAAGA TGCGCGCGTT ATTGTTATTG ATGAAGTTCA AATGGAAATT GATCAATATA 3600

TGCAACCGGA AGAAGAGCTA ATTGGTGATA TGTCTAAAAA TATTTTGAAA TTATCAGAAG 3660

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CATTTAGTGA ACCAATATTA ACAGAAGATG CGCAAGATTA TTTAGAAACG CTTCAAGAAA    3720
AATTAACGAT TAAAGAAGTA AAAACAAGTA CAATTGAAAA TCGATTACAT CCATTAGAAA    3780
TTGTTCAAAC GCTTCAAGAA AAAACCACGA ATGAAATGAC AGTTACTGTT GACGTAGGGA    3840
GTCACTACAT TTGGATGGCT CGCCACTTTA GAAGTTATGA ACCGCGTCAT TTATTATTTA    3900
GTAACGGCAT GCAAACATTA GGTGTCGCTT TGCCTTGGGC AATCTCAGCT GCACTAGTTC    3960
GTCCAAATAC ACAAATTATC TCTGTTTCTG GGGACGGCGG TTTCCTATTT TCGGCGCAAG    4020
AATTAGAAAC AGCGGTTCGT TTAAAGCAAA ATATCGTGCA TATTATTTGG AATGATGGTA    4080
GTTATGATAT GGTTAAATTC CAAGAAGAAA TGAAATATAA TCGATCCTCT GGCGTAGATT    4140
TTGGTCCAGT TGATTTTGTG AAGTATGCTG AAGCTTTTGG AGCCAAAGGG GTTCGAGTTC    4200
ATTCACAAGC AGAATTTGCC GCAGCTTTAG AAGAAGGAAT GCAAACAGAA GGCCCAGTGA    4260
TTATTGATGT TCCTGTGGAT TATTCAGATA ATCmAGAATT AGGTAAAaCA TTGTTACCAG    4320
ATCAACTTTA TTAGGAGATG GAAAAATGAG CGAACAATAT GTTTATCAAC ATGGTACGCT    4380
AGGCGGTTTA ATGGAAAGTT TGATGGCAGG AACGGCAGAA ATTGGTACGT TACTCACGCA    4440
AGGTGATTTT GGAATTGGGA CATTAGAAGG CTCAAATGGC GAAATTATTT TATTGGACGG    4500
TACATTGTAT CATGCAAATC AAACTGGCGA AATTACTATT CTAGAAGGCG AAGAATTAAC    4560
GCCATATGCC GCAGTTACTC GTTTTCAAGA AGATGGCGCA TTCCCTGTAT CAACGGAAAC    4620
CGATGAAAAT ATTAAAGCAC AAATTTTAGA AAAAATTAGT CCTAATTTTT TTGCGGCAAT    4680
TAAAATTAGC GGTCTTTTTG CGAAGATGCA TGTCCGTGTG GCACCTAAAC AAGAAAAACC    4740
GTATCCACCA TTTGTAGAAG CAGCACGCAA TCAACCTGAA TTTACAGCGG AGAATATTCA    4800
GGGAACAGTT GTAGGGTTCT TTACACCTAA ATTATTTCAT GGTGCCTCTG CCGCAGGgTT    4860
TCATTTGCAC TTTATCAGTG AGGATCACCA ATTTGGTGGG CACATTCTTG ATTTTGGCAT    4920
TAAACAAGGG ACTGTTTCGT GGATGGAAAC AGCAGAATTG CGACAGCATT TTCCAGTTCA    4980
TGATGCTGAT TATCGGAATA AAGAAATTGA TATTGCAAAA GCTTTGTCCG CAATTGAAGA    5040
AGCGGAATAA CTGAATAACA AGGCACATTT CTCCACGscC ATTCAAGTTG ACTAACTAGG    5100
TCAACTTGAA TGGGCTTATT GCTGTTCGTC GCTTTTTGTT GTTATTTTTC AAAAAAAAAT    5160
AGTATCCTTT TTATAATAAG CAAATAACAA TTGGAAAGGA TGGCGTAATG GACACACTTT    5220
ATAGAAGTTG GCAATTGTCT GGTTGGCTCT ATCATGATAT TTTTGTTATC ATTGTAGCAA    5280
TTATTTTTAT AGTAATTAGT GGTATTTTGG TTATTTCCTT AATAAGAAGG CGGAGTACAA    5340
GGAGACTGGT TCCCTATGCG TTAATTTTAT TGGTTTATCT TGCAGTGGTA CATTTTGCTG    5400
GTTTAATCTT TTTCGGAATG TTTCGTTCAG TAACGATTGA AGAGAAAAGT GCGACGTTTT    5460
ATTCTGAAAA AACAAAAGGC TTAACTTCAA TCGAGCGAAT GATTATTCCA AATGGACGAA    5520
CGAATGGCAT TAGCACCAGT AACTCATTGT TCCCAAGTGG ATTTCnGTTA ATAGTCAGAC    5580
GGGCCGAACG AATGTGGnAG TAAACGTTTA AGTTGGCCGT GATTAATTTA ATGGnCCAAC    5640
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AGATCCATAG GGGGTTTTGA nAA 5663

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAACAGCATA GACAGCAATT GAGTTATGGC CmCgGTTtGA AGcwTwAAGG rAACgGCCaT 60

CAGArGAAaT ACGrATCGsA GcmCCmCCmT TAAACsCATC ATAATCAGCA GGTAAAGTAG 120

AAACTTTTTG TAAtTCaGTG AAAGaACCAT CTGTTyCATC ATATGAAAGA ACTGAAACAG 180

TGCTATCTAA TTCACCAAAT AAATAAGCCA ATGATTTTGT TGGGTGGAAC ACTAAATGAC 240

GTGGACCAGT CCCTGGCTCA GTCACGAATT GAGCGATTTC AGAAAGCTTT CCATCTAAGC 300

TAACATTATA CGTATACACA CGATCGGTTC CTAGATCACA GACGACTAAG CGTTGATCAG 360

GCGTCAAATC TGTGTAATGA ACATGGGCAT TGTTTTGGTT TTCATGAGGA CCAGTTGGCT 420

CTGTATGAAT CACTTTGTCA GCATCTTCCA AAGAACCATC TTCTAAGATA CGATACACGT 480

GAACGATACC TTGGTGATAA TTTGCTGCaT AGACAAGTTG TCgGTtyTCG TCaACAGCTA 540

cATAAcATGG CGGCGCACCT TCCtCaGTTA CTTTAtTCaA TAAGTTAAAA tGGTCCATTT 600

CTGGTTGATA AGCGGCAGTG CCACCTTCAC CGTCAACACT AGTGACGCTA AAAAGTTCGC 660

CCTTTTGACT CAGAGCAAGA TAGGTAGGAC TCGTTTCTTC TAACAAAAGT GTCGCTTCTG 720

TTAAACGACC TTGTGTCGTA TCTAATGCAA TTTTATAAAT GCCTTGGCTG GCTCTTCGAG 780

TATAGGTACC TAGTAAAATT TGTTCTAACA TCACAATTCC TCCAATTTGT TTCAACACAA 840

TCACTTTTTA TGAAAGTGCT TTTATATAAT GTAGTATACC aTAAGAAGTC TAAGAACAAT 900

AAAACTTTCT ATCTGAGATG TTCgCaTTTT AAAgtGGTTT GtGCtATTAT GaTGaGaGAC 960

tGTGaTGACa GTCaTTTTTT gaTTTTTAGA GGGGTGACGA ACATGTACGA CaATACgGAT 1020

AATAACGGgA CCGTTCGTTG TTCATTTTGT GGGAAAACaC AAGAAGAAGT AAAAAAAATT 1080

GTTGCTGGTC CGGGTGTCTA TATTTGTAAT GAATGTATTG ATCTATGTAA AGAGATTATT 1140

GATGAAGAAT TTTATGATGA AGCAGTCCGA GAATTAACGG ATGTGCCAAA ACCCCAAGAA 1200

ATTTTAAATG TTTTAAATGA ATATGTTATT GGACAAGAAC GTGCAAAACG CACACTTTCT 1260

GTTGCTGTTT ACAATCACTA TAAACGTGTG AATCAATCAG AAACAGCTGC AACTCAAGAT 1320

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TTCTTGGCTC AAACGTTAGC AAAAACATTA AATGTACCTT TTGCAATCGC TGATGCGACC 1440

AGTTTAACAG AAGCAGGTTA TGTAGGGGAA GATGTTGAAA aCATCCTTTT AAAATTACTA 1500

CAATCTGCTG ACTATAATGT TGAACGTGCG GAAAAGGGCA TTATCTATAT TGATGAGATT 1560

GATAAAATTG CCCGTAAGAG TGAAAATGTT TCGATTACTC GAGATGTTTC aGGTGAGGGT 1620

GTTCAACAAG CCTTACTAAA AATTCTTGAA GGAACAGTTG cAAGTGTACC ACCACAAGGG 1680

GGCCGCAAAC ATCCACATCA AGAATTTATC CAAATTGACA CAACGAATGT TCtCTTCCAT 1740

CGTTGGTGGG AGCATTTTGA TGGGAATTGG AAACCATGGT TTAAAAACCC GCCTTAGGC 1799

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGCCAAGTTC GTCAATAATC GGTCAGATTG TTTTCAATCA GGAAAtcAcG TTTTcGCCGC 60

TTCTTTCAGg TgAAAATTTT CGCCCAGCGT TCATAGCCTG CGCCnTTTtC CGGCGGCAAG 120

TTTCGCCTGA ATGTCAATCA GGAGATTGAC CTTTCTGCCG GTTCGCTTCG GCGCTGTTTT 180

TCCTGACGTC AAACGTCTGC GCTGGCTGGT AATTCTGGCG CGCAAGGCGG TCTTGGTATA 240

ATCGTCGCCC AGCCGGTTCA CCCTTGTAGG GCGATCCCAT CCGGGCAGAC GGAATCCGGG 300

ATTTTTGCCG TCCACAACCT CATATCCCTC AGCCCGCATC TTTGCCAGAA ATTCCTCATA 360

ATGATTGCAC TCTGGCAGCA GCCGGTCAAT GGCTTGCTGT AACTGCTTTT TGTGgCTGAC 420

GCCGTACTGC GCCGCCGCCA TTTCCTTTTG GGGCCTGGCT TTTTTCTTCG GATTCTCAAT 480

CACCGAAAGG CCGTGGGCGC GGCACAGTTC ATCATTCATG CGTCGCAGGA TAAAAGCGGA 540

GTTTTTCACG TTCTGGAATT TTGCGTCACA GTTCAGGTTG GTGCTGTTAA ATTCAATGTG 600

GGTATGGATA TGCCGCTTAT CCGTGTGGGT GGCCACCACA AACTGATGCT GCCCGCCGGT 660

AAATTTCATC GCCAATTCAC AGCCGATTTT GTGCGCCTCC TCCGGGCTGA CTTCATCGGG 720

TTTGAATGAC TGGATAATGC GGTACATGAT AATGTCATGC TTTTCTGAmC TGCTGCGCCC 780

GGTAAGCTGG GCGTACAGTT TTTTGCTGAT TTCAAATTCT TCGGCGGCAG TTTCCGGGCT 840

GCACATATAG GAGGAAACCA GTTCGCCGCC GTCTGTCTTT TCTTCTTTCT GGTCATAGTC 900

GTGGCGTTCT GCCATTGACT GCTGACGGGT GCGGTTTTTC ATAATCTCTC GTGGTAAAAT 960

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AGCATGGGTA GCCTACTTTT GCAAGCCATA TTTTGTATGC TTGATACnAA AGGGGGGCAG 1080

GATACAGCTA TGGATACGAT TTCAGCGATT AAGACCCGGA TACTCCGTTT ATGTGCGGAG 1140

CGCAACATTA CCATCAACAA ACTGGCTACG ATGTCGGCGC TGCCGCCATC CTCTGTCAAA 1200

AACATCTTGT ATGGAAAGAG TACCGATCCT AAAATTTCAA CCATCAAGAA AATATGTGAC 1260

GGTTTGGATA TGACGTTGAT AGATTTTTTC GATGCGCCCG AATTTGAAAA TTTAGArCCG 1320

GAAATTAAAT AGCGTTACCG CGCCGCGTCC CGCTGCCGCT GTGCCGTCCG TACCGCTTTA 1380

ACGTGGGTGC AGAGAAACTC GTTATAGTCC TTGCCCTGCT TCGGCGGGTT GGGGTAAACC 1440

AGCTTCACCC GCCTGGAAAG TTCCGCATCG TTCTGGATTT CCTGGGTGAG CCGTTCCATG 1500

CCCTCCAAGC CGGCCTTGTC ATTGTCGAGG CACAGACTGA CTTGGGTAAC GTGGGGGTGG 1560

TCGTGAAGAA ACTGTATCAG GGCGCGGGGG CCGGTTCCGC CCAGGGATAA ATAATGGCTG 1620

TCCCGTGGTT CGCCGCCGGA CAGCTTTACT AATGTGGCGA GGGAGAGCGC GTCAATAGGG 1680

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TCGTATAAAA TCCCGGCTTC CATGCACACG CCAAGCAGTT CCGGGTCAAT GCCGCGATCC 1920

TGCAAATAGC CCACAACAGC GGATGCACAT CGGCTGGCCT GGGGCAGTCG GAAGGGCTTT 1980

GGCTGTTTTT CTTTTATGGG CGGCGCTTTT TCGGGCGGTG GCGCACAGTA GCCGCACAGG 2040

GTTTCCACCG CGCCTACAAA GTCCATGCCG CGCACCTTGA TCAGATAATC AAGGGCCGTG 2100

CGCCCACCGA TGCCCCGGCT GTTCCAGCAC CATTTCCCGT TGGAGATTTT TAAGCTGTCA 2160

TGGGTTCTGG TGCAGTATTC GCGGGGGCCG CTTTTTTTCA GTTCCTGCGG CTCATAGGCC 2220

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GCCAAGTAAT CACCTCCAAA TATGAAAAAA GGGCGGCGGG AGCATCTTTC TTTTGCCCCC 2340

GCCGCAGTTG TTTACAGTGc TTCAAATTTC TTCAGCAGGT CGTTCACGCC CTGCCAGATT 2400

TCAGAGTAGC CCTGCCGCAA GTCCTCCACA TCCTGCTCAT AGAGGTTGTG GGTGCTGTTG 2460

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GCTTCATGGT GACGCGGAAT TTGCTGCCGT CACACCTTAG CTGCATGGGA AAGCCGCGAA 3180

ACTCGCCCAA ATCCACGGTT TTTTCCGGGT CGTCCATCAG CATACACGCT TTAATCACCG 3240

cTTCGCCCGC CGCCTTGCGC TCCGTGTAGG TCTGCCCCAT GACAGTCATG GAAAACGCAT 3300

CGTCCTTGAC CGGGTGGGCC TGCACGGTTG GCAAATCTGC CGTCAGCGCT TCGATTAACA 3360

GCTTGGTTTC CGCGATTTTC TGCGGGTAGT ATTTCAGCGC TTTGTCCTGC ATTTCGTACT 3420

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GTTGGGAGGT GTGGTTGGCT TTGAGCATTT TCAGCTTGGA AACCTGCACA TCCAAATCCA    3480
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CAGTGGCGTC CACATCCTCG GCAGAGCGGG CAGGGCTTTT AGAGGTCATG ATCTGACCGA    3600
TGAATTTCTG TTTGTTTTCC ACCAGCCCCC AGTTGTAAGC GTCGAATGTA CCCTTGGTGA    3660
CATACTTGAA CATTTTCACC GACGCATTCA TGTTGCCCTG GCGCAGAGAT CGGCCCGCCC    3720
GCTGTTCCAA ATCGGCAGGA CGCCAGGGGC AATCCAGGTC ATGGGACGCG ACAATGCGGT    3780
TCTGCACATT CGTGCCTGCG CCCATTTTTG CCGTGGAGCC GATTAAGACA CGCACCTGCC    3840
CCCGCCGCAC CTTGGCGAAC AGTTCTGCCT TTTGGGTTTC CGTGTTGGCG TCGTGGATAA    3900
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AAATCTCCGT GCTGGCCTGC CATTCCTGCA CGATATTTTT CACGCAGGCG TTGACCTTGC    4080
TGTCCGGGTC GTCGGGCAGG AGCGGATTTT GCAGCCGCTG ATCCAGCGCC AgCTTGCGCC    4140
CGTCCGAAGT AATCCGCAGC ATATTGTCGA TATGGGGGTC AACCTGCCCG CCGCGCACAC    4200
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TGACGGTGAT ATATTCCGCC TTTGGCACGG GGAGATTCAG CATATCGGCG GTCTGGATGT    4320
CGGCGGCTTC TTTCCAAATA GAAATAAGTT CCGGCAGGTT ATAGAATTTC GCAAACCGGG    4380
TCTTGGAGCG GAAGCCGCTG CCCTCCGGCT TTAATTCCAT CGCCGTGACC TTTTCGCCAA    4440
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ACAAGTTCTT AAAGCCGTGC GCCTCGTCCA CAAACAGACG GTCAACGCCC AATTCCTCAA    4740
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TTTTCTTTGT TTTCTCCATC TGCTTGATGG TGTAGCGCTC GCCGTCCTCC GCCTTTGCTT    4860
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CCAGCACCTT TGCGCCGGGG TACAGGCGCA AAAAATCGCC GCCCCATTGT TCCGTCAGGT    5100
GGTTGGGAAC GACGAATAGG GATTTCTGGT TCAGACCCAG CCGCTTGCCC TCCATTGCGG    5160
CGGCAATCAT TTCAAAGGTC TTGCCCGCGC CGACACAGTG GGCAAGCAGC GAGTTTTTCC    5220
CATAGAGCAT CCGCGCCACG GCGTTCTCTT GGTGGGTACG CAGGGAGATT TCCGGGTTCA    5280
TCCCAGCAAA ACGGATATGG GAACCGTCAT ATTCGCGTGG ACGGATGCAG TTGAATTTCT    5340
CGTTGTACCG CCTGCAAAGG GTTTCCCGAC GTTCCGGGTC TTTGAAAATC CAGTCCTTGA    5400
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ACGTTTCGCA CATGGCTTCC TGCTTCTGCT GGGCAATGGC GGTCTGCTTT TCGTTGAGGA 5460

CGCGCACCTC CTTTCCGTCC ACTTCTGTCT TATCAAATAT CCGTACATCC CGCTGGTTTA 5520

AGGTCTGCTC AAAGATTTCA TAAGCGTTGA TGCGCTTGGT GCCGTAAGTA GCATAGACGC 5580

GCACGTTATC CCGGTTGTCT GTGCTTTTTC CCTGCACGTT CCATTCGCCG GTGGTAGGGG 5640

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ATGCCGTCAG GTCTTTGGGC TGCACCTGTT CCAGCTTTTC GGCATTGATG GCAAACTGCG 5820

GGTTTTCCTC AGCGGCGGCG CGGGCAATCG CTAACTTGGC CCGGACGTTG CCGGAAAGGT 5880

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TGTCCCGGAT GCCGATCATG CCCCTGACGC GCTCCGTGGG GGTTTTGCCA AGGACGGCCT 6420

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TGCGTACAGT GGGGTCGGCG GGGATGCTTT CCAGTTCCTC GCCGTCTTGC CCGGAATCCA 6540

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GGATGCCGTC CTCTGTCTGC CCGACCTCCA CCCATTCCGG GAGTTTTTCC GGGATGCGGT 6780

CGCGCTTCTG GAAAAAGAGG ATGTCCGTTG TGACTTCGGT TCCGGCGTTG GCCTTGAACG 6840

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AGAAATCGTC CGGGTGGTCG GTGCGCTCAA ATCCGTCTAC CGTTATATCC GCCTTTTGGT 7140

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CCGCCAGTTT TTCGGGCAGC ATCCCGAAAA AGTTCCCGAT GCCCATAGAC GGCTCCAAAA 7260

CCGTCCCCGG CGTAAAGTCC ATCTGTTCCA CCGCATTGTA GATTGCCTGG ATAACGGTGG 7320

GGCTGGTGTA GTGGGCGTTG AGAACCGTGC TTTGTGCAGA CTGGTACTCC CCAGGGGTGA 7380

GCAGTTCTTT CAGTTCGGCG TATTCCTTTG CCCATTTTGG GTCGTTTGGC TCAAAGGCGT 7440

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TGGTCTTTTC GCCGCCTGCG CCTAAATTTT CATCGGTGAT GCGGAAGTTG TGGCGTTCCG 7620

GCTCCAGACG GAGCGGCTGT AAAATAATCT CGCTGGGGAA TACCCGGCTG TCCACTTCCT 7680

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GCTCCTGCTG GACTTCCTCT ACAAACTGCC GCACAAAGGG GATGCTTTCA CTGCGGAAAA 8280

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TGCCGTACTT GCCCAGCGGC ATTtCCTCCA TCTCGTCCTC CCCGTC 11266

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AATTTTAGTG TAGTAAAGAA GTACGTGAAT TTGATTTTGG ATATTGTATT AGGGATTTTA 60

GGAGTTTTCT TATTAGTATT TATGGCTAGT TATTTAGTTG ACCTCGCTAC ATATCTCATG 120

AAGCCAATGA CGCCGGATAA TTTTTCAGTT ATCATGCAAG AAATTATTTC ATTCTTTATG 180

TTATTTGAGT TTATTATGAT GATTCTTCGC TATATTCAAG AAGGACACCA TATTCCGATc 240

GTTATTgATT TTAATTgTTa ACCGCAATTT TACGTCAATT AATGGkTGCG CATGGCGATG 300

GCyTGCAGAC TTwATkGTtA wCTTTAwCAA TTCTTTTACT AGTGGTTGTG CTATTTATTC 360

TCGGGTTAAA TGGCAGCAAA TTTTAtACGC TAGGAAAAGC GAAAGTAGaA gAAGaTCACG 420

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AATGTTTTTG TTGACTGCTG AGTCTGCGAC ATCTGGCTCA TGGGTTAGTA GCAGAGTGGG 780

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TGATTACATT AGATAAAGCT TTTTTTGTAA CGGATTTTCG TTATaCGGAA CAAGCTGCGG 1680

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AACAAGCAAa CTGGTTTTAC TATcGTTAAA AACACAGGAC ATaTTTTTGa CGAAGTAGCA   1740
GATTTAGCTG AACGTTTGCA ATTAGATAAT TTAGCTTTTG AAGAAACGCA AGTTAGTTTC   1800
GCTGATTATA GCTTATTGGA AGAAATTTTA CCATGTGAAT TAGTTCCTGT AATGGGTTTG   1860
ATTGAAGAAT TAAGAGAAGT GAAAGATGAA GAAGAAGTAG CGATTATTGA AAAAGCGTGT   1920
GCCATCGCGG ATCAAGGATT TGCCTTTGTC TTAGAGATGA TTAAACCTGG AATGACAGAG   1980
ATTGAAGTGG CTAATCAATT AGATTTCTTC ATGCGTTCAA AAGGAGCCAG TGGTGTTTCT   2040
TTTGAGACAA TTGTGGCCAG CGGTCTACGT TCAGCGATGC CACATGGCGT TGCTAGCCaT   2100
AAAGTCATCG AAAAAGGTGA GTTAATCACT TTAGATTTCG GTTGTTATTA TGAAGGCTAT   2160
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TATGACATTG TTTTAGAAGC ACAATTAAAA GTGTTAGCAG AAGCTAAACC TGGGTTGACG   2280
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TtAAGAATCA TCCGTTGCTT AAAAGAGAAT CCTTAAGAGA CTTAGTGATT CATCAAATAA   3180
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CCTCAACCAG ACTTAAATGA ATTATTCCCA GAAGATGAAG ATGGAGAAGA GAATGAGTAA   3660
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AAATTGGCAT TCTGTCAAAG GTCGAAAAAC TGCCAGAAAC TATTTCAGAA GAAGAATTAT 4440

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AGCGTTTGAA AGAAGCAATG CTCTACTCAA TACACGCAGG TGGCAAACGA TTACGCCCGC 6780

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CGTCTCCGGG AGCTGCATGT GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGACG 7500

AAAGGGCCTC GTGATACGCC TATTTTTA 7528

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6682 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CAAAGAATAT TTTAGGAGGT TTTTACATGG CTGCAAAAGA AGCAAGTTTT GATGTAnTTT 180

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GCCTAGCGCT TCAATTACTA ACCCATCCGT TTCTGGGGTG TTTAATAATT CAAACATCCG 1680

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CTTTAAATGC TTGTAAATTT TCAACAGACA ATGCCCGCAA AACAGGATTA AAGACTGCGC 5940

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CTTTTGCCAA AGGGGTCAAT AC 6682

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GTAGCCTATG AAGTTGGCGC AATTTATCGT CAAACACCTC AGTTTAATGA TCCCGAACTC 14580

AAAGAAGATG CTTCAGATAA CGTGGAAAAT TACGTAACAG TGACTGTTGA AGATTCACAA 14640

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CATTTACCTT CAACATTGCC AAGTGGAGAA ACAGTTGCTG GAAGTCTAAC CAAAGCACAA 15480

CATGTTACGC GCCAATTAAA GAGCTTACTG GAAGGTCATG GTACGAGTGA AGCCATCAGC 15540

TATGCGTTGA CAACAGAAGA AAAATCCCGT CAATTTATGA TGAAAGAAAG TCAAACAACA 15600

CGTTTGCAAT GGCCAATGAG TGAAGAGCGT TCTGTGTTAC GTATGAACTT AATTTCTGGT 15660

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GCGAAAGCGT ACGATATTCC AGAAACATAT GTTGCTGAAT TAAACTTGCa ACAATTAGTA 16080

GCCATAGAAG CAGGCGGGGT TACTTATGAA GCAGTTTCTA AATTCCCAGC AGTTTCTCGA 16140

GACATTGCTT TATTAGTCGA TGAAACAGTT ACCAATCAAG AACTAGTTAA AACTATTTCA 16200

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GGTAAAATCA CATACCGCAT CGTTTGACCG TACGTTAATC CTTGGGAGTA AGCCGCTTCA 17580

AATTGCCCTC TTGGGACAGC TCCGATTCCT GAGCGAACCA CTTCAGAAAT GTAGGCGCCA 17640

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TCAATTCGTT TAGAAGTTAA CGCTGTTTTT AATTCTGGAT AGGAACCTAA TTCTTGATAA 18300

GTAAATTTGA TTCCTTCCTC TTGCGCTTTT TTCTCTAAGT TTTCTTTTGT CGTAGCAGAT 18360

TGTGCAACGC CGATTGTTTT TCCGTCTAAA TCTTTCATGC TGGAGAAGTT ATCCTCTTTG 18420

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TCTTTCGCAA TCAAGCGTGC AATATCTgGT TCCATTCCTT CAtTTTTGTn TGATCAGGAT 18660

TCATATAGCC AAAATTAGGA ATGCTTCTTT GACACCTACT TnAATnTnCC CTGCTTTTTT 18720

TAAT 18724

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAAAATTACG TGATTCGCTT AGCCTGACCA GACTTTTGTC TAAGTCTTAA AACTTGATAA 60

GTAATAAGAG GTCGGGACAG AAGTGCTTAA CTCCGAGAAC AAAGTAGGTA CTGTTCAACA 120

TCTATTTGCT TTGCAAATAG TGTTTCTCAG CAATAAGAAG AAATTTCCGA AAATTGTCAT 180

AAAACACAAC GAGGAACGAG TTGATGTTGC ATGATACACT ACACTCCGTT TCGTTCGCAT 240

CAATTTCTAA GCATGGAACA TGCTAGAATT GAAGGACCCG GTGTTCTTTA ATTTTTGGAG 300

ACCAAGTCCT TCAATTCTTA GTGATTTATC ACTTAGAGAT TGATGAGATC GGAGCTCTGC 360

GAAGTAGGTA TTGTTCATCA TCGAATCACT ACGTTCTTCG TGATTCTCAA CAATTTCGGC 420

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CTTCCATAAT TTCTTTTGCA GATTCATACG CACAAGGATA GCCCATTCGT GTCATGACTT 2520

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TTTGCACGCG CCGTTCTGTA TTTGTAAATG TCCCGTCTTT TTCTGCATAA CTGATGCCTG 2640

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TGGCGATCTG CTAAACCTTC TTTCAAAATC ACATGCATCA TGCCATTAGC AAATGCGACA 3300

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ATATCAGCAA TAGGATTAGT CATCGCACCA GAGCCTAAGG TTTGGGCTAA ACCATGGACC     3540
GAAGCCGAAT GACAAACACG GGCACAGTTA TCAACATTAT TGGTACCAAA AGCAGCACGC     3600
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GACAGATAAG TCATGGGCCC ATAAATCTTC GTAGGAATAC AAACAATCCC TTAACGTTGC     5040
GACAGCACCA ATTGGACCGG ATTGTCCACC GAAGTGAATA AATTTCAATG CTCGACCAGT     5100
TGCAGAGCCT CCGCCGTATT GCTCGCCATA AATTATTTCT TCTAATGGTG TTCCAAGGTT     5160
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ACCATCGGCA GTACCCATCT CTAAAAAGGC TTGTCCACCT TCTCTTAAAA TTACAGGAAC     5280
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ACTTGCAAAT GATTCAACAT TATTTACTAA TGTTGGTTGC AAATATAAAC CAACATCTGC 5340

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TGAATTTTCC CCACAAATAT AGGCGCCAGc ACCAGAAATA ATCGTAATAT CATAATTGAA 5460

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AAATAATCCC ACCAACTGAT TGTGGTACTT TGTGAAAAAA TTGCCGCTGG AATAATAAAT 7200

GCATTAGCGA CCACGTGTTG AAACCCACTT GGGGATTACA ATTCAAAATG AGAT 7254

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GGGGCCAATT TaGaAAATkG ACmATTGAAT AGAAAAGGaT GTGAACaAAT GGCaAAAGAa 60

ACAAATGTTA AgTTAGTCaC GGTGAGTGTT TTTGTGGCAA CATTTATGAC AGCCATTGAA 120

GGGACCATTG TGTCTACTGC GATGCCAACG ATTGTCGGCT CGTTACATGG CATGGAAATT 180

ATGAACTGGG TATTTTCAAT TTATTTATTA ACGAATGCGA TGTTAACACC GATTTATGGG 240

AAACTTGCGG ATAAAATTGG TCGTAAACCT GTCTTCATGA TTGGCATTAT CATTTTTATT 300

TTGGGCTCCT CGTTGTGTGG CTTTGCTCAA GATATGTTGA CTTTAATTAT TGCCCGCGCA 360

ATTCAAGGTG TGGGGGCAGG CGCAATTTTA CCAGTTGCGT TAACGATTAT TGCCGATATG 420

TATACATTGG ACAAGCGAGC GAAAATTTTA GGTTtAAACA GTGCCGCCTG GGGAATTGCT 480

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GTAACATTTG GTTGTTTAAG TTTGAGTGTG CTCTTTTTTG TAGCATTTGT GATGATAGAA 780

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TATGAAAAAA GTCTTAACGA TTGGGTTATC GATTCTATTA GTCGGGGCCA TCTTTTTAGT 1080

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TGGTTTTGGG ATTACTATCA CAACGACTAC GGTGACAGCA CAAAGTACAG TGGAGCCTGA 1200

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GGTGTCAATT TTTGGTGTGA TTTTAAATGc AGGAATGTTT GCGAAATTGG AAGCGAGCGC 1320

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CATCTAAGTA GGTTTTAACG GCTTGAATAA AGGCGGATTT TTGGTGGATG GAGTGTCGAA 2520

ATTGAATGCT TTCCTCCATG TACGTTAACT CATTGTCGGA TACATATTGT TTCATGTGCA 2580

ACACTTGTTC TTTTAAATAG TCATCTCCGT TCAACACTTG CGAAACGAGC TGTTTTTCCT 2640

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TCATTTCTGG TGAAAAACCT GCTTCTCTTA AAATGCCCAT CATTTGATTC AAATGGCGTA 2760

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GATAGAGATC ATAATAGTTT TCCATGAAGG CTAGTAAGTC AGAATACCAT TCACCACATA 2880

ATGCAGGTTC TTGAAAGTGC TCTTCAATCG CTTCAGCCAT ACTTTGAAGT AAGGCTTGCT 2940

TATTTTTAAA ATACCmATaA ATTGcGGGCG CCTGTACACC AAGCTGTTTG GCGACTTTAC 3000

GCaTAGAAAG TTGtTCTAAA GTGGGACTTT TTTCTAACAA AGAAAATGCG GCTGCAATAA 3060

TCGTGTCTTT TGATAATTTC GGTTCCATGA TTTTAGCTCC TATTAAACGT TATCTTCGTA 3120

AGTTTATCAA AAAGAAGGTA CACTTTATGA TAGGAAAAAC TTGTGAAAAA TTAACTTGTT 3180

CGCTTGTATT TTACCACTAA AAATGGTAAA TTATGAATCG GCCTTATTTT ACAGTGTTAA 3240

ATTGGTGAAG TCAATGAGCA AATTGATTTT TTTGTAATGG GGAAGAATTC GCAGACCAAC 3300

ACTGAAGAAG CAGGGAACTA TTTTAAGAAA GTAGGGATAA GATGGACCTT ATTATTCAAC 3360

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ACTTAGCTGT TGTAGGCTCA ATTTTCTTTG TGAGTAACTT AGTCAAGGAC GATCCAACTT 4140

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CTGTTGTCCA CGCAGATCGT ATTTTAGTAT TGGATAATGG ACGTTTAGTC GGGGAAGGCA 4980

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CATTTTTTAT GTCTTAACTA GTGCCGCTAG TTTCATTTAT AGTATTCTCT TTACACAAGT 5340

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ATTGGTTGGT GTCTTAATCA TGATGTTCCG TCAAAATGTG GAACTGGCAT GGGCCACAAT 5580

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AATGAATCGC TTTTATGATG TGAATGAAGG CGCCGTGACG TTTGATGGTG TGGACATTCG 6300

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AAATGAGTCA TTCTCATTTG CTTCTTTTTT TGCTATGCTA AATAGAAAAA GGAGAAATGT 6900

CAATGGAAAA AATGAGGAAT ATACGGCAAT TACGGCGCAC GTTTTTGTTG CTAAATACTT 6960

TATTTGTACT GAGTGTATTC AGAGAGAATC GATGGACAAA ATCGGCACTG CTTTTTTTGG 7020

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TGCTAAAATA AAAAGCAGCA GGGGGCGAGA AAACCATGGA AAAGCCnAAT nAACGCCnAG 7260

CTGGATTTAG AACGTACACG GGCCAATTAA TTTTAA 7296

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GATTAAATGT CCTTGCCTCT GTTTTTGAAA ATCCTAAATC AAGCCTTTCA CACCTATATC 60

TTTTCGGTAG TACATTCCAG GAAATGAGTA ATTATCCAAT GTTTGATAAA CTTTTTTGCG 120

GGCTTCTTCA AGAGTCGAAG CAGTTGCTTC TGCTAAAAAG ATTCGTCCGC CAGCCGAAAC 180

CAGAGCCTGT TCTGAACGAG TTACCCCTGC ATAATAGATG GTTGCACCAG ACATTTCTGG 240

CAATGGTAGA TTTGTCTTAT ATTGATTAGG ATAGCCTTCT GCTGCTACAA CAACACCAAC 300

ACTCGCTAAC TCATTCCATG CAATCGTTGG TTGCTCTTTC ACCAGCAATG AAGAAATTAT 360

TTCTGAAAGG GGACTCTCTA AACGTGCCAA CACAACTTGT GTTTCTGGAT CCCCAAATCG 420

AGCATTAAAT TCAATAACCT TGGGGCCAGT TGCTGTTTGG aTTAAACCAG CATATAAAAT 480

CCCTTGAAAC GGACGTTTTT CAGCCACCAT TCCTTTAGCA GTCGGTTTCA GGACTTGGCT 540

AATGGCTTGC TGAACCGCTT CTTCTGGGAC CTGAGGCACT GGTGTATAAG CGCCCATCCC 600

CCCTGTATTC GGACCAGCAT CCCCATCGAA AATCCGCTTA TGATCTTGAG CAATCACCAT 660

CGGATATACC TTCTCATTAG AAACAAAAGC CATTAAGGAA AATTCTTCTC CTTGCAAAAA 720

TTCTTCGATT ACAACCGTTT GACCGCTTGC TCCAAATTGT TGGTCCTCCA TCATCGCAAC 780

TAGCGCCCGT TTTGCGGCTG CTTTTGTTTC GGCAACTACT ACTCCTTTTC CAGCTGCCAA 840

ACCATCTGCC TTAATAACAA TTGGTACTCC TTGCTGTTCA ATATATTCTA AGGCAGGTGC 900

CAAACGTCGA AAGACCCGAT ATTCCGCCGT TGGAATCTGG TATTTTTGCA TAAAATCTTT 960

CGCAAAACTT TTTGAACCTT CAATTATTGC AGCTGCTTTC GTCGGGCCAA AAATCAGTAA 1020

TCCCGCTGCT TGAAAGGCAT CTACAATTCC TTCAATTAAT GGCGTTTCCG GTCCGACGAA 1080

TGTCCAATCA ATCTGATTAT CCTTCGCAAA TTGAATTAGT TCCGTTTGCT GCTCTTCACC 1140

GATAGGTACA GTCCGAATAT TATCACCACT CATACCAGGA TTACCTGGTG CACAATAAAC 1200

AGTCTTGACT TTGTCTTCTT GCTGTAATTT TTTGGCGATT GCATGTTCAC GACCACCACG 1260

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TTGCCATGCT TGGTCATTTT CAACAACTGT ATCCTGTTCT TGAATTAATA ACCCGCCCAT 1740

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TATCTCTAAA AAGATTTGAT GCATTTCAGC CGCAGTCGCT TGGTCCACTG GACGATTCAA 1920

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CAAAATCGTT TTTCCTGTTC CAATTCCACA TGGGTTCATA TGTTTAACAG CGACGACCGT 2040

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AGGATCAACC ACTGCTGTTA CGTCTTGATA ATTTTTTGCC GCTGAACGTA ACATGCTAGG 2460

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ACACTTTTAC AAATAAAACG AAGCGAATCA TTTCTTAACA ACGTGCCAGG AAGTAAGCCA 8460

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GTCTTTTTTT TGACCGTTTA AAGCTGTTGC TTGATCAAGA TATTCCACAA AAAGAACCGC 9660

AGCATTTTCT GTTTGATACA ACTTCTTCGC TTTTCCTGTA TACACAAGTG CTTTCTTTTC 9720

CATTCtTTCC CTCTTCTCGT TAGCTTCATG AACCCTATTC TTTCTAACTc AGCTGATTCA 9780

CATCaGACaA AAACTTACAT TAGTTACAAA AAAACaATAA TCGTTCGTGT TTGTCGAATG 9840

TAAAAATAAA AACTTGCTT GGAGCAAGCA TTTATTAAGT TACGTTCCAA ATACCAACAG 9900

TCTCAATTTC CTTTAACGTT TCTGATA 9927

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTCTGCmrT rCAGTAAGGG CGTTTTTGGC TGAAGCAAGA TATGAGGTGG ATGCCTGCAC 60

AGATGGAAAC GAAGCACACA CCAAGTTCTA TGAAAACACC TATCAACTGG TTATTCTTGA 120

TATTATGCTG CCCGGTATGA ATGGGCATGA ACTTCTACGT GAATTTCGGG CGCAAAATGA 180

TACCCCCATT CTGATGATGA CAGCCCTGTC GGATGACGAA AACCAAATCC GGGCGTTTGA 240

TGCAGAGGCA GACGACTATG TAACAAAGCC ATTCAAGATG CGGATTTTAC TAAAGCGGGT 300

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CTTCTGCCGG AGGATTTTAG GGTACTTTGT GACGGTACGG AGCTGCCCCT GACACGAAAA 420

GAATTTGAAA TCCTTTTGCT GCTGGTGCAG AACAAAgGCA GAACCTTAAC CCATGAAATC 480

ATTTTGTCCC GCATATGGGG ATATGACTTT GACGGTGATG GCAGCACAGT CCACACTCAT 540

ATCAAAAATC TGCGGGCGAA CTGCCGGAAA ATATCATCAA AACCATCCGC GGTGTAGGTT 600

ACCGATTGGA GGAATCATTA TAATGGAAAG AAAAGGGATT TTCATTAAGG TTTTTTCCTA 660

TACGATCATT GTCCTGTTAC TGCTTGTCGG TGTAACGGCA ACACTGTTTG CACAGCAATT 720

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CAATAACCAA TCCTTTGAGT TTTATATTGA AGATAAAGAG GGAAGCGTAC TCTATGCCAC 900

ACCGAATGCC GATACATCAA ATAGTGTTAG GCCCGACTTT CTTTATGTGG TACATAGAGA 960

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TATCTTTGCG CGGCAAATGA CAACGCCGAT CAAAGCCTTA GCGGACAGTG CGAATAAAAT 1140

GGCAAACCTG AAAGAAGTAC CGCCGCCGCT GGAGCGAAAG GATGAGCTTG GCGCACTGGC 1200

TCACGACATG CATTCCATGT ATATCAGGCT GAAAGAAACC ATCGCAAGGC TGGAGGATGA 1260

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CGGTGACTAC AAAGACCATT CTAAGTATCT GCGCGAATGC ATcAAAATGA TGGACAGGCA 1440

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CATAGCCGAA CCGCTGGACA TAGGGCGCAC GGTTGCCGAG CTGCTACCCG ATTTTCAAAC 1560

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CACGCCCCAG GGAGGTGAGG TACGGATATG GAGTGAGCCT GGGGCTGAAA AATACCGTCT 1740

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CATTCCAATG TGAATCATCA CAAACGGCAT ATGAAACAAT CTGGGGAAAA ACGGGCTTTT 2220

CTATGGGCGT TCATTATCTC GTTCACAGTC TGCACGCTGT TTTTGGGGTG GAGATTGGTT 2280

TCCGTATTGG AGGCAACACA GCTACCGCCC ATCCCTGCAA CTCATACAGG CAGCGGGACT 2340

GGTGTAGCGG AGAATCCAGA GGAAAACACT CTTGCCACCG CCAAAGAACA GGGAGATGAA 2400

CAGGAATGGA GCCTGATTTT AGTGAACAGG CAGAACCCCA TCCCCGCCCA GTACGATGTG 2460

GAACTTGAGC AGCTGTCAAA TGGTGAGCGG ATAGACATTC GGATTTCTCC CTACCTCCAG 2520

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TATAGGGCAA GCGGTCGTCA AAAGGCTGCG GGGATTTGGA TGCCGTGTGC TAGCCTATGA 4320

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ATACCCCGAT ACCTATTTTA ATTTTGCTGT TTCATAATGA AAGTATTTGA TTTTCTAATT 6420

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CCTTAGAGTT GTGTTCCAAT CAGTATTATC ATGCCGGTTT TTGAGTTTAA TATGCAATAA 7260

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TGCGTTAAAA AAAGTGTAGC TCCGCCGTGG GCATTATCCG CCCCGCTAAG CGCACTATCG 7440

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CCTAAGAAGC TTCCTGGCCy TTTTGTTTGT CGAATTTTGT TGAATGATAA CGAGAATTGT 7560

CGATGTCGCA GCCCGCCTTC ATCGGTTCGC AGCCCATGAA CTGATGAAAG GAGTAAACGG 7620

CTATGACCAA AGAATATTGG GTAGCGGTCT TAGAACAAGA AGATCGTnTG ATAAGTAA 7678

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4732 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AAACCACGGA TGCCTTTTGA AAATATTTTA AGTGAAAATC ACTACCAATC AGACAAATTG 1140

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GAAGTGATAT AACCATACGT AGGAGAATCA ACGTGAATAT CAATCGGACC AAATGAACCA 2400

ATCCCAATCG CTTTTAAAGG ATATTGTTGG AAAAATTCTA TTACTTTTTT CATTGTTTCT 2460

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ATTCATGGAA CTATTTGGGG CAAAGCGAAC ATTTTTTAGT GTCCGTTGTG CAATTTTTTT 3360

AGAGGATCCT TTTTTTATCA CTTGACCTTC TAAACGAACT TCTGGAAAAA TAGCAGCATA 3420

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CGCTAATTTC AGTTGGTTCA CCTCTGTTAA AGGAACATTC GCAGCACTCC TCATGGCAAT 3540

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(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GGGaaAATwt TTTTAtgkGc tATGGcGTAt TACtAGTTAC gTTGTTGCCC TAGTGTCCcT 60

TATTTAAAAt ATTTGGtGAA AAATCaGCGT TTATGGACcA TTGgATACGG CCcATTTCcA 120

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CGTTCATTTG CCAAGATGGC ATGAGTTACC AGATATTGAA TTATATATGG ATCAAGTGAT    600
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CTACAATCAA AAGCATTTAG CGTTTTTAAT TGCGATTACG TTGTTGAAAC AAGTGTTAAC    780
ATTGCCAGAA ATTAAGCAAG GCATTTTATT CCAAGGAGCT ACGGTTGGTA TTCGTGAAGC    840
gTACAATTTA TTTTGTCAAG AACAGGAACG AGCGATTTAT GTGATTGCTG CTCAAGCGCA    900
AGAAAAAGAA GTTCAGGCCA AATCACAAGA ACCTATGGGG ATTGAATATT TGGCTGTAAA    960
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AAGTGTATCA ACGTTTAGAG AAAGAAATCC CTAGTACTTC ATTACCTGaT GGTGCAACAA   1260
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TTTCTAGTGG TTTAAGTGGA ACGTATAATG TAGTTCGCTT GCTTGGAGAA CAAACCGAAG   1380
GACTAGATGT ATTTGTTTTA GATACAAAGA ACATTGGTAT CGGGGCTGGC ATTCAGGCGA   1440
TACGAGCAGC AGAATTAATT GAAACAGGAT TAGGATGGCA AGAATTACAA CAAAAATTAA   1500
CAGAAGAAGT AGCCAACGCA AAAGTATTTT TTAATGTAGC CACTTTAGAA TATCTACAAA   1560
AAGGTGGACG AATTGGTTTA GTCACTTCTA TTTTAGGGAA TGCGCTAAAA TTAAACCCCA   1620
TTATTTCTTG TAATGAAGAA GGCATTTACT ATACGGTGGC TAAGTCTCGC GGCCGTAAAA   1680
AAAGTCTTGA TAAAACGTTT GAGTTGGTGA CGAACTTTAT AGGTGAGGCA CCCCGTTTCC   1740
GTTTGGCAGT CGCTCACGGT GCGGCAGAGG AAGAAGCmAA AGCmATGATG GAACGCTTGA   1800
AAGCAGCTTT TCCACAAGCA GAAGAAATTT ACTTTGGAAC AATTAGTCCG GCATTAGTTG   1860
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AAATCCCCTC AAATTTTTTT GaGGGGrTTT TTCaTTTAAG ATTyCyCTTT TyCATAGrAA   1980
TATCaTTtAG CyGGaAAAAC aACGrAAATT wTwTTGaAAA TyTCACGAAT GTGTTACAAT   2040
CCATCTACAA AGGGGGAtTT TTTGTGaAAA AAGCAATAGC AGAATGTTTA GGAACATTTA   2100
TTCTTGTCTT TTTTGGGACA GGAACAGCCG TTCTAGGAAA TGGTATGGAA GGGATTGGAA   2160
CAACGGGGAT TGCCTTAGCA TTTGGGTTAA CAATCGTTGC TGCTGCCTAT AGTATTGGCA   2220
CAATTTCAGG TGCACATCTA AACCCAGCTG TTTCTATAGG AATGTGGCTT AATAAACGAA   2280
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TGACAACAAT GGAACTAATC TACTATGTAG TGGGACAAAT TGTTGGTGGC TTGATTGCCT 2340

CATTTGCTTT ATTAAGCATT CTAAAAGGTG CTGGTAAAAG TATTGAGAAC TTAGGTCAAA 2400

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TTTATCATTT ATTCTGCTGT TACTGATTGC GATTCAAATC ATTGGTGGCT ATTTCATTCG 3720

TGAATTGGAA GCCACTACAA TTTCCGATTT TAAAAAAAAT ATGGATTCCC AAGTTGTCCA 3780

ATTGTCAAAC ACGTTAAGTA CGCAGATGAG CAACAAAGAT CTCGAACGTA GTGACGTTGA 3840

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GAAAAAGAAT GATTATCGTG ATTTAAATGA CTTTACGAGT AAAAAATATC AAGCTTTAGA 4020

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GATTGGCGTC CTTTATGTGA AAAGTAATTT AGAAAATAAA TACCAAGAAA TTACCAACAC 4140

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TCAAGCCAAC GTCTATGAAG CGCCCATGAC TGTCAATAAG GCGCGCTTAA TGGGAATTAT 6000

CAATAAAGAG GGATTACAAT ATCAAGACGT TTCCGAAAAT ACGCTAACCA AACAAGGGCA 6060

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GCAGAAATTG TGGCTGCACA ATCGTATAAA GGAATTCCTT TTAGAGACGA CACGGCAAAA 7260

TTAAGTATTT TAGCAGATAC GTCAGGTGAA TTAT 7294

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nATTTCATCT AACTTTTTGA CGCCnTAACA CCCTATTATC ACTTTTTACA TCTTATTTCG 60

ATTTAAAAAT AACGATAAAA AGCCCGTTCC TAACAGAATT ACTGCTGAAA CATAATAAGG 120

GAAAAAGTGA TTGATATCAA ATAAAGCTCC TGCTGCCATT GGTCCTAAAA TATTACCAAA 180

ACTTGTAAAT GTCGAATTTA GTCCGTTGaT GGTTCCTTGT TGATCTCCAG CATGTTTGGA 240

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AAAAAAGGTT AATTGGATTA AACCCATTTC ACCTATTTTT TGGACGATTG CATCAAAGAA 420

AAACAACTGA CAAATCAACG CTAAAATACC ACTAACCGTA ATCACGATTG CTATTTCACT 480

TGTGGTAAAG CCAAAATTAA TAGTCGCCAT AATACTATAA ATAGATTCGA ACGCTTGCAG 540

GCCAAAAGAG GAAATTAAGA TAATCACAAA TAATGAGGTA AACATTGGAT TTCTTAAAAT 600

ATCCATAAAT GAACCTTTTT TCGCTTCAAC AGCGGCTAAA ATTCGTTTCT CTGGCTCCTT 660

CAAAACAGTT AATGTCAAAA TAAAACCAAT AAACGCTAAA AATGCGGCTG CAAAAAACGG 720

GGCGCGAATA CCTAAATAAG CaATAAAACC ACCAACTCCT GGTCCGATAA TAAAACCACC 780

ACTAATTGCG GCTGACACAA GCCCCATCGC TTTCGGACGT TCAGAAATCG TGGTCATATC 840

TGCCACAAAG GCTGTCACTG ACGGCATTAA TAAAGCGGCG GCAATCCCGC CTAAACCACG 900

AGAAATATAA AAACCGCTTT TCGCTTGGGC TAAACCAAAT AATAACTCAG AAATTGAAAA 960

CACCAACATG CCCGTTGCAA TCATTTTTTT CCGACCAATT TTATCCGAAA GGACACCTGC 1020

GATTGGCGAT GTGATTAATT GGGCAATCGC AAAAATAGAA ATCATCATTC CCATTGTGGT 1080

ACCAGAAAAA TGCATTTCTT CTTTTAATTG GGGAATTACG GGAATGACTA GGCCTACGCC 1140

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ATAGCCAATG TGTTCATAAA ATTGATGTGC TGCTGTACGC TGTTCCCCTG AATTTAAGCG 1500

AATCGCAGAC AAGTTACACT TTTTAgCTcC GTTcTAGTTT CGTCATTAAt TGtTTACCAA 1560

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AGGTCACGTC AACGGGAACT TCATAGCCCA ATTGTTCTTT ATTAATGATA GTTAACGCCG 1800

CTGCATCTGT TGGCTTCATT TTTCTAATCA AGGGTAACAC CCTCCTTTAC ATTCTTACTT 1860

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CCAGCCAAAA ACGGAATCAA TCGGTTTTCC TACGAGTACT TTTCCATATA ATTTTGTAAT 2220

CATAAGATGT GCCACTAGAT CCTCATCGTA TCCCATCATA TCTTCAATAT ATTTATTTTT 2280

ATTAGTCAGA TATCTGGAAC GATGTATCGG AGAAAAATGT AAATCGAAGG GAATCGGATA 2340

ACTCAAATTT ATTGTATCTT tTAATTGtAG CACAkGGAAT TCTAtCCCTT TTTTTGGkGc 2400

CCACTTATCT AAAATATTAA TTGTATAATC TAATAATTGT TTCTTCTCAT CAATAGTAAG 2460

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GATATATAAT CTTTGCGCTG CACCATAACC AGGATGCAGG CCTACTCCCA AAGAAACAGT 2820

ATCTGCATAA CTTTTGGCAA CATTTTCTGC ACGATTTAAT AATAACCGCC CCACTCCTTG 2880

TTTTTGAAAT GGTAAGAATA CATTGAAATC AGCTATTTCA GGATATAAAT TTTTAAAAGG 2940

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TGCCATAAGG nCCACGTCAC CGCTTCACCT AATTTCTCTT TCACTCGTTG nATCATTTCA 3360

GCTTGCGTTA AGTCTCGTGC AGGrAAATGT TGAACTTTAT CATTACTGAT TAAAAAAATA 3420

AA 3422

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCGGACCATC AAAATCACTT TTTTCCTGCT CTTTTnAAGA AACGAAnGGA CCCATGTCTT 60

TTCAGAAAAG TTTGTTACAA TnACAAGCGT AGAGAGGATG TTAGGGTATG GATAAAATGA 120

AAGCTATTAC TTTTTTTGAT TTnGATGGAA CTTTGTTAGA TGGAACATCG CAAATAACTC 180

CTGAGATTAC CGCAGCAGTG GCGGCCTTGA AAGACAATCA AATTTTACCT TTAATTGCGA 240

CAGGACGGAC CTTGTGTGAG ATTCAGCCAA TTATGAAAGC CAGTGGCATT GATTCTGCGA 300

TTGTAATGAA CGGGCAATTT ATTCATTATG AAGGAAAAAC GATTTATTCA GATGAATTTA 360

CAACAGAGGA ATGTGTTTCA CTGCATGAAC ATGTCAAACA GCGTGGTCAT GAATTGGCTT 420

TTTACAATGA GCGCCGTATT TTTTGTACAG GGCATACTGG CACAGTGAAA CAAGCCTATG 480

ATTATATTCA TTCAGCTGTT CCAGAAATTG ATCCCACAGG TTATGAGAAT GATGCCGTCA 540

ACATGATGTT GGTCTTAAGT CAACATGGCG ATGATGATGA ATATTACTAT GAGCGGTTTC 600

CTGAATTGAC CTTTTATCGC AATGGTCCTT TTTCAATAGA TATTGTTCGT AAAGGGGTCT 660

CTAAAGGCTC TGGTGTCAAA AATCTTTTTA ACACCTTGGG ATTAAACGGC ATTCCGACTT 720

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ATGCCTTTGG TGATGGCATC AATGATTTGG CGCTGTTTGA GGCCTGTGAT TATGGAATTG    780
CCATGGGTAA TGCGCGAGAA GAACTAAAAG AAAAAGCCAC CTTTATTTCA ACTAAAAATA    840
CTGAGAATGG CATTGTTAAT GGCTTGAAAA AATTTGATTT ACTATAAGAG AAAACTACCT    900
TCTTCTATTG ATGTACTTTA GAAGAAGGTA GTTCTTTTGT ATGTTCATTT TTCTTTTTCT    960
GCTGTGCACA GAGAGCTACT CCCACTACTT GAATCAGCAA AATCGCTCCC AACAAACAAC   1020
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GAAAACAATT AATTATTGAT ACATGCATTT TAGCTGGAAA AATTATGCTG GAAAGCGGAT   1440
CTGAAGTATA TAGAACCGAA GATACAATTA CTCGGATTGC AGCAAATGCT GGCGAGCCAG   1500
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CTTACCTCGA TTCATTCGCA GCCGCTTTTG TCATTGGTTT GTTGGCCTAT TTGGCTGTGC   1920
ATTTTCACTT AGCGGTCAAC ATCGATAATA TCATTATTGG TGCGGTAATG CCGTTAGTTC   1980
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TGCTAGTCAA ACCTTTGCAA ACTTTTTAGG AACGGTCGGG TTAGGAATCG CTAGTATCTT   2340
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GGTCAAAAAA TAAAAAAACA AGCTCATTTT CTGAGCTTGT TTTTTTATTC TACTTCTTCA   2640
AAGAACAGCA ACAAATCTTG TAGCGTTAAT TGTGCTTTTT CAGCAGCGTT TAAATCTTGA   2700
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CGATGGGTAA TCATTAAACA AGTTAAGTTC CCTTCTTCAA TCCGTTGTTC CGTTAAGTGC     2820
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GATAAATAAT ACTCCCTACA ACAATCGCCA TCAGCCGTTC ACCAAACGTT AATTCTCCAA     3600
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CGaTaAAACC AaTCCTAAAA TTTTCATGCG ATCCGTTTGA ATGCCAATCG AGCGAGCCAT     3780
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TAAAATAATT GGAATTTTTC CTTTTGTAAA CAGTAAACcA GTCACTAAAC CGGCAAGCAT     4080
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TGCTGAAACA ATCATCGCTT CTCCTACTTT CTTTGATAAT TAGTTAATCA ATTTCGATTT     4320
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AATCACATCT GTTTCCTTAG TCATCACTTG AACCGTTTGT GCAATTTCAT TACTTGATGG     4680
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CACAGCATAT GTTTTCACTG TCAATCCTTT GGCTTCAGCC GCTTTCTGCG CTTCAGCTAC 4740

TTGGTATCGA GAATTTTCTT CTGAGGAAGC ATAGAGAATA CCTATTTTTT TGGCAGCTGG 4800

TATCAATTCT TTTAGTAAAT CCATCTGGGC TGACAAAGGA GATTGATCAC TAACACCCGT 4860

GATATTACCG CCTGGCTTTT GATTGTCTTT CACCAATCCT GCACTAACAG GGTCCGTAAT 4920

GGCGCCTAAA ATGATTGGGA TTTCTTGGGT AGTGTTGGCT AAcGCTTGCG CAcTGGCGTG 4980

GCGATGCCAA TTAAAACGTC TGCCTTTTTT TGTACTAATT GTTGACTCAT GATTGCTAAC 5040

TTACTCTGGT CGGCTTGACC ATTTTGAAAA ATAATTTCTA AGTTTTTGCC TTTGTCATAG 5100

CCATTTTCCT TTAATCCTTC TTCGACACCT TTATAAATTT CGTCCAATGC GGGGTGACTG 5160

ACAAACTGCA AAACCCCTAC AGTAACTGTT TCTTTCTTTG AATTCGTCAC TTTTTGATTC 5220

ACAAAAAAAG CACCGATTAA ATAAATAGCT AATAAAGACA CGACAAACGT TAAACGTTTA 5280

TTTTTCATTT TGCATTCTCC TAACTGCCCT TTTGTTTGGC AACTTTTTCT TTTTAATAAT 5340

AAAACCATTA TCTATAGGGC GTTTCTTCCG TTGAAAGTGA AACTGAGATT CGTAATCCTC 5400

TGCTTAGTCA AAATCCAAGG AACACTTTTT TACAAATGTC AGGATTTAGC TGCGACGAGG 5460

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GCATCTACTC TGTCnCTTCG TGCCAATCGT AGTGCTTGTC AGGATTTAAC TGCGACGAGG 5640

ATCGCAACTT TGGTGAGAAT CGCAGGAGCA CTTTTCTACG AATGGGACAA CGTTCTCTTC 5700

GCTCACCTTG TACTACTCAT CATCTACTCT GTCACTTCGT GCCAATCGTA GTGATTCGTA 5760

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GAGGCTCGTT TTTCTTTATT TCAGCATATT TACCACTTAA TTGTTTCGGT TTCTTTCAAT 6180

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CGTCATTGAA ATTACTAATG CCATCGAAAA TCCCCTCTTT CTAATTCCTT AAAACTTTCT 6300

ACAATCTAAG TTTAACATAG CTAGCTATTA TTCACCAGTT TCTGGTACTG TATCAGTGCT 6360

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CGCGGTCTTT GCTGCTTCTT TTTCAGCTTC TTGCGCCGCT TTTTGCTGGT CTTTCAAAAC 6480

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GCCGCTAACA TTGTATTGCT CTTGTGCTTT GCCAGCATTA TAAATTAACG GATAGATATA 6660

CAGCGAACGA TGAAATTCAT TCATTTTATC TGAATTAAAC AGCTTCACCA TTTGATCGTA 6720

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CGATTCAACT TGAGCAGCTC GAATATTTTT TTGCATCGTT GGAATAAAAA TGATTGAGCC 6900

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TTTATTATGT CATTTGaTGG CGTATTTACT CATAGCATGG tTCATGAGTT GaCAGAAACA 7260

CTCGTAAGTG GCCGGATTTC AAAAATCCAT CAACCTTATG AAAACGAAGt CGTTTTAGTC 7320

ATTCGTGCGA AAGGTAAAAA CCATAAATTA TTATTATCAG CACATCCTAG TTATGCGCGC 7380

ATACAACTAT CTACAATTAC CTATAGCAAT CCGGAAACAC CTCCTAATTT TGTGATGATG 7440

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AACGCTGAAA ATTACCGTCG CGACGGAGAA CTATTAACAA CCTTCATGGC ACAAGTCCCA 8220

AAAGGAGCCA CCGAGGTGGA ATTACCAAAT TATTATGAAG AAAATGCACC GTTGCGTATC 8280

TCGCTAAATC CTGCACTTTC ACCTAATCAA AATGCACAAA AATATTTTCA AAAATACCAA 8340

AAATTGAAAA ATGCTGTCCG AGTTGTTAAA ACACAAATTC AGCAAACACA ACAAGAAATT 8400

TCTTATTTAG AGTCAGTTGT GGCACAACTT GAAATTGCGA CACCAATGGA CATTGAAGTG 8460

ATTCGTGAAG AACTGATTGA ACAAGGCTAT TTAAAACGTA AAAAAAATAA AAAACAAAAA 8520

CAGCCGAAAA AAAGCCAACC CGATCTTTTT TATGCCACAG ATGGCACACC TATTCTCGTT 8580

GGAAAAAACA ATTTGCAAAA TGATCAATTG ACTTTACGAA CCGCTAAAAA AACTGATTAT 8640

TGGCTCCATG CCAAAGATAT TCCTGGATCT CATGTAATTA TTCGTGACGC ACATCCTAGC 8700

GAAGAAACCC TTACTGAAGC CGCACTTCTA GCAGCTTATT TTTCAAAATA TCGACTTTCT 8760

TCACAAGTGC CTGTTGACTA TGTCCAAGTA AAACATGTGC ATAAACCCAA TGGAGCAAAA 8820

CCAGGTTATG TGATTTATGA AAACCAACGA ACGTTATATG TGACGCCAAC AGAAGAATCG 8880

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CGTACTGcCG ATTGATCGTA CGTTGTTTTT TTGCATTGGC AAAGACATTT ATCAAGTGAT 9000

AAATAACACA AGTAAGCTCA ATTAGTTTAC AAACTAGCTA TTTCTCtCTA TACTGACTGT 9060

TGGAGGTGAA ATTCATGGTC TTTTTACACA TTATTTTTGG GATGTTTGCC TTTATTGGCG 9120

CTTTAGGTTT AGGTGTCGCC TTCCGCGATA GCTTTACAGA ACTTTCAACA CC 9172

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTATTGATC GAGAAAATGA AATTCGAGAA TTTAAACCTG AAGAATATTG GAGCATTGAT 60

GGGAATTTCC AAAAAGGTCG CAAGAAATTC AAAGCAAATT TCTGGGGCGT AGATGGTAAA 120

AAGAAAAAAT TACCAAATGC AGAAGCGGTG AAAGAAATCA CTTCTCGGAT TGACGGTAAA 180

GATTACGATG TTACAAAAGT TGAGAAAAAA GAACGGAAAC GTAATCCTGC ATTACCTTTT 240

ACAACCAGTA GTTTACAACA AGAAGCGGCA CGTAAATTAA ATTTCCGTAC CCGTAAAACC 300

ATGATGGTTG CGCAACAATT GTATGAGGGA ATTGCTTTAG GGAAACAAGG CACTGTGGGG 360

CTGATTACCT ACATGCGTAC AGACTCAACC AGAATTGCTG ATTCCGCCAA AGCAGAAGCT 420

GCTGAATTCA TTGAAAAGAC cTACGGAGAT GAGTTTTCAG CACATGGCGG CCGCAAAGCA 480

AAAAATACGC AAGGTGCACA AGATGCCCAT GAAGCGGTTC GTCCGTCAAG CGTTTTAAGA 540

ACACCTGATG AAATGAAGAA GTATTTAGAT AAAGATCAAT TAAAATTATA TACTCTTATT 600

TGGTCGCGCT TTGTTGCTAG TCAAATGACA CCAGCGATTT TAGATACCAT GAaGGTCACG 660

CTTCAACAAA ACGGCGTAAC GTTTATTGCC AATGGCTCCA AAGTGAAATT TAAAGGGTTT 720

ATGCAAGTAT ATGTTGAAGG ACGCGATGAT GGTAAAGAnG ACAAGGAAAA ATATTTTACC 780

TGAAnTAG 788

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTATGATTAA GGCAACAACG CCCCAAGCAC GATATGGAAA TCCCACGCCA CGTGTAGCTG 60

AAACACCTAG TGGTATGCTA AATGCCaTTG GATTGCAGAA TCCAGGTTTA GAAGTGGTTA 120

TGCAAGAAAA ATTACCGAAA TTAGAAAAAT ACCCTAACTT ACCGATTATC GCAAATGTTG 180

CAGGTGCTTG CGAAGAGGAC TATGTGGCTG TTTGCGCAAA AATTGGGCAA GCGCCTAACG 240

TCAAAGCAAT TGAACTGAAT ATTTCCTGTC CCAATGTGAA ACATGGCGGC ATAGCTTTTG 300

GTACAGATCC AGAGGTTGCT TTTCAATTAA CACAAGCAGT CAAAAAAGTC GCCTCTGTTC 360

CGATTTATGT TAAACTATCA CCAAACGTAA CGGACATTGT GCCGATCGCC CAAGCAATTG 420

AAGCAGGGGG CGCAGACGGT TTTTCTATGA TTAATACATT GCTAGGGATG CGCATTGATT 480

TAAAAACGAG AAAACCTATT TTAGCCAATC AAACTGGCGG ACTATCTgGC CCAGCCATTA 540

AACCTGTTGC TATTCGCTTA ATCCGACAAG TCGCCAGTGT TTCTCAGTTG CCAATTATTG 600

GAATGGGCGG TGTTCAAACA GTGGATGATG TCTTGGAAAT GTTCATGGCA GGTGCTAGCG 660

CTGTCGGTGT TGGTACGGCC AACTTTACAG ATCCATATAT TTGTCCGAAG TTGATTGACG 720

GATTACCTAA GCGAATGGAA GAGTTAGGTA TTGAATCGTT GGAACAATTA ATTAAAGAAG 780

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CACGATGTTT TCTTGGATTT AAAATTACAT GATATTCCGA ATACTGTGGA AAAAGCGATG 1020

ACAAATTTAG CAAAATTAGG CGTTGCCATT ACTAATGTCC ATGCAGCAGG GGGCGTTCGA 1080

ATGATGCAAG CAGCTAAGGA AGGTCTAATC AAAGGGACTC AGCCAGGCGC TAAGGTTCCT 1140

GAGTTAATTG CTGTAACCCA GTTGACTTCT ACTAGTGAAG AAGAGATGCA CCATGATCAA 1200

TTAATCAACG TTCCTTTAGA GACAAGTGTC ATTCATTATG CTAAATGTGC GGAAAAAGCG 1260

GGTCTGGATG GTGTGGTTTG TTCAGCATTA GAAGCACGTG GTATTCAAGA AGCAACCAAG 1320

CAGACGTTTA TTTGCTTAAC ACCTGGTATT CGTCCAGCAG GAAGTGCAGT AGGTGACCAA 1380

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CGCAGGGATT CCACATGCGG CATGGGTAGC CGATATTTTA GGATTACCAA TGGTTTATAT 1800

CCGCAGTAAA GCCAAAGATC ACGGCAAAGG GAATCAAATT GAAGGCCGAA TTTCTGAAGG 1860

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AGAAGCGGCG GAACGTGAAG GAGCAACGGT TTTAGGCGTT GCGGCAATCT TCACTTATGA 1980

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AAGGTTCTTG TCGTCTGATT TTTAGTGTCA TTTTCAGTAA CCAGATTTAA CGGTAGGAGA 2220

ACTTAGGTCA TTTGCCGAGG AGCGTAATGA TCTAAGTTCn TTTGTTTGAC GTAGAAAAGA 2280

TGTTAGGATA GAGTTTTAAC ATGAGTTTTA CCTGATTACT ATGTGGAAAT GrAGGaAGAG 2340

TGTATGAAAA AAATAAAAAA TATGGACGTk GAATGGAGCT ATACAGGCCA ACGATGGACC 2400

CAGAACATTG GCATACGCTA TGTGACTGGT TTGCAGAAGG TGCTAAGTTT GCTTATCAAT 2460

CGCCAaTTGC TTTAGAAAAA GAAaGTGCTG AGACAGTAAA TTCTCAGATT ACGTTTCATT 2520

ATAAAAAAGA AGAATTCACT GAAAAAGAAT TCAAAAATAC GTTTCATTTT GTACCACCAA 2580

ATACGGAAAG TTACGTAATG TTTGAAAATG TTGCGTATCA TTTAACCGAT ATCCATTTTC 2640

ATATGCCTAG CGAACATTTG CTATCGGGAA AGCAGTATCC GCTAGAATTC CATTTGGTTC 2700

ATATGAACGA TGCTGGCGAA AATTTAGTTG TCGGTTGCCT GTTTACCATC ACAGAGGAAG 2760

AAAATCGTTT TTCAGAAGCG AATCATCCGA TGGACTGGGA AAACGGCACG CACCAACAAT 2820

GGTTTAATCC GTCAATCTTT TTACCAGAGG AGCGTCTACA CTACCATTAT GTAGGCTCGT 2880

TAACAACACC GCCAACTAAG GGTCCAGTGA AATGGTTTGT ATTTGATACC ATTCAAAAAA 2940

TGGATCAAGC CTTTTTAAAT AAGATTAAGG AAGGTATGTT GGCCTTTAAC AATCGGCCCC 3000

TTCAGCCGTT GAATGGGCGT AAGATTTATT TTTCAAATGA TTAGTGTGTG GAGGAAAAAG 3060

GGTTGAATAT TCAACAAATG AAGTATGTTG CTGCCATAGC TAACAATGGG AGTTTTCGGG 3120

AAGCAGCCAA AAAACTATTT ATTACACAAC CTAGCTTGTC AAATAGTATT CGAGAATTAG 3180

AAGAAGAACT AGGGATTTCC CTCTTTTTAC GTACCAATAA GGGCGCTTTT TTAACAGAAG 3240

AAGGAATGGT TTTTTTAGAA CAAGCAGAGA AAGTTTTAGT TCAAATGGAG TTATTGGAAA 3300

ATCGCTATCG CGAGACAGTG ACCAGCGAAC GATTCTCCAT CTCTTCGCAA CATTACGATT 3360

TTTTAGGTGA GGTAATTGCC AAAGTTCTTA AAAAGTATGG GGATCAATAT AAAGATTTTC 3420

GTGTCTTTGA AACCACGACC TTAAAAGTAA TTGAAGATGT CAAAGGATTT CACAGTGAGC 3480

TGGGGATTAT TTATTTAAAT GAACAAAATA GTGTCAGTAT TGAACGGTAT TTAGAACAAG 3540

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ATCCTTTAGC CAAGCAAAAA GAAATTCATT TAGAGGAATT AGTTCCCTAT CCACAAGTTC 3660

GCTTTAATCA AGAAGGAAGC AATTTTTCCT ATTTTTCTGA AGATTTAGTT GAAATTCCTG 3720

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AATCAGTCCA ATTGGTCGCT ACTTTATCAA AGAnTTAAAA GcGTTGTTtA AAAAAgAGGT 3960

AGATACCAAA ACATTTmGCa CTAAGGaTaA AAAGAAGAGg TCGGGACAGA AGTGTTTAAC 4020

TCCGAGAAAT AAGAAGGAAT TTCCGAAAAT TGTTCTTTAA TTTTCGGAGA ATTTCGGCTT 4080

ATTTCCGAAG GATTTGCTTC TGTTCCCGCC GTTTATTAGT TTTTGAGCGT GGAGCAAAAA 4140

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GTTkCTCTTT CAATTAATGT GACAGGCACT TGAATGTCTT CTATGATTTG AAGGTCTTGT 4260

TGCATCGTTT GTAATAACAC TTCACCAGCT AGTTTTCCCA TTTCTTTAAA GTC 4313

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTnTTnCAT GCGATAAATG GTATTCCTGG TTTATCAGCC GTGAAGCCTA AAGCAGCTTT 60

CTATATTTTT CCGAAATTGA TACGGCCAAA TTTGACTTTT ATGATGATGA AAAATTTGTT 120

TTaGATTTCT TACACAAACA TCATATTTTA TTAGTCCATG GTGGTGGGTT CAACTGGCAA 180

CAACCCGATC ACTTCCGTAT TGTTTATTTA CCGAAGATGG AAGACTTAAA AACTACAGCA 240

GATAAAATGC GTGAATTTTT AAGTACCTAC AAACAAAAAT AAAAGAACTA CCAAAAAATA 300

GCCTCTAACG AAGCTATTTT TTGGTAGTTC TTGTTTTATC AACAATACTA TTCTGCGGTT 360

TCACATGCTT TTTTACTAAT AATCATTCGG TTGGTATATT TTTCTTCCAT ATCAGGACTA 420

GGATTTGCTA CTACGATGAG ATAAGAATTT TCATACTCCT TCTCCACAAA GCCTGAATAA 480

TTTGTTTTTT CCCAAATGAA GTGAACCTTT TTCTCTTCGG CCATACAATA ACACTCCTTT 540

TTAATAAAAA TGAACCTATT TATTTTCTAA GAAAACCTTA GATAATGTTC TTGCAGTATA 600

TTATGCAATA AAGTACAATA AAAGCATAAT GCGAATTCGC ATATTTTGAC AAAATCCCCA 660

TTTTGCAAGG AAAATGGCCG ATATAAATAG GAGCTATTGT GATGAATTCT TTAGGTGCAG 720

TTATTAAAGA AATTAGAAAA AATAGAAAAT TGACACAGAA AATGTTATCA GAAGACATCT 780

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TGCAACAACT TTGTGATCGT TTAGGTGTGA CTGTTGATCA GATTATGCGT TATAAATCTG 900

GTGATGTGCA CGTTGTTACG TATTCATTTG AAAAAATGGC TGAATATTTT CGCCATAAAA 960

AATATCAATT ATTATTAAAT TATTTAAAGG AAAATCGTAT TGAAGAACAA TTGTATTTAG 1020

ATACGGACTG GCAAAAATAT TATTATTATT TAGGtAGTTG TGAATTGTTT GTTCTAAATG 1080

ATTATGAAAA AGCTATTGCT AGCTTGCGTA AAGGGTTATC TTTCACCTAT AAAGCCGATA 1140

AGTTAAATGT TTCTGATTTA GAGATTCAAT TAATTAGTTG TCTAGGTGCC ACTTATGGTT 1200

ACATGGGCAA TCGAGTAGAA GCAGAACGAT TTTTAAGTTT GAGTATTCAT TATTTTAATC 1260

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CAAGGGgACG TAAAAATTAT TCGTGAGGAA GGCAAATGGA TTGCCCCAGG TTTAGTCGAT 1800

ACTCATATTC ATGGTTACAT GAATCATGAC GTAATGGATA ACGATGCAGA AGGCATTAAA 1860

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ACCTTAGAAG AAGCTGATGT GGCAGTTGAA GCAGGCGCTA gCGTTTTTGT TCATGCATAT 2280

AATGGGATGC GCGGCTTAAA TCACCGTGAA CCAGGGATGG TTGGTGCATT GTTAACGTTA 2340

CAACACGTTT TCTCTGAATT AATTTGTGAT GGACACCATG TACATCCGCA AGCGGCTGAA 2400

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GGCGGTATGC CAGATGGCAA CTATAATTTA GGTGAATTTC CTGTTGTGGT AGCAGAAGGA 2520

ACGGCTCGTT TGGATACTGG GAACTTAGCA GGTAGTATTT TAAAACTAAA aGAaGCAaTT 2580

AAAAATGTAG TTGATTGGGG TATTGCAACA CCTGCACAAG CAATTATGAT GGCTTCATTA 2640

GTTCCtGCGA TTAGCTGTAA AATTGATGAT CAATGTGGCA TGATTGCAAA TGGTCGCGAT 2700

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TTATAATTCT TTTGGTAAAA TCGCAGAAGT GATTTCTTTG TTCTCGTAGG CAATAAAAAA 2880

ATCGATTAAT TGCTTGTCAA ATTGCTCAAT ATCCTCTTTG TAAAGGGAGC TAGGAATCAC 2940

AAAGGTTTGC TCTAGGGTGC CTGCTAGATA ATCGCCATCT AAACTTTGGG CGACAACTAA 3000

AAATTCTTGT TCGCGCCAAT GTTCCACATC TGTTTCAGAA ATGGTTTCTG GAGAGGCTAA 3060

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CTCTTCTTGA GGTTGAGAGA GGATTGCTTG CAAAAATGTT TGTGGTTTTG CATCGGGTAA 3180

TGTTTCTTTT AGCTGTTCAA AATCCAATGA AAGTTCCTCC TTATTGTTTG TTTAAAATAG 3240

TTACTGAAAA ATCAATGGGT GAATTTGTTT TAAGGCTTTT GGCTTCTAAG ATGATTTTTT 3300

CAGCCAACAA ATCGTTTCCG TTATATACAG GTGTCACGCG ATAGCGAACG GTTTCGCCGC 3360

GATTAAGAGC TGCCCGAATC TGATTTTCAT ATTTCGTCAT ATAAGGAGTG TTGACAGGAT 3420

TCTGATACAA GGTGGTTAAG TTACGTGGAT CATCACCACT GCCTCCCATT TGACGGCCGA 3480

TTAGGTGGCC ACGCGAATGA TTAGCTTTTC CTGAAATGAA ACCAGCTGGT CGAATATCTT 3540

TATTAGCGGA AGTTCCTGTA TTGACCATTG CGGGTTTTAA TAGCGCATCA GCGCCTGTCG 3600

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AAAATCAAAA AAGGCTTTTC TTTGAAAGAC TTGTTTTCTC AGATATGTTA CTATTTTAAT 4020

GTAGAAGGGa AgGGATAGTG GATGGCCTAT ATTGAAGTCA AAAATGAATA CAAGCGTTAC 4080

CAAATGGGAG AGACAACTAT TACTGCGAAT GACGGCATTT CTTTTGAAGT GGAAAAaGGA 4140

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AATTTTCCAG CGCAACTTTC TGGTGGTGAA CAACAACGAG TAACCATCGC CCGTGCGATT 4500

GCTAAAAAGC CCAAGTTACT TTTATGTGAT GAACCGACAG GAGCGATGGA TTATGAAACA 4560

GGGAAACAAA TTTTAACCAT TTTGCAAAAC ACTGCTCGTG AAACTGGAAC GACCGTCTTA 4620

ATTATTACCC ACAATTCAGC CATTGCAGAA ATGGCCGATC GGGTAATTCG AATTAATGAT 4680

GCGAAAGTTC GCGAAATGAC TGTGAATGAT CAGCCTAAAT TGGTTGCTGA AATTGAATGG 4740

TAGGTGCCTA AAATGAAGAA AACAGCGCTA ATTAAAACAA GCTTACGTGA AATTAGACAA 4800

TCTACTACAC GATTTTTATC GATTATGGGG ATTATTTTCC TTGGTGTAAT GGTCTTTGTT 4860

GGTTTGAAAG CTACTGGACC AGATATGATT AAAACCGCGA ATAATTATTA CCAGAAAGAG 4920

CAGCTTCCAG ATGCGCGAAT AATTTCTACA ATGGGACTGG AAAAGAAAGA TTTAACAACA 4980

CTACAGTCTT TAAAAGATGT CGAAACAGTT GTGCCGCGGT ATACAATAGA TGCCACGATT 5040

GGGCCGCAAA ATAATGCAGT AAAATTGTTT GGCTATCGAA AAAATCAAGC AGGATCGGTT 5100

AACTATCAAG TAGTTGACGG TCGGTTACCT AAACAAACAA ATGAAATTGC ATTAGATACA 5160

TTAGCGAAAA CTAGATATGA CTATAAAATG GGTGATAAAA TCACTTTAAA CGATGCAGCG 5220

ATTAAAGAAA AAGGGCTGAA ACAAACTCAT TTTACTGTTG TTGGATTTAT CAATTCACCA 5280
GAATATATTG ATAATACATC CAGGGGAACC ACAACGGTCG GGTCTGGAAC GTTAAACTTT 5340
TTTGGCGTGG TTTCGGAAAA AGCCTTTGAC AGTCAACGGT ATCCAGAATT GCTAATCTCA 5400
TTTCGTTCAT TAAAACATCA AAATACGTAT TCCTCTGATT ATGAAAAGAA AAGAGAGCAG 5460
GCCTTAAATC AAGTAAAAGA GGCACTGAAA AATCGGCCAG AAGAACAGGT TGCGGCTCTG 5520
CGTGATTCGG CTCAGCCGGA CATTAACCAA GGTCGGCAAG CGCTGGAAAC GGGAAAACAA 5580
GCACTTGCGC AGTTGGaGCA ACAACCAGGA ATTCCAGCTG AGATGCTTGA AAAGCAAAAA 5640
GACGAATTGG CTAAACAAGA ACAACTGTTG GCTGAAAAAG AAACAGAGCT AGCCAATTTG 5700
AAAGCCCCaA CGTATTATTA TTTTACTAGG GAAGACAATC CAGGATTTTC TGAATATCaA 5760
GATAACGCTG ATCGGATTTC TTCTTTAGCC ACGCTGTTCC CGTTGTTCTT TTTCCTAATT 5820
GCGGCATTAG TCAGCTTAAC TACCATGACA CGTATGGTTG AAGAAAAAAG AATGGAAATT 5880
GGTAGTTTGA AAGCTTTAGG TTATCGTAAT CGTGAAATTG CTTCGATTTT TATTACCTAT 5940
GCAACGGTTG CCAGCTTAAC AGGTGCATTA TTAGGATTGG CAGTTGGCTA TTATCTATTC 6000
CCTAAAATAA TTTTTGATGc CTACGGTCAA ATGTACAATA TTCCTGATTT AGTTACACCG 6060
TGGTACTTAA ATTACAGTTT ATGGGGCATC ATTGTAGCCT TAGCTTGTAC TGTGGGAGCG 6120
GCCTTAGTGA CATTAAGAAT CGATTTATTA AGTACCCCAG CTACCTTGCT AAGACCCAAA 6180
GCGCCGAAAG CAGGCCAACG GATTTTACTA GAACGAATCC GCCCTTTATG GCAACGCATG 6240
AGCTTTATTC AAAAAGTGAC CGCTAGAAAT CTGTTCCGCT ATAAACGACG GATGCTGATG 6300
ACCGTTATCG GAATAGCTGG TTGTATGGGG CTGTTAATTG TTGGTTTTGG TTTACGCGAT 6360
TCAATTGTGG ATGTCGCTAC AATTCAATTT AATAAAATCT GGCATTACCA AGCAGTCGTG 6420
ACTTTTAAAG AGCAAACAAC ACCTGAAGAG ACAAAAGAGT ATCAAGAAAC GTTGCGCAAA 6480
ATGGATGGTT TGAATAAAAC AATTCCGTTA TATTCAGAAA TCTTTAAAAC GAAGGGCAAA 6540
GGCGCACCAA CTCAAAATAT TACTCTTTAT GTGCCACAAG ATCCTTCGAA AATGGCTGAT 6600
TTTCAATTAT TTAATGATCG AGTCACTGGA GAAAAATATT CCCTCAACGA TGACGGTGTA 6660
ATCATTAATG AAAAATTAGC TAAATTATTT GGCTATAAAG TCGGAGATCA ATTAAATTTA 6720
GAAAATAGTG ATAATCAAAC CTATCACGTG AAAATTGCCG CGATTGCAGA GAACTACACG 6780
GGTCATTTTG TCTATATGAC GCCGAAACTC TACCAGACGA TGACGAAACA GAAGCCGGAG 6840
TATAATACAG AATTCCTACT TTTTGACAAA AAGTTATCCT CAAAACAAGA AACCTCAATC 6900
GGAGAGGCGT TGACAAAACA GCCGAAAGTG TTGAACATTA CGTTTTTAAC TGCGATGAAA 6960
GGTTCGTTTG ATGATATGCT GAAAAGCCTT GATATTGTCA TTTGGGTACT AATTGCTGTT 7020
TCTGGTTCTT TAGCGTTAAT TGTGTTATAT AATTTAACCA ACATTAATGT TTCTGAACGG 7080
ATTCGAGAAC TTTCCACGAT TAAGGTTTTA GGGTTTTACG ATCGTGAAGT CACCACCTAT 7140
GTTTACCGTG AAAACATTAT TTTAACGTTC ATTGGTATTA TTGTTGGCTG CTTCTTTGGG 7200

AAAATTTTGC ATCAGTATAT TTTAGCAACC GTTGAAGTTG ATTTAATTAT GTTTTCGCCA 7260

ATTATTCATT GGCCAAGTTA TCTGTATTCC GCAGTCATCA CCATGTGTTT CACGTTGTTT 7320

GTGATGGTCA TTATGCATCG GAAATTGAAG AAAATCAATA TGATTGAAGC GTTAAAATCA 7380

AATGAATAGC ACATTTTAAA AAaCGAGGAG TCCGTAGAAG TTCGATAATT CTAGGGCTGC 7440

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ACAAGGGGTT CCTGTGATGT GTGATGGGAC ATCAATCATT AAAATTGGTT CGTCAGTTGA 8460

AGAAATTGCG ACAGCAGCGG AACAATTTTT AGGAAAAACA ACGGAAGAAT TAGAAAATGA 8520

AGCACGTGAA GTATTAGAAG GACATTTACG TTCGATTTTA GGTTCAATGA CAGTGGAAGA 8580

AATTTACCAA AATCGTGATT AATTTAGCCA AAGTGtACAA GAAGTTGCCa GTGTTGACTT 8640

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ACAAGCGGAA TTGCAACGTC AAACAGAAAT TGCAGAAGCT TCAAAAGAAA AAGAATTGAA 8880

ATTAGCGTTA TACAAACAAG AACAAGATAT TGCCAAAGCC A 8921

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGCAAATGCA CGAGGAGGAA CAAAAGAATG GAACArGGAA CAGTAAAATG GTTTAACGCa 60

GAAAAAGGTT TTGGGTTTAT CTCACGCGAA GACGGAAGCG ACGTATTCGT ACACTTCTCA 120

GCTATCCaAG GTGATGGTTT CAAAACTTTA GAAGAAGGTC AAGCAGTGAC TTTTGATGTT 180

GAAGATTCAG ACCGTGGCCC TCAAGCAGTT AACGTAGAAA AAAACTAATA AAAAATAATC 240

CAAAAACACC TAACATGCGT TAGGTGTTTT TTTGTTAGAA AAAATAGAGA AGAAAAATGG 300

ACAAGCATTT TTCTTCTCTA TTAAATGAGA GCTTTATTGA TCACTAACTG TGGCAGTCAT 360

AATCATTGGC AGAATCATTG GATGACGTTC TGTTTGTTCA AACAAGAAAG GCTGTAAAGC 420

GGTCGTCATG GCTTCGCCTA ATTTTGCTTC GGTACAGTTT TTATCTTTCA TTGCTTCACG 480

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TGTTGCTACC GCTAAAACTA AACCTTCTTC AGATAAGATA CGACGATCCC GTAAAACAAC 660

ATTCCCGATA TCACCGACAC CATTTCCATC AACGTACACG TCATTAGCGT TGAAGTGACC 720

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ATTTTCTTCA GGAACCCCTG TATCTTGAGC GAGCGAAcAT GGATTTTTAA CATTCTAAAT 840

TCACCATGAA CAGGCATGAA ATATTTAGGC TTCATCAAAC GAAGCATTAA TTTTTGCTCT 900

TCTTGTCCAC CGTGACCAGA AGTATGGATA TTATTGATTT TTCCGTGGAT AACTTCTGCA 960

CCGGCTTCAG ATAATAAGTT GATTAAACGG TTAACGCTTG TCGTATTCCC AGGAATTGGT 1020

GAACTTGAGA AAACAACCGT ATCGCCTGGT TGAATACTAA TTTGGCGGTG TGTACCGTTA 1080

GCAATCCGAC TAAGCGCGGC CATAGGTTCT CCTTGAGAGC CAGTACATAA AATCATTGTT 1140

TCATTTGCTG GCAATTGATT CAGTTCCGCC GCATCGACAA ACGTTCCTTT TGGCACTTTG 1200

ATGTAGCCTA AGCGTTCGCC ATTGACAATG GCATTTTCCA TGCTACGACC AAAAACAGCA 1260

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ACGGGTGTAA AGTCAAACTT AAAGTCACCT GTTGCGACAA TGTTACCAGA AGGCGTTTTA 1560

ACCACAACGC CCAAGGCATC AGGAATACTG TGAGTCGTCC GGAAAAAGCT AATCGCTGTT 1620

TTTCTAAAAC GAATCACCGT ATCTTCATTA ATTTCGTGTA ATTCCGCTTC TCGCAATAAA 1680

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ATAACGAGTG CTTTGACTTT ATGCAAATTT TGAACGATGT AGCTATAATC TGGAATCACG 1860

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TCATCTTGGA ATTGTACCCC ATATGTGTTT TTTCCAATTT CGCCTAAACC ACCGATTGCA 1980

AAAACGCCAG TTTCGTTATT TTTTATGTTT ACTTTCATGT TAAAACTCCG TTAGAGTGAA 2040

GTCCGCATGT TCTTGCTCGT AAGCAAGATG TTTTTCGTCT AATAATTGAA CGTATTCAAT 2100

ATTGTATGGG GTATTTTCTT CAACTAATTG GCGCACGATT ACATCGCTAT CGGCTTCCAT 2160

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TGAAAAATTT GAAGAATCTC GTTTTAATAA AGTCAATGAA ACTTACACTA AAAGTTCAAA 3840

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GAATTTAATT GCTTTTATTG AATATATTTT TCATGCGCTG TTCTCGTTTA TGTTATTTGC 4020

CAGTGTCTTT ATGATGTATC CGCGGGCTGC GGTTTCGGCT TCACGGATTC AAGAAGCCTT 4080

AGACATGGAA CCAGCTATTC GTGAAGAAGA AGGCGTAACA GAAACAGCTA CTAAAGGCTA 4140

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TGGGAAATCA ACATTAATTC AATTGATTCC ACGGTTTTAT GATGTATCAG AAGGTGAAAT 4320

TTTAATCGAT GGAGTGAACG TAAAAGAGTA CAAACTTAGT GCATTACGCA ATAAGATTGG 4380

CTATATTCCA CAAAAAGCGT TACTTTTTAC TGGTACAATT GCTGATAACC TTCGCTACGG 4440

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ATTTGTTTCG CAAAAACCGC AAGGCTATGA TGAACCTCTT TCAGAAGGTG GCACGAACTT 4560

TTCTGGTGGT CAAAAACAAC GTTTaGCTAT CGCACGGGCG ATTATTCGCA ATCCGGAAAT 4620

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GCGTCTGAAA AAAGAAACAA CAGAATCTAC TGTTTTAATT GTGGCACAAC GTGTTGGAAC 4740

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AGAGGAGGAA TTAGCATGAA ACACGCCTTT TCTTCTATGA AACGAATCGG TCGCTATATT 4920

AAACCGTACC GAGTGACGTT TTATTTAGTT ATTTTATTTA CAATATTAAC CGTTGCCTTT 4980

AATGCAGCGT TGCCTTATTT GACTGGATTA CCGACGACAG AAATTAGCCG TAATATTGCG 5040

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ATTCCGTTGT CTCTGATTAT TTCCAGAACA ATTGTTAAAA TCTCCCAGAA ATATTTCCAA 5460

GGAATGCAAA ATTCTTTAGG AGAATTAAAT GTTATGTCCG GGGCCGAGnT CGAATTTTAT 5520

AAT 5523

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ACAGTCGATT TCGAGCACCG GCAACTTTTG CTACATCAAT GATAGACGTC ATTTTTTACC 60

TCCAAAGTGG AATGTATTCT TATAAGAAGT ATAGCATACA TTTTTTTGAA AATAGTGCTT 120

GACATGGGAA CATTCCCATA ATTTATCCTA AAGATGTAAA CGATAACAAT TTAATCAAGG 180

AGGAAGAAGA CGGATGACAA GAGGAGCATT AAAAATTGCA ACAATTGGTG GCGGTTCTAG 240

TTATACACCT GAATTAATTG AAGGATACAT TAAAAGAAAA GATGAACTGC CAATTAAGGA 300

AATTTGGTTA GTCGATATTG AAGCTGGTAA AGAAAAATTG GAAATCGTTG GGGCAATGGC 360

GAAgcGCATG ATTAAAGCTG CTGGTTTAGA TTGGGAAGTT CATTTAACAT TGGACCGTGA 420

AGCAGCCTTA AAAGGGGCGG ATTTTGTTTC AACACAGTTT CGTGTAGGAT TATTAGATGC 480

TCGCATTAAA GATGAACGGA TTCCTTTGTC CCATGGAGTA TTAGGCCAAG AAACAAATGG 540

CGCGGGAGGA ATGTTTAAAG CATTTCGAAC AATTCCTGTC ATTTTAGCTA TTATTGACGA 600

TATGAAACGC CTTTGCCCAG ATGCTTGGTT AGTGAATTTT ACTAATCCAG CTGGAATGGT 660

TACGGAAGCT GCAATTAAAC ATGGTGGTTG GAAAAAAACA GTTGGCTTAT GTAATGTGCC 720

GATTGGTCAT AGAAAACAAG CGGCCGAAAT GCTGGGAATT CCAGAAGAAG ACTTATTCTT 780

TAAATTTGCT GGAATTAATC ATTTCCATTG GCACCGCGTT TGGGACAAAG AAGGACAAGA 840

GCGAACACAA GAACTCATTG ATTTAATTTA CGGaCCTAAG CAAGAGCAAG AAAGTCATTt 900

GAAAAATATT TTTGATGCGC CGTTCCATTA TGAACAGTTA AAAGATTTAG GAATGTTACC 960

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GTATGAACGG GGCGAAACAA GAGCACAAGT GGTTAAAGAA ACGGAAGGTC GTCTGTTTGA 1080

ATTGTATAAA GATCCCAAAC TAGATTACAA ACCAAAAGAA TTAGAAGAAC GGGGCGGCAC 1140

ACACTATAGC GATGCAGCTT GTGAAATGAT TGCATCAATT TATAATGATA AACGAACGGA 1200

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ACCGAATTTT GCAGATGCGA TTAATAAAAT TGAAGAAACA CAACCAGAAA CAGTCACATA 1560

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TTTTTATAAA ATGtAAAATA GCGTAATGCG CCCCAAGCTG ATGTTTTTCG TGTCAATGTA 2040

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TACTAAAGTC CGATTCTCTC ATTTTAGGGT CAGAATTGAC AAAAGAAAGC AGAGGTGTTA 2160

ATGTGGGAGT AATTAAACGA GGAGGTATAA TTGTATGTTG GCATCTATCA GAATTTGGAT 2220

TGACTTTTTG ACAAAATAAA TTGAATAAAT CTTATCAAAA AGTCTGAAAT TAAAATTCAT 2280

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TCACTTTTAT ATCGACTAGG TTTTCAACAA GAAAATTTAC AGACAAAGAT ATCTTCTCTA 3600

AGTGGTGGCG AACATGAAAA ATTACTTTGG CGCAATTATT TATAGAACCA AATAATATCA 3660

TCTTATTGGA TGAACCCACC AATTTTCTTG ATTTAGACAC AATCCAAGCA CTTGAAGAAT 3720

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GTATTCTGCA ATTTCTGCGG CATGGGAGCC AGCAACATGT CCAGTGACAA ATGCAGCTGT 3960

AACATTGTAG CCTCCAGTAT AGCCATTAAT ATCTAAAAGT TCACCAGCAA AAAATAAACC 4020

ATTGACTAAT TTGCTCTCCA TTGTTTTAGG GGTCACTTCT TTGAGGGAAA TCCCACCGCC 4080

TGTGACAAAA GATTTTTCCA AAGGCAATGT TTTCGTAACA GTGAACTGAA AGTCTTTCAG 4140

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TTCTTGGTTA ATAAAACTAG AACAGCGGAG CGCGGCAGGT CCTGAAATGC CAAAATGTGT 4320

AAACAGCATA TCCaTTTGAT GATTAACTAA AGGTTTTCCT TTTTGGTTCA AAACAGTTAA 4380

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TTGGTTATTT GTTTGGCATG TATAAAyGTT GCGCAACTAT GATGCAGGAG TGTTGACTGG 5760

CAAACCTTTA GGATACTGGG GAAGCCAAGC AAGA 5794

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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TTATCTTACC TCAGAATATA GAGGAGATAA ATGAATATTT AGTTCAAGTA AATCAACGAA 4200

TAGAAAAAAG AGGGCAGCGA ATAGTGAATC GG 4232

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CGATTGCCTT AACAAGTTTT ATCGGTGTAT TATTTGCCTT AACCATTGTC AAACGAATTA 1080

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TGTTAAAAAA ATGTATCAAG ATTATTTGAA TTGTTTACCA ACAAAGGCTG TCCTAAATAA   3060
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TGAAAGAAAT TCGTTCAGGT ATGTCGAATG ATGATCCACG TACGCTTGAT AAAGGAATAG 22620

AAAAAGTAGT TGTTGGTGGG GCTGTTATTT TAGCAATTGG TGGGGTAGTC GCCTATGTTA 22680

TTACACAGGT AGGaGCTATT CGTTTTTAAA AGGAGGAAAA AAATGAAGCT ATTAGTAGAA 22740

ATGATAGTCA ACGGTCAAAC TGAATGGGAA GTTGTAGAAG AAGAAAATGC GCCACAGGCA 22800

ATTATTCAGA GTCGAGGAGG CTTTTCATTT GATGAGAATG GAGAGCTCAT TGTCAATGAT 22860

GATGAAATAA GTTATACAGG CGTGTTTGAG GTTTGCGAGA CTAACTTATT GGATTTCACT 22920

GTTAAGGAAG CAGAAATCCA TAGATTTTAT CACAAAAAAT TAGAAAAGCT AGGGaTAGAT 22980

CCTCTAACGT TTGAAAACTC GCmAGAAATA GCTAACTGAG CGGAGGGGaA GCnATGAGAA 23040

ATCCAAAAGG AACGACCGAT CAGCTATTTA AAAGTTTAGC TGAATACmAT CCmACmACgA 23100

aTGrAGCCAT GTCTAAAAtA GcGAAAGTCC tAGTCCCtTT AGGAATCgCT ATTTTAGGCA 23160

TTCTTTTTAT GATTGAATTG GCGAATACCC AAAAGAAATT TCAATCAGAA GACGGTGGTT 23220

TGACAATCGA GCTATTAACT AACATTGCAT TGAAGTATGT AATCGCGTAC GTCTGTATTA 23280

TGGGTTCTGG CTACATTATT GATGGCATTG TTTGGTTTAC AATTCAAGCA GCCAAATGGA 23340

TTAATTCCAT TGTAACAGCG ACAGGAACAA GTGAAGCGAT CCCACAAATG GAAAAAGTTT 23400

CTTGGTGGGC AAAACCAATT GTATTTTTCT TTCAAATATT TGCATATATT GCATTAATAT 23460

TATCTAGTAT TATTGCAAAT ATTCTTATTT TCTTACGAGG GATACAATTG TATATGATTA 23520

AAGCTCTTGC ACCGTTGTTT GTGGCGTTTT TTGTTCATGA TGAATTACGT TCGATTGCCA 23580

TGGGGTACAT GAAACAAATC ATGGCCTATG CGCTTCAAGG CGTTCTGTTG GTTCTATTAC 23640

TTGGGTTAAT TCCGATATTA ACAGCAAACG ATTATCTATC CTTTGAATCT CTTGAAGGTG 23700

GCATTTTGgC AGGTGCTGGA GCGATCATCA TTAATGTTAT GACGTACTTT AATTTAATTT 23760

TAAAATATGT GGCAGTGATT ATTCTTCTAG TTGGTTCACA AGGATTTGCC AAACGATTAG 23820

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AAAAAAATCT GGGGAATTAC AGTCAGAGAA TTTAAAGCGT ATGTTTGCTT TGTTTTTATA 23940

GGGATATTTC TTCTGTTAGA AGTATTTTTT TTGCCTGATC TTTTATTTAT GGTTTGTGCG 24000

TTAG 24004

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTTGAAACC TGTTGTTGAA TCCATGAATA CTACTGGTTG GTAATTTGGA nnGATATCTT 60

GTTTCATACG TTTTTTCGCT CCTTTGCCCT GATCCATTTG CTGTATCAGA GTTATTTTGT 120

CGGTATACAA CAATGCTATC TTACCATGTT TTCAGTTGGT ATGCAATTAT CTTTTTGGAT 180

TTCTTTTAAT TTGTTTGCCA AACGAAACAT CATGGAAAAC TTCAAATAAT TGTTGATTAT 240

TTTGGGTCCG TTTCAACATT TTTATGAATT GATCCGTATA TTCCAGCGAG TCTCCTGACA 300

TATTATTTCT CAATTTCCAC GTTTCTTCTA GTTGTTCTGG TGTCATTAGC AACTCTTCTT 360

TTCGCGTACT TGATTTTTTA ATATCAATTG CTGGGAAAAT ACGGCGTTCT GCTAATTCAC 420

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GAGATAAATG GAGCTCCATG TTGCCTGTAC CTTTGAATTC TTCATAGATG ACATCATCCA    480
TTCGGCTACC TGTATCCACC AATGCCGTGG CTAAAATAGT CAGACTGCCC CCTTCTTCGA    540
TATTTCTGGc AGCACCAAAA AATCGTTTAG GTTTGAAAAA CGCAGCTGGa TCTATTCCGC    600
CACTTAAGGT TCGACCACTA GGCGGGACCA CTAAATTATA GGCCCTTGCT AAACGAGTGA    660
TGCTGTCCAT TAAAATAACT ACGTCCCGTT TGTCTTCAAC TAAGCGCATT GCTCGATCCA    720
GAACCAATTC AGCAACTCGC GTATGATTTT GTGGTTGTTG ATCAAAAGTT GAAGAAACCA    780
CATCGCCTTT AACGCTTCGC TCTAAATCAG TCACTTCTTC AGGGCGCTCG TCAATTAACA    840
ACAGAATCAA TTCCACATCA GGATGATTTT CTGTAATCCC ATTAGCAATT TCCTTTAAAA    900
CACTTGTTTT TCCCGCTTTT GGCGGCGCTA CAATTAAACC ACGTTGCCCA AAACCAATTG    960
GGGCAAATAC ATCAATCATT CGTGTTGATA ATCTGCCAGC CGTTGTTTCT AACGTTAATT   1020
GTTTTTCAGG ATACAACGGT GTTAGCGCTG GAAAATGTGG CCGCTCTTTC GCTTCTTCAG   1080
GATCTTTCCC ATTGACACTT TCAACATGCA TGAGTCCATA GTAACGTTCT GATTCCTTTG   1140
GCGGACGCGC CTTGCCAGCT ACTTTGTCCC CATTTCTCAA TCCGAAACGA CGAATTTGAg   1200
AAGAAGAAAT ATAAAtGTCT TCTGCACTTG GTCCATAATT AATTGGTCGC AAAAAGCCAT   1260
AACCATCCTG AGAAACAATA TCTAAAATTC CTTCCATGAA GAAAAACCCT TGCTTCTCAG   1320
CTTGTGCACG AATCACAGCT AAAGACAATT CTTTTTTGGT CATTTGGCAT AATAAGGATT   1380
TTAAcTCTTt CGCGTAgCAT AAATATCTTt TAACGTACTG tTTTCCaATt CAGCCATgTa   1440
AATAGTCGCT CATTGATCCA CCTCAAnCGG ACCTTCTTGT TCTTCGGTTT CTAGCATTTG   1500
AATATCAGCG CCTAAAGCAG TTAACTTTTC GATAATGTGG TCGTACCCAC GTAAAATATA   1560
TTCTACATTA TAAATAGTGG TCGTACCTTC AGCCATCAAG CCGGCAGTGA CTAGGCAAGC   1620
GCCTGCCCGT AAATCAGAGG CGACTACTTC TGCACCGTGC AATTGATTTG GGCCATTTAA   1680
GATAATCATA TTGCCTTCAA CCGAAGCATC AGCCCCCATC CGCACCAACT CAGGGATATG   1740
CTTATTTCGT TGAGCATAAA TCGTATCAAT AATTTCACCA GTTCCTTGTG CTTTTAAAAG   1800
TAATGGCGTT AACGGTTGTT GCAAGTCTGT GGCAAAACCA GGATACGGAT AGGTTTTCAC   1860
CGTCGTCATT TTCAGATCAT GTGATGGATG AACTTCAATC ATGTCTTCTT CAATTGTCAT   1920
CTTAACGCCC ATTTCTTGCA ATTTCGCAAT GAAGCTTTCT AAATGCTCAT AAATAACATT   1980
TCGAACCTTG ATTCCTTCAC CCATAGCTGC TGCCATAGCT AAATAAGTCC CAGCTTCAAT   2040
TCGATCTGGA ATAATCGAGT GACGACAGCC ATGTAATTCT TCGACTCCTT CAATCCGAAT   2100
AACATCCGTT CCAGCTCCTC GAACTTTTGC ACCCATGTTA TTTAATAATG TAGCAATATC   2160
AATAATTTCT GGcTCACGCG CAGCATTTTC AATAATCGTT TTGCCTTTGG CTTTAACTGC   2220
GGCTAACATG ACATTGATTG TAGCGCCAAT AGATACCATA TCCATAAAAA TTCGGGTTCC   2280
TTGTAAGCCA GCTTCGTCTG TTCTCAAGTA CATCGCCCCA TGTTCGTTGG TTACATGAGC   2340
GCCTAATGCT TCAAATCCTT TGATATGTAA ATCAATTGGA CGAGGGCCTA AGTAACAACC   2400
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GCCAGGTAAG CCGACAACGC CTTCCCCAAA TCGACCAAGA AGTGAGCCCA TAAAATAATA 2460

GGATGCACGT AAGCTATTGA TTTTTCCTTT TGGCATTGGC ACAGAAACAA CTTCTGTTGG 2520

GTCAATAATT AATGTATTAT TTTCAAAAGT AATTTTAGCA CCCATAATTT CTAAAATTTC 2580

AATTAATGAG TGAACATCCT GAATGTCAGG AACGCCATCT AAAGTCACGG GCGAATCTGC 2640

TAAAATAGCA GCTGGAATTA AAGCGACCAC ACTATTTTTG GCGCCGCTAA TGGTTACTTC 2700

GCCTTTT 2707

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCACCTTATT GATAGCGCTT CCTTATATTG nAATAATGCG ATTTTCTAAA CAAAAAATTA 60

TAGGTGGTAT TGATAATGAA AAATCCGTAT GTCCAAATAA CCGACCAAGA ACAATATAAA 120

AAGTCAATTC GTCGAATTCC TCCAAAAGAT CCTAATATTT TTTTAATTGA GAGACCTACA 180

GCAGGTGAGA TTATTGCTCT ATGGTGGACA ACCTCTTCCC GTGGCAAATC AACTGATAAA 240

TATATACCAA AATATTTCAA GCGTATCTAT CGAGTAGATA TGATTAAACA ACGTAAACTA 300

TTCATCAAAG CTAACGTTAT CTCCGAAGAA AATAATACTT ATGTACTGAC TGAACTAGGA 360

GAAATGTTAG TACATAAATA CTTTTATATT ATTGAAGAGC ATAATAATTC TTCCAATGAT 420

TCTTTCAATA CTGAACGAAG AAAGTTAGCT GATAAAATTC TATATTCGCT AGGCGGTGAA 480

ATATAATGCA AACGGAAGTT AAAGAGTTTA TTGCTTTTGA TATTGAAACA ACAGGTTTAG 540

ACTTCCATCA GGATGCTGTT ATTCAGATAT CAGCTGCAAG ATACGTTGAT GGTATTGAAG 600

TTGATTATTT TGATACATTG GTAAATAGTG ACTACATTCC AGATGAAATT ACCAAATTAA 660

CAGGAATCAC TAATGACCAA GTACTAAATG CGCCAACTTT AGATGAAGTT ATGCCTTATC 720

TTTTTGATTA TTTAGGAGAT ACGATTCTAG TTGGACATAA TATAAAAAGT TTTGACTTTC 780

CTTTTTTAAA AGCAAAAGGA TATAATATTG CAGAAGGACA TGAAATTTAT GATACTCGCT 840

ATTTTGCAGC CACACGAAAG CATGGGGCTG TAAACAATCA ATTAACTACA TTGAAATTAC 900

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GCTTGGACTC TTTTGAATTA GATGATGATA CTACACCTTT TTTTGAAGGA ATGTCTTTTG 1080

TAGTAACGGG GGCATTTGAT GATTCTAAAT ATAACCGTAA ACAAATTGAA ACACTGATAA 1140

AACAACATGG CGGTAGGGTA TCGTCAAGTT TATCTGCCAA GACTGATTAC TTTATCCAAG 1200

GTATTCAAAT TTCTTCCCAA CTTAAAGACG GAAAGCACAG CAGTAAAGAA CTAAAATATA 1260

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CGAAGGTGTT TTACGCACCC CATCTGAAAT TAGTTCTATG AAAGCAAAAA AAAAGAAATA 1980

GTTACTTAAA TAAAGCAAAA AAGTTCTACG CCTAAAATTC GAATTTAGAC GTAGAACTTA 2040

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TCCGTTGTGC TCGTGTTTTC TTTTCACATA AAGCAAAGAC TGTCGGTCCA CTGCCGCTCA 2160

TCAACGCTGC ATCAGCGCCG TACTTCAGCA TGCGATCCTT GATTTGTTGC ACGATTGGAT 2220

GTCTGGCAAT CGTGACACTT TCCAACGCAT TGCCAACCGT TTGGGTCATC CCAGTATAAT 2280

CCCCATTTTC AATAGCTATT CTTAGTCCAG CAATATCTGG ATGGTGCAAT TCATCTACCG 2340

CTAAATCATT AAAAACGGTA CTAGTGGATA CACTAATTCT TGGTTTAACT AACACAATCC 2400

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AGCCATCCAC ACGTTTATGC AGAACATCTA ACCCAAGATT AATTTTCGCA GGAGCTCGTT 2880

CGATTATTTC CATCGGTTCC CTGATTCACC TTCCTTAATC TTTTGTCTAC CAACATTTTA 2940

ATCTTTTAGA TTCTATCATA TGTCCATGAA GAAGTACACC GAAGATTGCT CTTTCTCTGA 3000

CGACAGATGG CTGAAATTAA AAAGAGCTTA GGAACGAAGG GCTCTTCCTT CACTCCTAAG 3060

CGGACTTTCT AAATTATACG GCTTGACCGA TGAATTCGAT TTCAACGGTG CGTGTTAAAA 3120

CATCTGAATA GCTATAAGAT ACACGTTCAA ATGAGTTCTC GTCTGGATCC AAGTCAACAA 3180

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GAAAGAAGAC AATTCGCCCT TCTTGAAGCC AGTCCTCAGT ATCATAATCT TTTAAATAGT 3900

ATTTTTTCAT GCACTTATAA ATCACTGGCT GATATTGCCC ATATAAGGCT TGAAATTGTT 3960

CTTGGTCTCC TGCTAATGCT TGTTGAATCT GTTCTAACAT AAAAAGCCCT CCTTTTCGAT 4020

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GCACCTTGTG AAAAGACCAC CCATTGTTCA GCCAAATCAC TCGTTGCGAC TGTTACTTGC 4320

GTTAAACGAT CATTTTTTTC ACCAGCTAGA CGTTCAATAT AACTATCTGC TGTTTCATCT 4380

TCTTTGGTGA AAACCACGGT CAAAAGGTAC TTTTTGTACG TTTGCTGAAT ACCTGGGACT 4440

AATTGGGCAT CAAAGACCAC AATGATTTCC AACCCTTCAT ATTTGGCGTA ATTGGACAGA 4500

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TCTGGCCAAG CACCAATCAT ATTATAGCCA TCAACGATTA ACAATTGTTT TTTCATACAA 4620

TCGCCTTCTT CTATAATGGG TTGCGGCCAC GATAGACTTC ATACATTAGC AAGCCTGCAG 4680

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CGCCTTGTGT ATTCCAGCGA CGATAATCCG TCCCAGACAT ATCTGTACCA AAAATCCAAA 4860

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GAATCATTTC ATGAACAGTA ATGAAGTTAC CTAGGGATTT ACTCATTTTT TCATCGTCTT 6480

CACCAATTGT GACATAGCCG TTATGCATCC AGTAATTGGC AAAGGTATGG CCTGTTTTGG 6540

cTTCGCTCTG TGCAATTTCA TTCTCATGAT GTGGAAATTC TAAATCTTGT CCACCACCGT 6600

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CGGGACGTCC TTTCCCCCAA GGAGAATCCC AAGAAATTTC ATCTTCTTTG GCACTTTTCC 6720

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CCCCCACTTC TAATTCATCA ATCGATTGAT GGCTTAATTT ACCATAATTA GGGAATTTAC 6840

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CGATGAAAGC TAAGATATCA GGCATGTGGT CCATCACCCG AGGATGTAAC GTTGCTGGTT 6960

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CTTGTGAGAA GATTTCTTCT TCGCCAACAG GAGACCATCC TAGTAAAGCA ATAAAGTTGA 8700

ACATGGCTTC TGGTAAGTAA CCTAATTCAC GGTATTGTTC AATAAATTGT AAAATTGTTT 8760

CATCACGTTT GCTCAATTTT TTGCCAGTTT CTGAATTAAT GATTAAGGTC ATATGGCCAA 8820

AGACAGGTGG TGTCCATTCA AACGCTTCGT AAATCATTAA TTGTTTTGGT GTGTTCGCAA 8880

TGTGATCATC GCCACGTAAA ACATGAGAAA TTTTCATTAA GTGATCATCT ACTGCAACGG 8940

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CCTAACAGAC CTTTTTCATA AGGAAGAGTA ACCCCACCAA TAATTAAAGG TCGTTGCGGA 10020

ACTAATTGAT GAACATCAAA ACCTTGACCG ATTCGAATCA TACTAAGTCC TCACTTTGCT 10080

TAATTTTTAT CGTTTTTAGG ATGGTTATCC TTGCGATCAT TAATCCCGCG ACCCGCGTGC 10140

GCCGGTTTGG CAAAAATCAT ACGCCCAGCT GCGGTTTGTA AAGCACTTGT GACGACCACT 10200

TCGATTTGCT CATTCATGTA ATGCTGGCCA TCTTCTACCA CAACCATTGT GCCATCATCT 10260

AAGTAAGCGA CCCCTTGTTG ACGCTCTGTT CCGGCTTTTA CAACCATCAC ATTCATCGTT 10320

TCACCTGGAA TCACCACTGG TTTCACAGCA TTAGCTAAAG CATTAATGTT TAAAACAGGC 10380

ACATTTTGAA ATTCAGAGAC TTTATTTAAG TTGTAGTCAT TGGTCACAAC CACGCCATCT 10440

AATAATTTTG CTAATTTGAT TAATTTACTG TCTACTTCAG AGATATCCTC GAAATCTCCG 10500

TCATACATCT CAACGGAGAT ACCTTCTTCT TTTTGTAAAG CATTTCAACG CTGGTTCCCT 10560

GCCCTTTAAA ACTAATAATT TnAACTGTAC CGCCCATGCC GACAACACGT CTCGGAATAT 10620

TAATTAAGCC ATAACT 10636

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAAnGGGTCT TTTTTCGAGT AGACGTTTGA TnTTAGCGTA TCCAAGAAAG GAAAACCCtA 60

ACATAAAaAT TTTTTATTTA CGAaGGAGAC CGATTTATAT GGAAAAGAAA GAATTTCACA 120

TTGTAGCAGA AACAGGAATT CACGCACGTC CAGCTACTTT ATTAGTACAA ACTGCAAGCA 180

AATTTAACTC AGATATTAAC TTAGAATACA AAGGTAAATC TGTTAACTTA AAATCAATCA 240

TGGGCGTTAT GTCTTTAGGC GTTGGTCAAG GTTCTGACGT AACAATCACT GTTGATGGTG 300

CTGACGAAGC TGAAGGAATG GCAGCAATCG TTGAAACATT ACAAAAAGAA GGATTGGCTG 360

AATAATGTCT GAGATGCTAA AAGGGATTGC CGCAAGTGAT GGCGTTGCTG TTGCTAAAGC 420

TTACCTGCTA GTTCAACCTG ACTTGTCTTT CAACAAAACT TCCGTAGAAG ATACTGATGC 480

AGAAGCAACT CGCTTAGACG ATGCTTTAGC AAAATCTACT GAAGAGTTGC AAGCAATTCG 540

CGACAAAGCA GCTCAAAGCC TTGGTGAAGC AGAAGCGCAA GTTTTCGATG CTCATTTAAT 600

GGTTTTATCT GACCCAGAAA TGGTTGGTCA AATCAAACAA AATATCCAAG ACAACAAAGT 660

CAATGCAGAA GCTGCCTTGA AAGAAGTTAC GGATATGTAT ATTGGTATGT TTGAAGCAAT 720

GGaCGACAAT GCTTACATGC aAGAGCGTGC aGCAGATATT CGTGACGTTG CCAAACGTAT 780

CTTAGCACAT TTATTAGGTG TGACTCTTCC AAATCCTTCA ATGATTAACG AAGAAGTAAT 840

CGTGGTTGCC CATGACTTAA CACCTAGTGA TACTGCACAA TTAGACCGTA CGTATGTTAA 900

AGCCTTTGTG ACAGACATCG GCGGACGTAC TTCTCACTCA GCCATCATGG CTCGTTCGTT 960

AGAAATCCCT GCAATCGTTG GTACAAAAGA AATTACTGAC AAAGTAAAAG CAGGCGATAT 1020

TTTAGCAGTG AACGGAATCA TTGGGGATGT TATTATTGAC CCAACAGATG CTGAAAAATC 1080

TGAATTTGAA GCAGAAGCAA AAGCTTATGC AGATCAAAAA GCAGAATGGG ATAAACTAAA 1140

AAATGCAGAA ACAGTGACAG CTGACGGCAA ACATGTTGAG TTAGCTGCAA ACATTGGTAC 1200

ACCAAAAGAT TTAGAAGGCG TACACAAAAA CGGCGGCGAA CTGTTGGTTT ATATCGTACA 1260

GAATTCTTAT ACATGGATTC ATCTGACTTT CCAACTGAAG AGGACCAATA CCAAGCGTAT 1320

AAAGCAGTTC TTGAAGGAAT GGAAGGAAAA CCAGTTGTGG TTCGTACAAT GGATATTGGT 1380

GGGGACAAAG AGCTTCCTTA CCTAACATTA CCACACGAAA TGAACCCATT CTTAGGTTAC 1440

CGTGCATTAC GTATTAGCTT ATCAGAACTA GGTGACGGCA TGTTCCGTAC ACAAATGCGT 1500

GCATTATTAC GTGCGTCTGT TCATGGTAAC TTACGTATCA TGTTCCCAAT GGTTGCTACT 1560

TTGAAAGAAT TTAGAGCAGC GAAAGCAATC TTTGAAGACG AAAAACAAAA ATTAGTCAAC 1620

GAAGGTGTTG AAGTTTCAAA CGATATCCAA GTAGGTATTA TGATTGAAAT TCCAGCAGCT 1680

GCCGTATTAG CTGATAAATT TGCCAAAGAA GTTGACTTCT TTAGTGTTGG AACTAACGAC 1740

TTAATCCAAT ACACAATGGC GGCAGACCGT ATGAACGAAC GCGTTTCTTA CTTATACCAA 1800

CCATACAACC CATCAATCTT ACGTTTAATT AAAAATGTAA TTGATGCAGC ACACGCTGAA 1860

GGTAAATGGG CTGGTATGTG TGGTGAAATG GCGGGCGATC AAACAGCTGT TCCATTACTA 1920

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TATGAAAGCA CATCGACAAT TGTCGATGTG CTTTTTTATT GTTGCGATTC ACGTATTTTT 2160

TTCTTGAAAT AATAAATCGT GCTTCCCAAA ATGAATAGAA AAACCAGCGT GATGCTACTC 2220

ACCAGTTTCC AAGGGAAATT GGTGTGTTTT TCAGGTGGGA GGTTGACGGC GGTAGCATTG 2280

TATTTTTTAG CTTCTTTTTC TTGGATGACT AAGTGTTTTT CCCACGAATA GTCTTGATAG 2340

CCATCGTTTG CTTTGATTTT tACAGTATAA TTTCCAGGAA CAAAAGGTTG TTCCTTTAAG 2400

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TAGCGAGGTT TGGTTTCTTT TTCATAATAC AAAGAGGCAT CGACTTGTAA TTTTTTAATC 2520

ATAGCCGCTT GTTTGTTTTG GAGATTCATT AATACGCGGT TACGACCGTT AGCTTGATCG 2580

GTTTTTACTT CATTTAAAGA TAATTCTGGC TGAACAGGTT CATCTGTTTC ACTAAGTAAG 2640

ACACCGACTA CATAAGAAAA ACGATTATTG ATGGCCACAC CGTTTTCTGA GTGAGCAGGT 2700

TGTTCATCTG ACTTTTGTTC AAAGTAGAGT CCTCCTAAAA CGTACCCATT AAATGGTTTT 2760

TCCGGTAAAG TAAGCTGACA TTCAACAGTC TTGGTTGAGT GTTTAGGTAG GTGGATTTCT 2820

TTTGGCAATT GCGCAATCTC ATTAAAAGTA AAAGGTGCAG ACGGATCTTT TTTTGTTTCA 2880

GCATGAGAAT AATCTGCCAA GCCATTATCA TTAGTAATCG CTGCATTGGC TGAAGCTAGC 2940

ACGGTAATGT CGTTGGCTGT TTGATTCGTT AGTTCGATTT GTAGCTTTTG TGTTTGGTTT 3000

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AAAATGATGA CGCTAATAGC ATGGAGCCAT TTAAAAAGCT GCTGATTCAT AGTGTGCACT 3180

CCTTTTTGAC AATTTTTTAT AACAAGGTAT TGCATGAAGT TGTTTCATGC AATACCTTGT 3240

TTGTTTTCTT TTAAAGTGGT GTATCATCCA AAATCCAAGT AAGCGTTGTT TTATATTGTT 3300

TAGCTGCAAC TTTTTTCGTT GTCGCAGGAA CAGTTAATTG AATGCCTTGA GCAGCGGTcg 3360

sTCCGCTACC AAAAGCTAAT GTCCAAGTGC CCATTCCTGT TGAAAGAGCG GCAGTCGCCA 3420

CAGGAGAAGT GGCGGCACCA GTTGGATCCA AGGTTACTGG GACCGTTAAT GGCGCCAAAG 3480

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CAAGATTTAG ACCACGTTTG TCAGTTACTT GAACATAGTT TGGCACGCTA ATTAAATCGC 3660

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TTTTAAAAAA GCTAAATCCT AATTAGAGGG GTGTATCAGA AAGAATCCAT TGTAATTCGG 4080

CAGTGTAAGA TTCTTTGACC GTTAAATTAA GGTCAGGAGC AACGCTTAAA AAAAGTCCAT 4140

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TTTGTTGGTT CCAAGGAATT TCTACATTGT TATCGTCCGT TGCGGTGTGT TGATAAACTT     4200
CGGTTGCTAA AGAGGAGAGA GGAAAATCAC TGCCATTTTT TCGATAAATG AAAGCTTGCT     4260
GGATCGTTTT ATTTGTAGAA GTTGAATGCA TGGGCTGACT CTCTCTTACC AACAAATGCC     4320
ATGGTGTTTT TGCAACTCGA CCATCGGCAA TGAGGAAAGG AGCGCTGATG GTCGATGGTG     4380
AGTATATGGT TCGTTTGCTG GGGAAAGGTA AATTTTTAAA GGAAACTGTA GTTGGCATCT     4440
GCACAAAACG GAGGGTACCG TTTTTGATAG GTAAAGATTG TTCTTTAGTG ATTGGCGTAA     4500
TTGcGTTCCG CCACCATCAT TGCCAGTAAC CGTGCTAGAA AATAAAAGAA ATTGGTTTAT     4560
CCATTCTTCT GTAACCGTTG CTGTATATTG TAAGGTGAAT TGTGTATTGG CTTCCGTAAA     4620
ATTATCTGCT GGCAGCGAAT TATGATAACT CCAATACGGC AAACCAGTGG AACTATCAGT     4680
TAAAAGTTGA AGCCCAGCTA TTGGCGTACT TAAACCTGCT GCTGATTGTT TTGTTAATGT     4740
AGCAGCTGAA AGTTGGGACA GTCCTTTAGG CACCGTTGCT CGTAATTGCT GATTCATCCa     4800
CGTTGCTGGT TGATTGGTTA AACGTGTGGT TAACGTAAAA CGAATGATTT GACCACTTAC     4860
GACAGAGTTT GCAGCTTCCC AGAGCCCTTG TGCATTTTTC CGCTCAATGA TTTGCGTAAC     4920
CGTTAGTTGA GGCACAGGAT AAGCAACTGT TTGAGAAACA GTAGAACTGG TTAACAAAGG     4980
CAGGCCAGTG CGATTGCTGA GACCTTGGAC CCACAAGCTG ACCGTTTCTC CCCCTTGGAA     5040
AGTGGGTAAA TTAGCAAATT GAAAATGGCC ATTGGAATCT AAGGACGTTG TGGAAATAGA     5100
ACCACCATTT ATTTGTACTT TAACTTGATA GGTTCCGTTA GATACTTGAG AATCTTTACC     5160
TGAAAGTTGA GTTGAGCCGG CATTGGCGAC TACGTTTGTG ACTGGTTGGA TTGACCAATT     5220
GACACTTTGG TCAGCTGAGG GGCTGCTTTG AATATAGTCG GTTGACGTTT TTGAACGAGC     5280
AAAGACAATT GTAGAGAGCG TGTCGCCATA TTCTAATGGT GAAGCTAACG ATGTCGAGAA     5340
ATTTCCGGCT GCATCGACAG AAATCCCTTT CACCACAATG GGGGTAGTGG TGCCATCATG     5400
GCGGTTCAAG GTTAATTGAA CAGAGTAGTT ATAGTTTGGG TCTTGTACTT GTTGAATGGT     5460
CCCTGTTACA GTAGTGTCCA GATGATTTGG TTGAGTTAGT TTGGCTGGTG TGACTTGAGG     5520
AACGGGATAA TTACCTAAAC TAAGTTGAGC TTTGCTAATT ATGCCTGTTT TTGTATTATT     5580
CCCAATGATA ATATTAATTG CGCCTAATCC aGTGCCGACA TCTGTAAAGG TTCCTCGAAT     5640
CGGATAGTCT TTGCCGTTAA GAGCAGGAGG GATTGAAATT CCTCGTTTAT AAAGTGCGCC     5700
CACATCAAAC GAAATGGCGG CAGACCATTT GGTTCCGGGA AGTAACACCA AGGTGCTACT     5760
TGGAAAAGTC AGATAAACAG AATGATAAGT GCTACTATAA GAGAGcTGAC GCCGTTAGTT     5820
GAACTGTGAA TATCTTGAGT GGCTGTTCCT GGATAACTGA CAGTCCCTGT TAAAAGAGTC     5880
AGAAAATCTT GTTGCTTTAG AGTGTCGTTA TCTAACTGGC TTGAAATTTC TGTAGGAAGT     5940
TGAATAGCAA TAATCGGTCG ATCATTAATT GCTAAGCCGA TAAGTGTCAC ACTGTATTCA     6000
TACGAAAGTG TGATAATATC TTGGTTATAC GTTCCCGTGC TTAAGGTACT TTTTAAGGTG     6060
CTATTACCAA CAGAAACACT AGCTGGCGTA GGTGCCATAG GTTCATCGTT TTCAGAGGAA     6120
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GCATGGGTTT GCTCGGTTTC TTGTTCCACG ATATCGGTTG CTTGAGTTGT TTGTTGTTCT 6180

GTTGAAACTG AAGTAAATGT TTCACTAAAA GTAGAGGCGT GAGTTGTAGG GTTCAGTGTT 6240

TCAGAATGAG CTATCAAAGG TTGAGTCAGC GATAAAAAAA GCCATGATAT GATGCAAGAA 6300

AAGATTCCCC ATACGAACTT ATTCAAAACC ATCCTCTCCT TTTTTGaTAT TATATGtATA 6360

ATGACGAAAA TATATAATGT GTAAATATTA AGTACATACA TTCTATAATG GGCCATnCAT 6420

AAAGTAAAGC GATTACATCC GATGGTGnAC AGGATATTTT GTTCACAATC TTTTAGTGTT 6480

TTAAAGAGGG AAATTTCTCG AAATTCTATG CGTTTTnAAT CCGGGAAAGA T 6531

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTTCGGGAA AGAAACACCT ACCATTTTTG ATGTTTTGGG CAGGGAATAG GAGGTAATAC 60

ATGGAATGGA GTTTTCCTTG GCTATCAATA GATGGCGACA GAATGTACGA TGATAGCGAC 120

TTCTCGAAAT TTTTTGAGGG TCTTTTTTCT TATGGCGTTT CTCTAACAAC AGCTAACGCA 180

TTAAAGGTTA CTGCCAGTCC TAATGGCGGG ATGAAAGTAC AAGTAGATTC AGGCTATGCA 240

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AGTATGCAAG ACAGGACGGA TAGTATTGTG GTTCGCGTGG ATAAAAGTGT GCGAGATGTA 360

TTTTTAGCTG TTAAAAAGAA CGATACGACA GTAACCCGTA CATCGGACGT TTACGAGCTA 420

CAGTTAGCGA CAATAAGAGT GCCCCGAAAT GTTTCTAGTA TTACAGGCGA TTTAATCACA 480

GATAAACGGG CAGATACGAA AGTATGCGGG TATTCTTCGC CGTTTCAAAA GGTTAACGTT 540

TCAGGGTTAG AAGAGCAATA CGGTACAATA CTAAAAAAAA TTGCGGAAGC CAACAAGACG 600

AGTTATGAAA AAATCCTAAA TGATTTTAAA AACTATGTTG CAAAAGCGCA AACCGATATG 660

GATTCTAATA TTGAAGAAAT TATCCAATCA GGTAATGGAA AGGTAAGTGC TTTTGATGTT 720

TTAATTCACG AATGGTTTGC AGCTTTAAAA AATGAATTAG ATACAAATCA AGCATCAAAT 780

TTACAGAATC AAATCAATGA AATGAAAGCT ACTGAAGAGT TACCAGCTAT AGAACATAAT 840

TTACTCGGTT ATCCTAATGT ACAAGTTTTG TATTGGGAAT ACGGTATTGG CCTATCAGGA 900

TTAGCTAATG AGCCAACAGG TCTAGGCGGT AGCAATGTGA AAAAGATTCC TCACAGTGTA 960

GAATATCTTG ATTTATTCAG TTTCAAAGTT AAAGTGCCAA TGAACTTTAA ATTGGTAAAT 1020

CCAACAGTAA CAAAAATAGA TAGTCGAACT ATTCGCTTTA TTGAAGCATT TAAAGTTATA 1080

GAAATTAAAT TTTAGGAGGA AAAGAATGTA TACATTTAAA AAAGGTGATG CAGACTACCA 1140

AGTCATGCTA AATGAAAATT TTAAAGAGAT AACTGATTCT TTCGAAGATG GTTTATTTGT 1200

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GACAATTGCG GGCATAGGGG TGTCAGTAGT TGTCTATTTA TTTACAAAAT ATTTAGGAGG 2220

TGTATAAGAA TGATTCTACC AGATAAGTAC TACAAAATTA TCAAATGGGG CGTGCTAACA 2280

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GTATCAGCAT ATAATTTAAA AGACAAGGAG AAATAAAAAT GAAAAAGAAA ATTTTAGCAG 2460

GAGCGCTTGT CGCTCTGTTT TTTATGCCTA CAGCTATGTT TGCCGCAAAA GGAGACCAAG 2520

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TGCTGTATTT GTTGGCTTAG GTAGTGCTGG AACTATTGTG ACAGATCATT TTTTATTCCA 6240

CACACCATTG GGCATAGGAA AAGTTCTTTT TCTGTTGCTG TTATTAATAG GTaTAATTGG 6300

CTTAAAAATG GTAACTGGrA ATAAAGAGGA GGAAACAAGA TGAGTTGGTT ATACTTAGTT 6360

ATTGCAGGCT GTTTTGAAAT TTTTGGCGTA GGTTCAATT 6399

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3956 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AACAGGAGGA AAACTTGATG GGCATTCCAA TCACCATTGT TTCTGGCTTT TTAGGCGCAG 60

GAAAAACAAC CTTAATTAAC CATGCGCTTG CGCAATCACC GTTTCCTAAA GAAGAAATTA 120

TTATTATTGA AAATGAATTT GGTCAAACAG GCGTTGACCA CGCATTACTT TTACAAACCA 180

CGGAACGAAT TATTCAATTA AATAACGGTT GCATGTGCTG CAGCTTACGA GGAGATCTTC 240

TTGCCTCTTT ATCAGCAATC TTAGAAGTGT ATCAAGAAGA ACAACAACCC ATTGCCCAAG 300

TCATTTTAGA AACAACGGGC ATTGCTGATC CGCAACCAAT CATTCAAACA ATTTTAACGA 360

CCCCGCACAT CAAAAATCAT TTCTATATAG ACAGTCTCTT AACGGTCGTT GATGGGCATC 420

ATTGGCAACA ACAGCTTCAA GAAGCCGAAG CCATCAAACA ACTGGCCTTA GCAGATCGCC 480

TCTTTTTTTC TGTCAAGGAA CCAGCAGACA GCACTCAGCT ACCAACGTTC CAAGAAACCC 540

TTCGTACCAT TAATCCTTTT GCTGATATTT TATCCTTTCA AGCCAACGAG CCTCTTTTGG 600

CTAGTGACTT TTTTCAATTA AATAAGTTTA CGGCAACACT TACAGAACAC GAAATGACTC 660

ATTCCCCGCA TGAGCACGCC CACGAGCATC ATCACCATAC CTTTCACTCC CTCACGCTAA 720

CGGCGTCCTC AGCCATCAAC GAACCTCTTT TCACTCGTTG GCTTGATTGG TTAATGTATA 780

CGCATCAGGA AAAGTTATAC CGTTTCAAAG GGATTCTCGC CTTACAGGAG CATGACTTGG 840

CCATTGCCAT GCAAGGCGTC AACCAGCAAG TGGCCTTTCA AATGACGAAT CAACCCCCTC 900

AAGAAACGAC AATTGTTCTG ATTGGCAAAG AATTAGAGAC AAAAAAAATT CAAGAAACCT 960

TTCAAACCCT CAACAAAATA GCTACTCCGT AAATTAATTT TTTACGAAAT GGAGGTCCTA 1020

TATATAATGG AAAAAACTGA CTTATCTAGC GCTTATCGTC GACTGAAAAG TCCCAACATC 1080

AAAACACGAA AACGCGCACT TAAAATCATT AAAGAACATA AGCGCAATAA ACAAAAGAAA 1140

ATTGCGTAAT TCACTAAAGG AGCACACCTA TGAAAAAATT TACTCTTCCC CTGTTAGCCG 1200

CCTTATCGCT AATCCTTTTC GGCGCTTGCG GCAAAACAAA CACCTCTGAT AAAACCGCTG 1260

ACGGTAAAGA AAAACTATCC ATTGTCACGA CTTTTTATCC TATGTACGAT TTCACTAAAA 1320

ATATTGTAGG CGATGAAGGA GACGTCAAAT TGTTAATCCC TGCTGGTTCT GAACCACACG 1380

ATTATGAACC ATCCGCCAAA GATATGGCTA CCATCCATGA TGCGGATGTT TTCGTTTACC 1440

ACAATGAAAA TATGGAATCT TGGGTACCAA AAGCTGCTAA AGGTTGGAAA AAAGGAGCCC 1500

CGAACGTCAT TAAAGGTACC GAAAACATGG TCTTACTTCC CGGCAGTGAC GAAGACGGAC 1560

ACGACCATGA CCACGAACAT GGCGAAGAAG GCCACCACCA TGAATTAGAC CCGCATACTT 1620

GGGTTTCGCC TCATCGTGCC ATCCAAGAAG TCACAAACAT CAAAGAACAA TTAGTCAAAC 1680

TTTACCCTAA AAAAGCCAAA ACATTTGAAA CAAACGCAGA AAAATACTTA ACAAAATTAA 1740

CAGCCTTAGA CAAAGAGTTC CAAACAGCTT TGAAAGACGC TAAGCAAAAA AGTTTTGTTA 1800

CCCAACATGC TGCATTTGGT TATCTTGCCT TAGATTACGG CTTAAAACAA GTGCCAATAG 1860

CTGGTTTAAC ACCTGAACAA GAGCCAACCG CAGGcGCTTG GCAGAGTTGA AAAAATATGT 1920

CACAGACAAC CAAATTCGCT ATATTTATTT TGAAAAAAAT GCCAACGATA AAATTGCTAA 1980

AACGTTAGCT GACGAAGCGA ATGTTCAATT GGAAGTCCTA AACCCGCTAG AAAGTTTGAC 2040

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TTTGAAAAAA ACAACAGATA CAGCCGGGAA AGAGGTTCAG CCAGAAACCT CTGAAAAAAC 2160

AGAAAAAACC GTGGCTAACG GATATTTCAA AGACAGTGAG GTGGCTGAGA GAACACTGAC 2220

AGATTACGCT GGAAATTGGC AATCCGTCTA TCCTTTATTA AAAGATGGCA CATTAGACCA 2280

AGTCTTCGAT TACAAAGCGA AACTGAAAAA AGATAAAACA CCAGCCGAAT ACAAAACCTA 2340

CTATGATGCC GGCTATCAAA CCGATGTCGA CCACATCAAC ATCACTGATT CCACCATTGA 2400

ATTTCTGGTC AATGGCAAAC CACAAAAATT CACCTATAAA GCAGCCGGTT ATAAAATTTT 2460

AAACTATGCA AAAGGCAACC GTGGCGTCCG TTTCCTTTTT GAAACAGACG ATGCCAATGC 2520

TGGGCGGTTT AAATACGTCC AATTTAGCGA CCACAACATC GCACCAACGA AAGCCGCTCA 2580

TTTCCACATC TTCTTCGGCG GCGATAGCCA AGAAAGTCTG TTCAATGAAA TGGACAACTG 2640

GCCAACGTAT TATCCAAGCG ACTTAAGCAA ACAAGAAATT GCCCAAGAAA TGATTGCGCA 2700

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AATTTCCGAA AATTGTTCTT TAATTTTTGG AGAATTTCGG CTTATTTCCG AAGGAGTTGC 2820

TTCTGTTCCC GCCGTTTATC AGTTTTTGAG CGTGGAGCAA AAATCCAAAG TGATTTTTGT 2880

CCCACGCTCC TCTCTTTTTT TATTTAGTCA AGCACACCTG kTCTGTTtCA AACGTCGCTA 2940

ACamTGGCGC AcTTCATCCG TTGATTTkGT ATTCATTAAT TGTGCTCTTA AATCACTGGC 3000

ACCTGGAAAG CCTTTGACAT AAATTTTAAA GAAGCGATGC AGCCCAACGA TGGAGCGAGG 3060

CACCAATTCC GCATATTTGT CTTGCAAATC CAATTGTAAA CGTAGCAAGC CCAGCAATTC 3120

TTGTGGCGTA TGTGTTTTGG GTTCTTTTTC AAAGGCATAA GGATTTTTAA AAATCCCCCG 3180

ACCAATCATG ATGCCATCTA CACCATATTG TTCTGCTAAT TCTAGGCCCT TTTGACGATC 3240

GGGAATATCC CCATTAATCG TAATTGTCGT TTGCGGTGCG ACACGGTCCC GAATAGCCAT 3300

AATTTGCGGA ATGACCTCCC AATGGGCATC CACTTTGCTC ATCTCTTTTC GTGTTCGCAA 3360

ATGAATGGAT AGATTCGCAA TGTCTTGCTC TAATAAATGC GTGATCCACG CCTCCATTTC 3420

CGCCATTTCA GTAAACCCAA TGCGTGTTTT GACACTAACA GGTAAGCCAC CTGCTTTGGC 3480

AGCGTCAATC AATTCAGCCG CGACTTCTGG GCGCAAAATT AGCCCGCTGC CTTTTCCACG 3540

CTCAGCCACG TTAGGCACAG GACAGCCCAT ATTTATGTCT AACCCTTGAA AGCCCATCTC 3600

CGcTACGCCG ATACTCATTT CACGGAAAAA TTCCGGTTTA TCCCCCCAAA TATGTGCCAC 3660

CATCGGCTGT TCATCTTCTG TAAAAACGAG GCGCCCGCGT ACACTATCTT TTCCTTCAGG 3720

ATGACAATAA CTATCCGAAT TAGTAAATTC TGTAAAAAAC ACATCTGGTG CCCCAGCTTC 3780

TTTCACGACA TGACGAAAGA CCACATCAGT GACATCTTCC ATCGGTGCTA AAACAAAAAA 3840

GGGCTTTGGC AATGTTGCCC AAAAATTCTT GCTCATCTTC ATATACTCCG TTTCTGATTT 3900

TTTCyTTAwT TTCAACGACA AwTGTCGACA TAATCTGGGG CGAAACAATG CTAATT 3956

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAnCAATTTT TGgATTAgCy GCTGGGTTTT CCAAnGnGTT TTTAgCkGCT AAAAGCGCTT 60

TTgGTAAcTC TGTAACGAGG AGGCAGTAAA nTGGTGCCCt TCACTTGGAG TGAACTTnyG 120

CGCTCGTtTG ACTACTTCTT GTAATTGGTC TTTATTTACA AGGGGTACTT CTTTTAATTG 180

AGCCATTGCA GTTTCCAATG CGTTTAGAGC CTCTGAGACT TCTTCTTTTG TCGCCGTTTC 240

TTTCGCTACG ATTGCTTCAG CCGCTTGAAT TGCTTCTTGC AATTGTTTTT CTGTTTCTTT 300

TGTAAATTGG TATCCTTCTT CCGGCTTTCT TCCTCGGGCT TGAGCGATTT GCTCTTTTAA 360

GGTTTCCTTA TCAACGGCGA CGGGTTGTTC TTTTAATTGT GCAAtTGcTT CACGCAATGT 420

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TGCTGCTAAT GACTCTTCGA GAACTTTTTT AGTTTCTTCG GTGAATTCTT GCCCATCACT 540

TGGTTTCTTC GCTAGCCCCT CTTGAATTGC TTTTTCTAAA TCAGCTTTAT TCGCTACATC 600

AGGCATTTTT TCCAACTGAC TTGCAGCCTT TTCTAGGTTT TCCGCGGCAG CAGAAACGTC 660

TGTCTGTGTG GCTTGTTCAT TGGCTAGAAC AGCTACTGCC TCATCTAAGA TTGGTTTAAA 720

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TGGCTGCTCA ACAGTTGTCG CACGTTTTAC GCGAGTTGTT TCTTTTACTT TAACTTTAAA 960

GGTAACTAAG TCCATTGAAC CATTTAACAA TTGTTTATTT CCTTGATTAC TAAGAACTAA 1020

ATATAGATTC TCCACATCAT TTGAATGTTT CCGATATTTA GAATAATTTT CCATTTGTTG 1080

TGTATTATTC GTGGTTGCAG GCTGACCGAC AAGTTCAAAT TTGCTAGAAT CAAAGGACAT 1140

TTTTGTGCTT AACGCATTAA TGTTTTTTAA GTCTTGACCT TTAAGTATAA AGGTTAATGT 1200

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CGCAATTTCT TCGACATCAG GTATCTCAAT CCCACCATCT AATTGTCGTA AAACATAACT 1320

GATATCATAA GCATCAATTA CCCCATTTTT ATTTAAATCA CCTTTTTCAA CATAGCCATT 1380

AAAGTCACTG TCCACAGATT CTAAGCCTGT ATAGTTTCGA TAACTCATTG CATCATTTTC 1440

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CTGCAAAATA TTTCCGTTGC CGGcATTGTC TCTTGGCAAG TATTCAATTT TATCCATTTG 1740

ATACTCCGCA CCAAGATCAA ATTTTAAAGA CAAGAAATTT CCATCACTTG GATTAGCGAT 1800

GCCTGTTGAC CAGTTCGTAT GCCAACCTGT ACTCAAATCT TTATCTGTTA ATTTCTTCAA 1860

TTCTGCGCCT GGTTGTTCTG GTAAATTACT TGTTGCTTTG ACTTGATTAA TTGTTTCTTT 1920

ATAGGGATCA TCTTGTGTTT TTCCTTTAAT CGGTTCACTC CATTCAGAGA CCCCGTTTTT 1980

TCCAACAGCT CGAACTCGAA AAGTATGTTC GCTTAGGAAG GAAAATCCAT CAAATGTTGC 2040

TGTATTCGTT TGAATATTTC CGrAAACAGT CCCGTCACGC TCTACTTCAT AGCTTGTTGC 2100

CTCAGTTACT TGATCCCATT GAAGAGTCAA AGAAGATGGC GTTGTTTTTT CTTCATTGAT 2160

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CTGATTCACT TGGAATTCTT TATCAAAATA ATATAGATTT GTGCCAGCTA AAAATTCTTC 2400

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GGsCGCTtCT GAAGCTAGCA AwTCAAGCGt GGTGCTtCGT tCATCAACAA AGnCTTtATA 2520

ACTTCCTTTt GTCGGTtCGA tAGTaACGGT CAGATCCCtT TTcGTTTGAT TTAGGGCCTT 2580

GACTATTTAT TTTAGTCGTA GCTGATTGCC CAGCTTCATA ACTAGTTGAA ATTCCGTCAT 2640

CTTCATACAT ATTAAAAGAA- GTGGTGCCAT TTGGATAAAT CAAGAAAGAT CGTTGATCTC 2700

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ATTCTAAAGC CATGGCCCGT ACCATTGGTA GTCCATCAAC TGATTCCTTG GCAATACTGT 3060

AGTTATAAGG CATCATCATT GATTTTAATT TTAGATACGC TCGGTTCAAA TCTGTGGCTT 3120

CTTGATCAAA AGCAAATGGC GTTTTTGGAT TGGAGCCCCA GCCGTCCATA TTTAGCTGCA 3180

CTGGTGTAAA AGTTTTCCAT TGGAAATCAC GTATGTTGAT CTCTTTATTT TTTCCACCAA 3240

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CTTTCGCAAT ATCCCGTTCT CCTTTTTTAG GATTTTTAGG ATCCGCTGGA TGGAGATTAG 3600

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TTGGCAAGAA CCACCCTAAC GGCATATCGT TTTTCTTATA TCGATCAATA ACTGCGCGTG 3780

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TTGTGGTTTT TTGTGGATCA TGACTTCCAA AATCATAGTT GCCAGGTTTC CATGTATTTC 4140

GAACAACGCC ATACCCTGCA GTTGACCAAT AAAATGGGTT AGGCGATGCT ACTCCGCCAT 4200

CTACCCAATT GTTCGTATTG ACAATCTGGA TAGCTGTTCC TTTATGCGTA AATCGACCAT 4260

TTTGAGTTCC TCCGCCAAAA TAATTTTCTT GACTACTTTG TTTTAACGTT TGTGTAGCTT 4320

TATCATTTTT AAAGGATAGC GGAgCGGTTT CTTCTAAAAT AACTTGATTC TTTTTCTTGT 4380

CTAGAACCTT CATTAAAGCG CTTTCTTTTT CGAACATAAT TTTTAAACCa TTATTTtCTA 4440

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TTATCGTATG ATGGTTTTTT TGTGTTTGTC AACGGTTAAT TATAGCAGCC ACCATTAACA 5220

AGTATTAACC CTTGATAAAC CTGTTAATTC ACTTATAATG ATGATTTTAT TGCGAAAATA 5280

TCTACATCAG AAAAAGAAAG ACTTTTTCAA AAATCTAATA CCTGTTGCTC AAATCTAGTC 5340

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GTGATTGATT TGACTTGCTG GTGTGAAAAG CAAACTAATG ATGATGCCAA CTATCAGTAC 5460

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CGAATCACTA AAAAACTAAA TTAACTGCGA AAATCAATGA CCATGCGCCC GCGAATTTTT 5880

CCTTGTTCCA TTTCTTCAAA AATAGCATTA ATTTCTTCTG GTTGACGTGT TTGACAAACA 5940

GGAACAACTT TTCCTTCTGC ACCGAATTGG AAAGCTTCTC TTAAATCTTG ACGGGTTCCA 6000

ACTAACGATC CGACTACGTG AATGCCATCA AGAACAAGAC GTGGAATAGA TAAATCCATT 6060

GTCTCAACAG GCAATCCAAC GGCGACAACC GTTCCTCCCG CACGGACTGC ATCGACTGCG 6120

CCATTAAATG CTGATTTAGC TACCGCAGTG ACTACTGCTG CATGGACACC GCCAATTTCT 6180

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CAAGTAATAG AGGAAGCTGG CTCTGATGCT AAATTTTCTG GCACTTTCAC TGcATAACCG 6480

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GAACGACAAA GCGTTTCTCG ACCAGAAGTA CAATATTCGC AATGCCCGCA GCCTTCATAA 6600

AACCATGCAA CAGATGCACG ATCACCAATT TTTAAACTAG TAACGTCTTT TCCAACCTCC 6660

GTCACAATCC CAATTCCTTC GTGACCTAAG GTACAACCGC TAACATCGCC AAAATCTGCA 6720

TTCTTAACGT GTAAATCCGT ATGACAGACA CCACAGACTT CCATTTTCAA CCGCGCTTCA 6780

TTATCTTTCA ATGGACGCGA TTCTTTTTCA ACAATTTTTG TTGTTTTTCC TTTTGCTGCG 6840

ACAATTGCTT TATACATGGT TCTTTCCTCC TTGTTTCTAT TGTGAATCAT TGAACAATAA 6900

TAGTATAATA CTACTTTCCA AAATAAGGrA CACCAATGAC TtGCGTAAAT TAACGCTAAT 6960

TTGaCAATTT ATCCTkGCTA GACAGCTAtc TTCCCTTATG TCATAGATAA TTCATACTGG 7020

CATGAnTTTC TCTGCATAAT TGnCAACTAT TTT 7053

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ACTTATTTTA CTAACGTCGT GACGCTAAGT TTAGGTGGAC TTGTAGCGAT AGTGATGTAT 60

ATCGATCGAA TTTATACGCC GATAGCCATA TTTAATGTTT TATTTGTTCA ATATAATTTG 120

GnATAAAGTA GCCTATCAGC GCTTGGAAGA TTTTTATAAA AAAGAAGATG ATCCTGACTT 180

AGCGGTTTCC GGCAAAGCGT TACCTGAAAT TCAAACAATT TCATTAAAAG ATGTGTGTTT 240

TAGCGTAGAT AGTCAAACGA TTATGTCCCA ACAAAATCGA CAATTTTCAA TGAATAAAAC 300

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TTTGGAAGAT TATTATGAAA AAGTTTTTTA TTTATCTCAA GATGTGCCAA TATTTCAAGG 480

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TATGTATCGT TTTCAGTTGG GGGAACTTTA TGAACGGTTG CCGGAAGtTT AAACACTATt 600

GTGAGTGAAA AAGGAtGAAT TTTTCTGGTG GTGAAAAACA ACGGATTGCT TcACACGCTT 660

AGCATTTACA CAAGCAGAGA TCCTTATTTT AGATGAGGCG ACTTCTGCaT TGGACGAAAA 720

GnCCGAAGAA AAAGTGTTAC AAGAAGTACA AAAATTTACC CACAATAAGT TGACTATTTT 780

GGTTACTCAT CGACCTAAAA CCCTGCGATT TGTAGATGAA ATTATTGATT TAAATGAGTG 840

AACTTGTTAG CTCTTTGGCG CTTCTTTTGC TACACTTTTT ATAAGAATTG AGAGAAAGGG 900

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CTTGGTCCAA GAAGGCATTT TTCCGTGTCA GACATTTCTG GATATCGCAG GTGGGACGGG 1080

ACGATACTTA CCTTTTTTTC AAGAGCAAGT CACGGAGTAT ACGCTAGCCG ATATTTCTCA 1140

GAGAATGTTG GAGATTGCGG AAGCAAAAGC ACAAAGCAAC GTTGTTTTTC TTCACCAAAG 1200

CCAAGAAAGA CTGATTGAGA CTGGGAAAAA ATTTCAAGTC GTTTTTTCAG CGATGAACCC 1260

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CATCGAAAAA ACGAACAGTT ATCTTACAAA ACTGTTCGTT TTTTTTGGTC TATTTAGCTT 2160

TCATCAGAGA GTAGAAAGGA ATCATTTTCT TACGATAACT AAAGAAAATA ACn 2213

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ACGTTCAGGA ACTGATACCC TAGATTTGCG CAAGTTGCAT CGTCCGCAAa GATATCaTCA 60

ATCACCACCA ACGCCGTGGC ATTATTTTGA TGAAGAATGT CATCAAAAGC CATGTAATCT 120

TCAGGTTTTT CTAACGCAAC GCTTGGTAAA ACAGTTAATC CTTGCATCAT CATTGCTTTT 180

TGATAACCAA AGTAACGTTC AAAGTACAAA CTTTCATGCG TTGTATTGGT CACAAATAAA 240

ATATTTTTAT GGCCGTTTTC AATTAAAAAT TCCGTCGCTT GTTTCCCTAA TAATTGaTTA 300

TCATTATCCA CGTAAACTAT TTCCGTTTCA TGTTGGTAAG GTTGACCGAT TAAAGTAAAG 360

GGAATGTTGT TTTCGTCTAA GTAATCAATG ACGGGGTCCT TACTATCTGA ATACACAAGA 420

ATAAAACCGT CCACTTGTTT TTGAAGATGC ATTCTTTTAA CGTTTTCCAA TAGTACATCA 480

AAACTTTTGG CAGTTGCAAT AGCAGTAGTC ATATCGTAAA GACGGGCTTC CTCGTTGATG 540

GCTTCCATAA TTTCTAAATA AAATGGATTC CCTAACCGTT CTTTCGAATC TAAAGGAGGT 600

AAAATTACGC CAATGGCACT TGAAATTCGT TTACCCAAAt TCCGTGCCGT CATATTTGGC 660

ACATAGCCTA AGTCATCCAT GACTTTTCGA ACTTTCTTTT TTGTCGATTC AGAAATACTT 720

GGATGATCGT TAATGACACG CGAAACGGTT GAAGTTGCAA CCCCCGCTTT CTTAGCGACA 780

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TCGCTTGTCC ATTAATAGAA AATGGAGCCT CAAAACCAGT CGTAGAAAAT AATACCATAC 1020

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GTTGGAGGAT TGTTTCGATA GGTGTCAGTT CATTAAAACG TATGGATAGT TCAGAAGCTG 1200

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AAGATAGCAA ATGTGACAGA ATGTCTAACT TTCCATCGCC AGATAAATTA AAGTAGGCGT 1320

GGTTCGTAGG ATTAAAAAGT GTTTCCTGTT TACTCCGTCC AGTACTGATC aTTCGTAAAT 1380

GATTATCCTC TAGCTGATAA GTGATGGTGG CCTCAATTGG TCCAGGATAG CCAGAAATGG 1440

TGTCGGTTAA ATGAAAAGCA ACGCCAATGA TATCCTTTTT TTCAAAGGGC TCGACTGTCC 1500

AATATTGAAA AGACCACCCC TTTGAGCCAC CATGGATATG ATGACCGTCG CTGTTTTGTT 1560

CTAATATTCC ATTTTGCCAA TGGCCATTAC GTATGCGTCC AGCAACTGGT CCAACAGTGG 1620

CACCAAAAAA GCTTTGATCC TTTAATACAT CTTGATACGA ATCATACGAT AAAAGGATAT 1680

TTTCCCAATG ATTATTTTTG TTTGGCATCA AAAGTTGATG GAGGCGCGCG CCATAATTGA 1740

GAAGAACGAC TTCTAAAAAG TCGTTCTTCA AAGTAATTTT TTTTAAGTTT GTGTTTGGAA 1800

TATCGGTTAC GGTGATACGA TTATCCTTCA TGATCAAGCC ACACTTTTTT TAAGTAATCA 1860

AACGTTAAAG CGCTCGTCTC TGGCACGATA GGCAACCCTT CGCCTAACTC TTCTTTGCGG 1920

CCAACGCCAA CAGGTTGCGC TCCACTAGCA AGAATCGCTT GAATCCCAGC TTTGGCATCT 1980

TCAATGCCAA GACATTCTGC TGGTGTCAAA TCAATTTCTT TCGCAGCTAA AATGAAAATA 2040

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GGCGTAATCG CTTGGATCAT TTCCAAGTAA TAATCGTTTT TCCGTTGCGC TAACTGGGCA 2280

AATTCTTCAG AAGAAAACGT GCCTTCTTTT TTTCCGTATT TTAACAGTAA CTGCAGAGAA 2340

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AATGTGGAAT GAGTAGGCTG TCCATGTCGC TGGTAAAAAG GGTGCAAATT TTAGTTGTTG 2700

ATGGTCCGTT TTCATTTGGG CAAAACCTTG AACAATCGCT AGCCAACTAC CAGTCATTGA 2760

GGTAATGTGT AAGCCATCTT CTGTATCATT ATTGTAATTA TCTAAGTCAA GGCGCGCTGT 2820

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TTTAGCTAAT TCGTCGTCTG CAATTTTGAG CGTTGTTTCT TCTTGGAATT TTAAATAAGA 3240

CTCACGGGTG TAACGTAGAA CCCACGCAGC GATGGTATTG GTATACCAGT TATTATTGAT 3300

ATTATTTTCA TATTCATTTG GCCCCGTTAC GCCATGAATC ATATATTGTT TGTGACGTTG 3360

GGAAAAGTGG ACCCGATCTG CCCAAAAACG AGCGATTGCT ACAAGTACTT CTAGACCAGC 3420

ATCTTTTAGA TAATCTTCGT CTCCTGTATA GTTGACATAA TTATAAATCG CATAAGCAAT 3480

CGCACCATTT CTGTGAATCT CTTCAAAAGT GATTTCCCAC TCATTATGAC ATTCGACACC 3540

AGTAAAAGTA ACCATTGGGT AAAGCGCACC CTTTAACCCT TGTTGTTGGG CATTATGAAT 3600

GGCTTGAGGC AATTGATTGT GGCGATATTT CAGTAGATTT TTAGTAACTT CGGGCTTAGC 3660

CAACGCCAAG TAAAGTGGGA CAGCATATGC TTCTGTATCC CAATATGTGG CACCTCCATA 3720

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AGGGTACAAG GTAGTCATTT CTGCAAATAA TTCGTTTACT CGTGTGATTT GTTGCGTTTC 3960

TGGCACATCA CGACTGGTAA CGACAAGCAC TTCTTTTGtG ATGGCGGTCG TTtCGCCtTC 4020

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AACAGAGGCT CCATCGATGA AATGGCGCAT GCCTGCAGTC ACTGTAAAAC GCTCTATTTC 4140

AAAGTTGTTA GGAATGGTCT TAGTCGTAAC AAAGCCAAGT GTTTCTTGTG TTTCAATAGC 4200

TCTTTCTTCC CAAAAATGTT CTTCATAATT GCTGTCTTCA TTTTGAACAT CGCCATCCAA 4260

TTTTGAGTGA AGAGTGATTG TGCCTGTACC TTCCAGCATT TCAATTGTTA AGTGGATGTA 4320

AGCTGCCTCT TTTTTTTCTA AGCTTAAAAA ACGTTCAAAA GAGAAGCGCA CTTTATTCTT 4380

CGGTGTTTGG ATGGTGAATT GCCGAGAAAG AACCCCGTTT TGCATGTCTA ATTCTAAAGA 4440

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TGCGATGAAA TTAATTGCGT TAATCACTTT ACCAAAATAT TCAGGATAAC CATTTTTCCA 4560

CCAACCAACA CGTGTTTTGT CTGGATACCA AACACCTGCT AAATAGGTTC CTTGATGGTG 4620

GTCGCCAGAA TAGTGTTCTT CAAAATTTCC CCGCATCCCC ATATAGCCGT TGCCAATGCT 4680

TGTTAATGAT TCTTGTAAAC GTAAATTTTC TTTATCTAAG TGTGTAGTAC GGATTTTCCA 4740

AGGATCAATT TGGAATAAAC GTTTGATTTG TTTCATGAGA ATCCCCCTCA GTGATTTTAT 4800

TGATAGGT 4808

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAGTAGGAAA CAGATATACT TAATATAGAA AATTCAGATG CACTTATTGG GAGGTTATTT 60

TATGCAACGA AAAGATGTTA CACCTAATTC AGATAAAAAA AGTTTATTGC AAAAATTTGG 120

GATTGGTTTA GCTGGCGGCT TACTTGGTGG CGCCCTTATT CTAGGAGGCG CTTATTCTGG 180

GATTATTCCC ACACCCAACG GCGGAAATAA TGCGGCGACG ACGACATCCA CTAATCACGG 240

CGACACAAAA GTCAGCAATG TAAGTTACAA TGTGTCTAGC GATGTCACAA AAGCCGTGAA 300

AAAAGTTCAA AATTCTGTGG TTTCTGTCAT TAATATGCAA AGTGCTAGCA ACAATTCTTC 360

GGCAGATGAT CCTTTTGGGG GATTGTTCGG TGGGAATGAA GGTACTCAAG ACTCTTCCGG 420

cAACAATGGT AACGATTTAG AAGCAGCCAG TGAAGGTAGT GGGGTTATTT ATAAGAAAGA 480

TGGTAAAACG GCTTATGTCG TGACAAATAA CCACGTCGTA GATAAAGCGC AAGGATTGGA 540

AGTTGTTTTA TCTGATGGTA CCAAAGTGAA AGGCGAATTA GTCGGAACCG ATGCTTACAC 600

GGATTTAGCC GTGATTAAAA TTTCTTCCGA CAAAGTTGAT CAAGTCGCTG AGTTTGGAAA 660

TTCTAGTAAA ATCACAGTCG GTGAGCCTGC TATTGCAATT GGTTCCCCTC TAGGCTCTGA 720

TTATGCTAAC TCTGTCACAC AAGGAATCAT CTCTTCTGTG AATAGAAATA TTACCAATAA 780

AAACGAGTCT GGTGAAcCAT CAATATTAAT GCTATTCAAA CCGATGCTGC CATCAATCCA 840

GGAAACTCTG GTGGTCCACT AATCAATATT GAAGGACAAG TCATTGGaAT TAACTCAGTA 900

AAAATTGTGC AATCAACTAG TCAAGTGAGC GTTGAAGGGA TGGGCTTTGC CATTCCAAGT 960

AATGACGTAG tCAACATTAT CAACCAATTA GAAAAAGATG GTAAAGTGAC GCGGCCAGCT 1020

CTCGGGATTA CGATGTCTGA TTTAACAGGT ATCTCTTCAC AACAACAAGA ACAAATTTTA 1080

AAAATTCCAA CTTCTGTAAA AACTGGCGTA GTGGTTCGTG GTGTTGAAGC AGCGACCCCT 1140

GCTGAAAAGG CTGGATTGGA AAAATACGAT GTTATCACGA AAGTTGACGG CCAAGACGTA 1200

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TTGCTGAACA AATCATTCCA AAACTTTCTT CACCACGTAA AACCCCTGGC CAAATCATTA 1560

AACCATCAGG CATCATTGCG CCTGGTTTGG CCACAACTAC TTTTTGTCCT GCTTTGATGT 1620

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GTGCCACATC GCCGACACGT TTTACTTGGT TTTCCGCCCC TTGATCGTCC GCAACGATGA 1980

CAAGTAAGAC ATCGCCAACG TGTTCTTTGT TATATGCAAA AATCATTTCT GTTCCTCCTA 2040

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TGGaAAGTTG CACTTACAAT TATTGAATTT TAGGCAATCC CTAATGCTGC CAAAAAAATA 2160

GATAATAGAA TAACCCCAAC TAAAAGTGTC GTTGTTTTCA CTTTTTTCCC TAATAACCAG 2220

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TGTAATGGCG TGGCGATTTT TCCAGAGCCA ACTTTGGCAG TTAACTCAAA CACGACATTA 2340

GAAGCCGTCA TCCCACCAAT AACCATTAAC CCTAAAATAG AGGCAGCTGT GGTAACTTTT 2400

TCGATTACGC CGCTATCTTC AACATCACTA AAAAATTTAG CACCTAATTT AAACCCTTTA 2460

TCCAAACAGA TATACCGTAA AGCAAAATGC GGAATATTGA TAATCAGTAA AAAGGCAATC 2520

GGACCAAAAA TATTTCCTTG TTTAGACAAT GAAATAGCTA CACCTGTTGC GATAACTTTT 2580

AAGGTCCCCC AAAAGAAAGA ATCCCCAATC CCAGACATTG GTCCCATTAA ACTAGTTTTC 2640

ACTGCATTAA TACTAGCTGA GTTAAATTCA TGATTTTTAG CATTTTCTTC TTCCATTGCT 2700

CCAGAAATTC CTAATAATAA GGTAGAGATA TGCGGGGTGA CAGACATAAA CTCTAAATGT 2760

CGTTCTAAGG CCGCTTTCTT CTCTTCATTA TTTTTATACA ACCTACGTAT AATTGGAGCC 2820

ATTGCATAAG CATAAGCTAA ATTTTGCATC CGCTCATAAT TCCATGATGC ATCTAACGTT 2880

AAAGAGCGAA AAAATACAGA CCAAAAATCT TTTTTAGTAA TGACAGATTT TGTGTTTTTA 2940

GAATTCATTG TCATCGACAA CAGCCTCCCT TGTTTGACCA TCACTCATAT TCATATATAG 3000

TAGGACAATC ACGATGCCAA ACAAAGCAAT CCCCACTACT GAAATTTTTA AATAAGCAGC 3060

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CATCGCAAAA CCAATTGCTG GaATaATACC TGCCGCAATA TCTAATCCaT GCGTAATAAA 3180

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TGAAACAAAA TCTGGTGGAT TACTTGCGCC AACAGGAAAT GCACCCATAA ATACCAACTC 3540

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TAATGGATCC TCAACCAACG TATTACTAGC AATCAAAATA CAATCTGCTT CTAAAAATTT 4140

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AACTCAGGTA ATTGTTTTCT AAACAACTTA ATCTTTTCTA GTGATGTCTC TTCACCCGTT 4440

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ACATTTGTTC TTCCATTTTC GTCACCTTCC CGATGGAGGC TGATCTAAAA GGCTTCTTTG 6720

ACTAAGAAAC TAGAGTCAAA AATGAATTTA GGACCCTTGC GCAGAACGCC CTTTTGTCCA 6780

GCTGATTCTC TCTTAATTTA ATGGTTCCTC TGGTTCATGA AAATTAGCCT AAGCTAGTTA 6840

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GACCGTTTTC AATTACGACA AAACTCGGAA TACCAAAAAT ATTCCACTCG GCAGCCACGT 6960

CAATAAACTG ATCACGGTCG ACTTCGATAA ATTGAAACGC TGGAAATGCT TCTTCAATTT 7020

CAGGCATGAC TGGTTTAATG AAACGACAGT CTCCGCACCA ATCAGCAGTA AAGAAGAAAA 7080

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CGTATGGATG TAACGACCAC AAACGCCGAT GACTGTACTT GGTACACCGT TATTAGTTGT 7320

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ATTTAGAAAA AGATTTGGAA CAATAGCGAT TTTGGCTATT GTTCCAAaTC TTTTTTATAT 10920

AATCCCGATT AAAGAACCTA ACAACCCAAA AATCACAGTA AAAATAATTA AAGCAATCGG 10980

CGTGCGTCCT TTTTTCAACA TAATAAAACA AAACAGCGTA AACACTAAAG GTAATAAATT 11040

GGGCATGATT GTATCAAACA ATTGTGTTTG AAGGTCTAAC TTAGTGTCTT TCAAGCGAAA 11100

AACAAAAGTT GTCGTTAATT GTACACTCTT CGGAATCAAC GCGCCCACCA CGGAAATTCC 11160

TACAATTGTT GCTGAACGAG ATAATTTTTT AGTACTTTCG CTTAAAACTG AAATTGCTTT 11220

GACACCCATT TTATAACCTA GATTAATTAA CCCAATTTTG GCAGCCATAT ACGGAATATT 11280

AAATAACAAC AAGAAAACAA TTGGTCCTAA GATATTGCCT TCTAATGATA GTTGTGAACC 11340

AATCGCTGCT GCAATCGGCA AAACGGTTAA ATAAAATAGC GCATCCCCAA TTCCGCCTAA 11400

CGGGCCCATC AACGCTGTTT TAATCGCTTG AATGGATTTT GGTGATTCTT TTGACTCTTC 11460

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TAAATGATTT TCCAAAGAAA GAGCTAAGTC TTCTTTATCA CGATGAATCT TTTTCAATCC 11580

TGGAATTAAT GAGTAGGTCC AGCCGCCTGC TTGCATTCTT TCATAATTAA ATGAAGATTG 11640

TAGCAGATAC GAACGGAACA TTATTTTTTT TAACTCTTTT TTTGTTATTA CTTTTTCGGA 11700

TATCATATCA TTATATGTTT CTTCAGATGC CATCTTCTTC AAACCCTCCA TTATTATTTG 11760

ATGCAGTGAC TGTATTATTT CTTTGTGCGT AAAATTCATA TAAAGCAATT GCGACAGCTA 11820

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TTGCATAAAC ATCAAATTTA TGCATAATTG GTGACATCGC TGTATATAAC AAGGTAATTA 12180

ACGCTTGCGC TGCAACTGCG AAAGGAACAG CCAAACcTAC GGTCACTTGT GGGTCAGATT 12240

TTGTGATAAT TGCTAACGCT GTTCCAATAA CTCCCCCAAT TACTACGTTA GGTGGTTGTG 12300

CACCGCCGAT TGCTACTGCA CCAATCCAAA CTAACTCTAG CGTTGCTCCA GTGATTAACC 12360

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TATGTGTCTG TAAGACAAGC TTATCAACCC CTGCTATCCC AGCCCAAATT CCTACCAAAA 12480

TTGCCTGTAC TAACATTTTT TTCCTCCTaT TAaCTTCGTC TACTTTTTAT AAACTGTTTC 12540

ACCATTTACT AAGGTTTCTA GCACTTCATA TTTCTCATCA ATAATTGTAA AATTACCTAA 12600

AAGCCCTAGT TTGATTTCTC CCATAGATTC GTTCACATTC AACAAACGAG CTGGATTTTT 12660

CGTGACTGAA TTAATAGCAA TCACTTCTGG AAGTAATGCT TTTTCAACAA GGTTGCGAAC 12720

CATATTATTT AAATGGTTCG TACTTCCAGC TAACTTGCCA TTGGCTAAAC GGACCACATT 12780

TTGTTCATCA ATAACCATTT CGATCCCTTT TTCTGGTTTT GGATAAACGC CTGGTTGACA 12840

CCCTTTGGCC CAGATAGAAT CTGTCACAGC AATTAAATAG TCCTTGCCTT TTAGTTTGGC 12900

TAACACACGT ACTAATGAAT AATCAACATG TACCCCATCA GCAATAATTT CAGCAAACGT 12960

TTCTTCACTA TCCAAAGCAG CAACTACTGC GGTTGGTTTC CGGTGACTGA TATCTTCCAT 13020

TCCATTAAAC GTATGGGTAA AACTTTTTGC ACCTGCTTCG ACAGCTGCCA TTGCTTGTTC 13080

ATAGGTTGCA GCCGTATGGC CAATTGAAAT GACTACATCA TGTTCATGAC AATATGTAGT 13140

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GTAAGCTTGC CACTCTTTGA TAAATTCATG ATTGGCATGA TTGGCATCCC CACCATGCCA 13500

ACCATGATCG TGAATATCAA TAAATCCTGG AAGAATGCGC TTTTCTCCGT ATTCTTTGTC 13560

GACAGCTTTT TCATTGTACG GTAGAATTGC AACAATTCGT TGTTCTGACA CTTCAACTTG 13620

AGCTGGTTGA AATTGTTCGT TAATCCATAC GTTTTTACTT TGAATAATCA TTCTTCCCAC 13680

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TTTAAAGGCG TCTACATCTG TTTTATTAAC GGCAACAGCG GTAGCTACTT GTtTTTGcCT 13860

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GCCATGTTTA ACAATTGTTG GCGCAGTGTA TCCTCAGAAA TTGCATCATT TGCGACTAAA 14100

ATTAAGTTGG CGCCTAAAGA ACCGTTCCAT TGTGTTGCGA CTTGACCATG AATCAAGCGA 14160

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TTGGATAATT ACTTGCGACA GTCATTGAAA TTCTAAACGG TGTGCCACCT AAAAGGTCAG 14460

TTAAAATGAC CACTGCTGGA CACGTCTCCA GCATAGAGTC AACGGCTTTA CGAATGTTTG 14520

ACTCTAATAC ATCAAGCCCT GTATCATTGA AAAAAGGGAC TGCCTGAACA TTTGCTTGCT 14580

CTCCTGCAAT CATACTAACT GATTGATGCA TTCCAGTTGA AAATACCCCA TGCCCCGTTA 14640

AAATAAGACC TATCATTTAT TCTTTCTCCC CTAACTATTT AsTrmGCTTA CTATATATTG 14700

GATAAGCAGA ACTTATTTCT CAAAGAGTGT AACAATTCTT GTGACAATTG AGTATGCTTT 14760

CCCATGATTT TGGACGATGa TTTCTATTTA AGAACATGTC CCTATACAGA TACAAGGCGT 14820

CCCAACTTAA AGATGCTTTT GAAAAAATGC TCGACTACAA CCGTGAGTCC AAACGAGCCA 14880

ACAAATGTAC CCATATACAA CACAAGAATA ACCAAGCTGA CTGGTTGATt GGTTAAAAAC 14940

GGGTGGACCA GTTTCAAGAC CACTTGAAAA ATAAAAACAT TCGCTAAATA ACTGCGATAC 15000

GCATAAgTGG CTATCCATTT AACCATTGGT AAAAGACGAA TCTTTTTGGC TATTCCTTGc 15060

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AAATAAGGTA GATCGTTCGG AGTCATCTGT GTTCCATCAA ATAAATTCCC TTGGACTGCC 15180

TGCCAAAAAA TAAAaAGaAA CAACAGAAAT AGTGCCACTC TCGTCTTTTT CAaGAAAGTa 15240

AAAATTTTCC CTTGATACTT CGCTGCGATG ACCCCGAAAA TACCATAAAT GAGATAACTA 15300

AGCCCTGAAC GATCTATTAA GTACCAAAGA GAAGTTTCTA CATATGGAAA AATCATTTTC 15360

TGGTACCAGA AGCACCAAAG GATATGCGCA CCGATTGTAA AAAAGACAAT TGGTAAAATC 15420

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AATTGCAACA TCATTACGGC ATACCATAGA TGTGCCGCGC CATCACCACT GAGAACTTTT 15540

CCTAGAAATC CTAGGGACGT TTCATAGGGC ATTCGTTGTT GTAAACTAGG AAAAGCGTAT 15600

AGATAGAGAC TGGACCAGAC CACGTAAGGA AGCACCAATT CATAAAATTT TTCCTTTAAA 15660

AATTCAAGAT ACGATTCAGC TTGACTCTTT AACACCATGT TGTAAATAAT TGCAAAAATA 15720

AACATGGGTG CCGAATATTT AGACATT 15747

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1536 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGCGTGAAAA GTATAAAGCT TTTGAACTGC CAnATAAGGT AGGAACTTCC CAGCAAAATA 60

ACCTnGTAAT TGACCATAAG CAAACAATGG CGAAACATTT CTTGAAAAAA ATTGTAACTT 120

GTAAAATTCT TCATAAGGAT CCCCAAAATC CCATCGATTA AAATCAATCA CACCGACCTG 180

CCTAGTTGGC AAGTAAATAA AATTTCCCAC ATGGAAATCT CCATGCTGAT AAACCACAGG 240

CCGTTGTTGC AATAACGGTA ATTGTTTTTC TAAATATGAA ATTATTGGCT GCTGGTACGG 300

CATACAAAAT TGAGATTCCT TATACTTATT TAGTTGGCTC TGCTTTTTTT CGTATAAATT 360

TTGCGCAATC TCTCTTTGAC TAATCCTTTC AGGCAACAAA AGCTTATGGA TTTTGTTTAA 420

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ATCGCTTAAG TCTTCACCTT CTAGATACGT TAATAACATG TATCCTTGTT CACTTTCAGG 540

AATAGGTGCA CATAAAAAAG GTTTAGAACT GGGAAATCCT AACGCCGCTA CTTTTTTGAT 600

AAATTGATAT TCTTGTTGTT TGGCTAATAA CTCTTCTTGT TGAAAAATTC GCAATAAAAA 660

GGTTTCTTGA TTTTTGGTAA CTTTAAACTT TAAATCAGTT GACCAACCAC GGTGAATAGC 720

TTCAACTTTT TGCCATTGCT GAAACGCTGG AATCTTCTCA AACGCCCTCA TTACTTTCGC 780

CTCCATTTCC CTATTGGTTT TAGTATACCA AAGAAAAAAG GCTGGAGACA ATTGGGGATA 840

AATTGTCTCT AGCCTTCACT GGTTATCATT TTCTAGTTTT CCTTATATAA AtCGTTCCAC 900

TCGTTACTAA GAAAGCTCCT CCTAAAACAA CCCAGAAAGT ACTAGGTACT TCTGCACCTG 960

CTTTTGGTAA TACTTTTTTG GGAAGCTGTT CTTTTTTCCC AATCATATTT TTATCAGAAA 1020

AAGCATGAGT ACTTTCTGTT GATTTGGTTC CCTGATTTGC TGATGAATTC AGCGAATTAT 1080

CTAAGGATGA CTCACTAGTA GTTTTTCCAG ATTTGTCTGG GTTTTGGTTT TGGTTTTGGT 1140

TTTGATCTTT TCCTTCGATT GGTCCTTCAC TTGTTTTTGT TTCTTTGTCT TTATCTGGTT 1200

CGCCACTTGT ATCTAGTTCT TTATCTTTAT CTGGTTCGCC ACTTGCATCT GGGTCTTTAT 1260

CTTTGTCTGG TTCGCCACTT GCATCTGGGT CTTTATCTTT ATCCAGTTCG CCACTTGCAT 1320

TTGGTTCTTT GTCTTTGTCT GGTTCGCCAC TTGTATCTGG TTCTTTGTCT TtGTCTGGkT 1380

CTTCTACATG TGGTTGATTT ATCTTGTGGT TATTTTCAAA TAAAGCACCT AATTGTAGCA 1440

ATGTTCGGTC TTCATTTAAT GCACTATTAA ATTGAATCCC CAAAGGCAGT CCTTCTTTTG 1500

AAACGTAAGT TGGTACACTT AATGCTGGAT GTCCAA 1536

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GCCAAATTTG GTGGATCGTG TCCGCTTGGG AnnGCCTTAT GGGTGGACCC TACGTGCCAT 60

TTGGGTGAAA ACTAGGCCAT ATTTTAAAnG GAATATCCGT GCTTTCCTTG GCCACCGTTC 120

ATAATCCATT TCCACTGAAC CGCAAAAAGA ATCGTATCCA GAGAGATGGC AAGGCCAnAC 180

AGAGAAaTTT TyCTTkGGaA CAACTTCAAG AAACAATTCT TGAAAAAGCC AATCAACAAG 240

TAGGCAGTCG CCGGaCGACT AAAGAAGTCA TTAAATTTAC TACTAAAAAT AAAATTGGAG 300

ATAAAATGAC TCTTGGTACG AAGAGCTTGT TAATTTTGCT ACTTTGTATG ATTTTTTATG 360

TAAGTCTTAC CTTTGTAAAG GGTATTTCAT TAACAACAGC TTTCATTCAT CCAGCGGAAA 420

CAATTCAACG TATATTTGTT CCTGAGAAAG TAGCAGGGAA GGATACAAAT GCTGTGAAAa 480

CGACTAAAAC TAAACCAGCT TCAACAAAAG AATCTAGGCA GCAGGAGGAA GTTCAGCCTA 540

GCCCAACGAA CGTACCAGAA AATAATAATA GCGAACAAGC TGTGTCAACG TATACTGTGG 600

AAGTTGGAGA TTCAGTCAGT TTGATTGCTG AAAATCACGG ACTCACTATA GAACAACTTC 660

AAACTTTGAA TCCAGAAATC ATTGAGGTAC CTATTTATCC TGGACAAGTG TTGAAATTGA 720

AAGAGGTGAC TGAATAATGC GCGAGGTAAA ATTAATTTTA GCTGaACAGT TTTCaTACTT 780

AGGCsTTGCa CAACGAATTG CTAAATACAG TAATAAAGCA TTATATCAAa GCCACATCTT 840

aGgAAATTTA TGGCAAATTT TAAGTCCTTT AATTCAGTTA GGTGTCTATT ATTTTGCTTT 900

TGGGATTGCC CTTGGTGGTG CTCGAACCGT AAAAGGAGGA GTATCCTATA TTGCTTGGTT 960

GATGGTAGGA TTAAGTACAT GGATTTTTTT AAGTACAGTA ACAAAACAAG CTTCTAGTTC 1020

TGTTTATATG CAAGTTGGCA TGGTCTCTAG AATGAAGTTT CCAATAAGTA TTTTGCCAAT 1080

GGTTAAAATA TTTTCTGAGT TACCAAGTTA TTTTGCATTC ACTACGTTAG CAGCGATTGT 1140

GTCAATCTCG ACAGGTGAAA AGATTTCTAT TTATTGGATT CAGCTACCTT ACTATATTGT 1200

AGCGATGATT ATCTTTTTAT ATAGTTTTAG TCTAATTAAT TCAACTATTG CTGCATTAAT 1260

TAGGGATTAT CAAATTTTCT TGAATTCTAT TATCCAAGTA TTAATGTATA TGTCAGGGGT 1320

CTTTTGGGAT TTGAGTACAA AGAATTTACC GTCTTGGTTA TCAAAAATTC TTATGTTGAA 1380

TCCTTACGCA TATATTATTA ATGGATTTCG AGATACATTT TTCTATAAaa GATGGTTTTT 1440

TGAAGATAAG CCCCAGCTTG TTGTTTTTTG GCTAACAACA TTAGTAATAT TTATCGTAGG 1500

AGCTCATTTA CATGTTAAGT TCAGAAGTAA ATTTGTTGAT TATATGTAAC ATGTGAAGAA 1560

GTAAAACCAC CGTATACTGA CAAGAATACG GTGGTTTTAC TCTTTAATTG ACAATAGCCT 1620

TCTCTTTAAA GAGAAGGCTA TCTAACGAAT CAATATTATT ATTTTAAAGT TGGATCAGAC 1680

TATTTCTAGT ATTCAAGTAT TTTTCATTTA AGCGATGTAT TCCCTACCTC TAATACATCC 1740

TTGTATCTCT CTAGACACGC CAgTTTTGAA TAAAATCATC AAAACAAyTG AATGGTTCGT 1800

TTAAAAATAT TTTTCGTGTT CTAATTATTA TAACATAAAA CTCGTCAACT GACCACTAGC 1860

TGgACGAGTt CATAATTTkT CCAGATAAAT AGACAGCCGT TTTCCGCCGA CTGTCTAAGA 1920

TTAAGATAGA TTTGTAAAGA AGTGgAATAA ATGgCTTCCT ACTATCTCtT TATAACAkGA 1980

GGrAAAgAAA ACkGCaAAaG ATAGCTGTGT TTTTTGAAAA AAAGATCAGC TGGTTTCCGC 2040

CAGCTGATCA TCCGTTGAAA AGAGATATAA AGAAGTGAAT AAAGCTTGCT TTACCTCTAT 2100

TTTATACCAT GTTTTGATTC AAATAACTAT TCAGTATTAG TTATACTTAA ATAATAAATA 2160

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CAAGCAGGAA ATCAGCCAGT TGCGTTAGTG ACAACATTAA GTGATGAAAT TAATCGTTCT 2340

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CTTGTTATAT CACATAACAA TGAAACAAAT TACACAGAAA AAGTGGTTGA GGCACTGCAG 2460

GAAACCAAAA AATTAGGTGC AGAAACGGTT TGTTTTGGCG ATATAGATAT TGAACAAAAT 2520

GGTGCTTGGG ATCGCCAAGT TGCGTTAAGT GCTGGACTTG AACCACAATT ACCTCTTTGG 2580

CAGGAAAATC GCGAacACTT GTGAAAGAAT TCTTGGCAAA AGGGTACACA GCAATTATCA 2640

AAACGGTCAG CAAAGAGGCA GGCATTCCAA TAAAATTTTT AGGAGAACCG TTAAATGAAA 2700

CATTTATCAC GTACCTTAAA GAGCATCAAT TAGATATTTG CGGAGAAAaC GGGGAGTACC 2760

ATACGTTGGT AATTGACGGC CcGCTATTTA AAAAGAGGCy CAtTATTATm CTcAGGAATT 2820

aTGAAgcCTT ATGCTaTyCT TgATtATtGA TGCTTAAaTG AAaGTAAaaG GACACAAGCT 2880

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AAAAGAATTA ATTAAAGAAG CCCAAATTGC GAAAGATACT CGAAAGATTC CAGGAAAACT 3060

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AGAACCGTCT GCTGAAACAA AAGAATTCAA AGTGAAAAAA GTGATTGATT AATAAAAAAG 3180

CAACGAATTT TTCTAAATTC GTTGCTTTTT TATATTTTTT TACACAAATG ATACAAAAAG 3240

AATATCAAAA TCAAATAAAT GATTAGTATA CTTGAAGaAA CAAATAGGAA GCAAAGCAAA 3300

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GTTTGAAGTA GCCTATTTCC GTGATATCCA TGAAATACCT TATCAAGAAT TATGGGAAAA 4020

TACCAAGAAG AAAAAAATCT ATTATTTTTG ATATATGTAT TGTGAAAAAC GTTTCTTTTA 4080

TTCGAGTATC TAAGCAAGCA TACTAGTGTA TTTCAATAAA ATACCATGAT GTTCATAGGT 4140

TTTATAATTT CAGCTCACAG ATTTTTGTTC AATAAGAAAA AAATTACAAC TAAAATAGAA 4200

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GGTCTCCTAA ATCTTTTCTA GCTTGTTCTT CAGAATATGA ACCATCAGTA GCAATGTTAT 4620

TTACTTGGTC TGCAGTAACT TTATCATGTT TTGCAACCTT CAAGCCACTT ACAGATTTGC 4680

TCGCTGCTTT GCCATCAGAG AATGAAACAG TAATAGATGC aAGAAGATCA CCACCCTTGA 4740

CATTTGTCCA AGATAGAGTA GTGGTAGAGA TGCCTTGGAT ATCTGTTGTA GAAGAAGAGG 4800

CTGGTTCACC TAAAATTGCT TTTACTTCAT CTTCTGTAGA ACCGCCTTCG CTGCTGTTCA 4860

TAATATCACC GACATTAATT TTATCGTAAG TkGCTTTTAA ATCAGAGTTA TCTTTCGATT 4920

TATCTTCTGr TTTCTTTTCA GAGCTTtCTT TTTTTGTATC ATTTTTTGAA CTATTCGTAG 4980

CTTTTGAAGA AGAGGCTTCT GTTTTCACTT CTTTGGTATC ATTGCTTGCT TTTTTATCCT 5040

CTTTGCCAAG ACCACTACCA GCAATCCCCA GTACAATAAC TACTACAACC CAAAACCAAA 5100

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GCCTTCCACC ATTTTTTGTT GGACGTTTTT TGACAAGGCA TTTTTAACTA ATTCTTTAAA 6660

CGATAATTTT CCTGAACGTC CCACATTGAA ACGTTTTGTT TCGGTGTATT CAATATCACC 6720

TACGCGCCAA ATGCGAATAC TTGTGCCAGT AGCTTGCAGT TGTCCGTCGA CTTCTGCATC 6780

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TTTTTCAATT GTAAAGGGTA AGACATTTTC TGGTAAAAAT TCGCCACTTA ATCGACCAGC 6960

CAAGACAACT GGATTATGGC AATAATAACA GTATGTGGCA GCCGTTGTTG CATCGGTGAC 7020

AATTTGAGCG CCACAGCTTG GACAATTAAA AATTTCCATT GTGCCTACAT CTGCAGTTGT 7080

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GTTGGGATAG ACATGTACAA CAGAACCATC TGTTAAAACA TCGTCCGTTC CTTTACGATT 8520

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CAAATGAAGA TAAATTTAAT TCTGAAATTC TTTTAGCAGA TACGGGCTAC GGTCAAGGTC   10500
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GAATAATGAA GAAATTATGG ACTATnTTTT 17250

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7947 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AAGAATGACA AAAAAATGTC CGAAGTGCGG GAACGAATTC GATGCAGAAT TAACGACCTG 4980

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ACCAACTGAA TCCATTTCAG ATTCTGAAGA AGGGTTAACA AGTGCAGCGT CGCTAGAGGC 5760

ACCGAGCGAC GCTGATGCAA CCGAGGGAAA AGTTTCAGAT TCAGGTGTGA TACCACCGAT 5820

GAATGAAACT GGGAATGCTC AACCAGCGCC TGCTCCGAAG AAACCATCAA AAAAAGTAGT 5880

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AATCAAGCCC TGATGAAATT AAACAAACCT TTGGCATTAG TAAAGCTCAA TTTAAACGCG 7860

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TTGGcTCGTT GGrACAATCm AAAGAAA 7947

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GCACCAGCGT GGTTGGATCA TTCTGATCAC CCGTTTCATT GGCCCGATAC TGGTGTTTAT 60

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AAGATGTTAG AGATTTTATC CaAATCATTA AAGAAAATTA ATGGATAATC TAGCCTTGAT 780

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GGGTTCCTGA AATGTTGAAT AGAACCACAG GAATTGCTGA AATAGTTGCT GTAAATAAAC 1020

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GCTTC 7865

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4023 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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TGTTTGGAAT GGACCAATGG GCGTATTTGA AATGAGTAAC TTTGCCAAAG GAACAATTGG    3180
TGTTTGTGAA GCGATTGCTA ATTTAGAAGA CGCAACAACA ATCATCGGTG GCGGGGACTC    3240
TGCTGCTGCA GCAATTCAAT TAGGCTACGA AAACAAATTC TCTCACATCT CAACAGGTGG    3300
CGGAGCAAGT TTAGAATTAT TAGAAGGCAA AACTTTACCA GGTTTAGCTT CTATTAACGA    3360
TAAATAATCA GTTTAAAAGA CAATATTTTT AAAAAAAGAA AAGGATGTGC TTTTCATGCG    3420
CAAACCAATT ATCGCTGGTA ACTGGAAAAT GAACAAAACT TTAAGCGAAG CACAAAGCTT    3480
TGCAGAAGCA GTAAAAAATG CTGTTCCATC AAACGACGTT GTTGACGCTG TGATTGGATC    3540
TCCAGCATTA TTCTTAGCTC CTTTAGCTTG GAACCTAAAA GATTCTGAAG TGAAATTAGC    3600
TGCACAAAAC TGCTACTGGG AAAACGCTGG TGCCTTCACT GGTGAAAACT CACCAGCTGC    3660
AATTGCAGAT TTAGGTGTAG ACTATGTGAT TATCGGACAC TCTGAACGTC GCGAATATTT    3720
CCACGAAACA GATGAAGATA TCAATAAAAA AGCCAAAGCA ATCTTTGCAA ATGGTATGAC    3780
ACCAATCTTC TGTTGTGGTG AAACTTTAGA AACGTATnAA GCTGGTAAAA CAGCGGAATG    3840
GATCGAAGGT CAAATCACTA AAGGCTTAGT TGGTTTATCA AACGAACAAG TTGCTTCAAT    3900
GGTTATCGCT TACGAACCAA TTTGGGCAAT CGGAACTGGT AAATCTGCAG ATGCTAATAT    3960
TGCAGATGAA ATCTGTGGTG TTGTTCGTTC AACAGTTGAA AAATTATACG GCAAAGAAGT    4020
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TTC 4023

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GGGCGGTGTC ACTGCGTCTA TTTTCGGTTA TCGGCCAACC TTTTTCATTA CTGGTACGAT 60

TTTATwACTC GTTTTTGTTT TGAGTCTCGT CTTTGTCCAT GAAGAGTTTG TGCCAATTGA 120

AAAAAATCAA GCCGCATCTG GGAAACAAAT TTTAAAAAAA CTAGAACATC CCCACGTGAT 180

TCTTGGAATG TTTATTACGA CATTAATCAT TCAAGCTTCC AATAATTCAA TTAGTCCCAT 240

CATCAGTTTA TATATTCAAC AATTGTTGGG TGGTCACGGA AATGTCACCT TAATTAGCGG 300

AGTCATTGCT TCTATTCCAG GGATTGCAAC GTTAATAGCC GCCCCTCGTT TCGGCCGGTT 360

AGGCGATCGT ATTGGCAGTG AACGCATCTT GACAATTGGC TTAATTTTAG CCATTTTTGT 420

TTACCTACCA ATGGCCTTTG TTCAAAATGT CTGGCAGCTT GCCATGCTTC GTTTCTTAGT 480

TGGGATTTCC GATGCCTGTT TACTACCAGC TGTTCAAACG TTGATCACTC GTTATTCCCC 540

AAGTGACGCT GCAGGTCGTA TTTTCAGTTA CAATCAATCT TTCCAAGCGA CAGGAAATGT 600

GATTGGTCCT ATGATTGGTT CAAGCGTATC TGCCGCTTTC GGTTATCGTG GGGTCTTTAT 660

TTCCACTTCT TGTCTGGTTC TCCTTAACCT TCTATGGGTT CGTCGAAGCA CCGCCGAATT 720

AAAAAAAGAG AAAAATGATG ACTAAGTTAT ACACAGAAAA GTTATCCACA ATTTGAATTT 780

TTAATTTTTC TCTTTTTCTT ATTTTAAAAA AAATAGGCAT ATAAAACAAA AAAGAAAAGC 840

GGATATTTAC TGGTTTTATG ACCAGCATAT CCGCTTTTCT TTTGGtTAAC TATACGCTTT 900

TTGTTTCACA ACTCGTGAAA CTTTTTAGAC GTATTGTAGT TCTTTTTCAT CTTGGTAGGC 960

GCGATCAATT AAGCCGCCCC CTAAGCATTC CATCCCATCA TAAAAAACAA CAGCTTGACC 1020

TGGAGTGACT GCACGCGCTG GTTCCTTAAA CGTAACGGTT GCTTTTGTGC CATCTTCAGA 1080

TAAGGAAACA TGCACTGGAA TATCTGCTTG ACGATAACGG AATTTAGCCG TACAGTCAAA 1140

CTCTTTTGGc ATTGGTGTAT CAACAGTAAA ATGAACCTCA CTAGCTTCTA AATGTGtTGc 1200

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CCCAATCACA AACCATGGTT CTTGTGTTTT ACCGCCGCCA CCAATTCCTA AGCCTTGGCG 1320

TTGACCGATA GTATAATACA TCAGACCATC ATGTTGTCCT TTGATTTCGC CATCTTCTGT 1380

CACCATGTTG CCTTTTTTAG CTGGTAAATA ATTACTCAAA AATTCTTTGA AATTCTTTTC 1440

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AGCAATTGCA CGAACTTCTG ATTTTTCCAT GCCACCCAAT GGAAACATTG TTTTTGCCAA 1560

TTGGGCTTGT GATAATTGGC TTAAAAAATA GGTTTGGTCT TTATTATTGT CAATTCCACG 1620

TAACATATGC ACTACGCCAT TTTCATCTGT TTCTACTTGC GCATAGTGGC CAGTkGCAAC 1680

ATAGTCAGCG CCTAGTTGCA TAGCATAATC TAGGAATGCT TTAAATTTAA TTTCTTTATT 1740

ACACATGACA TCTGGATTTG GTGTCCGTCC TAACCGATAT TCTGCTAAAA AATATTCAAA 1800

CACACGGTCC CAATATTCTT TTTCAAAATT GACCGAATAA TACGGAATCC CAATTTGATC 1860

CGCTACTTTT GCGACATCTT TATAATCCTC AGTTGCGGTA CAGACACCAT TTTCGTCTGT 1920

ATCGTCCCAA TTTTTCATAA AGATCCCAAT TACATCATAG CCTTGCTCTT TTAAAAGCAA 1980

CGCTGTGACA GATGAATCGA CACCGCCACT CATGCCTACC ACGACACGCG TTTTGCTGTT 2040

ATCTGCCATT TTATCACCAT CATTTCAATT AGATTCTGAA ATCATCCACG ATTTGAAGGT 2100

CGTAACTTTT CAGTGCTTTT CATTATACTA TTTTTTTGAA ATAAGTAAAG CAAGCCGGGC 2160

GTATAATGAG AAAACACTTG GAACAAAGAC ACAGCCAACA AGCTATTGCT TTCAAATAAA 2220

CAGAAAACcT GmAGGAACAA GCTACTTTCG CTTGTkTCTT CAGGTTTCTC TAAATTATTC 2280

TACTTTCT 2288

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTAATTTTT GGGAAaAAAT TwCCaAAGGC TAAGGaTaGk TAAAtTGgGG ACCwTATTTg 60

GAATaTTGaT TAAATTCTGA CCACTTAATT GtCTTTkGAA AAggTTATGC TAAAGTTACT 120

TTGTAATcGA ATGaGGAGGG CTATCACATG GaAGAAAAGA ATTGGCCTGA GTTATTTGCT 180

CGTTATCTTA TTGTCGAAAG AGGCTATTCA GAAAAAACAA AAAAAGCATA TCAAGAAGAT 240

ATACAACATT TTTTTTCGTT TTTAAAGACT TCAGGTAATG ACAATTATTT GACTGTGGAA 300

CATTTGGATG TTCGGGCTTA TTTGAGCGAA TTATATGATC AGGAATATAG CCGCAATTCG 360

ATTAGTCGAA AAATTGCCAG TTTGCGTTCT TTTTATCAAT TCTTATTAAA AAATGAAGCA 420

ATCCAAGAGA ATCCTTTTTC CTATGTTCAT ATGAAAAAGA AACAGTTACG GTTGCCCCGT 480

TTTTTTTATG AAAAAGAAAT GGATGCATTA TTTGAGAGCG CACAAGGGGA GCAACCGCTT 540

GATTTGAGAA ATCAAGCATT ACTAGAAGTT CTGTATGGGA CTGGTATTCG GGTCAGTGAA 600

TGTGCGAACT TAACGGTGGA CGCAGTTGAC TTTCAAGCTT CTGTTTTATT GGTTCACGGA 660

AAAGGAAATA AAGACCGTTA TGTGCCTTTT GGTTCATTTG CACAAGACGC CTTAAAGGAT 720

TACTTAGAGA ATGGCCGCGC GCTATTAATG ACAAAATATC AAAAAAAACA TCCGTATGTC 780

TTTGTTAATC ATCATGGTGA ACAAATCACG CCAACAGGGA TTGAATATGT CTTAAACCAA 840

CTAATTAAAA AAAGTTCATT AAATGCGGAA ATTCATCCCC ACATGTTACG CCATACATTT 900

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GCGACACATT TATTAAATAA TGGCGCCGAT ATGCGGACAG TTCAAGAATT ATTAGGACAT     960
GCTAATTTAT CAACAACTCA GATATATGCG CATGTGACAA AAGAAAGTTT ACAAAAAAAT    1020
TATCGAACGT TTCATCCTCG TGCATAATGG AGGTAAACGT CTAGGAGGAA CAATAATGGT    1080
TGAATCACAA TTTCACTCTA CAACAATTTG TGCAGTTGAA AAAGATGGAA AATTTGCAAT    1140
GGCTGGTGAC GGCCAAGTAA CAATGGGCGA ATCTGTCGTT ATGAAAGGTA CGGCCAAAAA    1200
AGTGCGCCGT ATTTACAATG ATGAAGTCGT TGTCGGTTTT GCAGGAAGTG TGGCAGATGC    1260
CTTTACATTA GAAGAAAAGT TTGAAGGAAA ATTAAATGAA TACAACGGAA ACTTAACGAG    1320
AGCTGCGGTT GAGTTArCCC AAGAGTGGCG TACACAACAG TCTATGCAAA AATTAGAAGC    1380
TATGCTGATT GTGATGAATA AGGAAGAAAT GCTCTTAGTT TCAGGAACTG GGGAAGTCAT    1440
CACACCAGAC GATGGTATTT TAGCAATTGG tTCAGGCGGT AATTTTGCTT TGTCCGCTGC    1500
AAGAgCCATG AAAAACTTTG GCGATAAAGA AATGCCmGCG AAAGAGATTG CTAAAAATGC    1560
CTTAAATATT GCTGCAGATA TCTGTGTATT TACGAATCAT AATATCATTG TAGAAGAATT    1620
ATAAGCGAGG GAAAATCCAT GAATGAATTA AACAAAACAC CAAAAGAAAT AGTCAAAGAA    1680
CTAGATCAAT ATATTGTTGG ACAGCAAGCT GCCAAAAAAT CAGTGGCGGT AGCTTTACGT    1740
AACCGCTATC GTCGCTTGCA ATTAGAAGAA AATATGCAAC AAGATATTAC GCCTAAAAAC    1800
TTACTAATGA TTGGACCAAC AGGTGTTGGT AAAACTGAGA TTGCTCGTCG TCTCGCAAAA    1860
ATTGTCAATG CGCCTTTTGT AAAAGTTGAA GCAACCAAAT TTACAGAAGT AGGCTATGTT    1920
GGTCGGGATG TCGAATCAAT GGTGCGGGAT TTAGTAGAAA ATGCGATCCA AaTTGTTGAA    1980
AAACAACAAT ACAGTCGCGT GTATGCGCAA cATTAAAAAA GGCCAATCAA CGTTTAGTCa    2040
AAGTATTAGT GCCTGGAATT AAAAAAGAAC AAAAACAGGC TGGCGGTAaT CAATTTGAaC    2100
AAaTGATGAA CATGTTTAAC ATGGCTCAGC AACAGCAAGA AGCACAAGAA GAAGTAACGG    2160
AAGATATTCG AACGAATCGC CGAACAATTT TGGAACAGCT GGAAAAAGGT CTATTAGATA    2220
ATCGTGAAGT AACAATTGAA ATTGAAGAAC CGAAGAAAAC GATGCCAGCT ATGAACAATG    2280
GCCTAGAACA AATGGGTATC GACTTAAATG AAACGTTAGG CGCTCTGTCA CCAAAGAAAA    2340
AAATCGAACG TACTGTAACG GTGAAAGAAG CACAAGAATT ATTAGTGAAA GAAGAATCAG    2400
CAAAAATTGT CAATGACGCT GATATTCATA GTGAAGCTAT TCGTTTAGCT GAATCAAGCG    2460
GAATTATTTT TATCGATGAG ATTGATAAAA TCACCTCTAA AAGTCAACAA AATTCGGGCG    2520
AAGTCTCTCG TGAAGGAGTA CAAAGAGATA TTTTGCCGAT TGTTGAAGGC TCCCAAGTTA    2580
ACACGAAGTA TGGTCCTTTA CAAACGGATC ACATTTTATT TATCGCTTCA GGTGCTTTCC    2640
ACTTGTCAAA ACCAAGTGAC TTGATTCCAG AATTACAAGG CCGCTTCCCA ATTCGAGTTG    2700
AATTAGATGA TTTAACGGCG GATGAtTCGT AAGTATCTTA ACTGAGCCAA ACAATGCTTT    2760
AATTAAACAA TATGTAGCAT TAATTGGCAC AGAAAATGTT TCAGTCATCT TTACAAAAGA    2820
AGCAATTGAA CGGTTAGCAC ACATCGCTTA TGATGTAAAC CGTGATACAG ATAATATTGG    2880
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GGCGCGTCGT TTACACACAA TTTTAGAGCG TTTATTAGAA GATTTATTAT ATGAAGCACC   2940
AGATATGCaA ATGGGTGAAA TTACGATTAC CGAAGCATAT GTCAATGAAA AATTGAATGA   3000
CATTGTTCAA AATGAAGATT TAAGTCGTTA CATCTTATAA AAAAGGCTGG AGGAGAAAAG   3060
ATGGCTACAT TATTAGAAAA AACACGTCAA GTGAACGAGC TTTTGCAAAA AAACAATCTG   3120
TTTGACGTAC AAGCAGAACT TCCGTACAAC AAAATGGCAA TGATTTTAGG GGATATTTTA   3180
GAAAGTAATG CGTATATTAT TAGCAGTTCA GGGGATTTGT TGGGGTATAC TGAAAAATTA   3240
GATGTTAATA ATGCCCGTAT CAAAAATATG TTTAAAGAGA AAAAATTTCC TCAAGGATAC   3300
ACCGAGGCCG TGGATATGCT CAAAGTAACC GAAGCCAATA TTCCAATAGA TAGTGATTTA   3360
ACTGCATTTC CTTTTGAATC ACGAGAGCTG TATCCGTTTG GTTTAACCAC TATTGTGCCT   3420
TTGTACGGTG CTGGCAAACG CTTGGGTACG ATTATTTTAG CGCGTGTTGA AAAATCCTTT   3480
AACGAGGATG ATTTAGTGTT AGCTGAATAT AGTGCGACCG TTGTCGGCAT GCAAATTTTG   3540
TATCATCAAT CCAGAACAAT TGAAGCAGAA GTTCGCAGTG CGACTGCCGT GCAAATGGCC   3600
ATCAACACTC TTTCCTATAG TGAATTAAAA GCCGTCCATG CCATTTTTGA AGCCTTAGAT   3660
GGCGAAGAAG GTCGTTTAAC TGCTTCAAGT ATTGCAGATG AAATAGGCAT TACTCGTTCC   3720
GTAATTGTGA ATGCCTTAAG AAAATTAGAA TCAGCTGGAA TTATTGAATC ACGTTCTCTT   3780
GGTATGAAAG GGACTTATTT AAAAGTATTA AATCAACAAT TTATTAAAGA GTTGGAAAAA   3840
TAAGCAATTG CTCGTATCAA CTAGGAGGAC AACGCAATGA CTGTACAAAT TGAAAATGAA   3900
TTTCTAATCG CAACATTTGC TGAAGAAGGA GCAGAATTAG TAAGTTTACA ATCAAAAGAA   3960
ACCGGCATTG AATATATTTG GCAAGGAAAT CCTGAATTTT GGGCCCGCCA TGCGCCCGTA   4020
CTTTTTCCGA TTGTCGGTCG TCTAAAAGAA GATACGTATA TGTACCAAAA TCAAGCGTAT   4080
CATTTAACTC AACATGGTTT TGCTCGTGAT CAAGTATTTG ATGTGATTGA AAAAGGTGGA   4140
GAAGAAGTTT CTTTTTCACT AAAATCAACA AAAGAAACCA AGAAGAAGTA TCCTTTTGAT   4200
TTTGAACTAG TGATTACTTA TACATTAGAA CATCAAGAAT TGACTGTAAA CTACCAAGTA   4260
GAATACACAG GGAAAGAAGA GATGTATTTT GGGATTGGTG GTCATCCAGC CTTTAATGTA   4320
CCTTTAGAAT CTTCACTAAC GTTTGAAGAT TATTATCTAA GTTTTTCACC TAAAAAATCA   4380
CGGACACAAA TTCCCTTAGC AGGCCCGTTT ATTGATTTAG CGAATAAAAC GCTAGCCCAA   4440
ACGAATACCA GCTTTGACTT AACGCATCAA TTATTTGAAA ATGATGCAAT GATTTTTGAA   4500
ACAAAAGGTC AAACAGCAAT TACGATTGCC ACAGACGAAA GTGACCATCA AGTCACTTTG   4560
AGTTATCCAG AAATGCCTTT TGTGGGGATT TGGTCACCGA CACCGAAAGA AGCGCCTTTT   4620
GTCTGTATCG AACCTTGGTG CGGGATTGCT GATGCTGTCG ACGCAACTGG CCAACTTGCT   4680
GaAAAAtTTG GCATCaATAA GTTmCCAGCT AACGAACTAT TTAAAmCACA GTATATGATT   4740
AGTGTAAAAT AAAGAAAAAG GCTGTGAACA TTATTTGTTC ACAGCCTTTT TCTTTATTTT   4800
TTTTGCACGT AAGCCAAAAG AAAGACGACT TTCTGTTCCA TTTTTAATTC GCTGAATGTT   4860
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TTCACGATGA CGGACAAAGA TAAAAGTAGT CAAAGCAATC GCAATCACGG TTAATAACCA 4920

GTTAAATGTT GGTAAAAATAG CTGGGACAGT GAAAGGCAAA ATAATAGTAG AAAGTGTAAT 4980

TAGTACAGCG CTAATCATAC TTGTTAAACT CACCATACTG GTTAGATACA GACAAATCAC 5040

AAAAATAAGA GCAGAATAAA TAAAAAATGT GGGGCTGTAT GCTAATAACA TGCCAGCGCT 5100

AGTGGCTACG GCTTTACCAC CTTTGAAATT GGCAAAAATA GGGAAGGTAT GCCCTAAAAC 5160

AGCTGCTACC CCAAAGAAGA GCGGATTCAC GCCTTGTAAA CCAAACAAAT AGGGTAATGA 5220

AGTGGCTAAC GTTCCTTTCA AGATATCCAT TAATAATACC GTAATTCCGG CAGGTTTCCC 5280

TAAGACACGA AATGTATTGG TTGTTCCTGT ATTCCCACTC CCAAATTGGC GTATATCTTT 5340

TTTAAAGAAA AGTTTACCAA TCCAAACACC TGAGGGAATC GAACCTAATA AATAGGCAAC 5400

AAGTAACAAA ATGACGATTT TCATCAAGTT AACCTCTTTC TTATTCAAAC TAGGATTTAT 5460

TTTATCATGA ATAGAAAAAC GGAACAACGT CTAATAACTA AAACAAGAAA AGTTTTTCTT 5520

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CAAAGACGTC TAATCACTGG TTTGAaAATT AGTTATCAAC GAAGATACAA TATATATGTA 5640

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TTGATTGCCT TGAAACCACA AATTGTTTAT GTGAATGACA TCAATTTAGC TAGCTCAGAA 6360

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AAACTATTAA AArACCAAAA ACTGTTTTGT TTGAAGTGGC TGCCTTACCA GACATTTATA 6600

GTTTTGGTAA TGGGACATTT TTAAATGAAT GGATTGAACC AATTGGGGCA AAAAATGTTT 6660

TGGCCAATGA AAAGGCTGGT TnCCAGTGAC A 6691

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20072 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTAnGGTAnC CAATCGTTCC CCGGTAAATT TGGACAGTTT TAATCTGTTC CACAAACGAT 60

nAACGGCTCC GTTTGTTAAT AACTGCCGTT CTAACATCTT TTCTAAATTG TGAAACAATT 120

TCTTGTTTGG CATAGGGCGG ATCCAATAAG ACCAAATCAA ATTGTAACTT CTCTTCATAA 180

AACTGTTCTA AGGCACGATT AGCATCCATT TTTCTAACTT CAAATTTTTC TGGTTCTTTT 240

GTAATCGCAA TATTTTCTTT AATTACTTTT AGTGCAGCAA AATTCTTTTC AATACAAATA 300

CTTTTGTCCA TTCCACGAGA AACGGCTTCA ATCGCTAACC CGCCACTTCC TGAATATAAA 360

TCCAGCGCCA TTCCGCCATC GAAATATGGA CCAATCATAT TAAAAATAGA TTCTTTTACT 420

TTATCTGTTG TGGGCCTAGT ATTGTCGCCA TCTAACGCTT TCAAGCGCCG GCCACCATAT 480

TCTCCAGAAA TAACACGCAT TGTTTCGACT CCTTTATCAA TCATTCTTTT ATAATTCATT 540

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AGACATTCTC TGCTAAGCGA ATCTCTGTAG ATAATTCCTC TACTACATAG CCGTCGTCTT 660

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CACTACTCTC CGTGATTTGC CTATTTTCTG GTCGTTTCTC TAATAAGACT AACACACCTT 1440

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GATTCATGAC ATAAATCGCT TGGTTACTTT GAACAGGATC GAAGGTCATT GACTGCGTTA 1860

TATCAACTGG CAAAGGAGAA CCTTCATTTA ATTGATACGG CATTTCCGTG AGCAACGTTT 1920

CTTTATTGAC ATAATTAACT GCCATTAAAC CGCCTGTCCG CTGATTAAAA AATAACACCG 1980

CAAAACTGCC ATTATCAAAA GCAACCAGTG GTCGATAGTT CATATCTTCT TCCATCAGCT 2040

CGACATCGTA AGCTTCATGA TGAAAATTAA ATGCAAAATT CGAATAAATC GTCATTAAAT 2100

CAGACAAGTC AGCAAGCTTC ATATCTATTT TAAACGGTTC TATCATTTTG TCATTGTTAA 2160

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TCAAACCGAA CGTCCATAAT TCATACGTAC GACCTGTTTT AATTTTTTCT TTAGGATTGC 2280

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TCACTTCTAA TAACAAATCA CCTGAGCTGA TTGcTTCGCC TTCTTCAACA TAAATGTGAT 2580

CTACCGTGCC CGCAAAACGT GCTTCGATAG TCGTTTCCAT TTTCATGGCT TCTGTAATCA 2640

GCAACGGCTG ACCTTTTTCT ACTTTATCGC CACGTTTGAC CAATACTTGT AGAACAGAAC 2700

CAGACATCGT TGCGCCGATT TGTTCTTTAT TAGTTGGTTC CGCCTTTTGT TTTACTTGAA 2760

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AAAATACTTG TGGATACATT AAATAACTTa AAACTTCTTC CAATTTAGGT TGaTACCCAA 3060

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GcCGCTCTGT GAAGGCTGGT CGACCTTTTA GAATAATTCG TTGCAGCTCT TTCGGGAACC 3180

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TCACTGTGTG ATATATTTTT TTGATTTCAT CCCAACGGTG CCCTAAGCCT ACCGCTTTTG 3420

CTTGCTGCTG TAGATTAGAG TATTGCCCAC CAGGCATTTC ATGCATATAG ACTTCTGTTT 3480

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GATTGATTTT CTGTGCATTA TCAATGTTAA TAGTTGGCGT CCGTTCACCA TTGACTAAAG 3600

CATAATATAG ACTGTTCATA CTTGGCTGGC TAGTTGCGCC ACTCATCGCA CTCATTGCGA 3660

CGTCAACAAT ATCAACGCCC GCTTTAGTAG CTGCTGAATA TGTGATGATC CCATTGCCAC 3720

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AACGATAAGC AGCTTGTGGT TTCAATAAGC CAGCCATATC TTTAATCGCA ATGATTTGTG 3840

CACCTAAATT TTCCAATTCT TTAGCCATAT CAAGGTAATA TTGAACATTA TATTTTGCTC 3900

GGGCTGGATC ATTGATGTCC CCAGTATAAC AAATTGCTGC TTCCGCAATT TTTCCGGTAT 3960

CCCGAACGAC TTGAATACTT TTTTCCATTT GAGGAATCCA GTTTAAGCTA TCAAAAATTC 4020

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TGAAAATAAC AGCTCGCCAT TTTCATTCGT GACACCTTTT TCTATTAGAT TATTTTTTkG 18720

GTCATACAAC GAAAATTCAG CACCTGcTAA ACGTTTCACC TCATTATTTT CATCTACTTT 18780

TTCyACTTTT AACTGGkTTn CTAAACGCGt ATTTcTTTTt tCAAGCGAAT CGTCTGkGTT 18840

TGTTCTAcTT AATTnCAAAT GGAaCTGGTG TTGCATCTAA CTTGTAACCA GTTGGTGCTT 18900

TTGTTTCAAT GAATGCATAC TGACCAGCTT CCAAACCAGC TAAACGAATT TGACCTGCTT 18960

GATTGGTGGT TAATGTTTCT TGAACAACTT GTTGTGTTTT TGTGTTCACG ACTTTGAAAA 19020

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ACCTGTTCCA TCACTACTCT CGTCTGCTGT GATGTAGGCA ATATCATCAT CTTCCCAaGC 19140

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AATATTTTCA TTTGGAATCG TTTCTAAATA AATATAATAG GCATTTTTAT TGGAAAGATA 19260

ACTGCCCGTG GCTGTTGGTA TTCCTTCAAA TTTCTCTGCT TCATAATTAA ATCCAGATTC 19320

AGAGGCATTT TTTTGGAAAA ATTGACTGGC ATCATAGCTA TATTCGTCAT GTTCCAAATT 19380

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TTCAAAATCT TCTGATAAAT TTTGATTATA TCGTAGCTTC AGTTGCAAAT CTGCTGAGTA 19740

ATCTGTAAGC GTTTGTAAGG CTTTAATCGT CCAAGTACCA TCATCGTTTG GAATCACTTG 19800

AAGTGCGTCT CCAATTTCAA AAGGTGTCAT TGAATAGGAA TATTTTTCGC TAGCCATCCT 19860

TAATGTCATC GTCTCTCCGC TTGCTAATTC AGAGATTCCT AATGACAAAG AAACTGTCGC 19920

CCAATCTTTT GTAGCAACAA TTTCCGTTTT TTCCCCCGGn yATTCAACAG CTATAGACCG 19980

GATTTGTGTG CCACTTTCAT TATCCATTGC ATAAGAAATA ATACTTGTAT TAGATCCTAT 20040

AATAGTAAAG ATAATTAAAC AAATCGAAAA TA 20072

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTGAnACAGA TGGAGTnnGC ACTGGCTATA CAGTAAGATA TGATCTTGGT GGAGAAAAAG 60

AnAAAGACAT AACAGTCAAT TTACCCGGAG CAGaATTACC ACTTAGTTTA AAAGTAAAAG 120

CACATTACAC AAATGGATTA CCACTTGAAG CGGGAAAAGA AGTACGCTTA AGAAATTTAA 180

CAGATGGATC AACAGAAGTA mTTAAGAAAC ArGTAGACGC TAACGGAGAA GTTGTATTTA 240

CTGAGCAAGA TGGTATAAAA AAGGAAGTAA ATTATGGTAT TGAAACAGAT GGAGTAAGAA 300

ATGGCTATAC AGTAAGATAT GATCTTGGTG GAGAAAAAGA AAAAGACATA ACAGTCAATT 360

TACCCGGAGC AGAATTACCA CTTAGTTTAA AAGTAAAAGC ACATTACACA AATGGATTAC 420

CACTTGAAGC GGGAAAAGAA GTACGCTTAA GAAATTTAAC AGATGGATCA ACAGAAGTAC 480

TTAAGAAACA AGTAGACGCT AACGGAGAAG TTGTATTTAC TGAGCAAGAT GGTATAAAAA 540

AGGAAGTAAA TTATGGTATT GAAACAGATG GAGTAAGAAA TGGCTATACA GTAAGATATG 600

ATCTTGGTGG AGAAAAAGAA AAAGACATAA CAGTCAATTT ACCCGGAGCA GAATTACCAC 660

TTAGTTTAAA AGTAAAAGCA CATTACAC 688

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nGATAAGGTC CTATAAATAG nCCGGATATn TTTTTATTAT TAAGATCTAG TACTTTCCTC 60

TTACTATGAG TGTACTAGAT TCTTTTTTTG CCAACTTTAA AGAACTAGAC CAATTTTCGG 120

TTTTTAGATT TTTGTTGACA AGTACCTACT TTTAATTGTA TGATTGTTTA TGTTTCTACG 180

GAATATATTT ACAAAGGAGG TATATAGACC AATATCGGAT AGCGCCAGAC CTGAACGTTC 240

AGGTGACGAG GAGAGAGCTT ATCGAAGATT CGGCGGGTGG CTCTAGGGAC TGCACTCTAC 300

AGATAACAAA GAAAAACTAA TTGTGAAGTT AGAACAAAGC GGTTATCACG CAGGTAGAAA 360

CATATAATGG GATTTGCTAG TTAAACAGGA CCTAGTAAAT ACAGAATTTC AATTGGAAAG 420

TAGGAATTAG CATTATGTGT GGAATTGTCG GAATGATTGG AAAAGAAAAT GTCACGGAAA 480

GTTTGATTCA AGGATTAACA AAATTGGAAT ATAGAGGTTA TGATTCTGCT GGGATTTGTG 540

TGAATGrTCm AAGCCAACAG CCCCATGTAG TTAArGCAGT TtGGGGgCAT TkCCsATTTa 600

GCAGCAAAAT TAACGCCAGA AATCGATgGA ACAGTTGGTA TTGGTnCATA CTCGTTGGGC 660

CACTCATGGC GAACCAACTG TCGCCAATGC ACATCCCCAT GTTTCAAGCG ATCAACGCTT 720

TGCATTAGTG CATAATGGTG TCATTGAAAA CTTTGAAGAA TTAAAAGAAC AATTTTTAAG 780

TGGTGCTCAC TTAATTGGTG ATACAGaTAC TGAAATCGTC GTTCAATTAA TTGcTCATTT 840

TGCTGAAAAT GGTTTTTCAA CAAAAGATGn CTTTTAAAGC GGCTTTAGCm GAwATTaAAG 900

GTTCATACGC TTTTGCATTA ATGGATAAAA TGGaCCCCAA TATTATCTAT GTAGCGAAAA 960

ATAAAAGCCC GTTACTTATC GGTCTAgGTG mAGGCtTaAT GkTTATtTGT AGTGaTGCGA 1020

TGGcGATGAT TAAAGAAcCA ATCAATTtGT TGAGATtGTT GATGGTGAGA TTGTAACTGT 1080

TACAGCGGAC AAAGTAGTAA TCGAAACGCC AGAAGGACAA GTAATCAACC GAGAACCTTT 1140

TGAAGCGCAA TTAGATTTAA ATGACATTGA AAAAGGAACA TATCCGTTTT ATATGCTCAA 1200

AGAAATTGAT GAACAACCTG CAGTGATGCG CAAAATTGTT CAAGCGTATA CTCAAGGTGA 1260

AAAAGTGACT TTAGATGAGG CGTTACTGGA AAAAATTAAT CAATGTAACC GAATTTACAT 1320

TATTGCTTGT GGGACAAGTT ATAATGCAGG TTGGGTCGGA AAATCTTTAA TTGAAACGAT 1380

TGCCAGTATT CCTGTGGAAG TTCATTTATC AAGCGAATTT GGCTACAACA TGCCTATTTT 1440

ATCTGAAAAA CCGTTCTTCA TTTTCTTAAG TCAAAGTGGT GAAACGGCAG ATAGTCGCCA 1500

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CGTGGTAGCA GCTGTCATGG AAACCTTGAT TGATGAAAAA CAACAAATGA AAGCCTTGGT 1800

GGAAGATTAT CTGACGTATA CTCGAAATGC CTTCTATATC GGGCGAGGAG TCGACTATTA 1860

TGTGTCGATG GAAGCGGCCT TGAAGTTGAA AGAAATTTCC TACATTCAAG CAGAAGGCTT 1920

TGCGGCAGGT GAATTGAAGC ATGGAACGAT TGCCTTAATT GAAGAAGGAA CACCTGTGAT 1980

TGGGATTGTG ACAGATGCCA AAGTCGCTGC CCATACAAGA GGCAATTTAA AGGAAGTCGA 2040

AAGTCGTAGA GCAAGAAATA TTGTGATTGC TTTGGAATCC TTGGCAAAAC CACAGGACCA 2100

ACTGATTATT CCAGATGTTC ATCCGTTACT TTCTGCCTTA GTTAGCATTG TTCCAGGTCA 2160

ATTATTAGCG TACTATGCAA CCTTACAAAG AGGCTACGAT GTTGATAAAC CAAGGAACTT 2220

AGCCAAAAGT GTAcTGTTGA ATAAATCAAG AACCTGAGAG AAAGATGTTC AACGGGTTTT 2280

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AAAAGAAAGA TATTCAGTCA AAAATGAAAG ATTCCAAAGA AATTCTTTTT TTCCGTTGAA 2400

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ACAAGAATTT ACTACCTTTG CAATGACACA TCCTGCAGGT AACTTTTTAG AAACACCCGA 2640

AATGAAACAT TTATTGGAAC GACGTGGCTG GCATTGTGAA TACGTTGGCG TCAAACGAGA 2700

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CGACATTGAC GGCGGAATTT TGATGGATTA TACAGATAAA AAATGTGTAG AAGCCTTTTT 2820

CACAGGCTTA AAAAAATATG TGAAAAAAAA TGATGGCCTT TATTTAACCT TTACTCCAAA 2880

TAAACAAATT TGTTTACGTG ATTTTAATGG CGGTGAAGTT GAAAAGGTCA ATCAAGAAAC 2940

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TGGTGCGCCA CGTTGGCTGT TTGTCAAAGA TATGGCTGGA TTAACAGAAG AAGATCTTTG 3060

GAAATCTTAT GGAAAAGATG CTAAATATGA CATCAAGAAA ACATGGGAAT ATGGAGTAAC 3120

AATCCGAGAA CTTCgTTACG AAGAGCTACC TCTCTTTAAG AAATTAACGG AAGAAACAAG 3180

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TGgCGAaCGA gCGAAtTTAT GGTGcGGACT AAcTTTGCTA CTTATTTaGA AAATCTTCAT 3300

GAGAAATTAC GCAAATTACA AGAGACGCTC AACGAAgTCA ATGAAGCGTT AATTGCCAAT 3360

CCTAAAAGCC GTAAAAAAAA TAACCAGAAA CGTGAATTTG AAGATGAAGT TCGTACCGTG 3420

CGCAAACGGA TTGACGAGGC TAAAGAAATG AAAACATCAG ATGAACCTGA AATTTTAGCA 3480

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CCTGAATATA TTGAAAAAGA ATTGACTGAA GCAAAAGGCC ATCAAATCGA TGCTGTTCAA 5220

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CCTAAAAGCG AGGACGTGCC ATTTTTTCGG TTTCAGAAAT TTGCTGAATC TGCTCTAATT 5340

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TAGCGAGGCG CATCACCTGC GATATTTCTT GAATAGACAA TAAAAATGCC AAAACTTAAG 6300

AGAGAAGCAA GTCCTAAATA CAAGATACAA TAAAGGAAAC TTAAGCCTAA GTTGATTTTG 6360

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CATTGGAGGA ACCAAGGATT GAGGCCAATT AAAGTAGCTA CTAAAGAGGA ACCCCAGCTA 6900

ATTTTTTGGT CATTGATGAT ATAAATTGCC aGTATGCTTG TGAGAGATAA GATAAGACCT 6960

GTTAGAATCG GTGTGGTCAA GCCCAGATCT GTCAAATGAC GACTTCCTTG AACAAACCAT 7020

GAGAGAAATT CACTGCCCCA ACGTGCGTAA GTCGTACCAA AATCTGTCAT TCCAGCGACT 7080

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TGTCCTAGCT GTGTTTTGaT ATATATTGGA TCAGCTTCAG CTAGGaTTAA TAAGTCAGAA 7680

CGGGcATGTC TAAAACTATG AGATGAAATT CtTTCAATAT TTGcTAGTTC ACATGTTTCT 7740

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AGTCCTTTTT CATTGATATT GCCAGGTTTT GCAAGCCAGT TAATCCATTG CTGATATTTG 8340

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TAGGGkTTAA ATATACTACA TTATTAATAT AGAGACCTTT CTGATTTcTG GGCATCATAG 10140

GTCTATTCTG TAGTTTAGTT CAGGATAATT AGCCATCAAG CTTTCCAATT TATn 10194

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nATTGGTTGG TACAGGTATT nGAATTGGTT nGCTCCCTTG GCATCAAAAG GTTTGCmAAT 60

tCGtTAAwTT mTyCAGATTG GTAATATCTG aTAACTCGkT GtAAGAAcAA TCaATAGAAA 120

aTAGATTTGT ATTTTgGCTG CTAACAtCTA GAACAGTTAA TTGATTGCTC aAACAAACTA 180

AAATGGCtAG ATCAACATTA TTAGTAACAT CTAAAACGGT TAATTGATTG TAAGAACAGT 240

CTAAAAGATG TAACCTAGTA TTTTGGCTGA CATCTAAAGT AGTTAATTGA TTGCTAGAAC 300

AGTCTAAATT CCTTAAATAG GTGTTCTGAG TAATATCCAA GTCTGTTAGA CGATTTCCAC 360

TACAAGATAG AGTCTCAAGC ATTCTATTCT GACTAAAATC CAGATTGGTC AAATTATTAA 420

ATTGACAGCT TAAATCAGTT AATTGTTCTG CATACTTGAT ACCTTTCAAG CTATCTAAAT 480

TTTTATTAGT GACAGTAATT TTTGTTAAAC TTGACATATC TGCAATAGTC AATTGATCCT 540

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TCGTTTTGAA TACGTGCTGC AATCACTTTT TGACCATTCG CTAATTGTAA GCTGGCTTTC 1740

TTTAAATGAA GCATCGCTCC CTGATTAAAG GGTTCTTCAT CCTCCGTAAG CATAATCGCA 1800

ATCACGCGCG CATATTGAGG AGTTAAGCCA GATTTCTTTT GTTTCACTTC CGTACTATTC 1860

TTTCGAACAA AGCGCAGAGA GCCCAGCTTT ACTCCGGAGA AAGCCGATTC AGGTGGCGTG 1920

GATCTCAAAT GTnATCGGTT TCTCTTCTTT CCCCTTGGAG GGGGAATTTC CTTAACGGCC 1980

ACCTTTnATT TTTTACTAAC TCACGGAATG GGGGCTTTCA AACGGGCATC GAACTTAnGG 2040

GGGAACATTG GnA 2053

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GCAGTCGAGC CTGTTGGTCC ATAAAAATCG GTGTATGAAA GCAATTCTTT TTAGATATTT 60

TTGACTTCCC AATTTGATAT ACTGCGGAAA GTATCTGAGA ATTTATTTAA CACATTTTTT 120

ATTTACTAnA GAAAGTAAAG ATCaGAGCTG TGCaAATAGA AATGATTAAA AACATCCCaA 180

TATCATCATC TAATGTTTCA AAAACTTCAA CAGGTTTCAT AAAATGTTTA ATTATTTTTT 240

TCATTGtATT CaCCTCAAAA AGAGAATAGA ATGAAATATT CTACTTATCC ATTGATATAT 300

CTAACGATTG ACTTACAAAA TTGAAATAAA AGTCTAAAAG TCAGTTGGTG TGATTATTAT 360

TATAATACAA AAAAGACCTC CATTCTTTTA AGAATAAGGT CTTTTTTTTC GTAGTCGCCT 420

TCTAGGCAAA CTAATTCAGT TAGCCGTATT CTAAACTCAA TAAAATGTCA AATACTCATA 480

GGTGTATTTT TATCACAAAA TTTACCACAG ATTTGCGGTA TTATTTACAT ATCTTAGATT 540

ATTAAAAATG ACAAAACAGC TATTTAATGC GTATTGTATG ATTTTTTTGT TCCTTAAATT 600

GTTATGGAAT TTCAGATGGG GAGTGGCAAA TATACGAAGA AAATTAACTA TTTATAGCGG 660

TTTTATTTTA TTAGAGAGTC TCGTTAGTTT TAGTATTGTA TGTGTGATAG CAGGGATATT 720

CTCCCTGACT ATTACACAAT TAATTCAGCA AAATTATCAA CGGGAGCAAG AATTAACGCG 780

CACTCGTCTA GGATACGAAG CAATTTTATT TTTAGAGCAG ACGGGTGATT TACGTTTCAA 840

AGAGCGGATA TATCAAGGAG AAACTTACCG ATTTTCTTTG ATGGAGAACG ATGGAAGAAG 900

GATACTAAAA GTCACAGATT CAAGAGGAGC GATTTTGATT GGTCAATAAA AAATATGCGG 960

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GTTTTACGAT GTTAGAGTGT TTAGTAGCAC TAGTCGTTTT AAGTTGTATG TGTCAATTGT      1020
TTCAGTTGAT GATTCAACAA AGTTTTATCG GAAATCAATA TTTGAAAAAC aATGATTCGA      1080
AATCCTGGCa TATTTTTTTA ATTCAATTAG AAAAAGAATG TCAAAAGCTC GTTTTCCAAA      1140
CAGGCTCTGC TCcAAGAGAT TTCTTTCCTC GACTCAGAAA CAAACAAGAC TATTTCAATT      1200
CAAATCaAAG AAGATAAAAT TATTAAGCGA GTCAATGGTA AAGGCTATCA ACCGCTGTTA      1260
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TTTACTTCTG GAAAAACATT TGATAGTTTT TTTCCGATAA AGGGAGAATT TTAATGAGGC      1380
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CAAATTATTA GATTTTAGAA GAAAGACAGT AAAGGCATTG ATTATTCTTT CTTTTTTcGT      1800
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GTCATTGGAT ACTTCTTTTT TAGATGCGTA TATTGAAAAT GGTGAAAATA TTTTAGATGA      1980
TTTTCAAGTA CGAGTACTTG ACGGAGTACC TAATCCAGAG ACAGTGAAAC AATTAGAAAC      2040
GCTGTATCAT ACGATTAAAA AAATTGATTT AGCTCCTGAA GATGTGCGAC GCTTGTCCCA      2100
ATTACTTTTG CTAAAAGGAA CGAGAAAAGA GCAGCTTCAA GCAAATCATC AATTGACGCC      2160
AGACGGTATT GGCTTTTTGT TTGTTTATTT AGTAGAACAA TTAACAAATA AATCAGAGCC      2220
ATTAAAAATT TTAGATCCTG CTTCAGGAAT GGGAAATTTA CTGTTAACGG TTCTGCTGAA      2280
CCTTGAAACA GCTGGTTACA AAGTTTCTGG TTATGGTGTG GATATCGATG AAACACTTTT      2340
GGCAGTATCT TCTGTGAACA ATGCTTGGTC ACAAGCCAAT ATTCAGTTGT TCCATCAAGA      2400
CGGATTGCAA GATTTGTTAT TGGATCCAGT TGATTTAGCA TTAAGTGACT TGCCGATTGG      2460
CTATTATCCA AATGATGAGC GAGCAAAGGG ATTTGCTGCT GCTGCGGAGG AAGGCCATAG      2520
TTATGCGCAT CATTTATTAA TGGAACAAGC CATGAAATAC GTGAAGCCAG CAGGGTTTGG      2580
CTTATTCTTA ATCCCGACCA ATATTTTAGA GACTGAGCAA AGTGAATTCT TTAAAAATTG      2640
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AGAACAATCA CGTAAAAGTA TCTTGCTTGT TCAAAACAAG GGTGCAGATG CTGAGCAAGT      2760
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CTTTAAACAA TTTGAAGCTT GGAAAGCTTC AAATTTAAAA TAAAATAGTA ACGAAGAGGA      2880
GAAAATTATG TCTAAAACAA TTGCAATTAA TGCAGGTAGT TCAAGTTTAA AATGGCAATT      2940
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AGATTCTATC TTCACAATTA AATATGGTGA AGGACAAAAA TATGAAGTAA TTGTTGATAT 3060

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TAAAGATTCT GTTGTTATTA CAGACGAAGT ATTAGAAAAA ATTGAAGCTT TATCTGAATT 3240

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AGAAATCATT AGCGTGGCAG TCTTTGATAC GTCGTTCCAC ACAACAATGC CAGAACACAA 3360

CTATTTATAT AGTGTACCGC GTGAATACTA TGAAAAATTT GCTGCACGTA AATATGGGGC 3420

ACATGGAACA AGTCATCGTT ATGTCTCTCA ACGTGCTGCA GAAATGTTAG GTCGTCCAAT 3480

TGAAGACTTG AAAATTATCA CTTGTCACTT AGGAAATGGT GCTTCAATCA CTGCAGTTGA 3540

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GACTGATGTG CAAGACATGG TTGATATTTT AAACAAAAAA TCTGGTTTAT TAGGTTTAAC 3720

AAATGGTTTA TCAAGCGACA TGCGCGATAT TCAATCAAAT CTAGATAAAC CTGAAGTTCA 3780

AACAGCATAC AACATTTTTA TCGATCGTAT TCGTAAATAC ATTGGTAGCT ATGTCACTGT 3840

TATGAATGGC GTTGATGCGA TTGTCTTTAC TGCTGGAATC GGTGAAAATG CAGTTGGCGT 3900

TCGTAAAGAT ATTATTGATG GCATGACTTG GTTTGGTTGT GAAATCGATG ATGACAAAAA 3960

TAATGTACAC GGTGAAGAAG CAGTTATCTC AACTGATGAT TCAAAAATCA AGCTTCTATT 4020

AGTACCAACT GATGAAGAGT TAATGATTGC CCGTGACGTA GAACGTCTAA AATAATTAAA 4080

CGAACACACC TTGTGAGATG CTCTCACAAG GTnTCTTAAT AGGTAAATAA GAAGAAACTG 4140

AGCCAACTAT CAAAAGTGAT AGTTGGCTCA nTTnCCTT 4178

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CAAAATCAGC CACCTATGGC CAGTCTATCC TGCCAAAGCG TTTTTTATTC TTCATCGGTT 60

GCTTTTTCTw GTTCACGATA kTTtcTCaTT TyTTTGCTGA ATAATTCACC GTTACTAGGG 120

GGCGTATATG TAATAGCATT CGCTCCGGCG ATAATGGTTT CATGAATACT CGATTCAGTT 180

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GTCGTAAAAA TAATTGATTT TATTTTACGG CCAAAAATTT TAATGCCACT GGCTTGCCGA 660

ATAATCTCTG GCATTTTTAC AATATCTTGT TTCAGCGGCG TCATAATTTC TGGAATCCAC 720

TTTTCGCTCA TTGTCATCAT TCCTCCATGC TTAACGGTCG TATTTATTTA AATTGTATTC 780

TTCAATTACA TGAATGATCT TATCAGCGTA TGTAGGATCC GTTGCGTATC CAGCATCTTG 840

AAGCGCTTGT GCAGCCTCTT TATAATTTTT GGCTAACAAG ACTTTTTCAT ATAAATTTGG 900

ATCCCAATCG ACCCCATCAA CAAATAACTT GGTATGATCT CGCATGGATT CTTCCCAATT 960

GTCATAAACT CGAAAATCAC CCTGAATCGT AATCCAGACC TCATTGACAT ACTCTTTTGT 1020

TTCTAAATTG AsTTTTGGTT GATTCCCATA TGCTTTAATC CCAAAAAGAT TGTTATATTT 1080

CGATGCTAAT TGACTkTGTC CAAAATTTGA TTCTAAAACT GCTTGCCCCA TAATAATACT 1140

TGGTAATACC CCGTAAGATT CTTGTAATTC ACGTGCATaC GGTGTGaTTT CAGCAAcAAA 1200

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TAACTTTGGC AAATTCAGCT GCTTTTTTCT TTTTTTCTGA TAaGTTGgCT CcACTTCATT 1380

AATTCCCCaC TTCaTCTTTT aTTTTCCgAt AAAATGTTTc aCTAtCTTTc ACTTTcgtGA 1440

tTGatTTCaT TTGtTaCTAt aACCGAATAA TTGTATCATT TTCACAGAAA ATTATCAACT 1500

TTCATCACTG CTTACGCTCG TGATTTCAGT ACTTGATTCA GTGGTAGCAG TTGAAGAAAC 1560

TGTACTACTT TCAGAAATTT CAGTGGATGA TTTCACTGTT GTTTCAGTTG ATGTGTGAAC 1620

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GTGTTGTGTG AAAAAGCTAT TACGATGAAC GCGGCAGAAT TAAAACAAGC CTTGGCAGTT 2760

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GACGAATTAC GTCGCTTGAT GGATGCTGGC AAATTTGGTC AGTTAAAAAT GATTCAAGCA 2880

CCATTTGGAA GTTACAAAGA ACCCGATCCT AAAAATCGCT TTTTTAATCC TGACTTAGCA 2940

GGCGGCGCAT TGTTAGATAT TGGTACTTAT GCGGTTTCGT TTGCTCGTTG GTTTCTCAGC 3000

TCACAGCCAG ACGTTTTAGC TTCTAGCATG GTTCCCTTCT CTACTGGCGT TGATGAACAA 3060

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ATATGtTTTG GAAACACCAT TAATAATGAT TGTCTGTTGA CGAATtGCTT CTGAGATGGT 5340

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GATAATCAcT TCGTCCCCAA CGTTCAAAAT GGCTTGAAAT AATAGATACA GCGCATATTT 5700

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ATAAGAGACA ATTGCTTGCT TTAATTCAGG AATGCCGCCA GAAGGTGTGT AATAACTTGC 5820

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TGATATGCCA TTAAAAGAAT GGCAACGTGT CATTGATGTC AATTTAAACG GTGTCTTTTT 21240

GGGTTCTACG AC 21252

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GCATATCAAC AAGTCAAAGA ACGATATGAA ATTTTACAAA AAGAAGAAAA AGCCTTAAAG 60

CAACAACTGG CTTCTTATCA TGATttCTAT GAAACGTTTT GCTTGGCTGA AGAAGTCTTA 120

TTGGCGGTTA TCCAAAGAGA ACAAGCACGT CAACATTTGT TAAATGCTTC ATCATTTTTC 180

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AAAGTTCCTA AGGACGAAAT AGCTCTTACT TTTGAAAATC CTACGAAGGC GGAAATTGAG 300

ACGGATATAC CAGTTAAACT AGCGAATAAT AAATTGGTGC AGCCGTTTGA AATGTTAACA 360

GAGATGTATA GCTTACCAAA ATATGAAGAA GTTGATCCGA CACCTGCGAT GATGCCGTTT 420

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CAGAACCAGC TGTAGTAACG TTGTATACGA TGCGTTTTAC CTTCCATAAC TTGAAAATTT 2700

TGACGAAAGC TGAGCGAACA GGTAAAGATT TTGATTATCT TTATTTAGAA GATGGTCGTT 2760

ATTCTCTAAA CACAGTCAAA AGTGCCATTC ATACAAAAAA CTCTTCCGAA CTTGAGCCAG 2820

CATTATTAGA AGTGATTTGT GATGTTTTTG CCTATCTGGA AGAGGGCGGT TTACCACAAG 2880

CAATTGATAT CCTTTATGAT CGAGCATTTT TACAGCAACA ACGAAAATTG GCGGATGAAT 2940

TGGGCTATGA AGAGTTAACG AAGGAAGTCA TCGCTTTTAT TGATTTAACC AATCTATCAA 3000

CGATGGCTAG AGGGATTGTT CAACATCAAA ACAGCAACTT TTTATCAACC GTACTTTCTA 3060

GCGCTGGCAG TATCACAAAG AAAGAACTGT TGACCTATGC GGAAAAGTCA CTTGTAGAAT 3120

TTACAGCATT TGTCAGAACA ACGAATTACG GACAACTATT AGAAAAGATT ATCAATAAAG 3180

AAACCAtGAa TTAAATTTAT TGGCTTTtGA AAAACTCAAA GATGATTACC TGACCTCAAt 3240

GTATGAaAAC GGTCGAACGG TCGCTTTtGG ACCGCTCCCA TTACTAGCCT TTTTGAATGC 3300

GAAAGAGGTT GAATGGAAAA ATCTACGTTT AATTTTGGTC GGAAAACATA GTGGGTTCTC 3360

AAATGAAAAA ATTCGAGAAA GGATGCGAAA AGTCAATGGG GTATAAAATT GGTGTCATTG 3420

GAGACAAAAA TTCAATCTTA CCATTTAAAC TGTTTGGCTT TGAGGTCCAT CATGCCATTT 3480

CAGAAATGCA AGTTAGAGAA GCCATTGAAA CTATGGCGAA AAATAAGTTT GGGGTCATTT 3540

TCATAACGGA AGAAGCCTCT ACTTTAGCAG AAGAAACGAT TGAACGATAC AAAGAACAAG 3600

TGACACCAGC GATTATTTTA ATCCCAAGTC ATAATGGTAC AATCGGAATC GGTTTAAGTG 3660

AGATTGAAAA AAATGTTGAA AAAGCAATTG GACAAAATAT TTTATAATGC AAAGGAGAAT 3720

GAGCGTGCAA ATTGGAAAAA TTGTCAAAGT TTCAGGTCCT TTGATTTTAG CTGAAAACAT 3780

GTCAGATGCT AGTATCCAAG ACATTTGTCA TGTAGGAGAT TTAGGCGTTA TCGGAGAGAT 3840

TATTGAAATG CGAGGCGACG TCGCTTCGAT TCAAGTATAT GAAGAAACAA CAGGCATTGG 3900

ACCAGGAGAA CCAGTTATTT CAACAGGAGA ACCATTATCT GTTGAATTAG CCCCAGGTTT 3960

AATTGCCGAA ATGTTTGATG GTATTCAACG ACCATTGGAT ACATTTCAAG AAGTAACCCA 4020

CAGTAACTTT TTAGGCCGTG GCGTTAAAAT TGATGCGTTA GATCGTGAGA AAAAATGGAC 4080

GTTTGAACCA ACTGTGGCAG TTGGTGAAGA AGTGTCGGCA GGTGACATCG TCGGTGTGGT 4140

TCAAGAAACA CCGATTATTC AACATAAAAT TATGGTGCCT TTCGGCGTTT CAGGAACGAT 4200

TGCCGAAATT AAAGCAGGTG ACTTTGCCAT TGATGAAACA GTTTACTCAG TGGAAACGGC 4260

TAAAGGAACG GAAAGTTTTA GCATGATGCA AAAATGGCCC GTTCGGCGGG GACGTCCCAT 4320

TTTAGAAAAA CTAAGTCCCA AAGTACCGAT GGTGACCGGA CAACGCGTAA TTGATACCTT 4380

TTTCCCAATT ACGAAAGGCG GAgcGGCAGC AGTTcCAGGA CCATTTGGCG CTGGAAAAAC 4440

AGTCGTTCAG CACCAAATTG CTAAGTGGGC CGATGTCGAC TTAGTCGTTT ACGTTGGTTG 4500

TGGGGAACGC GGGAATGAAA TGACAGATGT TTTAAATGAA TTTCCAGAAT TAATTGACCC 4560

AACAACTGGT GAGTCTTTGA TGAATCGGAC GATTTTAATT GCGAATACGT CAAATATGCC 4620

GGTAGCGGCA CGGGAAGCCT CGATTTATAC AGGGATTACC ATTGCAGAAT ATTTCCGTGA 4680

TATGGGTTAC TCAGTCGCAA TTATGGCGGA TTCTACTTCT CGTTGGGCAG AAGCGTTACG 4740

AGAAATGAGT GGTCGGTTAG AAGAAATGCC TGGTGATGAA GGCTATCCAG CCTATTTAGG 4800

TAGTCGCTTA GCTGAATATT ATGAACGAGC AGGACAAGTC ATCGCGTTAG GAAAAGATCA 4860

TCGTGAAGGA AGCATTACAG CGATTAGTGC GGTTTCGCCA TCTGGTGGGG ACATATCAGA 4920

ACCTGTCACT CAAAATACGT TACGCGTTGT TAAAGTATTC TGGGGCTTAG ATTCCCAATT 4980

AGCACAAAAA CGTCATTTTC CTTCTATTAA CTGGTTGCAA AGTTATTCTC TTTATTCCAC 5040

AGAAGTAGGG CAATATTTAG ACTTGGAATT GCAAGGAAAC TGGGCCgCTA TGGTAGCTGA 5100

AGGGATGCGG ATTTTACAAG AGGAATCTCA ATTGGAAGAA ATTGTTCGCT TGGTTGGGAT 5160

TGATTCCTTG TCGGATAAAG ACCGTTTAAC gTTGGAAACA GCCAAATCAT TACGGGAAGA 5220

CTATTTGCAA CAAAATGCTT TTGATGACGT GGATACGTTC ACTTCTCGAA CAAAACAAGC 5280

GAAAATGTTG CAATTGATTC TAACTTTTGG TGAAGAAGGT CAAAAAGCCT TAAGTTTAGG 5340

CACTTATTTC TCTGAGTTAA TGGCGGGAAC AGTTGAAATC CGCGATCGCA TTGCTCGTAG 5400

CAAGTATTTA CCAGAAGAAG AATTAGAAAA ATTGGATCGT TTACAAGCAG AAATTAAAAC 5460

AACGATAAAA GAAATCATTG CTGAAGGAGG AATGACGAAT GATTAAAGAA TATCGTACAA 5520

TCAATGAAGT CGTTGGTCCT CTGATGATTG TTGAAAAAGT GGCAGGCGTA AAGTACGAAG 5580

AATTAATTGA AGTACGCATG CAAAATGGCG AAATTCGCCA AGGGCAAGTT TTAGAAATCA 5640

ATGGAGATAA AGCGATGGTC CAAATTTTTG AAGGAACGAG TAACATCAAT ATTCGTGATT 5700

CAAAAGTTCG CTTTCTGGGA CATCCTTTAG AATTAGGGGT TTCGCCAGAT ATGATGGGGC 5760

GCGTTTTTGA CGGCTTAGGT CGCTTAAAAG ATAATGGACC AGAATTATTA CCTGAGAAAA 5820

AATTAGATAT TAACGGCGAA GTTATCAATC CAGTTGCTCG TGATTATCCC GATGAGTTCA 5880

TCCAAACAGG GATTTCAGCG ATTGACCATT TAAATACCTT AGTTCGTGGT CAAAAATTAC 5940

CTGTTTTTTC AGCATCTGGC TTACCTCATA AAGAATTAGC GGCACAAATT GCCAGACAAG 6000

CCAACGTGTT AAATAGTGaA GAAGAATTTG CCGTAGTTTT TGCGGCCATT GGGATTACCT 6060

TTGAAGAAGC GGAATATTTT ATGGAAGATT TCCGTCAAAC AGGCGCAATT GATCGTTCAG 6120

TCTTGTTTAT GAACTTAGCG AATGATCCaG CCATTGAACG GATTGCAACA CCTAGAATGG 6180

CTTTGACAGC CGCTGAATAT TTAGCTTATG AAAAGGGCAT GCATGTCTTA GTTATCATGA 6240

CGGATATGAC AAATTATTGC GAAgCGTTGC GAGAAATTTC AGCAGCACGC CGTGAAGTTC 6300

CAGGACGTCG TGGTTACCCA GGTTATCTTT ACACGAACTT AGCAACGTTG TATGAACGGG 6360

CAGGCCGAAT TCGTGGCTCA AAAGGTTCCG TAACACAGAT TCCTATTTTA ACAATGCCAG 6420

AGGAGGATAA AACACATCCA ATTCCCGATT TAACTGGCTA TATTACAGAA GGGCAAATTA 6480

TCTTGTCCCG GGAACTATAT AAGAGCGGTA TCCAACCACC AATTGATGTA TTGCCATCAC 6540

TTTCCCGTCT TAAAGACAAA GGAACTGGCG AAGGCAAAAC GCGCGGGGAT CATGCaGCGA 6600

CGATGAATCA ATTGTTCTCA GCCTATGCAC AAGGGAAACA AGCCAAAGAA TTAGCTGTCA 6660

TTTTAGGAGA ATCAGCTCTT TCCGATGTCG ATAAAATTTA CGCAGCTTTT GCCCAACGTT 6720

TTGAAGAAGA ATATGTCAAT CAAGGATTCG ATACAAACCG TTCGATTGAA GAAACGTTAG 6780

ATCTTGGGTG GGAACTATTA AGTATGCTAC CGAGAACAGA ACTAAAACGA ATTAAAGAGG 6840

ATATGCTCGA TCAATATTTA ACTGAAGGGA AGTAGAAAAA TGGCTCGATT AAATGTTAAT 6900

CCAACCCGTA TGGAACTTTC CCGATTGAAA AAACAGTTAA CTACGGCCAC GAGAGGTCAT 6960

AAGTTGCTGA AAGACAAACA AGATGAATTG ATGCGACGGT TTATTGCGCT AGTCAAAGAA 7020

AACAATGAGT TACGTATTCA GGTTGAACAA GAAGTGACGG ATGCGTTATC AAATTTTGTA 7080

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AAAGTTGAAT TAGAAATTAT TGAACAGAAC ATCTTAAGTG TGCCAGTTCC TAAAATGATT 7200

TTTGATTACG ATGAATCGGT TCAAGAAGCA CCCTTAGATT ATGGCTACGT GAATTCAAAC 7260

AGCGAGCTTG ATCAAGCTTT TGCTAAAATT TCAAGCATTT TACCGAAATT ATTAGCACTT 7320

GCAAATGTTG AAAAGACGTG CCAATTATTA TCAAAAGAAA TTGAAAAAAC GCGTCGTCGT 7380

GTCAACGCCT TAGAGTATAT GACGATTCCA CAATTrGArG AAaCAaTTTA CTmCaTTCmA 7440

ATGAAATTwG rAGrAAATGA ACGTGGcGAA ATTACACGTC TAATTAAAAT TAAAAGCATG 7500

AACAAgAAAA TTAGTGGTTA GGAAGAACGA GTGCGAAcCa GTTGGTAGCT TTCGTGCTCG 7560

TTTTTAATAA AAAAGGGAGT GGAAAAAATG AAAAATGAAG AACGCCGCAA AGCGATTGCA 7620

CTGAATTGTC AAAAATACGA AAGTGACTAT GCTCGCTTGG TGGAACCAAT CAATGaGCTA 7680

CTGTTAAACT TGGGAGCGGC TATTTCAGAA GAAGCCgCGA AcAAATCATT CTGAATGTAA 7740

AACGATATCA TCACGGCGTG AAATATCTTC CTGAGTGTCA TTTAGATGAA AGTAACCAAT 7800

TTATCGAAGA TGGGCTTGAA GCTCTTAAAA AGGGAGATTT AGGCAACGGT GCGTTACAAC 7860

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TTGATGCCCA CCAAATGTTG GCAGAACGTT TtACGAAGTT GTTGTCTGTA CaAACGGATA 7980

ATGATAaCAA ACAATAAGrA AAATACCCTk GGTTTATTAA GTCGACTTAG TAAACCAAGG 8040

syATTTTTTT AACTGTTATT GATTAGGGTA TTCAGACACC TGTAATTGCC ATAACTTATC 8100

TGTCACTGAA GCAATAAACG CAGCACTCTT AGCATTATCA GGTCCTTTAG TAAAAATTGC 8160

TAAAGCAAAG GGGTGAGGTG TTTCTAAAAT CCCCATATCA TGAATAAATT CATCATAGGA 8220

ACCAATTTTA TGAGCAACTT TTCCTTGAGT TGTGGGAGTT TCCATTCTTT CATGGAAAAC 8280

ACTTTGTTTC ATAGAATCAT AAATCGCTTG GTAATCTGGT TTTGTTGCTT TTTCAGTATA 8340

TAATTTTTGT AGAATAACAA GCGCATCTTC AGAAGAAAAT TGTGGCTCTT CaATCGAAGG 8400

TGTCTTGTGC AAATAACGCT GATACATTTC TCGTTTTGCT TTTGCATCAC CACCCAATGT 8460

GTCATAGAGC ATATTTTTAG CGATATTATC AGAATAGGTG ATGGCATATT CTTGTAACGT 8520

TTTTAATGGA TATTCTGGTT GGATATTATA GGCAATGATC CCcAGTTCCT TCTTCATAAT 8580

CTTCTTCGGC GTTATAGGGA ATCAGGTCTG TCCATTTTTT TTGACCAGAA GCAACCGTGT 8640

CGGCAACTAG CATCGTCAGG GGCACTTTAA TAGTACTAGC TGTATAAAAT TCATGTTGGC 8700

CATTCACGGA ACGCTGTTCG CCAGTT 8726

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GTAAAGACTT TTCACAAGTA TCAAAGAAAT CCGTCGTTAA TCTTTACTAT TCGACAAACG 60

AACACCCTCT TGCTCAGCAA GAGGGTGTTT TTTTGTGTAA TTAAGTGGAA AATCAACATT 120

GACTTTTTTT GAAGTCACAT AAGTGTGAAA ATTAGGTTTT TGGACAATGA TTCAGAAATC 180

TTTTGAAAAT TGAAGGTGTG AGGAAATTTA GAAAGATAAA AAGAGGGAGT ACTGAAAACC 240

GAAATTTCAG TTAAGTGCTT GGATCAAGAA ACAAAAACTA CGTTAkTTTG TCAATATCAG 300

TTGAAATTGG AGAAGAAGCA GAATGGGGTG ATAGTATTGG CAAATTAATT ATTTAAGGTC 360

ATCGTTACAG GATTTTTGTT TTTTATATyC aATCmAAAAG AAATAAATAC AAAGaACACA 420

GATAAGTATT TTAGCAAGTA ACCAATAAAT AGCAGGACTG TTGGTGCTAT AAGAATACAA 480

GAAAATAGTA GTAAACTTAA TTGAGAATCG TTTGCTATTT AAATAGTGTT CTTTTCCTTT 540

TAATATATAT ACGATAAAAT AAGTATATTA ATTGTAAaAG GACATGATAA TTATGGAAGA 600

ATTAGAATGG AATwwTTTTT aTGTTTGCTA TAGTTTTGAG GGTAGTGATT CTTTTAATAA 660

CTGTCAAGAT AGTAGATTAC TTTGnGAATA CTCCTGAAGT ACAAATACAG AGAAAACTTC 720

CTGAGTTTGA AAAAGTGCCA CCTTATGATC CAAGAGATAA TTCATTTCTG ATACAAATTA 780

TTCTTTAAGT AATACAACGA CTAAGTTTAT TTACCAAACC ATTACAATAA GAAAAGGTGC 840

AAGTATACCT AATTACTATT GGTATGATGA TGGTCAATTT AGAGGAAATC TAAAACTTCA 900

ACGTTGGCAA GACTACGGAG AAGATCCAAA CATAAGAGGA TATATCTGTA CTTATGGAGG 960

CTACGTTACC AATGGTTCAA GCCCGGCGCA AAGAATTGTC GATATTAATG AACAATAGCT 1020

ATTCTAACTT TATGTAATAG GAGGGAGTAA TCATGAAAAA AATCGGGTAT TTTAGTTGTA 1080

TTATTTTTTT CATGTTTTTG GTAGGTTGTA GTAATAACAA AAAAGAAAAC GGCAATCTTT 1140

TGAATGCCAG TTCGTTTCCT TTAATACTCA CCACGATTAT TGAAAAAGAA GAAGACCTAA 1200

CGAAAGGTTC AATTTTTTTC AACAAGGATA AAACCATGAC GCTTGAAAAA GAATATTTAG 1260

TTAATCCCAA TAATGAAGAC ACAAAAAAAA CAAGTAGAAC AGAAAAAAAG GTATATAAAA 1320

ATATTAAAAT ACAAGAAAAT AAAGAGAGCT ATGAAATTAT AGGTCAATTG GACAAAAAAA 1380

CGAAAAAAAT AGAGTTTAAA AAAGTTGATG AAGGTAAACG TATATCTGAT GCAGAAGGTA 1440

ATGTGTATGG TGATTTTGGT GGTAAATAGG ATAGTTAAGT CATAAAAAAG AAGGCTAAAA 1500

ATTTTTATTT TTTTCGTCTC TATACTTTCT GATGTTAGTT TTTTTACCAA CATCAGAAAG 1560

TATAGAGACG TTTTTGTGTA ATTAAACAAA AAATCAACAT TGACTAAGAC CAGAAATACT 1620

TCCTTTAGTG CTCCGAGTTG CTCTAATATA AGACACCAAA TTGATAACCA TTTGCTTGAT 1680

AAAACTCTAT TAATTGTGGC AATGCTTGTT TTGTTAATTC CTTATCTACT GAATCATGCA 1740

TTAAGACTAC TCTAATATTA TAATCCGGAT AAACCTCAAG TGAATGTTGA TGGAAAGCGA 1800

GCATTTCTGC GACTGTAGTA GGCTGTCTGT CTAACGGCTC CGCATCTCCA ACCATCGCAT 1860

TCCAGTCAAT CCAATGGATG CCAAGTTGTT TGAATAATTC ATCAGATTTT TCTGTACCTC 1920

CCCATGACAT ATGACCTCCT GGGTATCGCC AGAGAGTTGT TTGAAATGTT TCGCCCAATA 1980

TTTTTTTAAG AGAGTTCTCC ATGGTTGCTA TTTCCGCTTG TATTTCTTTA GTGTTGACAA 2040

TCCCGTTTGG ATATAACGTT GCATAATCAT GAGTTGAACT ATGAAAGCCT ATTGAATGTC 2100

CTTCTGCAAC TTCGCGTTTC ACTATCTTTT GATTTTCGGA AGTTAGGGTA TTTCCTACAA 2160

GAAAAAAAGT TGCGTGGACG TTATACTTTT TTAATGTATC TAGGACTTGT GGGGTtATTT 2220

GATTATTAAC GCCATCATCA AAGGTTAAGA ATACTAATTT TTCACCTTTG TAAGGTTCTT 2280

CTCCAGTTAT ATATTTTCTG ATTTTGTCTG CTGAGTAAGC ATATTTTTTT GATGAAATAG 2340

TCATGTGTGT TGATTCCTTT TCTAACTTGG TCGGGGAATC TTTTTTTGCA GTTGAATTTT 2400

TAGTCGATGT CTGCGTAGTA TCATCATTTT TACTTGTTAT CTTGGGTTGA GTTAATAGGA 2460

ACGTTTGAAT GAAAACAAGA ACAATGAGGA TTAACGCACC TAAATnATAC ATACCCGTnT 2520

ATTTTGAATT T 2531

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ACCGCCGCcG CCAArGAtGa AcGAAAATAT CTcGAATCCA CCAAAACCAC TACTGCTAAA 60

TCCGCCGCCA CCGAAACCGC CAAAGCCaCC aGCGCCGcCA CCGwAATTAG GATCAGTTCC 120

TGCATGGCCA TATTGGTCAT AGGCCGCTTT TTTCTGTGGA TCACTTAATA CTTCATACGC 180

TTCAGAAACT TCTTTAAATT TTTCTTCCGC ATCGGCTTCT TTGTTAATAT CTGGATGGTA 240

CTTTTTGGAA AGTTTGCGGT ATGCTTTTTT AATTTCATCA TCTGAAGCAC CTTTTGCTAA 300

TCCTAGCACT TCATAATAAT CTCGTTTCGT CGCCATTGAC TTCCCTCCAA CTTTCTTCAA 360

ACTTTACAAT GTGTTTAGAA CCAGCCAAAT TCATCGATTG CTTTCGGTCT CTCTGGTTGG 420

ATTATCTGTC ACACCTTGAA TCAGTGTTAC TAGCTGTGAA TAGGTATTTT CAGCTTGTTT 480

AACATCGTTG TAATCATACC ACAGTTCTTT CAAAACCTAA ATAGTTTCTT GCTAACTTGA 540

TTGTGGTTGA TTTTCTCACA AAAGACAAGG GACTGGGACA TTAGTCATTG TACTAATGAT 600

CCAGTCCCTA AAATCaATTG TTATTGATTA TTTGTCATCA CCATTTACTT CTTCAAAATC 660

AGCATCAACA ACATCATCAG CGCCACCTtG gAGCAGCTTC AGGgATTTTC TTGTGCTTGT 720

TGTTGCGCat TGgTTCGTAA AGTTTTACTG TTAAGTTTTG GACGATTTCA TTTAATGAAT 780

CACGTTTTGC TTTCATTTGT TCGATATCGT TTGCTTCGAT GGCTGCTTTT AATTCATCAC 840

GCGCATCTTC TGCTTTTTTC ACTTCTTCAG CATCTACTTT GCCTTCTAAT TCTTTCAATG 900

TTTTATCAAC AGTGAATAAT AAAGCATCTG CATCGTTACG TAAGTCAACT TCTTCTTTAC 960

GTTGTTTATC TGCTTCAGCG TTTGCTTCAG CATCTTTCAC CATACGTTCG ATTTCATCAT 1020

CAGATAAACC TGAAGAAGAT TTAATCGTGA TTGTTTGTTC TTTTTGAGTG CCTAAGTCTT 1080

TCGCACGAAC ATTTACAATC CCGTTTTTAT CAATGTCAAA GCTTACTTCA ATTTGTGGCA 1140

CACCACGAGG AGCTGCAGGA ATATCTGTTA ATTGGAAACG ACCTAATGTT TTATTATCAG 1200

CGGCCATtGG ACGTTCACCT TGTAAAACGT GAATATCAAC AGCTGGTTGA TtGTCAGCAG 1260

CAGTTGAGAA TACTTGTGAT TTACwTGtTG GAATCGTAGT GTTACGATCa ATTAATTTTG 1320

TAAATAcGCC ACCCaTTGTT TCAATCCCTA ATGACAACGG TGTTACGTCT AATAAgACAA 1380

CGTCTTTAAC ATCACCAGTG ATTACACCAC CTTGGATTGC AGCACCCATT GCTACTcTTC 1440

GTCAGGGTTA ACTGATTTGT TTGGTTCTTT GTTTGTTTCT TTGCGAACAG CTTCAACTAC 1500

AGCTGGAATA CGTGTTGAAC CACCAACTAG GATAACTTCG TCGATTTCAG AAGGATTTAA 1560

TCCAGCATCT TTTAAGGCTT GACGTACTGG TACTTTTGTA CGTTCAACTA AATCACTTGT 1620

TAATTCATCA AATTTTGCAC GAGTTAAGTT CATTTCTAAG TGCAATGGTC CTGcTTCGCC 1680

AGCAGTAATA AATGGCAAGC TGATTTGTGT GCTTGTTACA CCTGATAAGT CTTTTTTCGC 1740

TTTTTCAGCA GCATCTTTCA AACGTTGTAA TGCCATTTTA TCGTTAGCTA AGTCAATGCC 1800

ATTTTCTTTT TTAAATTCTG CAACCATGTA GTCAATGATC TTATTATCAA AGTCATCCCC 1860

ACCTAGGTTG TTATCACCGG CTGTTGATAA TACATCGAAA ACGCCATCGC CTAATTCAAG 1920

GATTGACACG TCGAATGTAC CACCACCAAG GTCAAAGACA AGAATTTTTT CATCTTTGTC 1980

TGTTTTATCT AAGCCATAAG CTAAAGCTGC TGCTGTTGGT TCGTTAACGA TCCGTTCTAC 2040

TTCTAAACCA GCAATTTTAC CAGCATCTTT TGTTGCTTGA CGTTGCGCAT CGTTGAAATA 2100

TGCAGGAACT GTAATAACTG CTTTTTCAAC TTTTTCACCT AAATAGTCTT CAGCAAAACC 2160

TTTTAAATAT TGTAAGATCA TTGCAGAAAC TTCTTGTGGT GTATATGATT TTCCTTCAAC 2220

ATCAACTTTG TAGCCAGCTT CACCCATGTG ACGTTTAATA GATGAAATCG TGTTAGGATT 2280

TGTAACAGCT TGACGTTTTG CTACTTCGCC CACTTgAATT TCACCGTTTT TGAATGAAAC 2340

GACCGAAGgA GTTGTGCGGT TACCTTCTGG GTTTGCAATA ATTTTCgctT CGCCGCCTTC 2400

TAGTACTGCG ACAGCTGAGT TTGTTGTTCC tAAGTCAATA CCAATAATTT TACTCATAGT 2460

GAATATCTCC AATCTGTATT AGTTTTCTAT AATAATATAT TTTTAATTAA CGTTTGTTAT 2520

TGTGCAACAA TGACCATTGA TGGTCGTAAC ACACsATCTT GTAATTTGTA CCCTTTTTGT 2580

AGAACTTCAA CAATGGTATC TGCTGGGGTT TCTTCAGAAG CAGGGACTGT TTGAACGGCT 2640

TGATGTAAAT TTGGATCAAA GGTTCACCCA TTGCTGGGAT TTCTTCAATT CCTTCTTCTT 2700

TTAAAGCCAC AGTAATA 2717

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAATTTAGAA ATGAGGACTA CTGATGATTT TATTACAAGC AAATCAAGTT GCCCGGCATT 60

TTGGCTCGGA AACATTGTTT GAAAACATAC ATTTAGAAAT TGCAACAAAA AGTCGGATTG 120

CCTTAGTTGG TCGTAATGGT GCTGGAAAAT CGACTTTTTT AAAAATCATT GCAGGCATTG 180

ATGCTCCCGA TAGCGGAACC ATTGCCAAAA ATaAAACTGC TACGTTAGGT TATTTAGCTC 240

AAAATACCGG CTTAGAATCA GATAAAACCG TTTGGGAAGA AATGACAAAA GCCTTTGCTG 300

ACATCCTAGA AATGGAACAg CGTATGCGAG aATTAGAAAC TAAAATTAGT GAAATGGAGC 360

CAACCACTTC CGTTTATGAA GGAATTTTAA AAGAGTACGA TCAATTGCAA CATACGTTTT 420

CTGAAAAAAA TGGCTACGGC TATGAAAATG AAATTCGCTC AGTCCTTCAC GGCTTTGGCT 480

TTGATGAATC CTTTTACACG AAAGATATTC AAACCTTATC TGGTGGTCAA AAAACCCGGC 540

TTGCATTAGC GAGAATGCTT TTACAAAAAC CAGACATTTT AATTCTGGAC GAGCCTACAA 600

ACCACTTAGA TATCGAGACG CTTtCTTGGC TGGAATCTTA TTTGCCAAGT TATGCCGGCG 660

CCCTATTAAT TGTTTCCCAC GATCGtTATT TTTTAGATAA GGTAGTTAAT GAAGTTTATG 720

AACTGAGTCG CAAAAAAATG ACTCACTACA AAGGaAACTA TTCCAAATAC TTAGAGTTAA 780

AAGCAGAACA ATTAGCCAGT GAATGGAAAG CGTATGAAAA GCAACAAGAA GAAATCAATA 840

AGTTAGAAGA TTTCGTTGCC AAAAATCTGG TTCGTGCATC TACAACGAAA CGTGCACAAA 900

GTCGCCGAAA AGTATTAGAA AAAATGGACC GTTTAGACCG ACCTCAAGGA GATGAAAAAT 960

CGGCGCATTT TCTTTTCGAT AGTGAAAAAG TCTCGGGAAA TGTTGTTTTA CAAGTCGAAG 1020

ATGCCGCCAT TGGTTACGAC CAAGAACATA TTTTATCCGA ACCTATTCAC TTGGATATTC 1080

GTCGCAAAGA AGCCATTGCC TTAGTCGGAC CGAACGGAAT TGGTAAATCC ACTCTCTTGA 1140

AATCAATTAT TGACCGCATT CCTTTCATTA AAGGAAGTAA AACTTTTGGC ACCAATGTTT 1200

CTGTAGGTTA CTATGACCAA GAGCAAGCCA ATTTACATGG CAATAAAACG GTCTTAGCGG 1260

AATTATGGGA TGAACACCCA ACCACACCTG AAAAAGAGAT TCGAAGTATT TTAGGCGGCT 1320

TTCTCTTCAG TGGAGACGAT GTTGAAAAAA CGATTCCTTT ATTAAGCGGT GGCGAAAAAG 1380

CCCGTGTGGC ATTAGCAAAA CTAGCGATGG ATCGTGACAA TTTCTTGATT CTCGATGAGC 1440

CAACCAATCA CTTGGATATC GATAATAAAG AAGTTTTAGA AAATGCGCTG ATTGATTATG 1500

AAGGAACCAT CCTCTTCGTT TCCCATGACC GTTACTTTAT CAATCGAATT GCAACAAAAG 1560

TTGTTGAGCT TTCTGAAAAA GGCAGCAAAC TTTATTTAGG CGACTATGAT TATTATTTAG 1620

AAAAGAAACA aGAGGAAGAA GAAATCGCTG CCCTCTTAGC TAATGAAGAA GCGGCGAAAA 1680

AACCCGAACC AGTTACAGCC AAAAATACCT TTTATCAAAA CAAGGAGCAA CAAAAATTAC 1740

TCCGTACTTT GCAAAGAAAA ATAACACAAG TCGAAGAAAA TCTTGCTCAG TTAGATACGA 1800

CAATTGCACA ATTAGAAGCA CAAATGAGTC AACCAGACAT TCTAGAAAAT CATGTTGAAT 1860

TGCTGGCTTT AAACCAACAA TTAGATGAAG TTCGTCAGCA ACAAGATGAA CTACTTGAGC 1920

AATGGGAAAA TTTCAGTTTA GAATTAGAAG AAATGGAAAA TAACAATTAA CGGAGGGATT 1980

CACTATGGCT TCCAAAAAAA TCAGTTTAAC GAaGCCCAAA TATCAACAAA TCGCCGTTGA 2040

TGTTGCGGAA AAAATTGCAG AAGGCAAATT ACATGTTGGA GATAAAATCC ATGCCCGTTC 2100

CACCCTAGCT AACCAATACC AAGTGTCGCC AGAAACAGCT CGCAAAGCCA TTATCGTTTT 2160

AGTTGATTTA GAAATCGTTA AAGCCAAACA CGGCAGCGGC TTCTATGTGG CATCAAAAGA 2220

AAAAGCGCAG GACTTTGTGA CACAATATCA AGACGTTCAA ACGATTGCTG AAATTAAAGA 2280

AGAATTGCTA GATAGCGTAG cGAAACAAAA AGAAGAACTT ACTCATTTTT CTAGCATTCT 2340

AGATACTCTT GTTGAACAAA CAAAGCGTTT TGATTCTTTC AATCCAATGA ATCCCTATTC 2400

ATTAGTTTTA ACAGAAGAAG CTGCTTATCT TGAGGCGACG ATTAGCGAAA TGAATTTTTG 2460

GCAAAACACT TCGGCAACGA TTATCGCCAT CAAACACAAA GAAGAGCTTC TGGTCTCACC 2520

TGGTCCATAT GCAAAGATTT CGTTGAACGA CACACTTTAT TTTGTTGGAC ATGACGAATC 2580

AACCTTACAA CGTGTCCAAA ATTTCTTTTA TCCTTAAACA AAAAAGTGAC TACTTATCTT 2640

GCGGTAAATA GTCACTTTTT TTATTTATTA TTTCTATTTT TCATAAAAAC CCACTATAAA 2700

ACCTAGTTAA AATACTGTTT TTCTTCATTT TCAGAAAGAT TTTCATCTAA TTTGACAAAG 2760

TGACAACTTT ATAGTAGTCT GATGTAGTCA CTTTTTTTAA TGAGGAGGAA CAATGATTTG 2820

CCAAAAGTAA AAgTAAATCA CCTTACCAAG ATCTTTGGtA AGAAAACCAA ACCGGCACTT 2880

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GGAAATATTT ATATTGATGG ACAAGATATT TCTTCTTTAG ATAAAGAAGG ATTACGTGAA 3120

GTACGTCGAA ATAAAATGAG CATGGTTTTC CAAAACTTTG GTCTTTTCCC CCATCGAACT 3180

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AGTCAATTAT CTGGTGGGAT GCAACAACGT GTCGGCCTTG CTCGTGCCTT GGCTAACGAT 3360

CCAGAAATTT TATTAATGGA CGAAGCGTTC TCTGCTCTTG ATCCGTTAAT TCGTCGTGAA 3420

ATGCAAGACG AACTATTAGA TTTACAAGAA AATGTCAAAA AAACCATTAT CTTTATCACA 3480

CATGATTTGA ATGAAGCTTT ACGAATCGGC GACCGGATTG CTTTGATGAA AGATGGTCAA 3540

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TCTCACCAAT TTCCATGGCA CACCTCGTTT CTATTTTCAG CTAATCTTTT CAACAAAAGT 16860

TTTGTAATAC 16870

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3905 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CGTTTCTTGG TGGAGCAAGC AGATGCTTCA AGAGCCAAAA GAAAAAAAGT GATTGATAAA 120

CTAGCGGCAG TAATGATTCT ACAAAATTAT TTAGATGCAC ATAGCCGATA ATTATCGAGC 180

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GTTCACTTGG CAATCCAGTA ATGGCCACTA TAACCAAGGG ATAAAGGAAG AATGCCTTCA 3900

CCGAT 3905

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GCCAAAAACA AGAAAATCAT TTCGTACTAT TGAGTTAGGT GATGCTGCAG TACAGATTAT 32760

AAAAGACC 32768

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7964 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AGTAGCAAAT TCAACCCGAT TCCCGCCTGG TTCACGAATG TATAAACTTT TAAAATATCC 6660

ACGACTTACA TACATTTCAA TTTCCCAGCC TTGTGCTAAA GCGCGCGTGT GTAGTTCTTG 6720

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GCTTGTTTTA TCCGACGTTG TTTGATGAAC AGAAAAGCTT TCCGTCTCAC TTAAAATAAT 6840

CGTATTGCCA ACTGCTTGCC AACCAAGAAA TGTTTCAAAA AAGGCCAAGG TTTTTTCAGA 6900

ATCTGGCACA TGAAATTCAG TAGAGGCCAA ACCGATAATT TGAACCGCTG CTGGAATGTC 6960

GTTAGAAACA ACGAGTGTTT CTTTTAATGG ATTTTCAGGA ACTTCTGTCA GGATAATATG 7020

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GGCTAAATAA TTTTTTTCTT CATAGCGGTT GCCTAATAAG GGCACGATAA AAAAAGTTAC 7200

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TTGATTTACG GTATTTTTGA CAAAACGTAA GCCTAACAAT TTTGTATAGA ATGATTGGTT 7320

TTCTTGACCA TGACGCGCTA ATAGTGAAAC ATGATGAAAT TGAGCATGCA TTTTGAGTTC 7380

CTCCTCTAAA TAACTATGTA TACTTACTTA AAGTAAGTAT AGTGCTTCTG ACATTTTTTG 7440

ACAACTATTT AGTTTGATTC AGAAGGCTGA CATAGCCAGA AACmAGAAAA AGTGTTAGAA 7500

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TTTGATTTAC CAGAAGAATT AATTGCTCAA ACCCCACTAA AAGATmGCGC TAGTTCACGA 7620

TTATTAGTTG TAAATAAAGA AaCAGGGGAC ATGGAGGATA AACATTtCCA TGATATTCTT 7680

GATGAATTAC AGCCTGGGGA TGCATTAGTC ATGAATAATA CACGGGTACT GCCGGCCCGT 7740

TTATATGGAG AAAAACCTGA AACAGGCGGT CATTTGGAAG TTTTACTTTT AACAAATACA 7800

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ATTCAATTTG GCGATGGTCG CCTAAAAGCG GTGGTTAAAG AAGAGTTGGA ACATGGTGGT 7920

CGAATCATTG AATTTAAATA TGATGGTATT TTCTTAGAAA TTTT 7964

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AGAAGTGAAA AGAGCTTTTG ACTTACGCTn nTATTATGAG GAACGAACCT TTCAGGCTGG 60

GAAAATAAGG AGGTATCAAA AGAATGAATT TGTTCAAaAA GArACAATCA AAGArACAGA 120

CGTTATCTAG TAACGTTGAA AAAGTAGATA AAAAAGTAAA AAAACGTGTA CAGCAACAAG 180

CAAATCCTAC CGTACAGGAG AGTATTTTTT ATACGAGTCA GTTTGAAGAA GnGCTCATGC 240

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CTGTAGAAGA AGaTCmATTA AACaCGGTAA TGGGGTATGC AGAAGGGTTA AATACACTAG 360

ACAAAAAATC TCGGTATCaG CTGCTGGTTG TTAATAAAAG AGAAGAAGAG TCGTTGATGG 420

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TTTTCACCAC AAAAAGTTCG TCCATGAAAC AAGCTAACAA AGAGTTAGAA GGAATCATGC 600

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CGAACGCGTT AATGGATGAA ATAAAAAATA ATGGCCAAAA GTTATTTAAT GGCCTATTTT 1140

CAGTTTTCCT AATTGCAGAA ACAGAAAAGG AACTTTTAGA AGCTGTTGAA TCGGTGAAAA 1200

ACGTAGGAGC AACCTGGCAA GTTGTGTTTG ATACGGTAGA CAATTACAAA GAAGAAGCAC 1260

TCAATACTAT CTTACCGATT GGAAAACCTT ACTTAGACGT TGAAATGAGT TATATGCGtG 1320

ATCTAACmAC mACmAATATt GCTACACAaG TACCTTTtAC CAATGTGGrA TTACAAgCCC 1380

AcAGGTCAGT TTtATGGCCG GAaTCmGTTG ACGAAGAaCA TGATtACTAT tGrCCGAAAA 1440

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CGTATGAACG CTTTGAAAAC AAAGAGACAG AGCCAACATT AGTCGATTGG TTTAGAATCT 1860

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CCTGATTATC AGTTGAAAAC AATGCAAAGT TTAGAGACAG ATAAGAAATC GAGTTATTTT 3600

ATCGAAaGAGG AACAAGCAAA GCATTATCAA GAGaTAAAAA AAGAGTTAGG CTACCAAACA 3660

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CGCTGGTTAT CGAAAAaGAG AAAGTAGCTA GGTTAACGAT TCGTGGTGTG AaTACCCTTC   3900
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GTTAGGAAAA AGCATTTACC CTACTATGGG AAACGCCAAT CAATGGGTGC ATAACTACAG   4860
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CTCTGATGGT AGTTTTGTCA TTTCTGAAAT GAATGTCAGT GGTGAGTATT CTATGAATTG   5040
GCGTGTCTTA AAAAAAGAAG CAGGCGAATA CTTTATGCGC CTAAACTAAA AAGAAAGGAA   5100
CCAATAAGAA CAATGTATAA TATGGAAAAA TTAAGTAGAT ACAAGAAAAT TGGCTTTATT   5160
GGTGGCAGCT TACTGCTTAT TGTGCTTATT TTTTTGATTG GGCTTAGTGT TGGGCAAAGA   5220
AAACAAGTAA ACACCAATGA AAAACAAGTA AAAGTCGAGA AAAAAGAGGA ATTAACAACA   5280
AGTACGGTAA AAAAATTTTT GATTGCGTAT TATACAAAAA AAGATCTTGG TGAAAATAGA   5340
AATCGCTATG AACCTTTGGT GACAAGCGCC ATGTATAACG AATTAGTGAA TGTAGAAAAA   5400
CAGCCTGTTA ATCAAGCGTA TAAAGGCTAT GTAGTCAATC AAGTACTTGA TACGTATAAA   5460
ATCTATATTG ATACTGAAAA CAATGAAGTC ATTGTGGACG TCACGTATAA GAATACACAA   5520
CGAACCAAAC GAAATAATGA TGAAGGAGCG TTGAAAAATC AGAGCAATCA AGAAGCGATG   5580
AAATTAACCT TTGTAAAACA gGCGCTAATT TTTTAGTGGA TAAAtGGCAC CAGTAACACT   5640
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TACCAATGAA TTmCAAGAGG AGCCAAATTC TTATAATACa CATGTAGTAA CGACAGAAGA 5700

ATCAACAAAG GAGAGTGCAA ACAGTGGGGA AAAGTAAAGT AAGTGAATTA GAAAAAAAGA 5760

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GGTGGAACAA AGAGAAATTG TACACCGCTA TTATGTTTTA GGTACTAGTA CTTTAGATAA 6780

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AACTGTTGAT TGCnG 7215

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTTCGCCTA AGAGATTCAC CATAACCACT GATTGAAGTA ATTGGGGTAA CCCAATGCCC 60

CAATTGCTAA TCCCTCGAAT ATGCGCATCA AATTGACTAA ATGAGCAAGC TTCAATAGAG 120

TAATGACCTG AGTTATGAGG CCGTGGCGCT AATTCATTGA CGTACAACTC TTCTGAATCC 180

GTTAAAAACA TTTCGATAGC TAAAACCCCA GATAGATTTA ATTCCTCAGC AATGTATTGC 240

GCCAATTCCG CTGCTTTTTG TTGCACATTC TCAGAAATTC GTGCTGGCAC AATTGATTCA 300

TGCAAGATAT TCTTTCGATG AATGTTTTCA GATACAGGAA AGCTTTGGTA ACCATGCTTA 360

TTCCCTGCAA CGATGATTGA AAGTTCTTTA GTGAAAGGCA CCCACTTTTC TAATTCACAA 420

GTGGCGTTAG cTAATAATTT AGTCGCTTGG GAGAAATCCT CTTCGCATTT TAAGACGACT 480

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TGTCCCCCAC CTATAATGCC AATAGTTGCT CCTACTTTTA AAGGTTTATT CAAGTTGTTC 960

CCCACTTTCC ATAACCGCTT TTTCCAATGA TTGTCGTCTT GCTTGGATTC TTTCTGCTAA 1020

CTGTAAATCA TCAATACTTA GTATTTCTGC AGCTAATAAC CCAGCATTGG TAGCACCTGC 1080

TGAGCCAATC GCAGTTGTTG CTACAGGAAC TCCCCCTGGC ATCTGCACAA TAGACAACAG 1140

TGAATCAATA CCGTTTAACG TTCGTGTTTT AACTGGAACA CCAATGACAG GTAAGGTTGT 1200

CTTTGCAGCT ACCATCCCTG GTAAATGGGC CGCTCCACCA GCGCCAGcgA nTAATAACCT 1260

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TCATCGTTGC CCaGTCTGAG GTACTTCCCa TAATCACAGC GACTAATGGT TtCATGAATG 1440

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GATGGCTCAG CAATTACCCT GTTTAGCCAA GGCAATTTTT CCCTTACCTA TCCTGAAAAA 3060

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GATTTAAGCC TGGGCCGAAA ATCAAAAGCG ATTTTCAGCC CAGGCTCTCT TTTTATTTTT 3600

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AATACTTTTT CATCTTCTTT CTCCTATAAC TCTTCATTTT TTTATGCTCT TACTTACAGA 5280

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TTTTCCAACT AAGTCTTGAC CATCTTCTAA AATCGTATGT GTcGCCAGAA ATCACATAAG 5460

AATATTCATC CTGTTCATGG CGAGCATATC CAGCTAAAGG CCGT 5504

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GTTGCGACTA AACTATAGCC AATTGCTGAA AAACGCTTAG CAATTTCTAA CGCCTCTTCT 60

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TTTGTTTCAT CAGCAATGGT GAAAAGTACA GCCCCATAAC TTGGCAAATG CAAGCCAGAT    120
GCTTCAAAGG CTTTATACAA GGCTTTTTCT AAATAATAAT CACTACCCAT AACTTCCCCA    180
GTTGATTTCA TTTCAGGCCC TAAGTACGTA TCTACTTTTT GTAGTTTCGT AAAGGAGAAT    240
ACAGGGGCTT TCACATGAAC TTGTTTACTT TCAGGATATA ATCCATCTTG ATATCCTAGG    300
TCAGTCAGTT TCTCACCAAG AATCGCTTTT GTAGCAACTT GGGCCATCGG AATCCCTGTG    360
ATTTTACTTA AGAAAGGAAC TGTTCGACTC GCACGAGGAT TCACTTCAAT CACATAAACA    420
CGATTTTCAT GAATAACAAA TTGAATATTC ATCATACCTA CACAGTTTAA ACCAAGTGCC    480
AGTTTTTTTG TATAATCGGC AATTGTTGCT TGAATTTCTT GAGAAAGATA CTGCGGTGGA    540
TAAACCGCCA TTGAATCACC AGAATGCACG CCAGCTCGTT CAATATGTTC CATAATCCCT    600
GGAATTAGTA CTGTTTCACC ATCACAAATG GCATCAACTT CACATTCTTG TCCCAATAAA    660
TAGCTATCAA CCAAGACAGG ATGTTCTGGA GAAGCTTTGA CTGCATGTCG CATATAATCT    720
TCCAAATCCT TTTGATTTTC GACAATTTCC ATTGCACGAC CACCTAAAAC ATAACTTGGA    780
CGAACTAAAA CGGGATAGCC GATACGATCA GCAATCACGA CTGCTTCTTC TGCACTTGTG    840
GCCGTATCTC CTGGTGGTTG AGGAATCGCT AACTCTTGCA AAGCTTGTTC AAATAAATCA    900
CGATTTTCCG CACGATCTAA ATCTTCAATC GTTGTTCCAA GAATTTTAAC GCCTTGTTTT    960
GTGAGCGGCT CAGCTAAATT AATCGCTGTT TGTCCACCAA ATTGGACGAT CACGCCAATC   1020
GGATTTTCTA AATCAATCAC ATTCATGACG TCTTCTAAAG TTAATGGCTC AAAGTATAAT   1080
TTATCAGAAA CAGAGAAATC TGTTGAAACT GTTTCAGGAT TACTATTCAT AATAATTGCT   1140
TCATAACCAG CCGCTTGGAT CGCTTTGACA GAATGAACCG TTGCATAATC AAACTCGACC   1200
CCTTGACCAA TGCGAATGGG ACCAGAACCT AATACTAGTA CAGAAGGCTT TTTCGAAACA   1260
TTGCTTTCGT TTTCCACTTC ATACGTGCTA TAAAAATAAG GCGTGTGTGA TTCAAACTCT   1320
GCAGCACACG TATCCACCAT TTTATAGACG GGCACAATTT GATTGGCTCT GCGGAAGTCA   1380
GCGATGGCTT GTTCTGTTTG TCCCCAAAGT GCTGCGATTT TCCGATCAGA AAAACCATTT   1440
TGTTTGGCTT CTTTCAAAAC AGCTACGTTG TCCACGTGAC TTTCAAGGGC TGTTTCAATT   1500
TCGATAATGT GTAAAAGTTT ATCCAAGAAG AATAAATCAA TTTTCGTTAA ACTTTGTAAT   1560
TCTTCGATGC TATATCCTCT GCGAATGGCT TCTGATAAGT AGAACAATCG ATCATCTTGC   1620
GCATGGACCA TTTTCTTCGT TAATTCCAAA TCACTGACAT GACTTAGTTC TGCTAACTCG   1680
TTGTGATAAG CACCAATTTC TAAAGAACGA ACTGCTTTTA ATAAGGATTC TTCAATATTG   1740
CGGCCAATTG CCATGACTTC CCCGGTTGCT TTCATTTGCG TTCCTAGTTC TCGAGCACCT   1800
TTTTCAAATT TGTCAAAAGG CCATCGAGGA ATTTTGGAAA CAACATAGTC CAAAGCTGGT   1860
TCAAATTCGG CATAAGTGGT TCCAGTAACT GGATTTTTCA TTTCATCTAA TGTTAAACCA   1920
ACAGCAATTT TTGCAGCTAA CTTCGCAATG GGATACCCTG TGGCTTTACT AGCAAGTGCA   1980
GATGAGCGAG AAACACGAGG ATTCACTTCA ATcACaTAAT AwTTAAAGcT ATGCGGGtCC   2040
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AArGyTAATk GAACwTTACa GCCACCTTCA ATTTTTAATG CACGAATaAT TTTCAArGAC      2100
GCATCTCGCA ACATTTGGTA TTCATAATCT GATAAGGTTT GACTCGGAGC AAAAACAATC      2160
GAATCCCCAG TGTGAATGCC GACAGGATCA AAGTTTTCCA TGTTACAAAC CACAATCGCA      2220
TTATCAGCCG AATCACGCAT CACTTCATAT TCAATTTCTT TAAAACCAGC AATACTTTTT      2280
TCAATTAAAC ATTGTGTAAC TGGTGATAAT TTCAGACCGT TTTCAGCAAT TTGGCGGAGT      2340
TCTTCTTCCG TATCACACAT GCCGCCGCcT GTTCCACCTA AAGTAAATGC GGGACGAACG      2400
ATAATTGGAT AGCCAATTCG TTTGGCAAAA GCCACGGCTT GTTCCACCGT ATTGACAATT      2460
TCACTTTCTG GAATCGGTTG TTCTAATTCT TCCATCAATT GTTTAAATAA ATCACGGTCT      2520
TCCGCTTGGT CAATCGCACT GAGCTTTGTT CCTAGCAATT CTACATTTAG CTCATCTAAA      2580
ATTCCTGATT CCGATAATTC CATCGCCATA TTTAATCCAG TTTGACCACC TAATGTTGGT      2640
AGAAGAGCAT CAGGACGTTC TTTTCGCAAA ATTCTTGAAA CAAATTCTAA AGTAATCGGT      2700
TCGATATAAA CATGATCCGC GATTTCCTTA TCGGTCATGA TAGTCGCTGG ATTTGAGTTT      2760
ACTAAGACAA CTTCATACCC TTCTTCTTTT AGCGCTAAAC AGGCTTGTGT GCCTGCATAG      2820
TCAAATTCTG CTGCTTGTCC AATAATGATT GGTCCTGAAC CAATCACCAT GATTTTCTTG      2880
ATGTCCGTTC GTTTTGGCAT TAGTTTTGCT CCTTCCATGC ATCCATTAAT TCCATAAATT      2940
CGTCAAATAA ATGAAGACCA TCGTGCGGTC CTGGAGCCGC ATCTGGGTGA TATTGCACAG      3000
TAAAAGCAGG ATAATCTCGA TGACGCACGC CTTCAACCGT TCCATCATTG ACTTCCACGT      3060
GGGTCACAAG TAATTTTTCT GGATCAATTG TTGCTTCATC TACGGCATAT CCGTGGTTTT      3120
GTGAAGTGAA ATCAATGCGT CCTGTTGCAA TTTCTCGTAC AGGATGATTC AAACCGCGAT      3180
GTCCAAACTT CATCTTATAC GTATCCGCAC CATTCGCTAA TGAAAATAAC TGATGACCTA      3240
AGCAGATGCC GAAAATCGGA ACTTTTCCTT GGATTGCTTG AATCATTTCA ATAGCTTCAG      3300
GCACATCTTT GGGATCTCCA GGCCCATTTG TCAACATGAC ACCATCGGGA CTTAATTCTA      3360
AAATCTCTTC GGCCGTTGTA TTATAAGGCA ACACGGTTAA GTTGCATTGC CGTTTTGATA      3420
ATTCTCGCAA AATACTATGT TTCAACCCAA AATCAACGAC GACCACATTA CGCCCAATAC      3480
CTGGACTCGG ATAAGGCTTA GTGGTGGAGA CTTGTGCCAC TTGATTTTTC GGCATGACTG      3540
TCGCTTTTAA TTGATCAAAC GCATGCGGCA AATCATCCAC GGCATCAATG ATGCTCCCTT      3600
TCAkTGTTCC AGCTGATCGT AACTTACGAG TCAGCGCACG CGTATCAATT CCTGAAATTC      3660
CCGGAATCCC TTTGCGCTTT AAAAATTCAT CCAAGGTCAT TTGTTGACGC CAATTTGAAG      3720
CAACCCGCGC ATGCTCTTTA ACAATGACAC CTTTACAGGT TGGTGCaATG GATTCATaAT      3780
CaTCTCGGTT GACCCCGTAA TTCCCaACTA ATGGATACGT AAAAGTAATC ATTTGTCCAT      3840
TAAAACTTTG GTCAGTAATT GCTTCTTGGT AACCTGTCAT GCCAGTAGTA AAAACAACTT      3900
CTCCTACTAC ATTGCCtTCT GCaCCAAACG CTTTTCCTTC AAATACTGTT CCGTCTTCTA      3960
AAATCAATAA CCTTTTCAAA CCTACTGCGC CTCCTCCGAC CAAGCTAATG CTCCGTCAAC      4020
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AAATGTCATA AGTGTCTTTC CTTTGACTGT CCACCCTGTA AATGGTGTAT TGACAGCCAT     4080
TGATTCAAAT GCTTCTGCAT CAATTGGTGC AGCTGTTGCT AAGTCAAAAA CTGCAATATC     4140
TGCTGGTGCA CCAATTsTTA GTGTTCCTGC GTTTAATCCA AAAATTTCTG CCGGTTTCAC     4200
TGCCATCCAA TCAATCACTT GTTCTAATGT GAAAATGCCT GTTTCGACAA AGTTCGTATA     4260
AATCAATTGG AAGGCCGTTT CACTACCGAC AATACCAAAA GGTGCGTTTA AAAATGATTG     4320
TTGTTTTTCT TCTAAACCAT GGGGCGCATG GTCGGTAGCA ATACAGTCAA TCGTGCCATC     4380
TAACAAGCCG TCAATCAATG CTTGTCGATC TGCTAAACCA CGTAATGGCG GGTTCATTTT     4440
CCAAAACCCT TCGTCACCAG GAATATCCTC ATCGACTAAA ATTAAATGGT GTGGCGAAAC     4500
TTCGGCTGTT ACGTGAATCC CTGCTTTTTT AGCATCTCGA ATAACGCGCA CGCTTTCTTC     4560
TGTTGAAACA TGACAAACAT GATAATGAAC GCCTGTTTCT TTCGCTAAAG TAATATCCCG     4620
AGCAATTTGT GAAGCTTcCG TTGCACTTAA AATCCCTGGT AGGCCTAATT TCTTAGAAAC     4680
TTCTCCTTCA TGCATCACAC CACCAAATAA TAAAGATTCA TCTTCCGTGT GCGCAACAAG     4740
TGCCATATTT AATGCAGCCG CTTCTTTCAT GGCTAAGTAC ATCGTTCCTG CCGTTTGGAC     4800
ACCAACACCA TCATTCGTAA ATGCAAAGGC GCCCGCTTCT TTTAAGGCCT TCTGATTGGT     4860
TAAAACTTCA CTCCGTAGCT CTTCTGTAAT GGGGGCATAT TGTAAAACTT TCACGACTGC     4920
ATCTTTTTGA ATTAAGTCGT AAACCTCACT TAATTTTTCA GCCGTATCTG GTACTGGATT     4980
CAAATTGGGC ATTGCGCAAA CCGTAGTAAA ACCACCGCGA GCAGCAGCTT TACTACCCGT     5040
TTTAATCGTT TCTTTATACG TAAAGCCTGG TTCTCTAAAG TGAACATGCA CATCCACCAA     5100
GCCTGGCGTG aTTAGTTGCC CGTTCGCATC AAACACTTGC TCAAAAtCTG CTTCGTCAAA     5160
CGATTCCCCG ATTGCGTGAA TCACACCATT TTCTAGCCAA AGTGCTGCCT CAATCAATTG     5220
ATTCTCTTTT TTGATGATTT TTCCATTCTT AATTAACGTC TTCATTTCTC CACCTAGGCC     5280
TTTCCATGTA AAATTGCTTC CAAAATTGCC ATGCGCATAA AGACTCCGTT ACTCATTTGC     5340
GCGACGATTC TTGATTGCAG ACTTTCCACT AATTCATCTG CCAGTTCAAC ATCCCGATTG     5400
ACTGGCGCTG GATGCATAAT AATTGCGTGT TTCTGTAAAC GAGTTGCCCG TTCGTTGGTT     5460
AAACCATATT CCAAATGATA GCCTTCTTTT GAAAAACTTT CCTTACCATC ATGACGTTCG     5520
TGCTGCACGC GAAcAACATC ATCACATCGA CTTTTTCAAC AATTTCATCT AGCGGCACAT     5580
ATTGTCCATA GACATCAAAC TGATGATCGT ACCACTCTTC TGGACCTGAA AAATAAATTT     5640
CAGCGCCTAA ACGGTTTAAT AACTGCATAT TTGATTTAGC AACGCGAGAA TGTGTAATAT     5700
CTCCCACAAT CGCCACTTTC AAGCCTTCAA ATCCACCAAA TTCTTCATAA ATAGTCATCA     5760
GATCCAATAA ACATTGTGTA GGGTGTTGTC CACTCCCGTC CCCACCGTTA ATAATAGAAC     5820
ATTGAATCGT TTTACTTTGA ATCAATTCAT CGTAATAATT TTCTTTACCA TGACGAATGA     5880
CTGCTACATC TACACCAATT GCCGACATCG TTAGTACTGT GTCGTATAAC GTTTCTCCTT     5940
TTTGAACAGA ACTTCTACTT GCTTCAAACT CAATCACTTC TAAGCCTAAT TTTTTCTCAG     6000
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CTACCTCAAA ACTTTTATGT GTTCGAGTAC TATTTTCAAA AAACAAGTTT GTTGCAAAAT 6060

ATTGACGTTC TTCTGGGTGC CATTTTGCCC CCTGTTTAAA TTCTCCTGCG CGACGGATTA 6120

ACCCCATGAC TTCACGGTCG GTTAAAGCCT CAGCAGTTAA AAGATGTTTT AAACTAATTC 6180

GTTCAGATGT AATAATCATT CGTCCAGTCC TCCTACTGTT CTTCGCTACG TGCGTTTTCC 6240

GGTAAAATTA AATTCAAAAC AATTCCTAAG ACAGTTGCTA ATGCCATTGA AGACAATTCA 6300

AAAGTTCCTA CTTTGAACAC TAAGCCACCA ATGCCGATGA CTAAAATTAC TGAAGCAATC 6360

AATAAATTCT TTTTCTTATC AAAATTAATC TTATTATCGA TTAAGATTTT CAACCACTGG 6420

GGnAACAAAC CGA 6433

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5855 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATAGAAACCG CCTCTCTCTC GACACGCAAC TTGCGTGTTA TCTGTACGAT TTGTTTACAT 60

GTTGCATTGT AAACAGTTTT TAGGCAATCG TCAAGCAGAA AATAATTAAC gTTGCAtGAA 120

GAAACtAATA ATTGCAAAAA TAGCAATGTG AGCTGGATAG AAAATATAAA AGAAATTCCG 180

CATGCCACGG CCTTTTTCAC CATTATAAAG AACAATTGGA ATCGCTGCTA AAATCATCAT 240

CCATTGGTGG TTCACCCCGA ATAGTTCTTG GAAATTATAG CTGGCTGCTG AAATCAACGC 300

AACAACGCCA ATTGCTGAAA TTTGTAACCA CTTTTTGCCA TGGAATAAAT AAAAAGCTAC 360

GGCCAAGAGA ACAAATAAAA ACCCACCTTC TGTCATCATT AGTGATGGCA CAATCAGATT 420

GAAAATTTGG AAACCAATTA AGATAGCAGG GTTGCTTAAT ATGTCTGGAG AACTAAAAAC 480

AACGAGAGGT AGGGCACTGA TTAATAAAGG CACAATAAAC CAAAGAAGCC CTTTACCAAT 540

TTGTTTTTGT TTAAAATAGT CCATAGACTG CATGTAGACC GTACCTAAAA ATAACGTCCC 600

AAAAATATTA TTGATAATTA AGCCACCTGT TGAAAAATAC GCATTTAAAA AGCCGTTCAG 660

AATCCCCATA ATCCAGAAGC CTAACAATAA CCGGAACATG TATTTTCGCC GATTGCTTGT 720

GTGAATGAAG CCTTCAGAAC TTTCAAATAA GAAAATAGGT GCAGCAATTC GTCCAATCCA 780

TCCGAACCAA CCAGGCACGC CTAAAAAACT AAAAAATTGC AATAGATGGT CAAAGACCAT 840

TGAAATAACC CCAATGACTT TCAAATGAAA GCCAGTTAAT GTTTTACCCA TAGTATAAAC 900

GCCTCTCTTT CATAAAGAAC AATATAACAA AGTCCAGAAA AACCAACCAT TTATTTGCCT 960

AACAGTTATC TTACAAAATT GTTTGATTTC TTCAGCTTTT GATGAAAGAA AAAAGTGCCA 1020

AGACTAGTTT TTATAATTAT TCTATGCTAT AGTAAAAGTA CATTTTAATA AAAAACATTT 1080

GGGGTGCTGT TATGGCTGAG ATGATACCCA TTGAACCTGA TGCAGTTAGT ACTGTCGCAG 1140

GGAAATGCCG ATTTACTTTG ATTTTTCACG CACTCATTCT GTCCTAGGAT GAGTGTGTTT 1200

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GCAAGGGTTA GCTGTGAAGG CAAAATGAAT AGTATCCAAT TAAAAGCTGT GTCCTTTTCA 1860

CGAGAACAAC CCTTGTTTGA AAAGACAAAT TTAGCAATTC CTCAAGGAAC GTTTTCCTTA 1920

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CCGCTTGATT ACCAAGGAGA AATTTTGATT GAAGGAATGG AACGTCGACA ATTATCAACT 2040

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GAATTAGCGA CGTTATCTGG TGGTGAAAAA CAAAAAGCGG CGTTGACAGT TCTGCTAGCA 2280

ATGAACCCAG ATATTCTTTT ATTAGATGAA CCTTTTGCAA GTATTGATCC AACCTCTCGA 2340

AAACAATTTA TTCAAATATT AGCAAGACTC CATCAAGCAG GCAAAACGAT TTTGGTGTGC 2400

GACCACGATT TCAGCGATTA CGCTGATGTT GTGGACCAAG TCGTCACGTT GAAAAATGGC 2460

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GCGCAACAAG ATTTTCTAAT CGTCACGCAT CGGCTAGAAC CTCTCTCTGG CGTGAGCAAT 3120

TACCGAATAG AATTGCTGCA GCAACAACTG ATTATCTGGC AGGAGGGAAC CACATGCAAA 3180

TAAAGCAAAC AAATGCAGCA ATTTATGCTT CTTTGATTCT TATTTTGACC TTTGAATTAT 3240

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TCGGGACGTT TTGGTCTATT TATTTGCATG GTACGAGTAG TCAACAAGCC TGGCTTTTGT 3420

TTAGCCGAAC GTATGCCTTT GCCGGTTTAG GACTAGCTTT TGCTGTAGGT GTTGATTTTG 3480

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GCCTACTCCG TGGCAAAACG TTTCATTTTT GGTCGCCGAT GCTTTATGTT AAAACACTGC 3660

TCGTCGCTGT TTCTTGGCGA GATAAATATA CTGAAGCAAT GTCTGCCCAT GGCTATGAAG 3720

AAGGAGCCAC CAGAAGTCGA AAAGAGCATT TTGTGTcAGC AAAAGTCAGT CTGGGGCTTG 3780

CTATTTTGAT CATCATTTTT ACAAATTTGT TTATTTTTCT AACGTAAAGG AGAAACCTAT 3840

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AATTCAAGAT CATTACTATT TAAAACACTT TAGTCAACTT TATCGCTTGA TTGCGGCACA 4020

AACGCAACAA CCTCGATTGA AAAAATTACT CTTAACAAAT GCGGAAAATC TCGCGTTGGG 4080

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AATTGGTGCA CAGTTAGTCA AACAACACTC ACCAGAGCCA CTGTACCAAC GTTGGATTGA 4320

AACCTATGCT GGGGAGGAAG CGTACCAACA CGTCCAAGAG GAACGCCAAC TGTTAGACCA 4380

ATTATATGAA GAAAGTTCAC CACAAGAACA AGCAGCTATG ATCaCCGCTT TTGTTATCAG 4440

CaGTGAGATG GAATACGCTT TTTGGGAAAT GGCCTATACA CACGAAACCT GGATTGGTTA 4500

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TAATTGTCAG TTGCTTTTTT GACAGGGCGT GATAAGATAT TCAGTGACGC AAAATCTGTT 4620

GTAACTCGCT CAGTAATAAC AGAAACGCCT TGCTAAGAAA GGACTGTAGA AGCCTCATGA 4680

ATTATCCAGA ACCGATTGCA AAATTGATTG AAAGTTATAT GAAATTACCA GGAATTGGTC 4740

AAAAAACAGC GACACGGCTT GCTTTTTATA CAATTGATAT GAAAGAAGAA GATGCTAATG 4800

CTTTTGCAAA AGCGCTAATT AGTgTCAAGA GAGaTCtCCA TTTCTGTAGT aTTTGCGGAA 4860

ATATTACTGA AGAAGATCCT TGTGAAATTT GCCAAGATAA AAATCGTGAC CGTAGTATTA 4920

TTTTAGTAGT GGAAGAACCA AAAGACGTTA TGTCAATGGA AAAAATGCGT GAATATCAAG 4980

GCTTGTATCA CGTACTCCAC GGGGTGCTTT CACCGATGGA AGGAACAGGA CCAGAAGATA 5040

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TTTTAGATCC AAGAnATGAC AGAATGGATG AGCGAACAGA AGCTTTACTT TACGCAGCTG 5700

cTCGTCGTCA ACATTTAGTG GAAAAAATAT TGCCAGcTTT GGAAGCGGGT CATTTAGTCC 5760

TATGTGATCG TTTTGTTGAC AGCTCATTAG CCTACCAAGG CGCTGGACGT nGAATTGGGG 5820

ATGGCCCCCA TGCCTCAATT AATGCGGTTG CGGCA 5855

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GTTTCATAAC TGTACCAATT GGAAAAACTG ACATGGAACG GCGTAACTCT TTTTCTCTCA 60

TCTCCATCCT CCTCTCTTAG TTATTTCTTA GAATAACAAT AGAATGACAA ATTGTCAAGA 120

ACTTATGTTA GATTTTCTAA CATAAAACAA AAAACCTGAT AAATATGGAC TTTTCCATCT 180

TTTCACGGCT GATTTTCTCC TACTAATCAA AAAAATAGAA ATGATTTGTT TTTACAAATC 240

ATTTCTAATC AACTTACCAT TTTTTATTCT TTTTCGGATT CAGCCAACCA TTTAGACTTT 300

TTTTTCGCAA AACCTTTCAC GATATACCGA TTTTCATTTT CAGCATATTC TTCTGAAATC 360

ATTAGTGTCA TCCGGCGAAG TTCACTTAAT AGTTGTCCGT CAGTTGGGCT AATTTCTAAT 420

TGATAAGGCT CGAGTAATTC CATCATTTGG GCACGGATAG CTTGAACCAG TCGTTCTTTA 480

TCTTCAGAAA TTTTAGTTGA GATCAATACA TTGGGAAATA AGGTTGGGAC AAATTCTTTA 540

CTGTCCACTT GATCTCTTTT ATTATAAACC GTCAAGCACG GAATATTTTC CAACGCTAAT 600

TCTTTCATCA ATGTTTGAAC TGTGCGTTCA TGTTGTAAAC GATCTGGCGC ACTTGCATCC 660

ACCACATGGA GCAGTAAATC CATCGTCCGA CTTTCTTCCA ATGTCGACTG AAAGGCTTCA 720

ATCAGCTGTG TTGGTAAATC TTGAATGAAG CCAACCGTAT CGGTCAGCGT AACTTCCATG 780

CCTTGAGGCA ATTGCCATTT TTTGGTTAAA GGATCTAACG TTGCAAACAA TTGATCCTCT 840

GAATAAGTTC CTGCTGTTGT CAACATGTTG AGAATAGTTG ATTTGCCAGC ATTGGTATAA 900

CCAATCAAGC CAATTTGAAA TAGTTCTGAA TTTTGTCTTT TCTGGCGGCT TCGTTCACGA 960
TGAGCAGTGA CTTCTTTTAA CTCACGACGG ATGCCTAAGA TTTTATTCCG AATGTGGCGG 1020
CGGTCCGACT CTAATTTCGT TTCACCAGGC CCGCGTGTCC CAATACCTCC TCCAAGTCGG 1080
GACAACTGTT TTCCTTGGCC AGCCAAGCGA GGCAATAAAT AATCCAATTG TGCTAATTCA 1140
ACTTGTAACT TTCCTTCTTT GGAGCGCGCA CGCAAAGCAA AGATATCCAA AATTAATTGT 1200
ACACGATCAA TTACTCGTAC AGCTAACGCT TCAGATAACA GTTGAtTTTG ACGCGGTGTG 1260
AGCTCATGAT TAAAAATCAC AAGATCCGCT TCATAGGCAT CTGTTAAtTG AATTAATTCT 1320
TCCAATTTCC CCTTACCGAT TACGGTTTGT CGATCGACTT GTGGTCGTTT TTGCGTTAAA 1380
ACAAACACCA CTTCTCCATT AGCGGTTTCC GTTAAATTCG CCAGTTCTTC CATTGATGCA 1440
GAAAATGTCT GATAATTTTn TTCCGTTTCA ACTCCTACTA GAATCACTTT TTCATGAGTG 1500
GTCATCGCCT ACTCACTCTC CTTCTGTTGT AGCCATTCCG CTACTTCTTT TTCCAACTTG 1560
GGcAAATCTG TTGGcTGCTG AACCAAATTC CACCAATGCG CAGCCATTCG ATTTCTAAAC 1620
CAAGTCAATT GACGTTTGGC ATATCGCCGC GATTGCTGTT TGACTGTTTC AACCGCCATC 1680
TCTAATGATT GTTCACCAGA AAAATACGGG AAAAATTCTT TATAGCCAAT ACCTTGAGCT 1740
GCTTGTGCAT GTGGTTGCTG AAACATCTGT TTTGCTTCTT CCAACAGCCC TTCTGTCATC 1800
ATTTGATCCA CCCGCTGATT AATACGCTCA TACAATAAAG CGCGATCTGT TTCCAAACCT 1860
AACAAATAAT AATCATAGAG ACGAGCTGGT TTTTCCTTCG GGGTCAAAAT ACTATAACCG 1920
GTTTTATCAA AGACCTCTAA CGCACGAATC ACTTTTTTGC GATTATTAAA ATGGATGCTG 1980
TTAGCCGCTA GAGGATCCTT TTGTTGTAAT AACAGCCATA AGGCTTGATT CCCTTTTTCT 2040
TCCGCAAATA AATTGTACGT TTCTCTAATT TCAGGCGAGT CATCTATCTC ACGACTTCCT 2100
AGTTGAAAAT CATAAAGGAG TGATTGAATA TACAAACCTG TTCCTCCAAC GATAATTGGT 2160
AGTTTCCCTT TTTCAGTAAT TTCTTTGATT TTTTGACGAC CCTCTTTCTG AAAATCAGCG 2220
GCAGAATATG TTTCGCTGAC TTCACGGCAA TCAATTAAAT AGTGAGGAAT TCCTTCTTTT 2280
TCTGTTTCTG TGACTTTAGC GGTGCCAATG TCTAACGAGC GATAAACTTG CATGGAGTCA 2340
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ACCGCAGTGG GTCCTACAAT AACTAATACT TTCTCCAATT ATGTTTCTCC TTCTTCTTGC 2460
CAATTTTGAC GAGCAAATTT TGCTTCCTCA GGAAAATCAG TATGAACACC CGCCAATTTT 2520
AGCTGAAAAC AATTTTCCAT TTCTTCCATC CGATTAACAG TCCACGGCCG CAGCGGTTTG 2580
CCAATTGTGA TAAGTTCTTT TTCATGAGCC AACACCCAAG ACATTTTTGG ATGTAAACTA 2640
TCGACAAGCG CGAATGCCGG TCCCGCTTGA CTTAAATCCT CTGCAGATTC ATAAATAAAG 2700
GCAATTTCTG TCTTAGGATC AGCTTTTTTT AATTTAACTA AACTTGGAAA ATAAAAACTG 2760
GAATATAAAT AACGAAACGG CCAGTTTTTT TGCTTCATTT GTTGGACGAT TTTTTTCTCA 2820
ATTCCTTCAT AATGGATAAT ATCGGTTTTA AGTTCAATAT TCAAAAAACC ATTGAATTGT 2880

TCTTCTACAA GACAATTTAA AACATCTTCC AATGTTGGAA CACATTGAAC AGAAGGATTT 2940

TTCTGAAACC AGCTTCCAGC ATCTAGTTGT TTTAATTCGT TTAATGTTAA CTGTTGGATT 3000

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ACCCCTAAGT CTTTTAAAAG CGACTCTTCC GCTTGTGAAA GATAGACTTG ATTACCATAA 3660

CCACTTAATA AAATAGTATA TTGCGTATCA ATTAATTTTT GTAAATAATC ATTAAGATTA 3720

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ACACTTCGCA CAGACTCCAA GCCGTAATAT TTTGCAACAG AACGATTAAC TTGTGCATCT 3840

GAATTAGTTT TTACATGCGA TAAATGATTA GAATAAGCTG AATATTTTGT TGTATTACTA 3900

TATGATATAT CTGGAAACAC AGGATTGATA TTTCCTTTTT TCTCTTGCTC AACTAAATAA 3960

CTATATTGTT TTGTCAAATC TAATTTTGAC AAGAATACAT CACTTACACC AACCATTACG 4020

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CTAGCAAAAT AAGTAGCGCG AATCTTATTT CCTGGTGCTA AAGCCATTAA CGCTAAACCT 4440

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ATCACCAAAA ATGTAATAAT AATTGAGCAT ATAAATATCT TCTTTTTATT CAATTTAACT 5100

TtCATCTCTG CTTACCTTCC GCTTTTAGTT CATACTTAAC ATATTTATCC AAACCAGATT 5160

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ACAGCATTAA TAAAAGTTAA AAACATATTT GATAAaCTTA AAGTAAAgGm CAaTTTACCA 6840

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GGCATGAAAA AGTAAGCCCA AAGAATGACA AAAGCAGAAA TACAACATTC AAAAATCGCT 7320

AAATACCAGA ATTGAGAACC GAGATTTCTT TTATCTAAAT TTTCGTATTC TTCTCCCCCA 7380

ATTTTTAAAT AGATACCATC AATCCAGCCT AAGTGGAGAA ATCCAACATA TGAAGAATAA 7440

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GCGCCAACCT AAATTTTCCG kGTTGATTtG CAAaTGCcAC GTTtCACCTA AwTTAwTTTC 8400

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TACTTCATCA ATTTTTTTCG ACTGATTTTT TAAGGAATCC AACTGTTCTA AGATATTTT 8519

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTTGGGGGG ATAATCAAAT TCCCCTGnGT TCCGCCACAA GCCACACAAT GATGCCcATT 60

CTGGTCGTAC ACCAAACCGT TCTAACAATT GAATTTCAAA AATATTTGTA ATGATTTCCg 120

GATCTTTTTG CTCaTTTAAA GCGGATAATG CCATGTGGGT AAATTGAAAT AAGTTCGGAT 180

CATAGTGCTG ATCTTCAATT GCTGCATCGA CTAAGTTTAA AATATATGTT CCATATGCGT 240

TAATAAATAT GTCTTGTTGA ATGTTTCGAA AAGGTTGAAC TTCTTTGCTG CTATTGAGAA 300

AAGATAAGCC TTCTTCTCTA AAGTTTCCGA TGTAGACGGC TTCTGTAAAT GGCAGAATCG 360

CTGGCAAAAG AGGATTATTT TTTCGATGCG CACCTTTCAC AAAAAACATC AATTTTCCAT 420

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AAATATTGTG GTCCTTCTGG CATTTGCtCA ACGAGAACAT CCATCAAATG CTsCAAAATT 1020

ATTTCCTTCA GTGGCAGAAA TGGGAATAAT TTCTTTAAAG TCCATTTGTT TCGAATAGTC 1080

TTCAATAATA CTCAATAAAT CATCTGGATG GACTTTGTCA ATTTTATTAA TAATCAAGTA 1140

GACTGGACTA TTATTATTTT TCAATCGTTC AATAATAAAG TCGTCACCTT TCCCGCGTTT 1200

TTGATCAGCA CTTACCATAA ATAAAGTAGC ATCTACTTCA CGCATCGCAT TGTAGGCACT 1260

TTCCACCATG AAATCGCCTA AGCGGTGTTT AGGTTTGTGA ATCCCTGGAG TATCGATAAA 1320

AACAATTTGT GCTTCAGGAA TTGTATAAAT TCCTTGAATC TTATTACGAG TTGTTTGTGC 1380

TTTGTCACTC AtAATTGCAA TTTTTTGGCC GACAATTCGA TTTAACAATG TTGATTTnCC 1440

AACAnTTGGT CTGCCGACAA TGGGCTACGA AACCAGATTT AAGGTTCAGT TGTCATGGAA 1500

TnCGCCGC 1508

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ATGAAGTATT CAAAAGGACG GTACGTCCTT GTAGTCTTAG TAATGGTCTT GATTGCTTGG 60

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TTAATTTTTA TTTTGTCAGG TTTAGCGAAC GGTTTAGCTC AAGGAAATCG TTTAGCCGTA     120
GATCAATGGC AAGCGAATCA AGTGGTTTTA TCAAAAGAGG CCAATAGTAA TTTAAATGTA     180
TCAGTGTTAG ATGAAAACGT GAAAGAAACG ATTTCAGGAG GCAAAATTGC ACCGATTGGT     240
CAACAATCTT TAGCCATCCG CCCAGCAGAT GATAAAAAGG CTGAATTAAC GAATGTTAGC     300
TTATTTGGGA TTGAAAAAGA AAGTTTTTTA ATGCCAAAAG TGATTGAAGG AAACGCATTT     360
ACTGATAAAA ATCAAGTGAT TGCTTCaGAA ACATTGAAAA ATCAAGGATT TAAAATTGGC     420
GACAAATTAA CTGCAGGGAA ATATGATGAG CAATTAGAAA TTGTCGGCTT TATTTCTAAA     480
AGTAGCTATA ACATTGTGCC AGTTATTTAC ACTTCTCTGG ATACTTGGCG GTCAATTAAA     540
TATGGTGACA ATCCAGCAAT GGCCAAAATG GTTAATGGTT TCATTGTTCG CAGCAAGGAC     600
AACACGGAAG TTAAAACGAC TAATAAAGAC AGCCAAGTTC TTTCAATTTC AGATTTTATT     660
GAAAAACTGC CAGGATACAG CGCTCAAAAC TTGACCTTGG ATGGCATGAT TTATTTCTTG     720
ATTGTGATTG CAGCGTTCAT TATCGGTATT TTTATCTTTG TGATGACTTT ACAGAAAACA     780
GCAATGTTCG GCGTCTTAAA AGTTCAAGGG GTGCCAACTA GTTTCTTAGC AAAGGCAGTC     840
ATGCTACAAA CCGCTTTATT GGCTGTTCTA GGAGTGGCGA TTGGTCTTGC TTTAACGGGA     900
ATTACCGTGC TCTTTTTACC AGAAGCGATG CCTTATGCAA CTAATGGACC ACGCATGATT     960
TTGTTTAGTG TACTATTGAT TTTATCTGCA TTAATTGGCG GGGCATTTTC AATTCGAACG    1020
ATTGCTAAAA TTGATCCGTT AATCGCGATT GGAGGTTAGA GACATGGCAA ATGTTTTAGA    1080
AATGAAAAAT ATTTATAAAA AATATGGTGA AAAACATACA GAAGTGATCG CGTTAAAAGA    1140
ATTATCTTTT GCGGTTCAGC CAGGTGAATT TGTCGCAGTA ATTGGTCCTT CTGGTTCTGG    1200
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TGTTGGCGGG CAATCACTAA ATAAGTTAAC GAAGAAGCAA CGTTTGGCGC AACGTTTTCA    1320
AAAAATCGGC TTTATTTTAC AAAGCTCTAA TTTGGTGCCA TTTTTAACAG TGGAAGATCA    1380
ATTTCACTTA ATTGAAAAAG TTGATAAGTC ACGTAAAAAT AGTGAATTAA AAGAGCAATT    1440
GTTAGAGACG TTGGGTTTAA AAGAATTACG AAATAGTTAT CCTCGTGATC TCTCTGGTGG    1500
GGaAAGACAA CGGGTAGCCA TTGCGTGTGC ATTGTATCaT GAGCCAGACG TAATTTTGGC    1560
AGATGAACCA ACGGCTAGTT TAGATACAGA AAAGGCGTTT GATGTTGTCA AATTACTAGC    1620
GAAAGAGGCC AAAGAGAAAG ATAAAGGGAT TATCATGGTG ACACATGATG AGCGTTTGTT    1680
GAAATACTGT GATCGAGTGG TTCGTATTCG TGATGGTGAA TTGACAGAGT AACAAAACAA    1740
ATAAAAGaGA ACATGATCGG ATTGCTGGAG CAATCCGATC ATGTTCTCTT ATTTCTTTTC    1800
AATACAGAAA AGAACAGGTG GCTGATTTTT TTGATTGATA AACTCATAAC GTAAGACACT    1860
GTAAACATCT TGTGGTAAGG CTTGCGTGTA ATTCGTGACC AAATCAAGTT CCTCTGAACC    1920
ACCTTCGTGG CCATAATAAA CGACTAAAAT AATGCGACTT CCTTTTACCA AATGAGGCAG    1980
TAACCCATCT AACGCCTGTT TAGTCGTAGT GGGTTTTGTA ATAATTTCCT TATTACTTTT    2040
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AGGTAAATAG CCTAAGTTAA AAATAGCGGC AGTGATTTCT GTTTCTTCAT CTAGGACAGC 2100

ATGAAGATGT TCATGTCCTA ATGGAAATAA CGTAGTTTGT GGGAGTAAAT TAAGTTCTGT 2160

TAACTTTTGT TCTGTATTGA TCAACGCTTC TTTTTGGATA TCAAAGGCGA AAACTTCACC 2220

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ATTCAATGCC TTGTTCTTTC AAAATTTCTT CTGCGATAAC CCGTGGTTTC CCCAATGATT 5700

TTGCCACTTG TTCTTCTGTT TCGCCTTCCG CAACACGAGC ATCAAATAAC GCCTTGTATT 5760

TCGCAAGAAT AATAGCTTGA TCTTTTGGAT TTAATGCTTT TAAATAAATT TTCAGCTCAA 5820

TAATAAAATG TTCTTTATTC ATTCCGCTCC CTCTTTCTAC ACGATTCATT TCTCATCTTA 5880

AACTATAATT TCTTTTTGAG CGAATAACAA GAGGAATT 5918

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CATACCCGCT CAATCATGAG GAGACTGGCT AAAAGTAATC CTAGCGTTTG CATCTTTTTA 60

TTTTTATTAA AGAAGTGCCC TGCTAACCAA CCTTGTCCGC CATGAATCAA TAACGAAAAA 120

ACGAACCATT GTGGATAGCC TGACAATAAA TCAATTAAGC CACCGCTTAA AGCTCCGACT 180

GTCAAGCCAC CGATCGGACC AAAAAGTAAA CTAGCAATGT AAATCCCTGC ATCCGCCAAT 240

GTAACAAAGC CATTTGTTGC TGGGACGGGG ATAATAAAGA CCATTGACAC AGCCACTGTT 300

AAAGCGGTAA TTACTGCATA TAGACTAATT TTTCTTGTCA TTATCCGCCA CACCTCCTGC 360

TAGTAATCCT TCATGCCACA CACTTCCAAA AGCTGCATTT AGCTGGACCC CAGAAACAAT 420

GGCTTCATGA ACGTATGTTT TTGCTAAATC AACTGCTTCA ATTAACGGAT ATCCTTTAAC 480

TAAATTCGCA CCAATTGCAG AGGCAAAGGA ACAACCAGCG CCATCAATGG TGTGGGCCAT 540

TACTTTTTCT TTGACCAATT GAATATGTTG TTGTCCATCA TAAAAAAAGT CACGTGCTTC 600

TTGACCAAGC CAACGATTAC CACCTTTAAT CACCACCGTT GCCGCTCCTA AAGAGTTTAA 660

CTCTTCCGCC GCTTGTTGGA CTTCTTCGAC GGTTGTTAAT TTTCTGCCAA TGAGTAATTC 720

TGCTTCTTTT AAATTAGGCG TTATAATCGT TGCGAATGGA AAAAGTTTTT CAATCAATAA 780

CTGCATGTAT CTTTTTTCAT AAACTGAAGT CGTTTCTTTA AAAGCCAAGA CAGGATCCAA 840

CACCACCGGC AGACCTGCGT GCTTTTTCAA AAAGGTTACA ATTTGTAACA TACTTTCTTC 900

ACTGTGAATC AAGCCAATCT TGATGCCGTC TAAACTCCCG GcAGGTATGG AAGCGAGTTG 960

CTCTTTccAC CAAAGAAgTC TCaAGGTCAT GAATCTGAAA ATGATTCTTG GGGGCTGTAG 1020

CAAGGCAAGT TAAAGTTGAT AAGCCAAAGA CTTGATGATT TTCAAACGTT TTTAAATCTG 1080

TTTGAATCCC GCCACCTGAA AAAGGATCGG AACCGCCAAT TGTTAAAATT ATTTTTGTCA 1140

TTTGTTTCGC TCCTTTATAC ACTCAGTTAT CATACAAAGT TTTCTAAAAA GAAAAAAACAG 1200

CCAATTGGCA GATTTTTAGC TCAGCCACTT TTTAAGTCTT TCGTTATCTT TTTCCTTTCC 1260

AAAAAAAGAG TGACCTCATC CGTCAATGAA GTCACTCTTT CTTTGGATTT AACACTTATT 1320

CGTCAATGGC TGTTACATCA ATGTTTAATT CAAACAATTG TAATGGAGAA ACTAAACTTG 1380

GTGCGTTGTT CATTGGGTCA ATTGCTTTGC CGTTTTTAGG GAAGGCAATC ACTTCACGAA 1440

TATTTTCTTC CCCAGCCAAT AGCATTGCTA AGCGGTCTAG CCCTAAAGCA ATCCCTCCAT 1500

GTGGCGGGAA GCCGTAATCT AATGCGTCTA GCAAGAAACC AAATTGGTCT TGTGCTTCTT 1560

CTTTTGTAAA ACCTAACGTT TCAAACATTT TTTCTTGTAA TTCTCGTGTA TGGATCCGTA 1620

ATGAGCCGCC GCCTAATTCG TAGCCGTTTA AGACAACATC GTAAGCTTCA GCATACACAG 1680

AGGCTGGGTC TGTTGCTAAG CGGTCCACAT CCTCTGCTTT TGGTTGTGTA AATGGATGAT 1740

GAGCAGAAAC ATAGCGACCA GCTTCTTCAT CATATTCAAA CAACGGCCAA TCCACAATCC 1800

ACAAGAAATT GAATTTCGAT TCATCAATTA AACCTAATTC TTTACCTAAA CGTGTACGTA 1860

CCGCACCTAA AGCAGCGGCT ACGATTTCAG GTTTATCGGC ACCAAACATT AAAATATCAC 1920

CGACTTCTGC ATTGGTAGCA GCAATTAATT CATCACTAAC TTCTGTTAAG AATTTAGCAA 1980

TCGGTCCTTT TAAGCCATCT TCTTCAACTT TTAACCAAGC TAAGCCTTTT GCGCCAAATT 2040

GACTCACATA CTTACCTAAG TTATCCATAT CTTTACGAGA ATACTTATCT GCGGCGCyTT 2100

TTGCATTCAA AGCCTTCACA TGTCCACCAT TTTCCAACGC TGCTTGGaAA ACTTTGAAGT 2160

CTACGTCTtT CACTACCTCT GCAACATCAA TTAATTCCAT AGCAAAACGA GTGTCGGGTT 2220

TATCGyTACC ATAGCGTGCC ATTGCTTCGT CATAGCTCAT TCGTGGAAAC GGAACAGArA 2280

TCTCAATTCC TTTTGTCTCT TTCATCACTT CAGCCAACAT ATTTTCTGTA TATGTTTGAA 2340

TTTCTTCTGG 2350

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGAATTGGCC TCGATGACAG GTCTTCTACG AGGATACGTG CAACAATTAG ACGTCCCTGA 60

ACAGCGTGCA CTAACAGAAG AACTAGCCAA AATTTGCGAG TTAATCTACC ATGTCAATCC 120

AACGACCCGA ACAAAATTAA CAGTCACAGA GGACGAAATA GCCTGGCTTT TGGAACGTGT 180

CAATGCTATG AATGAACTGA CATACGAAGA AAATCGTCCT TTTGTTTTAC CGATGGGCAC 240

AATCTGTTCC TCTTATGCAC ACATTTTAAG AGCCAAAGCC AAAGATATTG TTCGTTTACT 300

TTATCGCATG GACTATGGTG GTAAAAAAAT TGATCCGCAG CTGTATGATG TAGTCAACTT 360

ACTCTCAGGT TACTTTTTCA TGTTAGCCTT GTACCTAAAT CAGCTCGAAA ATGGTGAAGA 420

AGTTCCCTTT GTTTCTCGCA ACTATTCTAT TTAAAAAGTA CACCGACCGC TAACGACGAA 480

TTGCTAGCGG TCGGTGTACT TTTATACAGG TAAGTACGCT TCTCCTTTTG CAAATAGTTT 540

AGCAGTACCA CCAATAATGA CTCGATTTTC TTTCACTTCA CAAGTTAAAA AGCCGCCTCT 600

TGGGGACACT TGATAGGCCG AAAGGGTCGT TTGATTGAGC CGTTTTCCCC AATAAGGAAT 660

TAAATTGGCG TGCGCAGAAC CACAAACTGG GTCTTCGTTA ATTCTTAGTT TCGGGAAAAA 720

AGTTCGTGAA ACAAAATCCA CCGAGTCTCC TGATGCCGTT ACAATGACTC CTACTCCTAA 780

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TTCCGCAACG GAATAATAGT TAAACAACAC AAAAGCCGTC GCTAATGTAG CATGTCCACA 1080

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CGTAAAAGCA GTCTCTGACA AATTATTTTC AATCGCAATG TTTTGCATCA CCGCTTCTGG 1200

CAACCATTTT TCCAAAACAT AAACAGCGGC GGGATTGCCT TTAAAAACTT CCTCCGCGAA 1260

AGCATCGACA ATATAATAGG GATAACTCAT TTTAATTCTC TCCTTGTATT TTTTGATAAA 1320

TGTATTCCGC GCAACACAAA TCCTCAACTG CTAAGCCAAC CGCATCAAAA ATCGTGCGGC 1380

CTTTCTGCTC CGCCTTTAGT TTAACTTTGC CAGTGACTAA TTCGCCGAGA GAACCTACAA 1440

TTTTTTCAGC TGAAAAGGCA CCTTCTGAAA TCGGAATTAA AAGATCCCCG CTTTCTTTTA 1500

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CGGCTTCTTG GACAGAAGAA CAACCAATAA AGGTACATTC GGGGTAATTG TGCTGTTGCT 1740

TAGCGATTAA TTTTCGTGCA CGTTCTGCTG TGCGGTCATA TATAAAAACC TTTTCAATCG 1800

CCCGAACGCT TTGTAGCGCT GCGAGATGAG ATGAAGCTTG TTGACCTGCA CCAATCAAAG 1860

CGATACTTTT TGCCTTTGGA GCTGCTAAAT AATCGGTTGC CAAAGCAGAA ACAGCTGCCG 1920

TGCGAAsCCA CGTAATCGCA TTGGCGTCCA TCATCGCGAC TGGTCTTCCA GTAGAACTAT 1980

CAAACAATAA AATTTGACCA AGATGCGAGG CCAAATTTTT TTGTGGATTT TCTGGAAAAG 2040

CTGTAATGAT TTTTGCCCCA AAAAAGCGAT TTTTTCCTAA GTAAGCAGGC ATTAATGCAA 2100

AAAGATTTTG ATTTTTCCCA TCTGGTAAAA CCTCTACATG GCGCTCACTT TGCGAAATTT 2160

TTCCTTTTTG CAACTCTGCA AAGCAACGTT TCATCACTTG AATTGCTTCG GAAAACGACA 2220

ATTGTTGAAT AACCCTCTCA TAAGAAATAA TGTCCATCTG AATTCCTCCC TTTGCGCTAT 2280

CATAAACCAG ACAAACAATA CACTCAATGC TATAATTGTA TGGAATACAA TTTTATAGAA 2340

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TCTTATCTGG TGCGCTTCAA AAAAATGTGA AATTGCCTTC GCAAAGAGAA TTAGCTGATT 2520

ACTTGGATCT GAATTTCACG ACGATTGGTC AAGCCTATAA ACACGCTATG GAAAAAGGCT 2580

TACTTTATAC CAACATCGGT TGCGGCACTT TCGTTTCTCC CAACGCGTTT CACTCAATTA 2640

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TGTCTAGCGC CCGCCGAATG ACTTTAGCTG AAATCATTCA GCAAGAACAC TTATGGGTAA 3180

TTGAAGATGA CATTCATTCT TTTTTAACAA CTTATGCACA GCAAGCAGTT TTACCAACGT 3240

TTCAAGAACT CTTACCTCAA CAAACGATTT ACTTAGCGGG GATGACAAAA TTTGTCTGTA 3300

CAGGcTTACG CATTGCGTAC CTTGTTTTCC CTCCGCTTCT TCGCCAAGAA ATAGAGCGTG 3360

CGATTTTTAA CATTAACGTT AAAACTTCTG GCTTTGATGC TGAAATTGTC ACCCAAGTCT 3420

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AAGAACTCTT ACCGACATTA AACGAAAAGA AAGGACATTC CCTATGAATT CATTGCCAAT 3780

ATTTGAAAAA GCAGTGGGCA CGATTACCCT GCTTTCCGAA GAAAAACAAA ATGCCGAATA 3840

TGAAGGCTTT TTATGTCAAG TTAATGAATC GCAACAACTT ATCCGCAGTC GCTTAGCCAA 3900

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GAACGAAGCC TTTGATGCAA CGGAAGCCCC TGAAATGTTA GCAATTGTCA TTGCTGATCA 4020

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CCTGAATCTG GGAAAAAAGC GGCATGTACT TGATTGACAG CTTCCAGCTT AGATAAATCT 4860

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GCTTTTATGT TTTTCAAACA TTGCTTTGTT TGCGTTTTAA CACAGCCAGC CACAACTCTG 4980

CCCGTTTGAG GATCTATAGG CAATTGTGCA GACAGATTGT TATAGTGAGA AAACGCGACC 5040

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TCCCCAGCTT GAGGTGCATT AGGGATAGTT CCTTCCCCAT TTGAAACAAG TGCCTCCATT 5160

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AAAATGGTCA TTCTGACAAT GTCACTCATC ACATGGTTGA TACTTTCAAC AACCGCTTGG 5340

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CCATATACTC ACGATAATTT TCCGAGAACG TATCCATTAG CGTATAAATT CGTTCAAAAT 5880

CATAGTCACG ACGAGGGTCA TCATACCAAA CACATTGAAT ACTTCCAATA ATTGGAAGAT 5940

TCGGGCTACC TGCTGGCACA TCTGTAAATG CTTTTTTCGA CATATTTGCT AAAGCATCAT 6000

CATATTGATA AATGCCAGAA TCAACATTGC CAGCGACCCA ATACCACGCA TCATTGGTAT 6060

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CCCAACCGCC TGTATCGACA TCATTtGCAT ACTCATCGCC GCCAAAATTG AAAATTTCAC 6360

TATGCGCGGA AAAATAAGCC ACGTACTTAC TGATAATCGC CTTTGTGAAA TTCACTGCCT 6420

TTTGGTTCCC TAAATCTACT GTTCGTTTTG AGCCATCAAA AGCGGGATTT TTAATCGCTA 6480

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GGTTGTGGTT GTATTTTTTA CCATTCACAT TGACCGACAT ATCATCCAAG ATAAACCGTA 6720

AGCCATCATT TCCTAAAATT AATTGGACAT CTGTGTACCC ATTTTGACTA GCTTTGGCCA 6780

CTAATTCTTC CAGTTGCTCC ACGGAAAAAT ATTTTCTTCC CGCATCAATG GAAAAGACAC 6840

TTTTTAAAGG TTGTGTTTGT TTCTCTTTTA AATTATCCAA AGCTGTTTGG ACCTCCGTTT 6900

GCCAAGTAGT CACTTGTGCG GCTGTATACG TTTTTCCCGC AAGTTCTGTG GCGACTGTCT 6960

CTTTTGTTGT TTGTAGTGCT TGAATCGTTT CTGGTGTATA GCTTTCTGCC TTTTCAATGG 7020

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TCTCTGCAAG AGAAACGCCT TTACTCTCTG CAATGGCCGT TTTTGTCCAA AGTAAATTAG 7320

AAGGTTTTAT CTGATTTAAA TCGTCTTCAT TATAGGTGCG ACCATCGCGA TCTAAGGCAT 7380

AGAGGAACAT GCCCCCTAAA TTATTTTCAT AAGAATAACG AGCTACTTTA TACATGTTAC 7440

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CACGCCAAGC CCGATAATAA ACCATAAAAT GTTTCTCTTG GGTCGGCTCA TTGGCTTGGC 8160

TGATCATTGG TTGATGAAAC AGACTAAATA AGATAAACGC CAAGCCAACC AATAACGAAA 8220

GACCCAGCCA ACTGACAATT GTTTCTCTGT TTTCTCCTTT TCTTGTCGAT AAATTGTTCC 8280

CCACTTTGAA CACCATTCCT TTCTGCACTC CGTTCATTTT TGTGTATCCA CCTAAAAAGA 8340

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ATCATTTTAT TCTGCCTAGT CCAAGATCCC ATGCATACAG AAACTAACTC AACTAAGGGA 9000

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GCAATACTAT ATCTATGTTG CCCATCGATG ATCTGCATTG TGGAGTTTAC TATAATGGGT 9240

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ACACATTAAA ATAACATTTT GGTTAACCAT CCATGTTTAT TAATTCGGCG ATTTTCACAA 10320

CAATTTTCCC TTGCGCTCGT CCTGTCAATG AATAATCTAC CGCTTCTTGA ATTTGGCTAA 10380

AAGGAACGAC TCGGTCAATT ATCGGCTGTA ATTTTCCCTG TTCAATAAAC TCAGTGAGTA 10440

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GCTCCAATCG ATGAATCTTG CGGGTAGCTA TTTTAAAGGC CCATTGTTTC CAAAGCGGCA 10560

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ACTTTCGCGC CTCTTTCAAA ATCTAAAATT CCTAAGGCGG GGATCCTCTA G 21591

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GAGATTGAAT AATCGTGGCA AGTCCTGCTG CTATAAATGT TGCTTGGATT AAAGAAGACG 120

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AAAGACTTGG TGAAAAACCA CCTGAAAGAT CACTACCTAA ACCAACTTCT ACTTGATGTT 720

GATGTACTAA TTTTGCAATC GGTGTTACTG CATTACCAAA ATAAGCATTA GAGATTGGGC 780

AGTGCGCCAC AGCCGTCCCT GTTTCATGGA ATAAATTCAT ATCTGCTTCT TCTAAAAAGC 840

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CAGCCAATAA ACCTAATACA TATGCAAGCC ATTGGTTGTT GGCAATTAAw GGAATTAAAG 4380

CCACCCCACT TGGTCCAATA GCAATCGCAC CAACATTACC GAAgGCCCCA ATCACCGCAC 4440

CACCAATACC ACCGCCGATA CAAGCAGTAA TGAATGGACG TCCTAATGGT AAAGTAACTC 4500

CGTAGATTAA TGGTTCACCA ATACCTAAAA TCCCAACTGG CAAGGCACCT TTAATCATTT 4560

CAACTAATTT TTTATCTGAT TTACAACGAA TCCATAATGC TAAAGCTGCA CCGACTTGTC 4620

CCGCACCAGC CATGGCCAGA ATTGGTAATA ACAAAGTCAT CCCTGTTTGA TTAATCATTT 4680

CAATGTGGAT TGGCGTCAAA ATTTGATGTA AACCAAACAT TACCATTGGC AAsAAGGTTA 4740

AACCAAGAGT AAAGCCAGCA ACCATGCCAC CTTTTTCTAA GACAACATTG ATAATACCAA 4800

CTAAGCCATT AGAAATAGCT CCGGCTACAG GCATGATTAA GAAAATAGTT GCTAAGCCAA 4860

TCACTAAAAG TGAAATGGTT GGCGTTACGA TAATATCAAT TGATTCTGGG ACAATTTTAT 4920

GCAATTGTTT TTCTAACAAT GATAATAACC ATACGGCAAA AATAACACCG ATAATTCCGC 4980

CTTGTCCTGC AGATAATGTT CCCCCAGTGA AAATATTACT GATTGGAGCA TCCGGATTCA 5040

TTCCTGTTAA CATTGTGACT GCCCCAATAA CACCACCCAA CGCTGGCGTT GCACCAAAAA 5100

CGCTGGCACT GTTAATCCCA GTGTAAAGAG CTAAATAAGC AAAAATCCCA TTTTTAATGA 5160

TATTTAAGAC ATCAATATAT TGTTGCCATG AAGCTGAAAT ATCACCAGCA ACAACTAAGT 5220

TAGACATAAC AGCTGCAATC CCGCCAATAA TACCAGCCCC AACAAAGGCA GGAATCATCG 5280

GAACAAAGAT ACTAGAAATG GCTTTTAACA CTTTTTTAAA TGGTGAAGTG TTATTTTGTT 5340

TCGCTTTTTG TTGTGCTTTC ATTTGAGCGG CTTTTTCTTC TACTAAATCT TTTCCAGATT 5400

TGCCTGCTGA AGCATCAGTT GTGGTGCCAT GATTAAATGG TTCTCCCAAT TTGACACCTG 5460

CTTGATCTAC CATTTCTTGT GCAACCTTGT TAACAGTCCC TGGACCAACA ACTACTTGTA 5520

ACGTATCATC TTCTACGACG CCCATAACGC CATCAATTTT TTTCAATCCT TCAATATCCA 5580

CTTTGTCATA ATCGCGGATA TCCATACGAA CACGAGTCAT ACAATGAATG ACTTTGTCCA 5640

CGTTTTCTTG ACCACCAACT TCTTTATAAA TCCCATCAGC AATGCGTTTA ATTCTTTCTT 5700

CTGCCATGTT AAAACACCCT CCTAATTCCT TAATTTAATG TATTCTTGAT AAAtTGaTTC 5760

CCGTCAATTA ATTTTTGTGT TGCTTCTTCT TTAGTACTAT CAGTTAAAAT CATTACAATT 5820

GCTAACTTCA CATTTTCTTC TGCTTCTACA AATTTAGTT CGGCAACTTC ATAACTACAA 5880

CCCGTTGCTT CCATAATAAT CCGTTTGGAA CGCTCCACTA ATTTTTCATT GGTTGGTTTT 5940

ACATCAACCA TTAAGTTATT ATAGACTTTC CCAATACCAA TCATGGAAAT AGTTGATAAC 6000

ATATTTAAAA TTAATTTTTG AGCTGTCCCA GATTTCAAGC GAGTCGAACC TGTTAAAAAT 6060

TCAGGTCCTG CATCTACTTC AATCGGCATT TGCGCATATT TACTAATTTC GGCATTTTTA 6120

TTACATGCCA CAGTTGCGGT AGCTGCTCCC ACCGTTGTAG CATATTCTAA ACCGCCAATT 6180

ACATAAGGCG TCCGACCACT GGCTGCAATC CCAACAACAA TGTCATTTGC TGATAATTTT 6240

AGATCAACTA AATCTTGACG ACCTAGTTCT TTTGAATCTT CGGCACCCTC TACTGCGACA 6300

GTCATTGCTT TTTGACCACC AGCGATGAGG CCTTGAACCA TCTCTGGCTC GACGCCAAAA 6360

GTTGGTACGC ATTCGGCTGC ATCTAAGACA CCTAACCGAC CACTCGTACC AGCGCCCATG 6420

TAGATCAAGC GGCCGCCTTG AwTGAAGCyT TTGaTGAkGG CTTCTACCAC TGGTTCAATG 6480

GCTGCTAATT CTTGACCCAC TGCCaTTGCA ACTTTTTGGT CTTCTTGATT CATTTTTTGT 6540

AAAGCTTCTT TGACACTCAT CTCATCTAAG CCCATTGTaT TTTCATTTCT 6590

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3660 base pairs
(B) TYPE: nucleic acid

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

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

GACATCTGTC AAAACGACCG ATGTCCTACT CTCTAACGAT TAAGATAGTC CGCTAAATGC 60

GTTTGTTTTA GTCTTTTATA AAAGTTAAAT ACTGAGAATT TATTGTGTAA TTCGTGTACC 120

ACTTTCTCCT TTGATTGCTT CCGAAGCTAA TTCTAAAAGC CCGATAATCG CCTGGCGGTT 180

TGGTTTACTT TCTGCAAAAC TGATGGCCGC TTCCACCTTA GGTAACATAC TACCTGGCGC 240

AAATTGATTT TCTTCTATAT ATTGTTGCAT TGCCGTAACC GTAACATCGG TCAAAGCTTG 300

TTGATTTGCT TGACCAAAGT TAACAAAAAC ATGTTCCACT GCAGTTAATA CCACAAAAAC 360

ATCTGCTTCA ATGAGTTCAG CCATTTTTGC TGCCGCAAAG TCTTTATCAA TGACTGCATC 420

TACACCATGA TAGACTGGaC CATCATAGGc AaTAGGrACC CCGCCACCAC CACAAGCAAT 480

TACGATTTGT CCTGgCATCA ACAAGTGTTC GCAGCCTAAC TTTTTCGTAA ATATCAATGG 540

TTTTGGnTGA AGGAACTACC CGTCGcCAGC CTCGaCCCGc ATCTTCyTGa TAGACGTTCC 600

CAGTTTCCGc CATCmACTGt TTGGckGTTT CyTCGtCATA ATAACCACCA ATTGGTTTTG 660

TTGGTTTTGT AAAcGCTGGG tCTTTTGGaT CCcACCACGA CTTGTGtAAT TAACGTAACA 720

ACTGGTTGTT CCCCTAAATT TCTGGCTACT AGTTCTTCAT CAATTGCTTG TTGTAAATGA 780

TAGCCAATAT AGCCTTGGCt CATTGCTGTG CATTCaGGAA ACGGCACGAC ATCTTCTGGA 840

GATTGACTCG TTTCCTCAAA AGCTAAGCGA ATTTTGCCAA CTTGTGGCCC GTTGCCATGA 900

GCAATCACCA CTTGATGGCC TTGTTCAATT AAATCAACAA TGGATTTTGC AGCGGTTTGT 960

GCTTTTGCCA ATTGTTCTTT CGAAGAATTT CCTAACGCAT TTCCACCTAA TGCAATCACT 1020

ATTTTTGACA TCTGTTTCCC TCCTAGCGCT TTGGTTCTTG TTGTGTGATA CAGTGAATAT 1080

TGCCGCCCCC ATAAACAACT TCTACCGTAT TAACGCCGAC AATTTTTTTA TCTGGGAACA 1140

TCGTTTGAAC TTGCTCTAAA GCCAAATGAT CATTTTCATC ACCATACTGT GGCACAATCA 1200

CGCCATCATT TGTAATTAAA AAGTTCATAT AGGATGCGAT ACAAATATCG CCGTCTTCTC 1260

GTGGCATGGT TCCTTCCACG AAATCAATTT TGAAGGAGCC TTTAATGGTT ACATTTTTGA 1320

CAGGACAGCA TAATTTGTGG ACTTTTAATT GGCGTCCTTT AGCATCAGTC ATTTTAAGCA 1380

AACGTTGATA CGCATCTTGT GCCGCTTCAT AAAATGGGCT ATTTTGATCT TCAGTGTAAA 1440

TACAAGCCAC TTCACCAGGT GCAATAAAAC AArCTACATC ATCCACATGA CCATTGGTTT 1500

CTTCTGGGTC AATTCCATCA CCTAGCCAAr GAaCTTTTTC AACATTTAAA TAGTCGCATA 1560

ATTTTtGTTC GATTGCTTCT TTTGAAAGTT GTGGATTTCG ACCTTCACTT AATAAGCACA 1620

TTTCTGTAGT CAAGACTGTT CCTTGTCCAT CTACGTGGAA TGAACCGCCT TCTAAAACAA 1680

AATCATCTGT ACGATAAGAA TCTACATGCT CAATTTCACA AATTTTTTGT GCAACCAAAT 1740

CGTCTTGGTC CCAAGGGAAA TATAAACCAT CTACTAATCC CCCCCAAGCA TTGAATGTCC 1800

AATCCACACC ACGGATTTCT CCATGGTCGT TAATGACAAA TGATGGTCCA CAATCACGAA 1860

CCCAGGCATC ATTGTTTGAC ATTTCGTAAA CCGTAATTTC TGGCGGCAAT TGGCGACGGC 1920

AATTTTGAAA TTGTTGTTGA GAAACCACCA CATTCATCGG TGTAAATTGA CTAATTGCTT 1980

TGGCCACATT AGTAAAAGCT TCTTGGACAG GTTTACCACC ATCACGCCAA TTATCCGGTC 2040

TTTCTGGCCA AATCATCCAA ACTTTCTCTT GTGGTTCAAA TTCTCCTGGC ATTCTAAAGC 2100

CATCTTGtTT AGGGGTACTT CCTACAATTC GTTTAGCCAT TTTCTTTCGT TCCCTTCTTA 2160

ATTTTTTTCA CGTAAATAAT TACTTCACCA AACAGAATAA AAATGATTGC CCCAATTGTG 2220

ATTGGTAATT TTTCATTTAA TGCTGCGGGA CTAAAATCTA AAGGcACTGC TGTGAAAATC 2280

AGTGAAATAA TAATCATAAT CATTGGCAAA ACCACTAAAA CTTTTAAAAA TCCTGGTTTT 2340

CCGTTAACTT TAAACGGACG TGGTGTATCG GGATCAATTT TTCTAAGCTT ATAAAAAGCT 2400

GGGAAAACTG GGATATACGA TAACAAGAAT AGGACGACAT TCAAGGAGAA AAAGGCCCAG 2460

AATAAATCTT GATTAGGTAA AATTGGTGCT AATACAATGA CCACCGATGC CACAATGCCA 2520

TTCATCAAAG CAGCCCCAAT TGGCATGTCA TTTTTCTTAC TACGTTTTTC AAAAAATTTA 2580

GGCATGTCAC CATTTTCAGC AGCATAACAA GCTGTATTAT TGACTCCTAA TGACCAAGAA 2640

ATCATGTTTC CGAACAACGT AAGAAGGAAT AGGAAAGCCA TCAACATAAT GAACCAACCT 2700

TCTGTCGAGC CTGTCAATAG TTTAAAGCTA TCCATCATAC CACTGCCGGT ACTAATTTGA 2760

TCGGTGGGAA TCGCTACCCC AATTCCAAAG GCTGAAAAAA TATAAATGGC CGCAATGACT 2820

AACCCCGCTG CTACAATAGC TTGTGGAATT TGCTTCTTAG GATTTTCCAT ATCATCTGCA 2880

AACGTACAGA TGACTTCAAA CCCTAACAAA TTAAAAATGA TTACAGAAAT AAAAGATAAA 2940

CTCCTTAAGT CAAACGTTGG CAGCATTGAT TTCAAGGTAA ATTCATTGGC AACACCTTTC 3000

GTCAAGGCTA CATACAATCC TAGCCCACCA ATTAAGACAG CTAAAACCAT CTTGATTACG 3060

GCAGCTCCAT TTAGAATCCA GATACTGTCG CTGACTGGAT AAAAACTAAT CCAAACCACA 3120

ATCCAAGTAA AAATTAATTC AACAATAATC ATCATCGGTG TTGAAAACTT AATACCTGTA 3180

ATTGTCGTTA ATAGTTCTGG CGTCATAACG GCTAATGAAG CTAGCCACAA TGGATAATTA 3240

ATCCAATAAT ACCAAGAAAC TCTGGCACCC CAACGATGAC CATATGCTTT GGTCACCCAA 3300

TCATAGATGC CCCCTTCACC AATATAAGTT GTTCCTAATT CTGATGAAAT TAACCCATAT 3360

GGCAATAGGA ATGCAATTAA TAAGAAAATC CACCAAAAAA ACTGAGAATT ACCAATTGCA 3420

GCAACAGGCG CCGCTGCTTC AGCAACGAAA ACCACACAGA TCACTGATAA AATGGCACTC 3480

GTTAAACTAA ATTTCTTTTT CCCCTCCATG AAGACTCTTC CTCTCTTTAT AAACTGTCCA 3540

CTGATTCATT TTTTCAATCA GTGGACAGTT GGCCGTTAAA TGCTTTGAGT GTCTAAGAAA 3600

ACTTCTAGTT CTTTTTTCGC TTCTGcTTGC TTGATTAAAT CATAAGGATT TTTgCTTCAT 3660

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs

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

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

AATGACAACA TTTACAAAAA AGTTTGAGGC AAAAATTAAA ACGGCGGACA wTAAaCTTaA 60

AGTAAAAaTT TTGTTTTTAA AAaTTGCGAA CTTAATAAGT GGGCTTTTTC TTTTTCGTTC 120

AACCATTATA AATAATCCTA ATGCGATTAC TGCAATAATG AACAaTAAaT AGGATTGTAA 180

CGAGCCaAAC CCGCTCTCTT GTCCGAGGAA AATCCCGCCG AAGAACGTCA TAATCGCAAT 240

GGCAATACAA GCAAATCCTG AAAAATCGAT TTTTTCTTTT GTTTTTGTAA TATCTTTTGG 300

TAGGAACTTT TCGCCAATTA AAATTGTAAC TAGCCCCACG GGAACATTAA TCCAAAAAAT 360

ATACGACCAA GAAAAGTTTG ATAAGATCAA TCCACCAATC CCAGGACCAG CAATCGCGCC 420

TAAAGAGACA AAGGCACCTA CTGCACCAAG CGCCCGCCCT CTTTCATTTA AAGGGAATAC 480

TTCCGTAATA ATTCCTGAAT TGGTCGCCAT GGTCATGCTA GCACCAATAC TTTGAACGAC 540

TCGCGCAAAT AATAGAAAGC TCAGCGATTG ATTAAAGCCA CAAAGTAACG AACCAATCGT 600

AAAAATAACC GTGCCAATTC GATAAACTTT TATTTTTCCA AAACTGTCGC CAATTTTTCC 660

AAATAATAAT AAACAAGCAC AGACAACCAT TAAATAAATA GATACGACCC ATTCCGCTTG 720

ATTCATGGGT ACGGACATTT CTTtTGAAAT AGTCGGTAAa GCAATATTTA CAATGCTGGA 780

ATCTAATGTA GACATGAAGG TAAACATAGC CACAGAAACT AAGATCC 827

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAGGCATGAA GTAATnGGGA TGGATTTATT AATCGrATGA AGyCAtATCa GGAAGAAGAA 60

GCAGTTTGCT TTACAGATCG TTTGAAAGAG CAGGTGGAGA AAAATGGCTA GAAAAAGTCG 120

TATAAAAACA CCGATTGcGG AACAAGCACC TACTATCAGA AAGAATAATT TTGAAGAGGT 180

TTGCTTAGGC TATACATTAG CAGAAGGGCA AGAAGAAGCG ATTCGCTGTT TACAATGTAA 240

AAATGCACCT TGTATTGCTA AATGCCCCGT GATGATTGAT ATTCCTGGAT TTATTTTAGC 300

TATTCGTGAA GGAAACATGG AACAAGCAGC CGATATTTTA AGTAAATATA CGAATTTACC 360

TGCTATTTGT GGACGCGTTT GTCCGCAAGA GAAACAATGT GAACAAGTTT GTAAATTAGG 420

GAAAGCCAAA AACTTTGAAC CAGTGGCAAT TGGCAAATTA GAACGTTTAG TTGCCGATTG 480

GGCATTAGAA AATCACAAGT TTCCTAAGAA AACAGCGGAA CCAACAAAAG GGAAAATCGC 540

AGTGGTCGGT TCTGGTCCTT CTGGGTTAAC AGTTGCGGGG GATTTGTCAA AGCTAGGCTA 600

CGAAGTAATT ATTTTTGAAG CGCTTCATGA AGCTGGTGGC GTATTAACCT ATGGCATACC 660

TGAATTTCGA TTACCGAAAA AAATTGTTAA ACAAGAAATT GCGAGTATTG AAGCCTTAGG 720

TGTAACAATA GAAACCAATG TGGTAGTAGG TAAAACGATT ACGATGGAAG AAATAATGTC 780

AGAGTTTGAT GCCTGTTATC TATCGGTTGG TGCAGGGGCA CCAAATTTTA TGGGAATCCC 840

AGGAACTAGT TTAAATGGGG TTTATTCTTC TAGTGAATTT TTAACACGAA TCAATTTAAT 900

GCATAGCTAT GAGTTTCCAG AATATGATAC ACCGATTAAA CGTGCTAAAA ATGTTGTTGT 960

GATTGGCGGC GGGAATGTTG CAATGGATGC CGCTCGTTCA GCCAAACGAT TAGGCGCTGA 1020

AAATGTGAAC ATTGTGTATC GTCGTTCGTT AGAAGAATTG CCAGCAAGAA TTGAAGAATA 1080

TCACCATTCC CTTGAAGAAG GAATTAACTA TTATTGGTTA ACGAATCCAA TTGCTTATTT 1140

AGATGACCAA CAAGGAAATC TAGCCGGTGT TGAATGTGTC AAAATGGTTT TAGGTGAACC 1200

AGATGCGTCT GGAAGACGAC GGCCAGAACC AATTCCAAAC AGCACGTTTA CCATTCCTGC 1260

TGATGCAGTA ATCGAGGCAA TTGGCCAAGG GGCAAATCGA GTCTTGTTAT CAACATATCC 1320

AGAAATAGAA CTAAACCAAT GGGGTTACAT TCAAGCTGAT CCTAAAACAG GAGCAACCTC 1380

AATACCTGGC GTTTTTGCTG GGGGCGATAT AGTCACAGGT GCTGCCACCG TTATTTTAGC 1440

GATGGGCGCT GGGAAAATCG CAGCTAATGC AATTGATCAG TATGTCAAAA CACAAAAAAC 1500

aACAGTCACA AGCAATGTTT AGGAAAGATA AAAGGTGAAA AAATGAAAAA AACAATGGAT 1560

GGAAACACCG CAGCGGCTTA TATTTCATAT GCGTTTACAG AAGTTGCCGC TATTTATCCT 1620

ATCACACCAA GTTCAACAAT GGCTGAGTTG GTAGATGAAT GGGCGGAAAG TGGTTTAAAA 1680

AATATTTATG GTCAAAAAGT TCAAGTTATT GAAATGCAAT CAGAAGCTGG GGCAGCGGGA 1740

GTAGTTCATG GTTCGTTAAA AACAGGTGCG TTAACCACTA CTTATACTGC TTCACAAGGT 1800

TTACTGTTGA TGATTCCCAA TATGTATAAA ATCGCAGGAG AATTGCTGCC TTCTGTGTTC 1860

CACGTGGCGG CTCGGGCAGT AACGACAAGT GCGTTGAGTA TTTTTGGTGA TCATGGCGAT 1920

GTgATGGCTA CCCGCCAAAC AGGTTTTTGT ATGTTAGCAG AATCGAGTGT TCAAGAAGTG 1980

ATGGATTTGT CGGCAGTTGC TCATTTAGCT AGCTTAGAAG GTAGTTTACC TTTTGTAAAC 2040

TTTTTTGATG GTTTTAGAAC GAGCCATGAA CTACAAAAAA TCGAAGTGAT TGATTATGAT 2100

GACCTGAAAG AAATGGTGAA TCAGGAAGCT GTAACTCGTT TTAGAATGGG AGGCATGAAT 2160

CCTAATCATC CCACTGTTTC AGGGACCGCT CAAAATCCTG ACATTCATTT TCAACAAAGA 2220

GAAACAGTCA ATAAAAATTA CGAAGAAATG CCAAAAATTG TTCAAAAATA CATGAAAAAA 2280

ATTAACAATC TTCGTGGAAC AACGTATGAT TTAACCGATT ATTACGGGGT TGAAGATGCA 2340

ACAGAAGTCA TTATTTCAAT GGGGtCGgct TCGCCAGTAA TCAAACAAAC AGTCGACTAT 2400

CTCAATCAAC AAGGACGCAA AGTTGGTTTT ATCAATATTC ATTTATATCG TCCATTTCCT 2460

ACCGAAAACC TTCTTGAAAA ATTACCAGCT ACAGTAGAAA AGGTTGCGGT TTTAGATCGA 2520

ACAAAAGAAT CGGGAGCCGA AGGGGAACCG TTATTGCTAG ATGTTCAAAG CGCTCTCTAT 2580

CAACATGAAA ATCGACCAAT TGTGATTGGT GGACGTTATG GGTTAGGCTC TAAAGACGTA 2640

GCGCCTAATC AAATTAAAGC GATCTATGAT CATTTGTTAT TGCCATTTAA AGAATTAAAA 2700

CAACGTTTTA CGGTAGGGAT CGTTGATGAT GTAACCTATC AATCATTGCC AGAAGAACCT 2760

ACTTTAGATT TAACGCCAGA TACTACCTTC CAAGCAAAAT TTTGGGGCTT TGGTTCTGAC 2820

GGAACTGTGG GAGCAAACAA GCAAGCGATT AAAATTATCG GAGATCATAC CGACCTTTAT 2880

GCACAAGCTT ACTTTAGTTA TGATTCTAAA AAATCAGGCG GTTTAACCGT TTCGCATCTG 2940

CGTTTTGGTA AAGAGCCAAT TACTTCCACG TATTTAATTG AACAAGCAGA TTTCATCGCT 3000

TGTCATAATG CTTCCTATTT GCATAAATAC GACCTGTTAA AAGGTTTAAA AGATGGCGGA 3060

ACGTTTTTAC TGAATACTAT TTGCGATCAA GAAAAGATTC ATCGTTTATT ACCGGCTAAG 3120

TTAAAAAAAT ATATTGGGGA GCACCAAATC AAATTTTATA TTATCAATGC GGTTGAGTTA 3180

GCTCGCAAAG TAGGCTTAGG CCGTCGGATC AATACAGTGA TGTCTACTGC CTTTTTTGAA 3240

GTAACAGATA TTTTAACGAA AGAGCAATAT TTACCGTTAC TTAAAGAAGA AGTGAAAAAG 3300

ACTTATGGAA AAAAATCAAT GGAAATTGTT GAAAAAAATT ACCAAGCGAT TGATGCTACC 3360

TTTGAATCGC TGCAAGAAAT TGTAGTTCCA GAAGATTGGG CAACCATTGT TTTAGAGCCA 3420

GAAAATCAAG AGTCGGAaGC TCCAGCTTTT GTGACAAATA TTTTAGAACC AATCAATCGT 3480

CaAGAAGGGG ATCAGCTGAC CGTTTCAGAT TTGATTGAAA ACGGAATGAA GGGCGGTGCC 3540

ATTCCTATGG GCACTGCGGC TTATGAAAAA CGTGGCATTG CGTTAGAAGT GCCTGAGTGG 3600

CAAATGGATA AGTGTACGAT GTGTAATGAA TGTGCCTTTG TTTGTCCACA TGCGGCTATT 3660

CGACCGTTTT TAGCGGATGA AGAAGAACTG AAAGAAGCAC CTGCAGGTTT TGCCATGCGC 3720

GAAATGCGTG GCACAGATGG GTTGATGTAT CGTATCCAAG TTTCTTTAGA AGACTGTACA 3780

GGTTGTGGTC TTTGTGTTCA GGCATGTCCC GTGAAAGACA AGGCGATTTT AATGAAACCT 3840

TATGAAACTC AGAAAGAGCA AGCGATGAAT TGGGCCTTTG CGATGACTCT TAAACAAAAA 3900

GCCAACCCAG TCAAAAAACT TTCTGTTAAA GGTTCCCAAT TTAACCAGCC ATTGATGGAA 3960

TTTTCAGGTG CTTGTGAAGG CTGTGGCGAA ACACCTTATA TTAAGTTGTT GACGCAATTA 4020

TTTGGTGATC GAATGATGAT TGCTAACGCA ACAGGCTGTT CATCAATTTG GGGTGGTTCG 4080

TCACCGGTGA CGCCTTATAC AACGAACGAA TGTGGCCAAG GACCAGCTTG GAGTAATTCG 4140

CTGTTTGAAG ATAATGCGGA ATATGGTTAT GGTATGTATA TTGCCAATCG AACGAAACGT 4200

CAACATTTAG CTAGTCTGGT TGAAGAAAGT CTTGCTAAAA ACGTCGGATC AGATTCACTT 4260

CAAGCCTTGT TAAATGATTG GTTGGAACAC ATGGCTGAAG GGGAAGGAAC ACAACAGCGA 4320

GCCACCAAAC TAGCGGCAGC ATTAAGTGAA GAAGCCGATG AAGATCCACT TTTAACAAAA 4380

ATTTACGAAC AAAAAGATTT ACTAGTGAAA ACGAGTCAAT GGATTGTCGG CGGCGATGGT 4440

TGGGCCTATG ATATCGGGTT TAGCGGCATT GATCATGTTC TTGCCAGTGG GGAAGATGTT 4500

AATATTTTTG TTATGGATAA CGAAGTGTAT GCCAATACAG GCGGACAAAC ATCTAAAGCT 4560

ACACCAGCTT CAGCCATTGC CAAATTCTCA GCGGGTGGGA AACATACCTC TAAAAAAGAT 4620

TTAGGGATGA TGGCAATCAC TTATGGGAAT GTCTATGTTG CACAAGTGGC TTTAGGCGCA 4680

AACTCAATGC AAACGATTAA AGCAATTGAC GAAGCGGAGC GGTACCCAGG CCCATCAATT 4740

ATCATCGGTT ATACCCCATG TATTAATCAC GGGGTCAAAG GCGGAATGGT TCGGACGTTA 4800

GATCAAGCCA AAGAAGCCGT TGAATCTGGC TATTGGCCAC TTTATCGCTA TAATCCAGAG 4860

TTAGTTAAGA AAGGCAAAGA TCCGATGGTC ATTGACTACA AGAAAACAGA TTTTGACAAA 4920

ATGCGTGATT TCCTTGAAAA ACAAACACGT TACTCTGCGT TGCATACAAT TAAACAGAAT 4980

CAAGAAGTAG TCGAACATTT ACTTGATAAA ACTAAAGAAG ATGCAATTGA ACGCTCTGAA 5040

AGTTATAACA AACTAGTCAC ACACATGAAA AAATAAAAAA ACAAAGCCTC TTACTTGAGA 5100

GGCTTTGTTT TTTTATCCAA TAATAATTTT TTCTGAAGGG TATTCGTAGC CTAAGTCACG 5160

TGTTTCTTTT GGTACAAAAA TCATTAAGGT ATAAAGCATA CCAATACGTC CAATAAACAT 5220

TAATAAGGCA ATCATTAATT TACCTACTGT TGTTAAATCG TCTGTAATAC CCAAAGAAAG 5280

ACCGGTTGTC CCAAAGGCAG AAGCGACTTC CACAATGATT GAAATCAAGG GCAGATTTTC 5340

AGTGGCTGAC AAAAAGACGA CAGCGAAAAA GCACATAATC AAAGATAACA TGAAGACGAC 5400

AATCGATTTT TTGACATCAT CGTCATCTAT TTTACGGCTA AAGACGCTAA TATCATCTTC 5460

ACTTTTTAAA AAGGCTAACA AATACAAGCC AATAATCGCA ACAGTCGTTG TTCGAACACC 5520

ACCACCAACA GAGCTAGGAC TACAACCAAT AAACATTAAC ACAGAGAAAA TAATCAACGT 5580

TGTAATTTGG AAGTCCCCTA AATCATTAAT TTGGAGGCCA GCGTTTCGTG TAGTCATCGA 5640

ATAAAACATC GAACTTACCC AACGGCCACT TTCATTCATT GTCAAAAATA GGTGATCTTT 5700

TTCTAATAAG TAAATCAAAA TAGTCCCACC AATAAACAGA ACAATAAACG CTAGCAAAGC 5760

AATTTTACTA AACAATGAGA AGCGGAAAGG CAAGCCTCGT TTCTTCTTAC GAAAGTTCTT 5820

TTTCTTAAAA TGTAACCACT CATGAATTTC CAGTAAAACG GGAAATCCAA TCCCGCCGAT 5880

AAAAATCAAG AACATAATTG CCAGTAAAAA GAGATAATCA TGAGCAAAAG GAATAATTGA 5940

ATCACCTGAA ATATCAAAGC CTGAATTAGT CACTGCAGAA ATAGCTTGAT AAAATCCATA 6000

AAATATCGCA TCTCGCCAGT TCGTATAATA ACCACTTATA TAAAAATAAA GCGAAAAGAG 6060

CGAGCCGAAG ATTACTTGGA ACCAAATTAA AATCAAAAAA GTGGTGCGGA TCAGTCGAAC 6120

AATTCCGCTC AGTCGCGGCT GATTCATGTC AGTCATAATT AAcTGACGTT GCTTTAATGT 6180

GATTCGCCGT TTTGATAAAA TAAAAAAGAC CGTTGAAATC ATCATAATCC CTAAGCCACC 6240

AACTTGGAAA AGAACCTCCA ATAAGACGAT CCCACGATCA TTAAAAACCG AATTAATATC 6300

GACTGTGGTG AGTCCaGTAA CACTGACTGT ACTGATTGCT AAGAAAAATA AATCAATAAA 6360

AGGAACATGC GAGTCAGGTT CTCTGAAAAT AGGGAGGCAA AACAATAAAT AAGAAATAAC 6420

CGTCATTAAT ATGTAATAAG CGACGATGAT TTGAATAGAT GAAAAATTTT TGCGAATAAA 6480

TCGATCGCTt cTctTTCGCT GTGCCAGCCA CAGCAAACGT GTATGGTTCA CTAGATaACy 6540

TCCCaATTCT AATTAAACTA mGTATACCAA AACTTTTCGC CTCAAACGAA TAATTCTGCC 6600

AGAAAATCCT TGAAATGACA AATAAAAATA AGAAATTCGT TAGAAATAAT TGGAAAACAT 6660

CCACAAACAA GCGAGAACAT GATATTTTAT GAAAGAATAG AAAAATAGGT TGTTCCCCAA 6720

ACAACTTATT AATAATTGGT CAGTTTGTCT AACGATACAA CTTTAAAAAG TAGTGGTAGC 6780

TTTTTTATTT CGGTTGATAT GTGAATGTGT TCACTTTATG TAACAAACTG TTATTTTTAT 6840

TCAAATGAAA AATAAGAAAT TGTGTTGGTA GAAATCAATA GTTTATAAGG TGGGAAAACA 6900

ATGAAAAAAG TGTTAATGGG AGTTCTTTCC CTAGGGTTAT TATTAGGTGC AGCAACAGGT 6960

TGTACAAGCG ATCAAGAAAA AGCCGCTGGT AAAACAAAAG CGTCTTCTGA AAAAACAGAA 7020

GCAACATCTG GTGCCTCTGC TAATGGTTAT ACAGATCCAA GTGAACTAAA AGACAGTTAT 7080

GATGTTGTTA TTGTTGGTTC AGGTGGTGCG GGGATGACCG CTGCATTACA AGCCAAAGAA 7140

GCTGGCATGA ATCCAGTTAT TTTAGAAAAA ATGCCTGTTG CAGGTGGGAA TACAATTAAA 7200

TCGTCTTCAG GAATGAATGC TTCACAAACA AAATTCCAAG AAAAAGAAGG CATTAAAGAT 7260

AGCAACGATA AATTCTTTGA AGAAACACTA AAAGGCGGTA AAGGAACCAA CGATCAAGAA 7320

TTACTACGTT ATTTTGTTGA TCATTCAGCT GAAGCAATTG ATTGGTTAGA TACAAAAGGr 7380

ATTACATTGA GCAATTTAAC GATTACAGGT GGAATGAGCG AAAAACGCAC ACACCGACCT 7440

GCTGACGGAT CAGCAATTGG GGGCTATCTA GTTGACGGTT TAGTACGTAA CGTTCGCGAA 7500

GAAAAAATTC CATTGTTTGT TGATGCTGAC GTCACAGACT TAGTTGAAGa AAACGGTCaA 7560

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AATTGAAAAA CTATGTTACA ACGAACCAAG AAGGCACAAC AGGTGACGGT ATCCAAATGA 7740

TTCAAAAAGT TGGcGGTGCG TTagTGGATA TGAAAGAAAT TCAAATTCAC CCAACTGTTC 7800

AACAAAGCGA TGCTTTCTTA ATTGGTGAAG CAGTTCGTGG AGAAGGCGCA ATCTTGGCTT 7860

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TCAATGCCTT ACCAGAAAAA TCAGCTTATT TAGTCTTTGA CCAAGGCGTT CGCGACCGTG 7980

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ACCAAGATGT TAATGCCAAA GATGACAAAC AATTTGGCCG GACAACTGGA ATGGAAGCTG 8160

ACTTAAGCAC AGCCCCTTAC TACGCAATTA AAATTGCACC AGGGATTCAC CACACAATGG 8220

GTGGCGTGAA AATCAACACG AAAACAGAAG TTTTACGTGA AGATGGCACA CCAATTAAAG 8280

GTCTATATGC TGCTGGTGAA TTAACAGGTG GCTTACATGG TCaAAACCGT ATCGGAGGCA 8340

ATGCAATCGC CGATATTATC ATTTATGGTC GTCAAGcAGG TACGCAATCA GCAGAATTTG 8400

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TACTGCTTTT TTGCTGAAAA TATAGTAAAA TACGTAAGGA ACTAACGGAA AGGTGTAGTG 8640

AACATGGCTC AATTATTTTT CAAGTATGGC GCAATGAACA GTGGTAAAAC CATTGAAATC 8700

TTAAAAGTAG CACACAATTA CGAAGAACAA GACAAACCAG TTGTTTTGAT GACCAGTGGA 8760

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CACGTGAGAC GGTTGAGGTT TATCGCCGAT ATAAACAAGT TGTTGAAGGG ATTAGCGATG 9420

CCGAAGAACT TTTAAGTGAA AACTTAGATG CGGAAATGGC CGAAATGGCG AAAGAAGAAC 9480

TTTCTGATTT GAAAAAAGAA AAAGAAGTGT TAGAAGACCG CATTAAAATT TTATTATTAC 9540

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AAGGGTGGAA AGCGGAAGTT TTAGAAGCGA ACGTCACTGG AATCGGTGGA TATAAAGAAG 9720

TAATTATGAT GATTTCAGGA GATAACGTCT TTTCAAAATT AAAATATGAA AGTGGCGCTC 9780

ACCGCGTGCA ACGAGTTCCT TCAACAGAAT CACmAGGACG GATTCATACA TCGACAGCAA 9840

CCGTTGTAGT TATGCCGGAA GCGGAAGAAG TCGAAATCGA ATTAGCTGAT AAAGATATCC 9900

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CTGTTCGATT AACCCATTTA CCAACAGGAA TCGTAGTCGC AATGCAAGAT GAACGTTCAC 10020

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AACAAGAAGC ACAAAGTGAA TATGATGCTA ACCGTAAATC GGCGGTGGGG ACCGGAGATC 10140

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TTTGAAGTCC TTAACTGGGC TTCTTCTTTT TTAGAGGCGC AAGGCAAAGA AGGCTACGCT 10380

ATTCACTATG TTTTTTTAGA ACGTAAAGGT TGGGATAAAA CGCAGTGgCT CCTGCATATG 10440

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GTTAATGAAC ATACTTTGAT TCCTAGGCCA GAAACAGAAG AATTAGTCGA GCGTTGCTTA 10620

AAAGCCAATC CAGATACTCC TTTGACGGTC GTGGATGTCG GAACAGGGAC AGGTGCCATT 10680

GCGGTTAGCT TGAAACTGGC ACGGCCCAAC TGGCGAGTTA TTGCCATTGA TCTTTCAGAG 10740

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GCGGCCCTCC AAGAATTATT GAGCGCCGCC TATCCACAAA AAACAATTAA AATTGAAAAA 11100

GATTTATCTG GCAACGATCG CCTCGCGATA GCCGAGTAAC TAAGGTTCTT CGTCGCCACT 11160

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TATCGTAGAA AATTTAGCTA TCGATCGTGC CAAAGAATTA TTTGGTGCAA AATTCGCGAA 12540

TGTACAAGCC CATTCAGGTT CTCAAGCCAA TACAGCGGCA TACCTTTCAT TGGTTGAACC 12600

AGGTGATACC ATTTTGGGGA TGGATTTATC AGCTGGTGGT CACTTAACAC ATGGTTCGCC 12660

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CAAATGCGCA AGCGATGACG AAAGTTTTCA ATCAAGCGCC AGAAGCTCGT TTAATTAGTG 13200

GGGCAACAGA TAACCACTTA TTACTGATTG AAGTGACAGG TTTTGGTTTA AATGGAAAAG 13260

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AATATCCATT ATATAACTAA CATCAGGGGA TAGCTGAAGC GCCGATTCTC TGGTACAAAT 13560

AAGAGTCGGA GCTT 13574

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTTACAGCG TTACTGAnAC AAGCAAAAGA CGCTTTAAGC AAATAAGCTT AAACAATCTT 60

TCACACCCTA CTCAAGGAGT AGGGTGTTTT TTTAATAACT CCGTTGGTAA CTTTCATCTA 120

TAAATGAAAA AACTTGTGAG AGCGGAATTT CTTCAGAAAG ACTTAACCAA TGCTCTTTAT 180

TCATATGATA GGCAGGAAAA TAGCCAGGTT GGTTCTTTAA TAAGGCAATC AATTCAGGCG 240

CAAGTTTAAC GGTTAAAATA GTGAGCTGCT TATTCTCGGT AGCGCCGAGC AGTTGTGCAT 300

CCAGTGGCAT AATTAAAGCA AACCATTTTG CATTTCTAGG ATGACGAAAG ACGAGATAGT 360

CTGGGTGTTT TTTAAAAGGA AAATCGGGCG TTATCTGATA ACGTTCTTGG ATATAGGCGC 420

TAATAGTTTC TTGAAAAGTC ATAGGTTTCT TCCTTTCGTT AAGGCTAGGC ATATCTATTT 480

ACATCATAGC AAAAATTACA TAAAATTACT TCGTTCAAAG GAATGGGAGG AGGGAGCAGA 540

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TGACATTAAT TTCAACAATT TTAGTAACCT TGGTGGCTGT AGAATTTTTC TACATTATGT    600
ATTTAGAAAC GATTGTACCA ACATCTGAGA CAACAAGCCG TGTTTTTAAA ATGGATAGGC    660
AAGAGTTACA AAGArAATCA GTCACTACAT TGTTTAAAAa TCAaGGAATC TATAATGGAC    720
TAATCGGTGC AGGACTTATT TATAGTGTCT ATTTTGCGCA AgCAACGATG GAGATGACAA    780
AATTTTTATT GATTTATATT ATTTTAGTGG CGGCGTACGG TAGCTTAACT AGTGATAAAA    840
AAATCATTTT AACACAAGGC GGTTTAGCTA TCGTGGCTTT GATTAGTTTA CTTGTTTAGC    900
CATCAGAGTT AATAGAGAGA GGCAGTCAAA TCGACAGAAA AAACACGGTT GATTTGACTA    960
TTTTTTATAG AATTGAGAGA GACAAAATGT GGTATACTTT GTTTATTAGA TAGGGAGGAA   1020
TTAAAAATGC TGAACCAAAA AGAAGTAAAA AAAACCGATT ATACTCAATT AATTTCTCTA   1080
TGGCGTTCTT CAGTAGAAGC TACCCATTTG TTTTTGAGTC AGGCAGATAT TGATAAAATC   1140
GAAGTGGTTT TACCTGATTA TTTTCAACAA GTTCAATTAA GTATGTGGTT AAATGAAGAA   1200
CAGAAaTGTG TGGGCTTTAG TGGAACAAAT CAACAAaCGT TGGAAATGTT ATTTATTGAC   1260
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TCAATTATCT TTGTTGATGC TAATAAACAA AATGAAGGGG CAGTGAAGTT CTATCAATCT   1380
CAAGGGTTTC AAGTAATTGG TGAATCAAAG GAAGATCCTC AAGGAAATCC GTTTCCTATT   1440
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ACCAACCAGC CTGGGTGGAA CAGTTTGAAG AAGAAGCCCA AGCGTTGAAA CAGATTCTAA   1560
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CTACAACCTA TGGTACATTA AAAAAGCAAT TGGCCCAAGC ACACCCCGAT AGCATTGATA   1920
AATATATGGA TGGCAAAGAT GCGTTCATTA AGAAAATAGA AAAAGAAGCG TTGAAGAAAT   1980
ATTGGGAAAA ATAAAAAAAG TTGCTAAGGC TAGCAACTTT TTTTTGGTTC TTTTTTGAAA   2040
AAATGATAAA GAAGACCACT TAAAAGAACA CCTAGAATAA TTCCAATCGC TAAATTATGC   2100
GTATAGACGA TCACACCCAC TGTCACGAGT AAAATAACAA TTTCAGTAAT TTCAAAAGTT   2160
CGGAAAAGCT GCAAACTTTC CCAATCAAAG GTGTCGACTG CCACTGTCAT CATGATCCCA   2220
ATCAATGCAG CTGTAGGAAT GGCTACCATC ACGGATTTAA AAACAAAAAT GAATAGAAGG   2280
AGGGTAATAC CTGAAATCAA AGTAGAAAGC CGTTTTCGTC CTCCAGATTT AACATTAATG   2340
ACCGCTTGGC CAATCATCGC ACAGCCAGCT TGGCCACCAA AAAAGCCGGT AATTATATTA   2400
GCGAATCCTT GTGCTTTAAC TTCTCGTTGG CTATCACTTT GGCTCGCTGT CATTTTGTCC   2460
ACAATGGGGA TCGTCAATAA AGATTCAATT AACCCGACCA TTGCTAAGGC AACAGAGCTA   2520
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GGTAAAATAA TCCACAACGT TTCTAAGTTG ACGGGTACAT TAGGCCAACG GATCGCTGGA 2580

TGAAACTGAC TCATTTCACC AAGATCACCT ACCGTTTGCA AATGACCTTT TAAAAAATAG 2640

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ACATCACTGT CTTGGGAATA AAGCGCATCA ATTTGTGGAT ACCTAAATAA CCTAAAATAA 2880

ATTGTAGAAA GCCTGTTAAA ATAGTCGCAG CAAGCATGTA TGACAAACCA TGTGCTTGAA 2940

TTAAGCCTGC aAGGACTAAG GCCATTGAGC CAGCAGACGC CGAAACCATT GCCGgACGGC 3000

CGCCCGTAAA AGTAATCACA AGTAAAGTAA cAGctGAAGC AAACACTGCA GAAAGCGGGT 3060

GAACACCAGC AATAATCGCA AACCCGATTA CTTCTGGTAA AATGGCGACA GAAGAAACGA 3120

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ACGGGGAAAT GAATCAAACT ATTAAAGACA CAGGCAATGA AAAAGCCAAC TACATACCAA 3660

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CTTTGCTTGA AACGTCCAAA TAAATAGACA ACTGCTACGA GTAGGACAAT CCGCATAATT 3780

TTAAAGAGCA TCGCAAGTTG AAcTGCGTTC TCATTGACCA TATTGGCACT GGCGACAACC 3840

TGACCAACTG ATTGTAAAGT CCCTCCGATT AGTGCGCTAC GAGCCAACAA ATTGGTACCA 3900

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AAAGTAATGA TTTGGCCTTT TTCTTCCTCA TCTGCTTGAA TTGCTGGAGC AATCGAAGCA 4020

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AAAGCCAGTT TTTTACCGAT CAAATAGGCA AAAATAATGG TCAGCGACAT TTGAATGAGA 4140

ATAAATGCGA CACCTTGTAA GCCAATTTGG GCAATCGTTT GAAAGGTCAC GGTGGTTCCC 4200

AATAAAACAA CAGAAAATTC TAGTAATTTA CTTTCGGCTA CTTTGGTTCC GCGATTTAAA 4260

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ATTGAAAAAA TCTCTCTTTC TTGTTCATTA CTTCCAGTAT AACGAAATTT TTTACATTTG 4500

AGAnATAAAT AGTTAAnATA ATATTTAT 4528

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CAATTTGCTT TGGGAGAACT ATACTTTACA AATGGTCAAT TTGTCGAGGC TATTACTCGT 120

TATCAAAGCA TTGTAGAAAG TGGGACAGCG CAAATCTCTG CTATTTCCTT GAATGAACGC 180

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GAAAGATAGG AAACGACGAT GTTTGTTAGT TTATCAGAAA AGAAAAAATT TTTAACTTGG 960

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ACGCACGATG CGATTTTAAA TAATGTTCAT TTTGTTGAGA ACGTAGAAAA AACCGATCGG 1080

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GACCGATTTC TTCGGAATGA TTGGAAACAA TTAAAATTCC TTTCGCAGCA TAGGCTCCAT 1800

CGAGTACAGA ATCAACAACA CGACTGAAAA CAAAGGACAC AATTAAAGTA TACATCATTC 1860

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CTAAAATTTT CCCACCAATT AATAAGAGCG GAATATTGAT TAATAATGTC GTATATGCTG 2220

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GGCCAGCAAa AAAACAAGGG AAcCGCAAGA GGTAGAATCA ATACCAGGGG CACGCGGGGC 3420

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AGTCCAATTT GGCAGTGTAG GTGAAGGGCT CACTATTCGG CATGATTCTT ATGATCGGCG 3540

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(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CCACTTAAAA GTAAGCCTCT TGCACTCGTT ATAGAACAAA TCAGTTATTG GAAGACGCCT 240

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GGATGATTGG GcGCTAATAG TTCAAACTGT CCAtCTGTAA AGACCGGATT GTCTTtCCGC 480

AACGCAATTA ACTTTTtATA ATAATcAATA CGGATgCGCA TcCGTTtCTT GGGCAGCCAC 540

ATTTATnnCT TGAAAT 556

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5998 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTTAAAAAA ACCATTTTTA CTATTTTTTT CACTTTTAGG AGCTATTTTT ATTTTAGCTA 60

GTTGTGGCAT AGGAAAaGaT GCTGTCACAG ATACTAAGTA CAAAGTTAGT TTGCAGCAAG 120

CTGCTGAAAT CTATGAAAAA GAAGCTGGCA ACAGCAAACC ATTAGTAAAT GTCCAATTTG 180

ATACAGAACC AGCAAGTGAC TACAGCTATA TCTTTACTAA CGATACAGAA ACACTTTACG 240

TGAATCCTGA AACAGGAAAA GTCACCAAAA ATACTGAAGC AAATCAACTT GGCGAAAACG 300

AGACAGCCTT TTCAGCTGCT GAAGTCAAAG AATTAGGCGC TGTTAACGAC GTTTTAGCCA 360

AAGCAAAAAA AGAAGTTGGA GGACTTTCTC CACGTATTTT GACTTGGAAG TTAACCAAAA 420

ATAACAATAA ACTTGTTTAT ACAGTAGATG TTAAAACGAC TACGGCAGAT GAAAAAGTTA 480

CCTTAGATGC CAATAAATAA GCACAAGCGT ATAACTTATC ACGAAATAAC CAAATCTTAA 540

AATACTCTTT GGGACAGAAA CTACGCATTA GGAAACCTTA ACATTTTCCG AAGCCGATCG 600

TTCTGTCCCA ATTTCATTCT TTTAAGTAAT AATAATTGTT CGTTACCCCT GCTACCGTTA 660

TACTTAGTTT AAAAGAAAAG ATGGGAGTAT CAATTCATGG TTTATACAGT TGATTTTAAA 720

GAAGTAGCCA CTATTGGTTT AGAAAGTTCA CCAGTGGCAC CTGCCCTTGC TGGACTAAGA 780

GCGAATGAAG CTCGCTATTT TTGGAATAAA TACAAACATC GCTTTACGAC CGTCCCTGCC 840

TCTGAAGCTC CAGAAACATT GGCCTGGATT GAAAAAATTT TATTAGAACG AGAATTACAT 900

TTCCCTTACA AGCCACTTGA AATTTCTTCT TTCACTTTAG ATGGCATAAA AATGGCCTAT 960

GTATTTTATG AAAACGGCTT AGCAGTTAAC GTGATGTACA CATTAGCTGA GGAAGGCAAA 1020

CGCGCCGTTG GGTTTAAACT TTCAGATGGT ATGGCAATCC CTGCAGAATT TGAAGGAAAA 1080

TTCAAATTTG CTCGTCAAAA ATCAAAATTA GCTGGAACCA TTCGCGGCTC TTATTTTGTC 1140

ATTAAAGGAA CCTATTAAAA AAATGCTTTT GCCCTTATTA TTAAAGGCAA AAGCATTTTT 1200

TTATTTTAAT TCTTCAATAT AGTTAAATAC TTGTTGTCCA GCAATACCGC CTTCACCGAC 1260

CGCTGTCGTG ATTTGACGCA ATGTTTTTTC ACGGACATCA CCAATGGCAT AAACACCAGG 1320

AATTTTTGTT CTCATTTCTT GGTCTGTTTC AATCCAACCA GCCTCATTCG TAATACCAGC 1380

TTTTTTAAAT GGTTCTGTTA ATGGATCTAG CCCCACGTAA ATGAACACGC CGTTTGCTTC 1440

AATTTCAGAA ACTTCATCTG TTTTGACATT CCGTGCTTTC ACACCTGTCA CGACCATTTC 1500

ATTGCCAACA ATTTCTTCGA CAACTGTATC CCAAACAAAG GAAATCTTTT CATTTGCAAA 1560

GGCACGATCT TGAATGATTT TTTGCGCACG CAATTCATCA CGACGGTGAA CAATCACTAC 1620

TTCAGAAGCA AATTGCGTTA AATAGATTGC TTCTTCAACT GCAGAATCGC CGCCGCCAAC 1680

GACTACTAAG CGTTTATTTT TAAAGAAAGC ACCGTCACAA ACAGCACAAT AAGAAACACC 1740

ACGGCCAGCA AATTCTTCTT CGCCTTTTAC ACCCAATTTT CGGTGTTCAC AGCCTGTTGC 1800

AATAATTACC GCTTTAGCTT CATAAGATTT GTCATCACAA ATCACTTCTT TATAGGATCC 1860

GTGGTCTTCA ATGCCCATCA CAATACCATA CGCATTTTCC GTACCAAATT TTTCTACATT 1920

TTCATACATT TTATAGGCCA ATTCTGGACC CATAATAGAA TCAAAGCCTG GGTAATTCTC 1980

TACCTCAGCA GTGTTGTTCA TTTGCCCACC AGGCGCACCG CGTTCAATCA TTAATACAGA 2040

AAGATTGGAC CGTGATGCAT AAAGTGCTGC CGTCATCCCA GCAGGACCGG CACCAATGAT 2100

AATTACATCA TACATTTTAT TTCCCCCAAA ATTTTAAGTA AGTTTACTTT ACTCCTTAAA 2160

CAATTTCTTG TCTACTTTTC TGCCCTTTTT TGACATTCGG AGTAGGTGTG TCTATTACGT 2220

AAGTTATTGT ACCACGGTTT TGTGTTTTCT AGGAGGGGGA AAAGAAAAGT TTAAAAATAA 2280

CGATCACAAC GAATCATTGA TTTTTAGAAG CCGTTGTACT GCCGCATCAG AGAATTCTTC 2340

TTTATCATTT TTTATGCATT CTTGTTGATT TTGCCCTTGT GGAACAAAAC GAAATACTGT 2400

AAATGATGCA GATAACGTAT CAGGATTACT AATCCGATGA AGACTTTTAT GCATCCGAAT 2460

AAGTTCTCCT TCTGCACAAA TTCTTGAAAT AATTTGCTGA TTTTCTAGCT CTTCTATTTT 2520

CACTTTTCCC GACTGCACAA GTAAAACTTC TTCGATTTCG TGATGCTTAT GCCAACCTTG 2580

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CACAGTTTTT CCTGGCAAGC TATTTATATG TATTTCAAAC TCTGGAAATA GAAAATAATT   2640
TACTTCTGTT CCATCTGGCT TTTTACGAAA GATGACCTCG TCTCTTGTTA AAATTTCTAT   2700
ATATTTCTGT AACATGGCAG GCTCCTTTTA ACTTTTTTTA TAGCCGAAAG CTATTCTTTC   2760
AAACTAAGTT TGAAGCTACT TTCTGAAAAT TCGAGTTCCT TTAAATATAC TTTTATTACC   2820
ATTTGAAAAT CACTTTTTTT AAAACAATTG ACTGTTCAGT ATCAATCTTc ACTAATCCAT   2880
CTGTTCACCA GAAAAAATAT AGTATTTCCG ATTATTCACG AACTTATTAT TCAACTTCAA   2940
AGGAAAATCA GTCAACATAC AGCCCACATA TCTAACATCA GAAACACTTC TACTTTTCTC   3000
AAGTACTGCT ATGGTATACA TTGACCTTAC TAGTAACATT ATAGCATCAA GTTTTAATCA   3060
TATGTAGATT TAAAAAAAAT GaTAGcACCC TAACAGaTGT TTTCGTTGCT CATTTAATTT   3120
ACATGATTAT TTTTTAGATG CTAATTAAAT GTTTGTCAGT AACCTGAATT TTTGATATTT   3180
TTATCCAGAT TACTTATGTC GGTTTATCAG TTGTGCTAAC AAAAAATGAT TGTTTTTAAA   3240
GATAATTTAA TTCATAATAT ATATAGAATG AAAAAAAGGA GGTTTTATTG TTGAAAGTTG   3300
CTATTTGTGA TGACAATCCA ACGTTaACCG AAAAAATAAA CACGATGCTA TTTAATTATA   3360
ACCCAAATAT ATTTGAAACC TATACCTACT ACAATCCTCT CAAGTTAGTC AATCAACTTG   3420
ACCAAGAAAA TTTTGACTTT TTTATTTTAG ATATAGAAAT GAGTGAAATG AGCGGAATAG   3480
ACTTGGCAAA AAAAATCCGA GAACGTGATA TTTTATCACC TATCGTTTTT TTGACGAGTT   3540
ACAAAGAATA CATGGAAGAA GTCTTCCAAG TACAAACTTT TGATTATTTA TTGAAACCGC   3600
tACGGAAGAT CGGTTGCACC AAGTTTTGGA AAAACTGAGA CAACAGCTAG AAAAAAAAAG   3660
AAATTACTTT GTATTTTCTA GTAACAAAGT TACTTATAAA ATACCAACCA AAGATATCAT   3720
TTATTTCGAA AAAGATAAAA GACAAGTATT GATTCATACA GTTGGAGAAa TCTACAAACC   3780
CtATATGTCA ACGAATCAGA TAAACGAACA ACTTGATACG AATTTTGTGC AAGTCCACTC   3840
TTCTTTCATA ATAAATTGCG CTTATATAAA AGAGTTAGGA AAAAATTTCC TATTAATGGA   3900
TTCTAAAGAA AAATGTATTG AAATACCAAT AAGTAGGCGC TTCAAAGCCG CCGCTCATAA   3960
AAGTATAGTT ATGTCCATGA GAGGAAAGAT ATAATGCTTG ATATAACATT ACGAAGCCTA   4020
AGTTTGTTAG TTTATTTATT TCTTATCTCT TATTTTTTTT CTAATTGGTC AACAGCTATT   4080
AAAAATCATA GAGAATTTTA TAATGTCATC TGGATTGTTA TAATCATATC AGCCATGGTT   4140
ACGATTATAT TATCCAATGC TTACATACCG AACATTTATT TACCGTATCT TAACTTATTA   4200
CTAAGTTTCA TTTTAACTTA CACTATTGCT ATGCTACACT CGGTCCCTTA TCTCGACTCG   4260
GCCGTATGGA CAATGACACT TATATCAATA AATTTAATCT GTGAAGTATT GTCGTTACAC   4320
TTTACGAAAA TAATTTTAAA TGCAGAATTA ACATCCTATG GTAGCCCTAC TTTTTTCATA   4380
ACTTCAATAA CAATTACAAC TTTGATTGGG GTAGCCTGGA TAGTCATACT TAAATTTTCA   4440
ATAGTTAAAG AAGCAAAGTC TGAATTATCG ACAAACTTAT CATTTATTGT GATTTTATTA   4500
CCTATTCCCA TACTATCAAT AATCATTTTA TTTGGGCTTT TAATAGGAAA CAACAATGAC   4560
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AAAATTTCTG AGATTACTAT TACGATTAGT GTCATATTTT TAAACATCTG TGTAATTTTT 4620

CTTTATAAAA TCACTATAGA ATATCAAAAA AATCAATATA ATCTTACTTT GAGAAAAAAA 4680

AATATCGAAG TGGAGTATAG AATTTTAAAT GAAATAAAGA GAAACAGAAC TAACGTTTTA 4740

AAATTAAAAC ATGATTTGAA GAATCAATAC TTAACAATCC TCGGACTTAT CGAAAATGAA 4800

GAAGTTAATG AAGCTATCGA TTATATTAAG AGTAGTTTTG ATATTTTAGA ACCACCAACA 4860

AAAACTTATG CTGCCGATGG AGTATTAAAC TACCTATTGA ATGAAAAGCT TGCTGAAGCA 4920

AGAAAGAATC AAATTAATGT TGATCATCAG ATATTTGTCT CTAAAAATAT AAAAATTAAT 4980

AATGACGTTC TAACTATTGT AATTGGAAAT ATAATTGATA ACGCCATACA AGCATCGAAG 5040

AGAATCAAGC CGATTGACAG ATATGTCAAT ATAATTATCA AGCAAGTCAA TAATGATTTA 5100

TTTATTGAAG TATCtAATAA CTATAATTCt GaAGAnATTT TTaCaAGAAA ACaTAGaAAA 5160

AATaAAGGtT TAGGaATGaA AAACaTTGaT GATCTCTTAC AACAATTAGG TGGTATTCAA 5220

CGTCACTGGA CGAAAGAACG TAGATATTTT GTAACTATAG TTATATTTAA TGTATACAAA 5280

GGAAACAAAT GCGGTGATAA CTAATCAAGT AAATCACCGC ATTTTTTAGT ATACTTCCAT 5340

GTCGCATAAT TTATCAGAAA ATTTCAAAAA TAACCAAACA AGCATCAATC CCATAATCGT 5400

TGAAAATAGG AACGTTATAG TTGGAAAATT CATAAGACCC ATAGCAGAAA AATTCGAATA 5460

TATTAGCATT AGTACCACTG ACGTTATTAT TGAAGCAATT TCCGATTGTT TCCAAATTGA 5520

AATTATTTCT GACAATATCA AAATTACGAA TAGTAGACTA CAACTTGTAA CTATGGTAAT 5580

AAGACCAAGG TAAATTTCAA AAAATAAATT TGAACTATGA AACTTCAAAA TTAAGTTAAG 5640

CAAAACCTCA GTCACAAATG AAATAAGAAG CGCACTTCCA AAGCTAGATA AGATTATCAC 5700

GTAAAAAGAA CTTGTTTTTT TTACGAGAAG CTCTTTTCGA TCAATCGGAA AAAGAAACGT 5760

TCTATTCCGG TGATTGCCAA CATAAAATCG TACAAGCTCT TTCCTTAGTA ATACAGCTCC 5820

ATAAATTGAT ATGCCGCACA TAGAAACAGT GTTCGATAAT GCTATAATTC CTTGAAATGA 5880

CGAGATCGTA TCAGCACTTT CATCAAATAT TCCCACAAAT GAGAAAAmCA TAAAAAATAA 5940

CATTTGGATT ACCAGTGTAA TTAAGAAAAC TTTAAACCAA CATTnTAATG GnnCTAAT 5998

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAATCCGTAG CAACATTTAT GGAGACAATT ACAGAAAAAT GCGGTGAAGC ACATCAAGAT 60

TGGGCAAAAA ACTTTCAGGG CGGnCTTTGC CAATACTTTA CTAACAACAG TGAAACGTGC 120

AAGAAGATGG TACTACCTTT TTATTAACAG GCGATATTCC AGCAATGTGG TTGAGAGACT 180

CAACAGCACA AGTTCGTCCC TATTTAGTGA TTGCnAAAGA AGACGAAGAC CTTGCTCAAA 240

TGATTGCTGG TTTGGTTAAA CGCCaTTTCG tTATATTTGC ATTGATCCTT ATGCCAATGC 300

GTTTAATGAA ACAGATAATC ATGCAGGCCA TCAAACTGAT AAGACAGAAA TGAATGGCTG 360

GATTTGGGAA CGGAAATATG AAATTGATTC ATTATGTTAC CCGGTCCAAT TAGCCTATTT 420

ACTTTATAAA AATACTGGGA TGACCGAACA ATTTAATTCA GATTTTGTGG AAGGCGTCAA 480

AAAAATTCTC AACGTTTTTA CAACAGAACA AGATCACGCA CAGTCACCTT ATTTATTTGA 540

ACGAGATACG TGGCGTCAAG AAGATACGTT GGTTGAAGCA GGGAAAGGAA CACCAGTTGG 600

CAAAACAGGG ATGACATGGT CAGGCTTCCG TCCTAGTGaT GATGCCTGCC AATATGGTTA 660

CTTAGTTCCT TCTAATATGT TTGCAGTCGT AATTTTAGGC TATATTCAAG AAATTTTCTC 720

TGATGTTTTA GAAGATGCTA CGATTGGGGC GATTGCTAAA AAATTACAAG AAGAGATTGA 780

AGAAGGCATC CAAACATTTG GACGAACAAA AAATCAAAAT AACGAAACGA TTTACGCGTA 840

TGAAGTGGaT GGCTTAGGCA ATGCAAGCGT GATGGaTGAC AGTAATGTTC CCAATTTAGT 900

AGCAGCCCCT TATCTGGGTT ATTGTTCAAC AGAGGATGAA CAATATTTAA CAACGCGTCA 960

AACCTTATTA AGTAAAGAAA ATCCTTACTT CTATGAAGGC AAATACGCGA AAGGGATTGG 1020

TAGCTCGCAT ACACCAGAAA ATTACGTGTG GCCGATTGCT TTAGCAATGG AAGGAATGAC 1080

AACCAAAGAT AAAGCAGaAA AAGAACGAAT TTTAGATTTA TTAGTTGCCA CAGATGCGGG 1140

GACTCATTTG ATGCATGAAG GTTTTGACGT AGATAATCCT GAAAATTATA CAAGAGAATG 1200

GTTTTCATGG GCTAATATGA TGTTTTGTGA ATTAGTTATG GATTATTTTG ACATCCGAGT 1260

GGAAAAATAG GAGGAAAAGT AATGACAAAG AAAAAAGTCT ATATTGTTTC CCATAGTCAT 1320

TGGGATCGTG AATGGTATCT GCCTTATGAA GrACATCATA TGCGCTTAAT TGAATTAGTG 1380

GATAATGTAT TAGATTTAAT TGAAAATGAT CCAGAGTTTA ACAGTTTCCA TTTAGATGGA 1440

CAAACGATTA TCTTAGACGA CTATTTACAA GTTCGCCCAG AGAAAAAAGA AGCCGTGAAA 1500

AAAGCTGTCC AAGCAGGCnA ACTAAAAATC GGACCATTTA GTATTTTACA AGATGCTTTT 1560

nAATTAGCTC TGAATCCAAT GTCGAACATG CTGATTGGGC TTAGAAAGCn AAATnGGGGC 1620

ACAGTCAATT AGGTACTCCC G 1641

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AGAGAAGGGA TCATATGTCA GCAAAACATA ATCATGAACA ACACCAGGAA AAACAGCCAA 60

CAATGTCCCA CGATAAAATG AATCACATGA ATCATGATAT GGCGCATGAA CAAATGGCTA 120

TGTCACACCA ACATGAAGGA ATGAAGGGAA TGGATCATTC AATGCATATG GGGAATTTTA 180

AACAAAAATT CTGGCTGTCA TTGATTTTAG CTATTCCGAT TATTGTTCTT TCACCAATGA 240

TGGGTTTTCA ATTACCTTTT CAATTTACTT TTCCAGGTTC TGATTGGTTG GTCTTAATTT 300

TAGCAACTGT GCTATTTTTT TATGGTGGGC AACCATTTTT AAGTGGCGCT AGAATGGAAT 360

TACAGCAAAA GAGTCCAGCA ATGATGACGT TAATTGCGAT GGGGATTTCG GTATCATATT 420

TTTACAGCTT ATATGCGTTT TACATGAATC ATTTTACGAA TCAGGCCCAC GTGATGGACT 480

TTTTCTGGGA ATTAGCCACT CTGATTGTTA TTATGCTTTT AGGCCATTGG ATTGAAATGA 540

ATGCTATTTC TAATGCTGGT GATGCCTTGA AAAAAATGGC TGAACTGTTG CCTGACACAG 600

TCAAGCGAAT GACTGAACAT GGGGAAGAAG AAATTCCTTT GCAAGATGTC CAAGAAGGTG 660

ATCGCTTGAT TGTTCGTTCG GGAGATAAAA TTCCGACAGA TGGTAAAATT TTGAAAGGAA 720

GCACAACAGT CGACGAATCG ATGGTTACAG GGGAATCAAA AACAGTAGAA AAAAACATTG 780

GTGACTCCGT GATTGGTGGA GCTGTCAATG GCAACGGAAT GATTGaAATT TCGGtAACTG 840

GCACGGGTGA AAATAGTTAC CTGTCAAAAG TTATGGAGAT GGTTAAACmA GcGCAATCGG 900

AAAAATCaAA ACTAGaATCC aTTTCAGACC gTGTAGCCaA GTGGTTATTC TATATTGCCt 960

TATTCGTAGG TGTGTTAGCA TTTATCGGTT GGTTAATGGC GACGAAAGAT TTGTCGCTAG 1020

CATTTGAACG AATGGTTACA GTTTTTATTA TTGCCTGTCC CCATGCGTTA GGCTTAGCAA 1080

TTCCTTTAGT GATTGCTAGA AGTACCTCCA TTGCTGCTAA AAATGGCTTA CTTTTAAAAA 1140

ATCGGAATGC ATTAGAACAA GCCAATAAGG TTGAATATGT GTTGCTGGAT AAAACTGGAA 1200

CTTTAACAGA AGGACAATTT ACAGTTACTG GCTTAGAATT AATGAGTAAG CAGTTTACTA 1260

GAGAAGAAGC ACTTAAATAT ATTGGGGCAT TGGAAAAAAA TGCAAATCAT CCGTTGGCAA 1320

TTGGGATCAT GAACTATTTA AtAAACAAGC CgTTCAACCT TATGAAGCCC ATAATCTGCA 1380

AGCTTTATCA GGCGTAGGAC TGGTTGCTAC TGTTCAAAAC CAAGAAGTCA AAATAGTCAA 1440

TGAAAAAGAA GTTGCACGGT TACAGTTAAC CTTCGATGAA ACAATTAAAA CAAACTATCA 1500

AGAGCAAGGA AATACCTTGA GCTATTTAAT CATCGCTGGT CAATTAGTCG CACTGCTTGC 1560

TTTAGGAGAT AAAGTCAAAC CAGAAGCTAA AACATTTATT GCAGAGTTAC AAGCGCAAGG 1620

AATTACGCCA GTCATGTTAA CAGGGGATAA TCAAACAGCC GCCAGTGCAG TTGCTAATTA 1680

TTTAGGAATG AAGGAATACT ACGCAGAGCT CTTACCAGAA GATAAAGAAA AAATTGTGCA 1740

ACAATATCTT ACTGAGGGAC ATCAGGTCAT GATGGTAGGA GACGGTATTA ATGATGCACC 1800

AAGTTTAGCC CGTGCTTCAA TCGGCATTGC GATAGGCGCT GGTACAGATG TAGCGATTGA 1860

TTCGGCAGAT GTTGTACTGA CGGATAGTGA TCCTAAAGAT ATTTTAAGGT TCTTAGATTT 1920

AGCCAAACAA ACACGACGTA AAATGATCCA AAATCTTTGG TGGGGAGCTG GGTACAATAT 1980

TGTCGCCATT CCTTTAGCGG CTGGGGTTCT TGCACCAATT GGGATTGTTT TAAATCCAGC 2040

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TGTTCTCTAT TTTTTTCTTC TTAAAAAAAT TTTTGCCTTA TTTGACGTAT TCTTATwACa 2220

AGGGAGTGaA AGGGGACGAT ATATGGaTTT CaAGGaATTA TTGgTCTTTk GAmCATAAAA 2280

ATATGTTGGA ATTGTTGGGA TTTACTGCCA ACAAGAGCAG ACATTTTCTG TTTTGGATGG 2340

CTGCCAGAAA ACTAAAGGTG AGCGACAAAA CCTCCATTGT TACATTCAAC GTTTTGAAAA 2400

AAAGCAGGAA ACGTTTAAGA TAGAAGGGCT TTGTAAGATT TATACAACGA CCAAAGGAAT 2460

TGTAAAATAT CGTGAATTAT GCGTTTGTGG CTTGGCTCGA TTTAGACAAA AATTTTGTTA 2520

TTTTATTCCC GAATTTTATA TTTTACGTTG TCTAATTGAA GAGCGAATCA ATTATGCACA 2580

ATTGACCCAG GTATTGGAAT TACAGGAATC AACTCTTCGG AAGAAATTTT CTAATATTCG 2640

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TGAATGGCAA ATTCGACAGT TAATCCTTTG TTTTTATTTG TTTTTCCAAG AAAGCTGTCT 2760

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TGTGATTCTT GAAGCACATT TTGGTGGTTG TTTTGGCAAG AGAGCGCGAA AGTATTTTAT 3060

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AATTAGGAGA AATTTTACAC AACATCATTT TAATTATCAA GAAATTCATT TATGTCGATT 3180

TTTAAGTACG CATATGAATA GTTTATTAGA CGGACAAGCA TGGTTGCCAG CTCATAAACA 3240

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GCTTTTAAAA CGCCTATATC CAGTCTTTAC TTCAGTAAAA GAACGGGAAT TGACGAGTTG 3360

CTATTTTTAT CACATCCTAG ATTTATTTAA CCCGATTTTA TATGAAAAAA AATATATTAT 3420

TTGCCTATTG ACGGACTTTC CTCCAGAAAA GGAACAAGCG TTGGGGCAAT CTATAAAAAG 3480

CTATTTCAGT GAAAAAAAGA ATATTACAAT TATTCATGGA AAACCAACGT ATCAACTTCA 3540

CCAAGTACAC CTCTTAATTG TCAATCATTT GTTTCAGATG AACGTAGCGC TTTCTTCTAA 3600

GACAGTGGTT TATTTGCCAG AGGAATTATC TCCTGCTTTT TTTGAAAAAG TCGAAGCGAA 3660

TCTATCGTAA GAAGTCCAAT TTTGTCTAAA TAGTGTTAAA ATGAAGAAGT AAGAGGAATG 3720

GATGAGGAGG ATATTAAAAT GAAACAACTG cAATTTGGTA CAAGTGACGA AACAGTTTCT 3780

TCGGTTATCT TAGGATGTAT GCGCTTAAAT GGTGCTGAAA ATCCTCAACA GGTAATTGAA 3840

ACTGCTTATG ATCATGGCAT TACATTTTTT GATCACGCCG ACATTTATGG TGGCGGCGAC 3900

TGCGAAACCA TTTTTGGTAA GGCCTTAAAA GAAAGTACCA TTCGTCGTGA AGATATTTTT 3960

ATACAAACGA AATGTGGGAT TCGTCAGGGC TTTTTTGACT TTTCAAAAGC ACATATTTTA 4020

GAAGCGGTCG AAGGGAGTTT ACAGCGTTTA GGTGTAGATT CAGTCGATGC ATTATTGTTG 4080

CATCGTCCAG ATACTTTAGT GGAACCAGAA GAAGTAGCTG AAGCTTTTCA TTTATTAGAA 4140

AAACAAGGGA AAGTTCGCTA TTTTGGTGTA AGTAACCAAA CGCCAGGACA AATTGAACTT 4200

TTAAAAACAG CTGTTAAACA ACCGTTATTA GCCAATCAAT TACAATTTGG CATCAAGCAT 4260

ACTGGTATGG TAGATCAAGG CTTACAAACA AATATGGAaA TATCAGGAAG CATTGATTAT 4320

GATCATGGTA TTTTAGATTA TTCACGGTTG AAACAAATGA CTATTCAAGC ATGGTCACCG 4380

TACCAATATG GTTATTTTGA AGGTGTCTTT ATTGGAAATG AAAAATTCCC TGAGTTAAAT 4440

CAAAAATTAA GCGAATTGGC TGAAAAATAT CAAACAACGC CAACTGGTTT AGCCAGCAGC 4500

TGGATTCTGC GCCACCCTGC TAATATGCAA GTCATCGCAG GAAGTATGAA TCTTGGTAGA 4560

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CGTTGATGGA AACAGTGTAG CCTTTCGTGC ATTTTTTGCG CTACATAACT CATTAGAACG 4920

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CCACATTCAG AACaGrATTT TATTCaGAAT ATAAAGCCGG ACGTTCAAAA ACACCGGGGG 5100

AATTTAAAGA ACAAATGCCG TATATTCGTG AACTTTTAGA AGGTTTAGGC GTAAAATATT 5160

ATGAACTACC TAACTATGAA GCAGATGATA TTATTGGTAC ATTAGnCCAA CAAAGTTGAT 5220

AAAGATGAAT TTGATGTTGT CGTGTTATCA GGGGACCGAG ATTTGACGCA ATTAGCGACG 5280

GACACTGTCA AAGTAGATAT CACTGTTAAA GGAGTTAGCG ATATTGAATC ATATACGCCT 5340

GAGCATATTG CTGAAAAATA TGATGGGTTA ACGCCTAAGC AAATTATTGA TATGAAAGGG 5400

TTGGCTGGCG ACACGTCGGA TAACATTCCA GGTGTAACGA AAATCGGTGA GAAAACCGCG 5460

ATTAAGCTGT TAAAACAATA TGGCTCAGTT GAAGGGGTTT ATGAGAATAT CGATGAAATG 5520

AAAAAAAGCA AAATGAAAGA AAACTTGATT AATGATAAAG AGCAAGCCTT TCTTTCTAAA 5580

CGTTTAGCGA CAATTGAAGT CAATGCACCA GTCGAAGTCA ATGTGGaAGA CTTGGcATAT 5640

GAAGGGAAAA ACTTAGaAAA ATTGGTTCCT TTTTATAAAG AAATGGACTT TAAACAATTT 5700

TTAGCTAAGT TGGACATTAC AGAAGAACCT GTTGAAATGG AAGATATTTT ATTTGAAGTA 5760

GTCGAAGATC AGTTAACCAA TGAAATGTTT ACAGACGATA TGGCTCTTTA TGTTGAGATG 5820

ATGGAAGATA ACTATCATAC GTCACCGATT GTCGGCCTTG CTTGGGGCAA CAACAAGAAG 5880

ATTTATACCA CGAATAATTT AGCTGTTTTT GAAAGTCAGC CATTTATTGA CTGGTTGATG 5940

GATGAGACAC GTAAAAAAAA TGTCTACGAT GCaAAACGGA CGTaCGTTGC ACTAAATCGC 6000

TATGTAGGAA AAATGACAGG GATTGCCtTT GATGTTTTAT TGGCTGCTTA TTTACTTGAT 6060

ACCAATGACA ATAACGCTGA TATTGAAGGT GTAGCACAAC ATTACGGATA TGATGCGATT 6120

CAATCTGATG AAGCCATTTA TGGAAAAGGG GCCAAAAAAG GCTTGCCAGA GGACGAAGAA 6180

GTTTTCTTTG GTCATTTAGC ACGTAAGATT AAAGCAATTC AATTTTTAAC AAGCAAATTA 6240

GATAGCGAAT TAACAGAAAA AAATCAAGCT GATTTATTCT ATAAAATGGA ATTACCACTT 6300

TCTCGTATTT TAGGCGATAT GGAAATAACT GGTATCCGTG TTGATGCCAC ACGCTTAAAA 6360

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CGTCGTCAAG CTAAAGCGGT GAATTTTGGA ATTGTCTATG GTATCAGTGA TTATGGCTTG 7020

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GCTTTGGGCC CAGAGCCAAC ACCAGACGTT TTCCAATTAG CTACTTTTCA ACA 8033

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CAGAAAGTCC AGCCATTTAT ACGCGAGAAT ATCAAGCCAA CAATGGCATC ATTGAATTTG 31380

ACATTCGTTC TGTCAATCAA GAAGAAATGA ACAAAATCGT GCAACGATTA CAAGAAATTA 31440

TGGACAAAAA GGAGAAATAA GTCATGTCAT TAAAACCTAA TTATTTAGAA GAACGCATTT 31500

GTTTAAACGT CTTAGCCAAT TCAGTAGAAA ATGCCCAAGC CTGTTATGAA GCAGCAGAAG 31560

GGCATGTTGT GTTAGGCGTC CTTTCAAAAA ACTATGAAAC CGATGAAGCA GCTATTGACG 31620

ACATGAAAAA ATACCAAGCA GCAACCAACA ACGCTTTATC TGTCGGCTTA GGGGCTGGCG 31680

ATCCTAATCA AAGTCAAATG GTGGCTCGCT TATCAGAAGT TCTACAACCG CAACACGTGA 31740

ACCAAGTCTT CACAGGTGTC GGcgCtTCGC GGGCCTTACT TCGTCAAGAC GAAACAGTGA 31800

TTAATGGCTT GGTTTCACCC ACAGGCAAAG TTGGCTATGT CAACATTGCG ACAGGTCCGT 31860

TAAGCTCTGG TGCGCCAGCG GCGGAAGTGC CTATCGAAAC CGCCATCAAA TTGTTGAAAG 31920

ACATGGGGGG CAGTTCCATT AAATATTTCC CGATGAAAGG CTTGGCTCAC AAAGAAGAAT 31980

ACCAAGCAGT AGCAGCAGCT TGTGCCAAGT ATGACTTTTA TTTAGAGCCA ACAGGAGGCA 32040

TTGATTTAGA AAACTTTGAA GAAATTGTTC AGATTGCGGT GGATGCCGGC GTTAAAAAAA 32100

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ACGTGAAAAC GTTACTAACC ATGATGAAAA ACACATTGAA TAAGTAGGTG GCAAAGATGA 32220

AAATTGCTGC GTTTGGTGAA GTCATGCTtC GTTTCACTCC GCCAGAGTAT CTAATGTTAG 32280

AACAAACAGA GCAGTTAAGA ATGAACTTTG TAGGGACTGG CGTAAATCTC TTAGCAAATT 32340

TGGCTCATTT TCAACTAGAA ACAGCATTGA TTACGAAATT ACCTGCCAAT CGTCTTGGTG 32400

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GCGATCATAT TGGTAGTTTT TTTGCAGAAA TGGGTTATGG AATCCGCCCC ACACAAGTAA 32520

CTTATCAAAA TCGCCATCAG AGTGCTTTTG GCATCAGCGA GGCGAAGGAC TACGATTTTG 32580

AGGCCTTTTT AGCGGAAGTA GATATGGTGC ATATTTGTGG TATTTCGTTA AGTTTAACTG 32640

AAAAAACTCG TGATGCTGCT TTGATACTTG CTCAAAAGGC GCATGCCTAT CAAAAGAAAG 32700

TTTGTTTTGA CTTTAATTAT CGACCTAGTT TGAATACAGC AAATAGCGCA CTCTTTATGC 32760

GTCAACAG 32768

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6027 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTATTTACA CCTGCATTGG AAGTCGAAGA TGCCGAAAAG AGTAGTTGGA CTTATCCCGT 60

TTATGGTTAT TTAGATAGCG AAAATCCTTG GGAAAAAATT GCGGCTTTAT TAAATAAACG 120

AACACAAGGC ACACCACGCT TTGCTTTAGA AAAACAAGCT CTTTCTTTAG CTCGTTTCGA 180

TCAATTGAAA ACCTATTTCC CAGCTAGCGA TTTTTCGCAT GATGTTACGC CTTTAATTGA 240

AAAACTTCAA TTAATTAAAA CAGAACCTGA AATTCAACGT TTACTAGAAG CTGGTAGTTG 300

GGCTGATGTC GCTTTTGAGA TTGGCTTCAA AGCAATTCAA GCAGGCGTTG CGGAACAAGA 360

AATTGTTGCA GAAATCGAGT ATCAATTAAA ACGTCAAGGT ATTCGCTCAA TGAGTTTTGA 420

TACGTTAGTC TTAACAGGAA AAAACGGAGC TAGTCCTCAC GGGGTACCTG GCGAAACAAA 480

AATTGAGCCC CATGACTTAG TGTTATTTGA TTTAGGTGTC GTTCATAATG GCTATTGTAG 540

TGATGCCACA CGAACAGTCA GCTACTTGGA ACCTTCTGAT TTCCAAAAAG AAATTTATGG 600

AATTGTCTTA GAAgCACAAT TAGCAGCAAC TGAAGCGGTG AAACCTGGTG TTACAGCAGG 660

cGAATTAGAT GATATTGCCC GAGGTGTAAT TACmAAAGCT GGTTATGGTG AATACTTTAA 720

CCATCGCTTA GGCCATGGCA TTGGAACCAC TGTCCATGAA TACCCATCGC TAGTTCATGG 780

CAATGATTTA GTCATTGAAG AAGGTATGTG TTTCTCTATT GAGCCCGGTA TTTACATTCC 840

TGGAAAAGTA GGCGTTCGTA TTGAAGATTG TTTACACGTA ACGAAAACAG GCTCCGAACC 900

ATTCACTAAG ACAACCAAAG AATTGCAAAT TATTCAATAG CATAAAAATA AAATGAGGCC 960

ATCAGTCAAC CGGACTGATG GCCTCATTTC TAAATTTTAA GGTAAGCCGC TGAACAAAAG 1020

CAACACGATC CGTTGCTAAC TTTCATAAGC TAAACGCTTG TTACCCTTTA AATTCTTTTT 1080

TTACGTCTTT CGCTGCATCT TTAACATCTT CTTTTGCTTC TGCAGCTTTT TCAGGAACAT 1140

CTTTGGTGGT TTCTkTTGCT TCATCGACAC CAGCAGAAAC AGTTTCTTTG GCCGCTGCCG 1200

CAGAATCTTT AACGTCAATA TAGATATCTT CTGCTGCATC TTCGGCAATT TCACCTAAAT 1260

CTTCTGCGTG ATCTTGAGCA TCGTCAGCTG CTTTTTTAAA TTGATCAGAT AAATCACCTG 1320

TTTGTTTTTT AAAGTTATCA AGCATGTCGC CAGAAACACC TTGTGCTTTA TCCAATGAAT 1380

CTTTTGTTTT TTCTTTGACA GAACCTGCCA AATCAGAGGC TTGATCTGAT AAAACGCCGG 1440

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CTTGCGCTTT GTTTTTTAAA TCATCTGTTT GATTTGATAA ATCATCACGT AATTCTTTAC 1560

CTGATTTTGG TGCAAGTAAT AATGCGGCAA CGGCTGCTGC TGTTCCACCA ATTACTGCyC 1620

CTAAGAAAAA TCCGCCTTTT TTAGCCATAA AAATCTCCyC CAATTAGTTA TTkGTTTTTT 1680

TATTTTTTGA ACGCATTGCT CTAAAAGCAG AACCGCCTAC TTTACTCACT nAAACCAGcT 1740

TTCGCTGtGC CTTTyCCTAC GGTTCCTACC TTTGTAATCA AATGTTTACT TGAGGTGTTC 1800

AATTCAGAGA CACTTTCGCT TAAATCAGCA ACGGCCGTAA ACAACGGATC AATCGTTGCC 1860

ACTTTTTGAT TCACATCTGT CAATAGTTCA TTACTTTTAA CAAGCAAGCC TTCCACTTGG 1920

CGACTCAATA CATTCACATC GCTAGTCACG ACTTTGATTG TTGTATTTGT TTCATCAATT 1980

GTATCTTCAA TTTTTGAAAC AACTTGAGAG ACTTTATATA ACACAAGTAC TAAAAAGATG 2040

ACTAAAACAA CAAATGcTAC CGCTGCAATT AAGGCAGCAA TTTCCCCACC TGACATATCA 2100

TTACTCCCCT CTGAAATTTT ATTTATAATC tTAGGATAAC ACCAACTTAT ATTTTTCACA 2160

ACTCATAAAG CTAAGAATGA CAATTTATTT TATAAAATTC TCATGCCCTT TTCTTTAAGA 2220

AAAAAAGCGT AAAATTTCCT TCTAACGAAT TGAAATTTTA CGCtTATTTT TATTTATTTT 2280

TCTTTTGGTT GCTCTTTTTT CGCTAATTGA GCACCTAAAT TAATAATGTA TTCTCGTAAA 2340

TTATCTTTTA CTTCTGGATG AGTCAAACCA TATTCAATGC TTGTTTTCAT AAACCCAAAT 2400

TTATCGCCAA CGTCGTAACG TTCTCCTTTA AACTCACGAG CAAAAACGCG TTGTGTTTTA 2460

TTTAAAGTGT CAATCGCATC TGTTAACTGA ATTTCGTTAC CAGCGCCTGG TTTTTGATTT 2520

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AAGTTATTTT CTAATTCAAC ATTTGAATCA AAATGATCTT CAATCGGACG TTTGGCTTTG 3000

CCTGTCACAA TTAAAATATC TTCGATTCCT GAAGCTAGTG CTTCTTCTAC AATAAATTGA 3060

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CTGCTTGTTG TACATCTTCG TCATTGTACA AGACATTGTA GATTGTTTCT GTGATTGGCA 3300

TTTCGACTTC TAGTTGTTGT GCCAATTCAT AGGCTGCTTT AGTTGTTGAA ACACCTTCCA 3360

CAATCATGCC CATGTTTTCT AAGACTTCAT CTAACTTATG GCCTTTTCCT AATAAATTAC 3420

CCGCACGCCA ATTTCGAGAA TGGACACTTG TACAAGTAAC AATTAAATCC CCAACACCAC 3480

TTAAACCAAT AAATGTTAAT GGGTTTGCTC CCATCGCAAC CCCTAAACGA CTAATTTCTG 3540

CTAAACCACG AGTCATAATT GCCGCTTTGG CATTATCACC AAAGCCTAAG CCATGAATCG 3600

CTCCGGCGCC CAAAGCAATA ATATTTTTTA AGGCCGCCCC TGTTTCTACA CCAATCACAT 3660

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CTGCTAAATT TTCGCTTGCT GCTGTAATGG TTGTAATGTC ATGAACAGCG ACTTCTTCTG 3780

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CTATCACTTC TGAAATCCGC TTATGTGTAC CTTGTTCGAG CCCTTTACTT GCATGAATAA 3900

TAATTGGTTT TGTTTTTAAA TGTTGGGCCA CTTCTTGTGC TACTGAACGA ATGGCTTTAG 3960

TTGGTACCAC AAACAGTACC GCATCAACAT CTACTAAAGC AGTGGCTAAA TCAGTGGTTG 4020

CCTGAATTGA AGTAGGTAAG ATTAATTCTG GTAAATAATG TTTGTTGGTG TGTTTGTATT 4080

TATTTCATCG ATTTGCTCTG GTTTATTCCC CAAATACAGA CCTCGTGTCC ATTTcGGCTA 4140

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GTGAAACTCT CCTTTCGCTA AACAACGTTA CTTCTTTAGT TTACCATATT CTTCAATCAA 4260

GTTGGATTAA GAAGTTGTTA TTTTTTTCTT TTGTTTCTCC CGATTGTAAA ATTTCAAATT 4320

GGGATTTCTT CTGCGAACGA TCACAATAAC AATTGCTGCC ACGAACATCA CTAAAGACAA 4380

CAATTGTGAG ACACGAATGT TACTAAACGC ATACAAACTG TCCATCCGTA AGCCTTCGAT 4440

GAAGAAACGG CCGAAAGAAT ACCATATTAT ATAACCTAAA AAGACTTCGC CTTCTTTTAA 4500

AAAGTGTGGC TTTTTGCGTA ATAACACTAA AACGATAAAG CCTAAAACAT TCCAGACAGA 4560

TTCATATAAA AATGTTGGTT GATGATATGT TCCGTTGATA TTCATGTTAT CAATGATAAA 4620

CGTTGGTAAA TGGAGATTTT CTAAAAATTG TCTGGTGGTC GCTGGCCCAT AGGCTTCATG 4680

ATTCATAAAG TTGCCCCAGC GACCAATTGC TTGCGCTAAA ATCACACTTG GTGCGGCAAT 4740

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TCGAACGTTT TTGTTGCATC ATAGCCCATT GTTTTCGCGC GGAAGTTCAT TGCTGCTACT 5220

TCAATGATAA TGGCCACATT TCGGCCGGTC TTAACAGGAA TACGAATCTG AGGGACATCA 5280

ACGTTAGCTA TTTCAACCAT TGCATCATCA CTACCAAGAC GATCATATTT CTTGTCTTTT 5340

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CCAAACAGGT TCATGACGTC AATAATTCCG ATACCACGAA TTTCAATTAA ATGCTGCAAA 5460

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TCGGGGATTT CTAGTCCTCT GGATACTATA AAGGCTGGAG TATCTTTCGC ACATAAACGG 5820

CGCATCACTA ATAAACGCTC TTCAGGCATC ATTCGTTCCG CAAAGGTAAT TTCTTtGCTC 5880

CCAAATAATT GTAAACGGTC ATGGGAATAA TAATtArAAT ACCCaGTTAA TTCTAAACCT 5940

GGCCGGGAAA TTTCACCAGT TTTAATTGTT CTATTTAAGC TTtCTtCATC TCCGTATACT 6000

ACTTCTAAAG AnAGATTTTC TACCAGT 6027

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CAACAGTCCC AGATGATAAG GTTCTGCTAC CATTACGAAA CTCTACATCA GTATATAGTT 60

TATCTGACAC TCGCATAATA ATTTGGTGCG GATTTTCAGT AAAGTAATTA TCTGAATTTG 120

ATACCAATTT TGTAACATAT GATTTGTTAG CAGTTATATA ACCTTTGGCA GkCyTTAATC 180

yAGGTAATCC GTTTTCGGTA TAATCAACAC TaAAACTTgA TTAATGTATC TTTAGAAACA 240

AACTCACtTT TTTACTGAAA TTTACATCTT GATAATAATA ATCATTTGTT TTCATAACTA 300

CATACTCTGG ATAATCATAT AGATAATCTT TGATGTTTGG CACAACTTTT TGTGCATAAC 360

TTTTATTAGC CGTTAAATAA CCATTTTGGG TAATCAAACG AGGAACTTGA TTTTCACGGT 420

ACTCGATTCC CACAACAGGA ACTAAACTTC CCTTGGAAAC AGCTGCTCCT TTATATAAGA 480

AGTCTGAATC CCCATAAAAA TTATCACTAT TTTTCATAAT AATTTGCCCT GGATTAACCG 540

TATGATAGTT AGCAATCCAA GATCCAGTAG CTACTACATA GTTCTTGTTA GCCGTGAAAT 600

AATACCCATT TGCCATCTTC AATCTAGGAA TTCCTGATTT TGTTTTCTCA ATAGCAGTTA 660

CTTTTAAAAC ACTGCCTGCA GATACTTTAT TTGCTTTTGT CTTGAATTCT ACATCTTTGT 720

AATAGGTATC TTCATTTCTA GTAATTACTT GTCCAGGATT AGATGTGTAG TAAGTATCTT 780

CTAATCCTTT ATATTGTTCA ACTATATTTT TATTTGCAGT CAAATATCCT TTCGCTGTTT 840

TCAATCGAAA TATACCGCTT TGAGTATAAG CTAAATCTTC AACTTCTACT ATTGTTCCCT 900

TCGAAACCTT AGACAACCTT TGCTTAAATT CTGGATCAGC ATAGAAATAA TCATCGCTTT 960

TCAAACGAAC TTTTTTAGGA TTTGTCGTAA AATACAAATC AATATTGCTT TGTGCCGCTA 1020

ATACATAATC TTTATTTGCT GTTAAATAAC CTTGGTCTGT GACCAATCGA GGAATTCCTG 1080

CTGAACTATA TTCAATCCCC TTAATGGTAA CTAGTGTATT TTTTTTAACT CGCCAACCAG 1140

GAGTTCTAAA CGCTACATCT TGGTAAAAAG TATCGTCATT TTTCATGATC ACTCGACCTG 1200

GaTTAGTTGT GTAATACTTA CTTAAGTcAG GCCCACTACT ATTACCCATA TTTAaaAAAT 1260

TACTATAGGT CwGGAAtATC AAACGGACGC CCTTcATAAT tAGCTAAACC AGGgAAATAC 1320

ATTTGCGAGA CCATTGCCAA GCAccTGgTC ATTATyCCmC TGCATGGAAC TATCTGGaGT 1380

ATATGGATAT tGCGCTACCC aTACTCTGTC TCTTCCgAAG GCGGAGGTGT CGATATAGCC 1440

ATTkGTTAAc CACCATTTGC CAACATACAA CGCATCATTT TTATACCCTA ATGCCTTTAA 1500

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TTGCTGGTTA AACGCAACAG AATTAGcATG cGTTTCGCCC ATTGTTTGTA AGCGTTGGAT    1560
CTTCCGCATC ATTAAACATT ATGGTATTTT TATCTAAGCC AGAGTTAGCC GCCGCCTGAG    1620
CAAAATATCT TGCTTCATCT TGTGtGTCGC AGCAGAGACA TACATACTAT AGTGATATGC    1680
TGAAACTTTT AAGCCCGCAG CTTTGGCATT TCTAATTTGG CCCGCAGCAT ATGGATTAAC    1740
ATACCAAGTT CCTTCTGTCA ATTTAACCGA AACACCTGTT ACACCATAGC TTTTAATTTT    1800
TTGATATTCA GCTACTGAAA TGTCTCCATT CCAACTAGAA ACGTCAATAA AATTCTTGCC    1860
AGGCAAATTA GGATCATTCG CATAGACGTT CGCAACTGTT GCTCGCGCTA CCCTAGAAGA    1920
AAGGCCGTTT TTCATAGCAT ATGTTCCTTT TTTATGGTTC GTTCCTTCAC GTGCTGCTTC    1980
TTGATAATCC GCTTCATCTT GGTCAATGGT CTTTTTTTCT ACTTCAGAGC TTTGTGATGC    2040
TTCTGTTTTA CTATCTGTTG TGTTTGTTTC TGAAACAGAA GAATGTTCTT CCGTTGTACT    2100
ATTTGTTGAA GAATCAAGAG ACTCTTCTTT TGTGCTTGAA GTAGAACTAT CTCTTTCAGA    2160
GGTATTTTCT TCTGTAACAG AAGATGTATC CTCCGTTGAA TTAGTCGTTG TTTCTGACGT    2220
AGCTTGAGTG ACCAAGCCAG TcTCCCCCGT TGTTTCTGTT TTTACAAGCT CTTCTCCTGA    2280
TGCAATCACA CTAAAACTAT TTAATAATAC AGTACAAATT AACATACCTG AAATGATTTT    2340
TTCATGAAAC TCTCCTTATA TATTTAATAA TATGTATCTT TCTTAAACAC TTGCCATTCG    2400
CTCTCGAAAA ATGTGTATCC TATAACCTTC AACTAATTGT TTTCACATTT TAAAACTAAC    2460
ACCAATTATT ATCTCATACC TTTATTTCAA ATTCAATTAC GCTTTTTTAA CATTCCTATA    2520
TCAATTTTTT ACTTTTAAAT GGTAAAAAGA TGAAAACAGA TCTTTAATCG ATTGTTTTCA    2580
TCTTTTATTT ATTTTTTAAG ATATTCTGTG TACGATTTTT TAGTATCAAC AATTAGCGCT    2640
TCATGATGGG GTTGGCGATC TTCCTCTGGT GGCAATTGCA TATAATCCCC AAAAACCTCT    2700
GTTAAGTAGC GCTTGTAGCC CACTGGTATT GGCATTTTTG TATCTTCAAA TGGAACAAAA    2760
ATAGCAGATT TAAAATCTTC CAAATGATAA ATATTACCCA TGTAGCGTGG TCCGACACAT    2820
AATTCTGTAA CATAAGGAGT GGAGCCGAAG GAATACTTAG TCATTCTTTT TTCAGCAAAG    2880
CGCCAAATAT GATAGCGAAC CTTTTTCGAT GGAAAGATAT TCAATAATAC CCGACTCCCC    2940
GTTGCTAAAA TGCCACCATG TTTTTCTGGT ACCACTTGTG AACAGAATAA AGCATAAATT    3000
AATGCCCAAA TTTTTTGTTT CTTCCTTTGA AAATTTCCTT TTGGCGCACC ATCTAAAGGA    3060
AAAATATCGA TAGGAATACC ATGAGGAATC GCTAATCCAT CTTGATAGGT TTTAATAAAC    3120
GTTGTCTGTG CATCCCTAAT TGTCATAAAT GAATTATGAT CATTATAAGT TTTTGAAGCA    3180
ACTAACAATG GATAACATTC TGTATCTGCA TATTTAGGCC AAAGCACTTT CaATTTTTCa    3240
TAATCTGGTC TTGGCATAAA GAAATCTAAG TCATCATCCC aTGGAATAAA ACCTTGACTG    3300
CGGATTGCTC CGATACAACC GCCTCCACAA AAATAACAGG TTAGATTATG TTCTTCACAA    3360
AAAGCCACAA AATATTTTGA CATGCGTAAA ACGACTTGTT GAATTTCTAC TAATTGCGTC    3420
TGTGTTGTTT GTTCCACTTT TCCTTTTCCT CCCTATTCAT TCTTTGCATA TTTAAATGTT    3480
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GTATAGAATA AAAAACGCAT TAAGTAGAAT GAACTTTTAA TAACTGAAAA CTGTTCATTT 3540

TGACGCAAAA TTTTCCAAAC CCAACTGATT GTATTCCATT TGTTAGAAGA TGTAGAGGTG 3600

GTTAGCTTAC GATAAATGGC TAATTTTTCG TTAATAAAAT AGACCGTATT TATTTCTTTC 3660

AAAATGTTTA ACCAAGTAGC ATAGTCTTCA TGTTTTAAAT CCGGCATTAA ATGGCGTTTA 3720

AGCAGATTAG ATTCGACTAC GACTGTTAAG CAGCCGATAG TATTTGTTTT TAAAAGATCT 3780

TGATAGGTTT GTGGTCCCTC ACTAAAATTA CGCTCATGAG TAATGTTGCC ATTTTCATTA 3840

CATACAAAAT AAGAACTACA TGTAAATAAA AGTTTTTTTT CTTCCATCCA CTTGACTTGA 3900

ACTTCTAATT TATTAGGAAG CCATAAATCA TCACTATCTA AAAAGGCAAT ATATTGTCCC 3960

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AATCCATCGT CAATTCTTCA CGTTCTTCAG ACTCATCCAA TCCTCTtGAT GATACTTTAT 4440

CAAAGAGAAT TTTGATGGTT tgAAGCAGAA TTTTCATATC CaATAGCAwG aATAATTCTT 4500

GATGTACAGT AAATCAAAGT TCAATTTACT ATTGTAGTCA GAAGCATACT TCCCATAAAC 4560

TTGGGCATAG CCAGTAATCC CCGCACGTAC ATTGTGACGT AAATAGTAAT TCGGGTTTTC 4620

CTGATTAAAT TGATCAACAA AGAATGGTCG TTCAGGACGT GGTCCGACAA TGGACATATC 4680

CCCGCGAATA ACATTGATTA GTTGTGGCAA CTCATCAATA CGTAAAGCGC GCAAGTATTT 4740

ACCAACTGTA GTGACGCGAC TGTCGTTACT TGTAGATAAG ACTGGGCCTG ATTTTGCTTC 4800

TGCTGTTGCC GACATCGTTC TAAATTTTAA AATCGAGAAC TCACGTTGAT CTAATGTAAT 4860

CCGAGTTTGT TTGTAAATCA CTGGTCCCGG TGAGGTTGCT TTGACTAAAA TGCGC 4915

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTAATGCAA TAGCTGCCCC TACAAGCGCT ACTCCTAATA AAGGTATTTT CATATAAACA 60

GCCATTACAA AACCAATAAC AAGATAACTA AAATATTCTT TTGCAGGTAA ATATCGCAGT 120

AGTAACCCTA TACCGACAGC TGGTAGTAAA CCTCCAGCAA CAGTTAATCC ATTGGTTAGC 180

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CATTCTGGAG TATACGATAG AATTGTATTA ATTAATGATG GACCGAAAAT TACTGCCAAT      240
GCTACTGGTA TGCCTGTTGT TGCTGCTGTT AAAAACACGC CAAACATTTG CATTTTGGTA      300
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ATGGTATTTC TGATAACATC TAGTTGGACC ATCAATAAAG CTACTGGTAT ACCAATAGAG      420
ATTCCTACAG ATGGTTTTTG CCCAGTAGTA ATTGTAATAA AAGTTGCTAC GATACTTGCT      480
GTTTGATAGT CAGGTATTGA AGCTCCTCCc AAAATTACTT ATTCCCaAAG ATAGTAACTG      540
TAAAGTACCa CCGATAAATA AACCTGtTGA TATATCmCCt AGGATTAATC CTGTAACAAA      600
ACCCGCTGnT TACCGGTTGA TAAGTTCCAA ACaTTGTTGA GTTTTTTTCA AAGTTAATAA      660
AAAATCCATA CAGCACAATT AATACTAATT GAAAAATACT TGCTTCCATT AATTTTCCTC      720
CTTAATTACA TCAAATAATT TTGAAAATTT ACCTTTTTCA CTTGTTTTGA TAAAAATCGG      780
GATTTGTTGA ATGTCTGCTT CGACTACCAC TGTTTTTCCA CCATCAAAGT TTTCTCTTGT      840
CCATAGGTTT GTCCAACTTT CACCTTTTGG TAAATAAACT TCTCGACTAG TCTCTTTATA      900
ATTTTCAATA GGCGCAACAA GAATCGCATC TCCAAATAAA TAGGTATCTT CAATATTCCA      960
AGCATTCTGA TCATGTGGAT ATTCATAAAA TAATGTTCTC ATAAGTGGAT CACCAAACTC     1020
ATGGGCCTGT CTCATCAACT TACTAATATA AGGCTTCAAT TCTTCTCGTA tTTTTATATA     1080
TTTCGtTAGT ATTTGTTCGA CTTCTTTACC ATAAGACCAA ATTTCATTTG GAGCTCCGGT     1140
AACCATTGAT CCTCCTCCAT GATCAGATAA TGGTTTGCTG TGTGGTAAGC GATCACCATG     1200
CATTCGTAAA ATAGGCGAAA ATGTTGCATA TTGGAACCAG CGGACTAGTA ATTCTCTAAA     1260
CTCAGGATCT TTAGGATCTC CTCCATGAAA TCCTCCAATA TCTGTTGTCC ACCAAGGTAA     1320
CCCAGCCAAC CCAACGTTTA ATCCAGTATT TACTTGATTA CGAAAAGCTT CAAAGCTAGA     1380
ATCAATATCT CCTGACCATA ACAAAGCTCC ATAGCGTTGT GCCCCTGCCC ATCCACCTCT     1440
TACAAGTGTA ACAACTGATT GATTATTTCC TAAACCTTCA GAAATCATTG ATAAATAATC     1500
GATTGGATAC AAATTCCCAA TTTGTAAATC gGTTCCTTTT TTATATCGAT AATTATCGAA     1560
ATCATATACA GAATACCCAG GCTCAGCTAC ATCTAGCCAA AAATATTTAA CTCCTTTGTT     1620
AACATAATTC TTTTTAATGA GGTTCCAAAC ATATTCTCGT GCTTTCTCAT TAGTCATATC     1680
AACAAAAATT GTATTTCCTT GAATTTGCAT TGTTAATCTA ACGCCACGAT TTACTTTCAC     1740
TAAGTAACCA TTTTCTAGAT ATTCATTAAA ATTCATTGCA TCAGTTTGTA CAGTAGGCCA     1800
TATGGAAATA ATTGGCTCTA CATTATATTC ATCTCTTAAT GTcTTAAAAA TTGTTCAGGT     1860
TGAGGCCAAT ATnCTcATCA AATCGATATT CACCTTGTTT AGGCCAATGG AAATAGTCAA     1920
TAGCTATAGT TGAAAGTTTT ATTCCCAAAG CATAGTATTT TTTTACAACA TCCATTACTT     1980
CATTTGGAGA TCGATAGCGT AGTTTACTTT GCCATAATCC CAATAAGTTT TCAGGCATTT     2040
TAGGAACTTT ACCAGTTAAA TCACTATAAT TTCGaAGTAT CTCTTTTGGG GTATCACCTG     2100
CAATTACTAC ATAGTCAATA TAATTAGTAG AAGCCATTTT CCATCGAGTC ATGTTTTTAG     2160
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CAAATGATAC CTCTCCTATA CCTGGATTAT TCCATAAAAA TCCATATCCT AAACTCGATA 2220

CATAGAATGG TATAGATACT TGTGAGTTTC TTTGAGCTAA TTCTAGAACT GTATTCTTCA 2280

AATCAAGATA AGATTGTTGA TATTGTCCCA TTCCAAAAAT CTTCTCACTT GATTCAGATT 2340

CAAATCTAGT TGTAACCTGA AAACCACCTT GTAAATTAGA GTGGTATTCT CTAGACTTCA 2400

ACTTCAGCGT TGAATTAAAA TCTTTAGTTA TTTCAATTGT ACCTGCATCT TCACTTCCGT 2460

CATCATGTTT GACAGCTCTC AATCTGATAA ACTCTTTTAA TAGCACTTCA TTTTTTTCAT 2520

TATAAAAAGT CAATCGGTCC CGATGGTCTA ACACAACTCT AATTTTCCCG TTTATTAATT 2580

CTGTCTTATT TTCGTCTTGA TTTATTATGA CTGTACCTAA AGCATCAGGC TCACCAATTA 2640

AAGAATTAAG TCTATTTTCA AAGTTCATAT CTACAAACGA TCTGACTCTA ACGGCATTTT 2700

CACCCCAAGC TTCTACAATC AATAATTCAT CATCAAAAGT TCTCcGAAAA AGATTTTGGT 2760

GTAACTTCAA TCACATCTTC CAACCCACTT TCAATTTCTT CTTAATTAGT TTGGTATATG 2820

ATAACAATAC TAAGTAATCG CAACAATACA AACGCTTTCC ATACGCACGC CTTTTGCTCT 2880

CTCTGTGTcm ACAAAAGGTT ATAGAtTAAT TTGTTTTCmC GAtAAACTAA TTAACTAAAA 2940

AAATAAACAT AAGATAATAA GCATCAATGA CTTGAAATTT ATTCGTTAGC ACGTTAAACT 3000

AATTAATAAA TAGACTATAA AACAGGCTCA GTAAAATGTC AACTGTAAAC GGCTATATTT 3060

TTTTTGGATA AATTAATTGG CTTTAGGCAA TAGGGAATCT TAACCTTAAT TnCACTAATT 3120

TATTCnAATT TAGGGGGGAA ATGGTTTCC 3149

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7019 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTcCCCkGC tTCyTTTyCC ATAAAAATAC yCTTTtCTAG ATATTTTAAa GCATTTTaTr 60

GAAACGTTtC ACCAAAATAT GAACATCTTT TTCTTAAAAA TAATTCTGTT AAATAACAGA 120

AAAAAGTCTG GTCAATCCGA CCAGACTTTT TAAATATAGA TAGTAAAATG TGTAATTTCA 180

GGGATCACCC CAAAACGGGC ATGAATGGCG GTCGTTCCTA AGCCTGTATT AACATATAGT 240

TGCGTTTCTk GGTCCAACTG ATACAATCCT CTGGTATACT TTTCTGCTAA AACATTTGTG 300

ATTGGATAAA AAGGAATCCA AATTTGTCCG CCATGGCTAT GTCCTGCTAA AACTAACTGT 360

GTACCCGTAC CAACAAATGC ATCCGCGACA TCTGGTTCAT GGGTCATTAA TAACGCATAG 420

TCATACGTTT CTCGATAGGA TAATGTTTCT GAAACGGAAG GATTTCCCAA TAACGAGTCA 480

TCTAAACCAC CAATAAAAAG ACGGCGTCCA TCTGCTAAGG TTACTGTTTC TCCTTGGTTT 540

TTCATAACGG TAAAGCCACT GGCCTCCATG aCTTCrnCAT ACACCGCAGA AGCACCGCCA 600

CCATAATCAT GATTTCCCCA AACTGCATAT TTTCCAATTG TCGCTTGTAA CTGTTTTAAC 660

TTTTCAATCA TCGGTTCTTT TTGTTGCGGA TTTTTGGCAT AATTGTCAAA TAAATCACCT 720

GTAAAAACGA TAATATCTGG TTTTTCACGA TTGACTTTTT TTATGACTTT ATCTAACCGC 780

TTCGTCTCAT AAAATTCTGA AACTTGTATA TCCGAAAGTT GCACAACATT CAATGGTTCT 840

CGTTGATTTT TCTTTCCCAA AGTCACCTGg ATTAACGTGa ACTAAATTCG GCTCAATCTT 900

CCACGcATAG ATTGGGaGTG CGaTAATTAA GaAAAAAAAT AAGAGCATTA TACTTAAACC 960

AATTTTTTTA ACCACATCAC TCGCTCCTTT CTTTTCTTTG ATTTCCGAAG ACTTAGTATA 1020

GAGAAAAATC TTCTTAACCA CAATCTAAAA CAAAGGAAAT TAAGGCTTTG TTAAACAACC 1080

TAAAGAATTT CCACAATCTC TTATCCTTTT CTTAGCTTTT TTATAAAAAA AGCTAGATAA 1140

TTTCATCTGT CGATGAAATT ATCTAGCTAG AACATTCTTC TCTTAATGAT GATGTTTTCG 1200

AAACGTTTGA TAACCAATTA AGCAAAATAA AATCCCCAAT AAAATCATTC CAGTTACTGA 1260

AAATAAGCCT GCTAACATCT TTCGCATCCT CTCTGTTGCT AATCTTCCTT ATTTATAGTC 1320

ACTATTTCTT GTTGTAAAAT TGGTTGAAAT AGACGACGTT CTGCTAATTT TCTTGcTAAA 1380

ATTGCTTCAC TTTTTTTCGT AAAGATACCT AAGTTATGGC GCTTGCCTTT CAAAGAGATA 1440

TAAGCCAGCC ATTTCCCAGA AGCGGTCTGG CTCACCCCTT TGTGTCCACT GCTATTATTT 1500

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CAGCAAGATT GTCCGCACGA ACACAGACAA TACGCTTTCA TTGTCTGTTG AATACTTTCA 1680

ATCCGTACCA CGACTAATTC ATGATAGTTT TTTTTCAACA TTGTTTGATA GCGGTGGTGA 1740

GCACATTTCG TTCGATACCC ACGAATTAGT TGTCTTCTTG AAGCTTCTGC ATAGCTCCCA 1800

CAAGAACAGC GACAGGCCCA AACAATCAGC CCTTCTTTTC TTTTTGCCGT TGGTGCTACT 1860

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ATTGAAAGAA GCAATAATTT TTGCAATAAA GCGGTTATAA TCCTCCCCAC CAGAAAAATC 2220

AACAAATACA TGAATCGTTT TTTCAATTGC GCAAAAAGAC CGATCATTTA ACAAACAAAA 2280

CATAAAATCA TAGTATAGAT GCACGCGTTC ATACATTAAA AATCGTTTTT GATACAGCGA 2340

CTCTGTCTTT TGTATAAAAC CATCTAAGGC GCGATGAATT TGAGGAAACC GCTCTTCAAA 2400

GAAACTGCTC TGCTTGGCGG GAATAAATGC AGCCACCGAA AAGTATAGGC GGTCCCAGCG 2460

ATAACAAATC AACTTTAATT TTTCTTTTGT TTCCACCGTA ATTCGCTTTT CAAAGAAAGG 2520

AATAACACTA TTCATATGAT CAATAAATTC GTCTAACATG GTTAACTTAT CTGGAAAAAC 2580

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AATGTTAGGC AGCCTTTCTT GATTACTTCC ATAAAAATAA TACAAGCATT GAAAACAAAA 2940

ACTTCGGATA TTTTTCTCTT CTCCAACCAA GCCTGTTGAC TTTAATTTAA TATGCCAATT 3000

AGCTAAAATC AGATTTAGTT TATACGAGAA GGCATAAATT TTGCTTTTGC TCATAAAATG 3060

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TTTTTGCGCA CTAATCAGTC CTTTAGCTGG AAAAAGAATT TGACTCCTTG AAGAAATCTG 3240

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AAGTAATTTA TCTCGGAATT CTTGGTCTAA TAATTCATCT AACAAAGTAG TCACATTTTC 3420

AACTCCAAAC TATCACGCCT TAAGTATCTA TTTTTTTAAC AAGACGTGAG TGTCAATCTT 3480

GCTTATTTTT TCCACAAATT TAAAAATGAT TCTTTCAATA TTTAGGAATC TTCATAGAAA 3540

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TTTTACTTTA AATTTAAAGA AAAGCTGATT TGTTTGACTA ATTTTCTGTT TCTTTTCTAG 3660

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ATCGACGTTT TTTCCACCGA CTAATTCTTG CCCAGTTTGT TTTAAATACC AATCAACAAT 4020

TGGTTTAAAG TCTAAAATAT ACTCATTAAT TCCCGCGTAA TTTCCATTAT CATCATACAT 4080

CGCTTGATAG TTATGCACTA CATAGGTATC TGGTCCGTGC ATTGGAACAT GAACGCGAAT 4140

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CAATTCCATT GGCATTGATT TTAAGAAATA ATTTAGCTGA TCTACGGTTA AAATGCCTCG 4380

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TTCCaCGAAT TTTTGTAATG TGCTTTCTAA AAATTGACGT GTTCCCtCCG CAATTAAGTT 4620

GCCGTTTTCA TCAAATGCTT CTTTAGCTTT CCCTAATAAA AACTCGTTCC CaGGCATCaC 4680

GATTGCATTG ACACCAGGTG CATCAAGAAT TTGACGGAGA TGTAATTGCG CACGCGAGGT 4740

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TCCAATGGGT AACCGGTTGT CGGATCCAAC AGATGGTGAT AGACTCGCCC AGCTTCGGTT 6000

AAACTTCTTT CATAAATGCC CGACGTCACA ACCGATTGAT TAGCCACTTC GACAAGTAAG 6060

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TGGACTTCTT TCAAATAGGc AATTAGTAAA TCAGCGATAT AGCCTTTTGc TAAAGCCCCC 6240

AGATCTAATT TCATTCCtTC TTCTTCCAAA AAAACCGTTT GTTTTAAGGG ATTtAAGTGA 6300

ATCTTTTCtG GATTAATTTT TTTCAAACAG GCTTTAATTT CCTCTTCTGA CGGGACACGG 6360

GCATCTTTAA AACCGATTCG CCATGTTTGA ACTAACGGGC CAATGGTAAC ATTCAAATGA 6420

CTAGCTGGAT CACAACTATG TTTTTTCCCT AATGCAATTA ATTGATACAA CTCTGGATGA 6480

ACGCTGACTG GTTTTTGCCC AGCTTGTTGA TTGACAGCCA TCAGTTCCGA AGTTGAATCA 6540

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ACAAATGAAT CATACGCCTT TATTTGATGC CAGTCAAGTC GTTTATATAT TTTTTTATAT 6780

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ACGCTTTTTT TATTATATTT TGAAAATAAA TATATAATTT TCTATATAAA CTAATTTCCC 6900

TTAGATAAAA TTGTTTCTTT CAATGTTTGA ATTGCTTCCA ACAAGATGCG ATTTTTATTG 6960

ATTTTTGCAT ACGCGCGGGC ATCTTGTAGT AGTTCTAAAA TTTGCTCTTG CGGCTTTTC 7019

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TATTTATTCT TTTAACGAAA CACACAATGA AGGTAAAGAG aCTCTtGGTG GTAAAGGGGC 60

AAACTTGGCA GAAATGACAC GCTTAGGTTT GCCGATTCCA CAAGGATTCA CGATTACAAC 120

CCGTTGCTGT ATGGACTATT TGGCAGATGC TACTTTCTTT GAAGAACACT TACAATCAGA 180

AATTTTGAAA GCGGTTAAAA ATCTAGAAAC TGAAACAGGC AAATCTTTTA CCGCGGACAA 240

TGAGATTCTC TTAGTTTCCG TTCGCAGCGG TGCTGccTtC TCGATGCCTG GTATGATGGA 300

TACTATTTTA AATTTAGGTT TAAATGATCA ACGTGTGAAA AAATTTGCGA CCTTAACCTC 360

TCCTGGTTTT GCTTTTGACT GTTATCGCCG ACTTATTCAA ATGTTTGGAG ACGTCGTCTA 420

TCACATTCCC AAAGAATTAT TTGACCAACA AAAAGAGCGC TTGGAACAAG AGCTCAACAA 480

AAAAATTACC GCTTTTCAAG AAGAAGATCA TTTTGCCTTG ATTGTCCGCT ACCAAGAAGT 540

TTTTGAACAA CATCAGGTGG TCTTCCCGCA AGACCCTGTC GCACAACTTT TTGAAGCAAT 600

CAAAGCTGTT TTTGATTCAT GGAATAATCA ACGTGCGGTG GTTTATCGAA ACTTACATCA 660

TATTGCACAT GATTTAGGTA CAGCTGTCAA CATTCAAGAA ATGGTTTTCG GCAATCGTGG 720

ACTAGACAGT GGCACTGGCG TTGTTTTCAC TAGAAATCCG GTCACAGGGG AAAATCAACT 780

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AGAACCCATT CGTCGTTTAC GTTTGACTAT GCCAAAAGTT TATCAAGATT TTCGCCATTA 900

CGCAGAACTT TTAGAATATC ATTATCGTGA CATGCAAGAT ATTGAATTTA CCATTGAAAA 960

TGAAAAATTA TATATTTTAC AAACAAGAAA CGGGAAACGA ACCGCCGCAG CTACGGTTAA 1020

AATTGCTTTA GACTTAGCCA AAGAAAATCG CATTACTAAA CAAGAAGCAC TGTTACGTGT 1080

GACACCTGAT ACGATTGATC AATTAATTCA TCCCGTGTTT GATCAAGAGA AACGACAACA 1140

CATGGAACGT TTAGCTATGG GACTTCCTGC TAGTCCTGGT GCAGCAAGTG GCCAAATTGT 1200

TTTTACAGCA GAAAAAGCCA AAGAACTGAC CAATCTAGGA AAGAAAGTCA TTCTTGTTCG 1260

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CGTGGCGGAA TGACTTCTCA TGCCGCTGTG GTCGCACGAG GAATGGGAAC TTGCTGTGTG 1380

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GCGTATGTGG AGAAGTCGGT GGTGATCCGC AATCCATCAC ATTTTTCCAA ACACTTGGCC 2520

TAAACTACAT CTCTTGCTCA CCTTATCGGG TACCTATTGC GAAACTCGCA GCTGCCCAAG 2580

CCAAAATTTT AACCGAACCG GCTGTGACTG AAGAACAAAT GGTCCTTCTT TAATTTAACG 2640

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CTATGTGAGC CAATAAACCC AGCTAAAGCT TTAAAAGCTG TATTAGTTAA ATAGTTCCAT 4020

TCTACGATTT CAAAGGTGCC AGCAGCTATC CGATAAATCA CATAGCCTTC TGCTTTCCCT 4080

TCTGACGAAT AATAAATCGC TTGATTATTT GGTTTACTTG CACGATTCAG CGTATAATCC 4140

AGCCACCAAG TTTCACGGAT CACACCACCA GAGTGCGCTC TTTGATTTTC aAGGTATACG 4200

TCTTTAATGA CCTCTTTACC GTCAGCCCAA GaAACTCGtT TAATGGTACC TGGAACTCgT 4260

TTAAcACGTG GCCaATCTTC CgTTTTAAtT GTATACTCTG CTTGTTCaAA TGTTTGTTCA 4320

TAGCCATATT GACGATAAAA TGGATATGAA AACGGTGCTA AGTAAGAAAG GGCAACCTTT 4380

TGTTTCGCTA AATCAGCCAA CATTTCTTTC ATAATAGCAG AGATGCCGCC TTCACCACGA 4440

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TTTTATAGGC ATTGAGCCAA GACCAGTTAT CCATACACGT CCACATATGA TATCCTTGAA 4920

CATTACTACC TTCTTGAATC GCTTGGTGCA CCCATTTCAA GTGATCTTGC ACGAATTCAA 4980

TCCGATAATC ATCTTCAATG ACTCCTTGTT CATTGACAAA GCGTTCTTCT CCtTCTACGC 5040

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ATGTATCATA AATACCTTTT TCGTAGATTT CCCAGCCACG GTAAGGATTC ATTTTTTTGC 5160

CAGGCATATC GTAGACATCA TAAAAATCTT CTGGAAGTAA GCCTTCTGGT CGTGTTTCAA 5220

CAGGTGTTTC TTTTGCTTTG GCACGACGTG GTTGATAGTA GTTTACTCCT AATAAGTCCA 5280

CAGTATTTTC AGCAATTATT GCTAAATCTT CTGGCGTTGT TTCTGGCAAT AAGTCATTTG 5340

cTTTCGCCCA AGCAACCATA TCTTCTGGAA AATGACCTTT AACAGCCGGG TCTAAAAACG 5400

AACGGTTAAA GAAACCATCG ACAAATTTAG CCGCATTTAC ATCGGCTTCG TTGTGCTCAT 5460

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CAAGATTATC CTTGGCCGTT GCTTCTTGAG CCACCGTACT CGCTGGAAAA CCAATATTTC 32760

CCGCCAAA 32768

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GACGTCGTCG CTCAGGATTT TGCTAAAATG GCCCAGTTTA CGTATCATTT ACAAGAAGCA 120

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TAAAATATTG GATGCCGTTA TTAAGTCAAG GGGGCGTTGT CACACAAATC GGGATTCATG 1560

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GTAATGGCTG TATCAATACG CCAGGAACAG AAGTTTCAAA AATCTTTGAT GTATCCTATG 1680

ACGGAATGCC GGTAATTATT TATGGACATA TCTATGATGA TGCACCAGGT GAATTTGATA 1740

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AACCTGTAGA TTACGGCGAA GAAGTATAAA AAGAGATATT AGGcAAGACC GTACTTTGGT    1800
CCAGCTGTGT ATCTGAAAAG TAAAAATTGG AGACGTCAGC GTAACGACTG ACGTCCCCAA    1860
TTTTTTATTG ACAAGCGTCA TAACCCGCTC TATGATACAA ACAGAACAAG CAATTTAAAT    1920
TGGGGGAACG AAGATGCCAT TTGTACATGT AGAATTAATT GAAGGCCGCA CAGAAGAACA    1980
GTTAACTAAT ATGGTCAAAG ATATTACAGA AGCTGTGTCA AAAAACGCTG GTGCACCAAA    2040
AGAGAATATC CaTGTGATTG TCAATGaATT GAAAAAgACC GCTATGCACA AGGCGGCGAA    2100
TGGAAAAAAT AAGTTTTCAG AGAATTTCTG TTGAATCACT TGCTTTTTCT GAAAATAAGT    2160
GGTTAAATAA GTGCATAAAT GATTGATGAG AAAGACAACT GAACTTGCCC GCGATCTATT    2220
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TGTTCAAAAT TAGGTGGAAC CACGATATTT TCGTCCTAGT ATTCGTTAGA ATACTAGGAC    2400
TTTTTGTTTT TTAACAAGGG GAACAGGTGG CTGTTTCGTT TCATTGTGAA AAACAGGAAC    2460
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GCTAAAAGTA TTAGCAACAG TTTAGCCAAA AAAGCTTTAG CTGGTAAATT CAATGGTGTT    2640
TTAATCGATT TAGATCGTCC TATCGTAGAA GATGGTTCGC TTGAAATCGT GACACCTGAT    2700
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CGCCGTCTTT TCCCTAACAT TAAATTTGGC GTAGGTCCTG CGATTGATTC TGGGTTCTAT    2820
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GAAATGATGA AAATTGTGAA GGAAAATAAC CCAATCGTTC GTAAAGAAAT CTCACGTGCA    2940
GAAGCGTTAG AATTATTTGC TGATGATCCT TACAAAGTTG AATTAATTAC AGATTTGCCA    3000
GAAGATGAAA TCATCACTGT CTATGATCAA GGCGATTTTG TTGATTTATG TCGTGGTGTT    3060
CACGTCCCTT CAACAGGACG GATTCAAGTC TTTAAATTAC TTTCAGTAGC TGGTGCTTAT    3120
TGGCGCGGAA ACTCTGACAA TCATATGATG CAACGGATTT ATGGCACTGC CTTTTTTGAT    3180
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CATTATCAAC CATCCAATTA GACTTCTTAT TACCAGAACG TTTTGACTTA ACTTATGTTG 4020

GCGAAGATGG TGAAAATACA CATCGCCCAG TTGTTATCCA CCGTGGTATT GTCTCAACAA 4080

TGGAACGATT TGTGGCTTAC TTAACAGAAG TTTACAAAGG CGCTTTCCCT ACTTGGTTAG 4140

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AGAAGTCGTT TTAGACAATA ACGGAAAGAT TGTTTCACAA ACCCCAATTT CCAAaGGGGA 5580

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TATGATTTTC CCTTATGAAG TAGGAGATGA CACTGTCTTT AAAGAATTAA GaAAAGCTTT 6120

TGCAGAATAT GGTATGGGAA CGAAAACTGG AATTGATATA CCAGGAGAAA CAACAGGAAT 6180

TCAArACAAG GACTTTAAGG ATTCGTCATC tGCGCCaCAA GGCGGTAATC TTCTTGACCT 6240

ATCTTTTGGA CAATATGAT 6259

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGCTGACTCA ATTAGCGTAA TGGAGTTTGT TTTAGAACTT GAAGATGAAT TTGGAACAGA 60

GATTTCAGAT GAAGATGCAG AAAAAATTGA AACAGTTGGT GCCGCTGTAG ATTATATTGT 120

GAGTAATTCA TAAAAAATAA TAAGACAAAG TCGATTAACA TTCCTGTTAA TCGACTTTTT 180

TTGCGTACAT AATGGTTATT TTATTAAGCA ATAAGGCTAT TTTTACACAT ATTTTTGTAA 240

AAAAAATCAT ACATGTAAAA AAATAACTGC GAAAAAAGTT ATTTTATCTT GCTTTTTATG 300

GAATAATTCT ATAAAATTAT GAAAAAACAA TGAGCTGTAA ATTAACATTG ATAAAAATTA 360

GAAAGTGCTA TCATTAAATA TTAGTTAATT TATATAATGT TTTTGAAAGG ACGTAAGGGG 420

TGCGTATGGA TGCAAGGAAA TGAACAATTA CTAGAGGTTT CAGGATTAGA AACAGCATTT 480

AGAATCAAAG ATGATTATTA TAATGCCGTC GATGATGTTT CATTTGAATT GAAGAAAAAT 540

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ATGGGCTTAC ATGATCCCAA TCATACCAAA ATTACTGGGG AAATTTTATA CAACAATTTA 660

AACTTAACTA CGTTTAATGA AACATTGTAC AACAAAGTCA GAGGAAACGA TATTGGGATG 720

ATTTTCCAAG ATCCGTTATC TGCACTGAAT CCGCTCATGC GAATTGAAGA CCAAATTAAA 780

GAAAGTCTCA CGTATCATAC CAAAATGACC GCACAACAAA AACAAGCACG GGCCATTGAA 840

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TTGTCTGGcG GcATGCGCcA ACGGGTGaTT aTTGcCATTG CAATCGCGTG tAAACCACCG 960

aTTTTaATTG cmGrTGaACC AACAACGGCC TTAGACGTTA CCATTCAGGC ACAAATTCTC 1020

GATTTGTTAA AAGATTTACm AGaAGAAAcA GGGAGcGGCA TTATTTTAAt TACCCATGAC 1080

TTAGGTGTAG TTGCGGAAAT GGCTGATCGT GTAGCGGTTA TGTATGCGGG TCAGTTTGTA 1140

GAAGTAGCCA CTGCTGAAGA ATTGTTTAGT CATCCGAAAC ATCCATATAC ACGTTCCTTA 1200

CTTCAGTCCA TTCCCCAAGA GAATTCAGAT GAAGAAGAAC TTCATGTGAT TGAAGGGATT 1260

GTTCCTTCGT TAACCAAATT ACCTAGAAAA GGTTGTCGGT TTGCCCCACG AATTCCTTGG 1320

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GTTCGTTGTA CATGTTATAA ACATTTTCAT TTTAGAGACG GGGAAGGGGA AGCGTAATGA 1440

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GATTATCGGG GCTAGGAACT CGATTTTAAT CGGTTTTGCC ATTACGATTA TTACGTCTAT 3720

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ATCATATAAT GACGAGACAA AACAGTTTGT ACATACTGAT ACTTCAAAAA TAATGGAAAA 9540

TCTGGTGAAC AGACAACAAG GAATTTATTA TTTTGGCTTT CCGACTTGTC CTTGGTGTCT 9600

AGAATTATTA CCAATACTAG ATAAAGAATT AGAGAAGGAA AGTATGAATG CTTATGCTGT 9660

AAATACTCGT GGTGATGACT ATACaGAAAA TGATGAkGAA TTATTACaAA AATTTkATCa 9720

AAAATATACT GGGGATGAGT CGCTTTCTGT ACCTTTTATT GTTGCTA 9767

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAAATCGTTT TGGATTTTTT CTCGGnTnCT TTCTATTTAA GTTATTTTAG TTGGATATCG 60

TTATTTAATA AGGCTATTAT ATGGTATAAT GATAATTAAC TGAAGTGTGG AGGAAATAAA 120

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CCGCTTGGTG AAAGAAGTAG GGATTACAAC AATCTTTGTA ACGCACGACC AAGAGGAAGC 1860

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GTTAGACGGC GCCAAAATCG ACGGCAAACA ATACGGCATT CCATTTAATA AATCGACAGA   5820
AATGTTATTC TATAATGCTG ATTTGTTGAA AGAATATGGT GTTGAAGTAC CGAAAACATT   5880
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TGCTGGTTTT GACTCGTTAA ATAACTATTA CGCAATTGGA ATGAAAAACA AAGGCGTTGA   6000
TTTTAATAAA GACTTAGATT TAACAAGCAA AGATTCACAA GAAGTCGTGG ACTATTACCG   6060
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AAAAGATGCT GAAGCTGGTG GCTATGAATA CGGTGTTGCA CCACGTCCTG AAAAAATCAA   6240
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AGTGGcTTGA TCAACCAGTG GGAAATGTGG AAGGGGATAT GACGATTCAA AATCCGAATG 7680

CCGTACGCCT CAAAGAACAT CCATATATAG aATTTATTAA TAACGTCCAA ATGGCTTCAA 7740

GCGGAACGGA TATTTCAGGG ACTGCACTTT TTAACAATGA AGGCAAAGGG TTTAATAACC 7800

AAATTACGAT GCGCGATATC ATTACCAACT ACATTTATCC AAATACCTTG GCTGTATTGC 7860

GTGTCACTGG ACAAGACCTC CGTGAAGCGT TAGAACAAAG 7900

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCCTTACATT TCATGTTATA AAATGTAACA TAGAAATTAA GAACAAAAGA TTAAGATCAG 60

TTGAAGTCCG AAACAGCAAA AGTGGCGAAA ATATGTTCGG TATGTTAAAC TAATAAGTGG 120

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GGGCCGGCGC AGTCCAGCGT 5480

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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TGTCACGGGT GACGAACGAT GTGGATGCTG TCAGCAATGC GATGCAACAA AGTTTTATCA 180

ATATTGTTTC AGCAGTCTTA GGTATTGTGA TGGCGGTAGT GATGATGTTC TTAATCAATC 240

CGCTGATGGC GATTTTTTCA GTGATTATGA TTCCGTTGTC TCTGATTATT TCCAGAACAA 300

TTGTTAAAAT CTCCCAGAAA TATTTCCAAG GAATGCAAAA TTCTTTAGGA GACTTAAATG 360

GTTATGTCCA AGAAAATATG ACTGGGTTCA GTGTCTTAAA ACTATATGGT CGGGAAAAAG 420

AAACCCTTGA AGGCTTTAAA CAAGTCAATC ATCGTTTAAA TGGTTTTGGT TTCAAAGCAT 480

CCTTTATCTC AGGATTAATG TTGCCATTGG TTCAGATGAC CGCTTATGGG ACCTATATCG 540

GGGTAGCTGT CCTTGGTAGT TACTATGTGG TTGCTGGTGT GATCGTAGTG GGGCAATTAC 600

AAGCGTTTAT TCAATATATT TGGCAAATTA GCCAACCAAT GGGGAATATT ACGCAGTTGT 660

CTGCAGCTTT ACAAAGCGCT TCAGCTTCGA CCATGCGGAT TTTTGAAATC CTAGATGAAC 720

CAGAAGAAGA ACTTAACGAA CAAGATGTTC CTTTGCCAGA ACCTATTTTA GGCTCTGTTG 780

AATTTGAAAA TGTCAGCTTT AGTTATGACC CAGAAAAACC GTTAATTCGT AATTTGAACT 840

TTAAAGTTGA TGCGGGCCAA ATGGTTGCGA TTGTGGGACC AACTGGCGCT GGGAAAACAA 900

CCTTAATCAA CTTACTGATG CGTTTTTATG ATGTAACAGA AGGCGCCATT AAAATTGATG 960

GCATTGACAC GAAAAAAATG AACCGTAGTG ATGTCCGATC TGTATTTGGA ATGGTATTGC 1020

AAGATGCTTG GTTGTATAAA GGTACCATTG CAGATAACAT TCGTTTTGGG aAGTTAGATG 1080

CCACGGaTTA TGaAGTTGTC GATGCaGCGA AAACGGcCAa TGTGGATCAC TTCaTTCGGA 1140

CAATGCCAGA CGGGTATGaA ATGGAaATCa ATTCTGAGGG AGATAACGTT TCCCTTGGtC 1200

aAAAACAATT GTTGACCATT GCCCgAGCGG TAATTTCTGA TCCGAAAATT TTGATTTTAG 1260

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CTGATTTAAT TCTTGTTATG AAACAAGGAG AAATCATTGA AAAAGGTACG CATCATGAGT 1440

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CGGTTGTAAA ATCGGTGATG GTGCTTTGAT TGGCATGGGT TCAACCATTC TAAATAATGC 2040

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TAGAAGAGCA AAGTCAAGGA TTTGACTCTG TAGTAGTCGT AACAGCGCAA CATCGCCAAA 2400

TGTTGGATCA AGTGTTAGAA GATTTTCAAA TTACACCGAA TCATGATTTA AATATCATGA 2460

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ATGCCCACTA TCAAAATGAT TTATTGGAAA AAATCCCTAC AGACCAACGC ATCGTGCTAA 2880

TTACAATGCA TCGTCGTGAA AATTTAGGCC TGCCAATGGC AAATGTGTTT AAAGCTGTTC 2940

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AAGTCCGTGA AATAGTAGCG GAACACTTAG GTGAATTAGC TCGTGTGCAT TTAATTGAAC 3060

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TGAATTTTTT ATCGGGGAAT GACGGTCTTT TTATTAAAAA CATTTAATTT TAAAGAGGTT 4320

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TGGCGCTTTT TTATCGTCGC AGAAGCATTA CTTTTTATTC TGGCGTTATG GCAAATTGTA 6720

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CCGGTGTTGC ACGAAGATTT GACAAACCGG GAACACGAAA TTTTAATGTT GATTGCACAA 8940

GGTAAAAGTA ATCAGGAAAT AGCTGATGAA CTCTTTATCA CTTTGAAAAC AGTTAAAACA 9000

CATGTTTCAA ACATTTTAGC AAAACTAGAT GTGGATGATC GGACCCAAGC GGCGATTTAT 9060

GCTTTTCAAC ATGGTTTAGC CAAATAAATA TCAGATAAAT CCATAAATAA ATTCTAGGAA 9120

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GTCAGAAGAA ATGAAACAAA ATTTTGCAAT TATTGGTTTA GGACGTTTTG GCGGCAGCAT 9240

ATGCCAAACT TTGGTGGAAG CTGGTCAAGA AGTTTTGGCC ATTGACAGCA GTGAAGACCG 9300

TGTCAATGAA TATATGAATA TTGCAACGCA TGCAGTGGTG gcTAACGCCC AAGATGAAAT 9360

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TATTCAAGCG AGTATTTTAG TGACACTAAT GGTTAAAGAG ATGGGGGTTC CCAATGTCTT 9480

GGCCAAAGCA GTCAATGAAT ATCATGCCCG TGTCTTAGAT AAAATTGGGG CAGACATGGT 9540

CGTTCACCCA GAGCGGGATA TGGGCATTCG AATTGCTCAC AAACTTGTTT CACGCAATAT 9600

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GGTAGCGATT CGCCGCTCGA AAACAGAAGT AATTGCTTCG CCAGATGCTT CTGAAATTGT 9780

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AAAAAATCGT TTTGGATTTT TTCTCAGGTC TTTCTATTTA AGTATTTTAG TTGGATATCG 10380

CTATTTAATA A 10391

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AGTATTAmTG TkGATAkGGA TTTATTAGAA GcAGsAGGaA TATATGAATA TGAaAnAGTA 120

CAAATAGTTG ATGTTAATAA TGGAAATAGA TTTGAAACTT ATACAATAGC TGGAGAGAGA 180

GGAACAGGGA TGATTTGCTT GAATGGAGCT GCAGCTAGAT GTGTATCAAC TGGAGATAAA 240

ATAATTTTAA TGGCATATTG TGAATTAAAT GAAAATGAGG TTAAGGATCA TAGACCTAAG 300

GTTGTTTTTG TCGATGATAA TAATAAAGTT GAAAGAGTAA CATCATATGA AAAACATGGA 360

AGGTTATCAG aTATAATTCT TTAGGTTTTG TAATGTTATT TATATATAGC TAGACTATTA 420

TTGAAATATT TATTGATTAC TAATTGGATA GATGTCAATA AAGTAGACAC AAAAAGAGAA 480

GATACTTAAA GATTTTCAAA GTAAAGAGCC TCCATTTCAT TTGGTGtAAG CATATCTCAT 540

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TCCAAATCCA ATTGTTGTAA GGTTTCAAAT GTGTATTGAT AGACAAATTC TACTTTCAAC 1140

GACTTATAAG TTGATTCAGC TACGGCATTA TCAAAAGGAC AGCCTTTATG ACTCAATGAT 1200

CGATTGATGT CAAAAGTCGT TAATAATTCA TCAATAGCTT GGTTATCAAA CTCTTTTCCA 1260

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GATAAGGCTT TTTTTATTTT TCTTGAGCCG TAGgCtTTCG GCTGAGGATA AATTCTTCAG 1680

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CGACTACTTC TTCAAGTTCT GATTCGTCTT TCTTTGGTTT TGATTGATAA TAATAGGACT     1740
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TTCTAATTGC TGGTTTCTTT TACGTAGTTC TAACAATTCT TTTTGTTCAG GCGTAAGATT     1920
ATCTTTTTCT TTGAATGAAC CACTCGTTTT AGATTGCTTT ACCCATTTGT CAAATGCTGA     1980
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GACTATTTGT TGCTTGAATT CTTGTGAAAA AGTTCTTCGT GTTCTCTTAG ATATAAAAAT     2100
TCCTCCTGGT ATGtTTTCTT CTAGTCTACA CACCTTAATT TTTCTGTCTA GTTAATTGTA     2160
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TCGGAGCCAT AACACCGCAG CATTCACAAC ACCTTATAAT TTTTGTCAAA AAAAGTGTTG     2280
CCATTCCnAT AGATGAAATT CTTCAATTGA GAGTGTAAAA TATTTTGTGT AAATAGAAAA     2340
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GGAACACGAT AACCGTCGAA ATGGCTATGG AACTAAAACG CTTAAAACCA GTTTTGGTGA     3480
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GAGTCAACGA GATATTGCCG CAACCGTCGA AGCTATCTAT GGCTTTGATA TTTCCCATGA     3660
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AATGATTTCA GATATCACTG ACGCTGTCCT TCCTGAATTG GAAGAATGGC AAGCCCGCCC 3720

CCTAGCAAAG TGTTATGCCT TTCTATTCGT TGATTGTATG TATGTTACTT TACGAGAAAA 3780

TTATGAAGCC AAAGAATATG CTGTATACAC CATTCTTGGC TATGATCTCA AAGGAATAAG 3840

GAGATTTTAG GA 3852

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATTGGCTAAG CGTTTAAACA AATGCGTCTT CTAAATAAya GGTTTTAATG ACATGACTTA 60

nTTCyCCTTT TtGtCCATAA TTTCTTGTAA tCGTgCACGA TTTTGTTCAT TTCTTCTTGA 120

TTGACAGAAC GAATGTCAAA TTCAATGATG CCaTTGTTGG CTTGATATTC TCGCGTATAA 180

ATGGCTGGAC TTTCTGCTTT TAATGCTTGG ATGACTTCCT TAGCGGTTTT TCTGCCGTCC 240

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CCGCCACCTT GCGCTACCAT GACTTCTACA GGCGTGCCGT AGTCCACGTT GTGCCCTTTA 840

GGTAAAACAA TCTCCCGCTG TTCGATTTTT TCTGTATAGG GATGATACGC GTGGTACAAG 900

CTGCCTTTTC CAATCAAGGC AGCCACCGAT TGGGCAATCC CCGCCGAAGC CGAGGAAACG 960

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ACTTTGGAGA CACCTAGAAT GGTCATTTTG CCAGAAGCAT TAATGACTTC TTTTAAGTGG 1140

AATTTTtCGT AACTAATTGT CATAGATTTG TCCTCCAATA ATTGTTTTGA TTGGGCGAAT 1200

TTGCTCTTTG GCTACTCGTG TCAATCCATT AGAATCAGTC AATGTTTTTT CTTCTGCTTG 1260

AATCGTGAAA ATCGTTAAAT CAGCATCTTT ACCTATTTCC AACGTGCCTT TTTGCGTTAA 1320

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GACCACACGG AGTTTTTCCA TCGTTGTGGC TAAATCATAA ACAGGACCAT TTTCTCGGTT 1440

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AGCTACGTGA AAATTGAAAC TATCCGTACC ATGCCCGATA TCAAATACGA CTCCTTTGTT 1560

GTACGCTTGC CAAGCGAAAT CTTTTATTTT ATCCGTTGCT TGGTCTAAGA TACCATTTTC 1620

TTTCCCATTA AAACAATGGG TTAGGACATC CCCTTTTTCC ATCAAGGCTA AAATTTCATC 1680

TAAATGAGGC GGTGCTGATC CAATGTGAAC CATTAAGGGA ATTTCTTGGT TCTCTTGCTG 1740

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ATAAATCTAA ATTTTGTCCA AGGCTTAATG AATTCTAATA ATACAAGTTC TTCTTCTATA 2340

ATACGCCCTA CTCGGTTTTT GCGTGAGTCT TGATGTGGTT CTAAAACGAC TTGTAATTCA 2400

TTTTTGTATT TTCCAAATGC ATCATTTCCC ACAACAACAT CTCCAGGTTG TAGCATTGCT 2460

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ATCATCTGCT GAGTGATATC TCCACGGCGA AAATGTTGAT TTTTTGTTAC GATTTCTTTT 2580

TCAATTTCAG AAGTCGCTTC TTCAAAAACA ATGGTCAATT CTGTTTGATA ACGATTCAAC 2640

TGACCCAATG CTTCTAATTC TTCGTTGGAA GCATAAGCAT TTCCAATAAC AACATCATCA 2700

ATTAAATTTG TTGCAAATAA ATGTTTAGCT TGAACAGTGA CTGGCAACTG TCTATGCATT 2760

TCTAAAGTAG GTAGCCCATC ATTCACATCC CAAGGACCAA TTTCACCTAC CTGTGATGAA 2820

ATAAAAGCAG CTGTCCGAAT ACCTTCCTTT TTAAAACGGA TGCTACATTT TTCAAAGAAA 2880

TCATACGGCA ATGCAGTTCC CGCTTGTGGA TAAAAGTTAT GACAACCATA TAAGAAAGGT 2940

CGATTCGCTT CATACGTCAA AATGTTATCA AGATAAGCGA CATCATTACT CATATTCAAC 3000

TCAATAGCCA CGCCGAATGG ATTAAACGTC AACATGGCTT CTTTATTTCC ATCAAACCCT 3060

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ACCAAAAATC ATTGCGCCTA AAATTGCGCC CCCAGCGATT GGTTTTTTCC AAATGTAAAA 5220

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AATAATTAAC GGGCCTAAGA AGCGTCCTGA GGCATTACCA GCCCCCATCA TCACATCCGC 5340

ACCAAAAGTG GAATTTCCTT GATTGATAGT AAATTTCCGA ATCAACACAA TTACGCCACC 5400

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TTGCTGTTCC ATCTATGAGA CCTCCTTTTT TCTATTTAAC GGTGAAGACA TTGTGTAAAT    5880
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GGAAGAAGCC ACTTAAAATA AATAATAAGA TAATGACACC AAGCATGCCG CGTGTCATTC    6000
GGGTCCACCC TAAATCATCG ACACCTTTAC CGATTAAGAT CCCTAATACA ACTCCTGGGA    6060
CAGCATTGCC CATGACTAAT TGAGATAATC CGCCAAATAA TGTTCCCCAG AAACCCGTCC    6120
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GTTCTTCCTG ATCCATAAAA CCAAATCCAA GAACAGTTTT CCCATCGTTA ATTGCTGTTA    7140
CCCCTTCTTC GATTGATCGC ATGCCATGTC TTTCGGGATA CCCGTATTTA GTAGCAGCCG    7200
TTAACGCTCC TGCACCACCA CTTCCACAGA AAGAAATGCC TAAATCAGCC TTTTCTTGTT    7260
GCATCACATC TCCTAAACGC ATATCAGCGC CCATTCCTGG AACAACAACC GCGCGACCAC    7320
CGGCTTGCTC CACTCCTTTT GCAACATTTT GTCCTTTTCC TAAACGATCT GCGATAACTA    7380
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CTGTAATCAT AACTTTTCCT CCTATTAATT GTTTTGTTTA GCAACTTCAA AATGAACAGC 7440

TAAAACATAC CATTCATCTT CTGATAACTG ACCAATTGCT TCTGTTGTTT CTTCTGCAAT 7500

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GATGGGTTCC GAATAAATCA CTATAAATAT AAAAATATTC ATCCGCTAAT AAAGGCAAGT 8760

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(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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TTCCTTTAGT TCTTTATCCG TAATTGTTGA ACTGTTAATT CCTTGTTCAT ACAATTGTCG 120

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ATGGCTTCTA ATTGTAAATT TTTTCCAGTT GTGCCAGAyA ATGCCCCATT rGCTTTATAA 1200

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kTTGGTTTGA TTTCATCTGG ACGTTTTGCT TCATTTCCAA CTAAAAAGGA TTTTCCaTTT 1440

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CTTCTATATG CACACGATAA TAAACATCAT ATGCGTTAGc tATTTCTCCA GTTAAGCGAA 2100

TTTGAATCGC TTCGAGCCGC AAAGACTTTC CGCTTGTACC AGACAATTGA TTATCTTTCA 2160

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GTCGCTCCGT TAGAGATGTT TCTGAAGCCA CCGTTTCTTC AGTAGTTCCC TTAGAGCGTT 2640

CCAAAGCGTA AGCAGAAATA GGGGTAACGA GAAATCCCGA CAACAAAACC GCTAACATAG 2700

AACTAGTTAT AACACTTTTT TTCATTAATT TACTCCTT 2738

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GATTGGACGA AAGTAACTAA TAAATCTGTT TTTATAACTG GTGCTTCAGG CATGATTGGG 60

ACCTTTTTAA TTGATGTGCT TATGTACCAA AATAAAACGA GAAATGCGAA TATTTCGATC 120

TGGGCGATGG GACGAACATT GTCGCGTTTA GAAGAGCGAT TTACTAGTTA TCTAGAAGAT 180

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GACTATGTGT TGCATTGTGC TAGTAATACA CATCCTAAAT CATATGCCAG TGATCCAATT 300

GGAACGATTA TGACCAATAT TGCTGGTACG CAGCATATTT TAGATTATGC GGTCAAAGCG 360

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TTTGTCGGTT TTCTGTTCGT TCATATTCTT TTGCTTGAAT ATATTCTGTT CGTTGATTTT 3060

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CTATTTCCAT ACATTTTTAT CTATATAACA TTTCCCAAAA CGTTGATATA AATGGATTAG 5520

GATGTATTCA ACACACGTCG TATTTTTATA 5550

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CAACGTTTGT TTACAGCCTG GGAGAAAGCT TGGAGTGGCA AAGCTTCAAT TTTAGCAGAC 240

ACCCTAAATC ACTTGGATGG GTTCCGTTTA TCTGATTACA AATTGCATGG CACTACAGAT 300

TATTTAGAAA ATCCCTTAAA CTATAATCGA ATGAGTCAAG AAACATTAAC GGTTATGTGG 360

GaAACCATCC AAAAAAATAA ACAACCATTC GTCGACTTTC TAACGCGCAA AGcGCAAtTA 420

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ACCAATTTGC AATTGAATAT TATGTTTTTT ATGCAATGTG TAAAAGTCAA TTGATTGAAG 26160

AATTTGGTAT GTGAATTCTG TAAAGGAAAT GCCACTTTCT AAACGACTAG CGACAATGTC 26220

TTTTGCCAAC ATCGTGTTGA CATTAAAGTT TTTCCCGTAA TCTCTTAAAA AATCTAATAA 26280

AGATAGTTCT GATAACCAAT CGTAGTTGTT CACCATTGTT ACCTCAGCAT CTTTACCAAA 26340

TAATTTTTTC ATTTGGTTTG AAAGACTGTC CACATTATGT TGCACAGCTT CCATCGTTTG 26400

TAAGACACGT TCGGTTGTTC GTCCACTTGG GTCACCAATT GTTCCAGTTC CGCCACCAAT 26460

TAAAATGTAT GGGTGATGAC CTGCTAATTG GAATCGTTTC ATCATCATAA AAGGAATTAA 26520

ATGTCCAATA TGCATGCTAT CTCCAGTTGG ATCGACACCG CAATATAGCG AAATGCTCGT 26580

ATTTTCTGTA AGTTCTCTTA GTCCTTCTTC GTTTGTTTGT TGATTGATTG CATCACGCCA 26640

TGCTAGCTCG TCAATGATAT TCATGTTATC ACCCTCCATA TTTATAATTA TCTCTTTATA 26700

GGAAATCGTT CATTTAACGA AACAAACGAT TAACACACTT GTTTTTACAC GATATCCCGT 26760

GTTTATTTCT ATGTATACAC GGGTTCACGA AATTTTCTTT GGTCTGCCAC GTATTCAAAA 26820

AAAGAATACA AAAAATCCCT AAGTCGTCGA AACGACTTAG GGACGAATTT CTCGTGGTAC 26880

CACCCAAATT TATACATAGT TTAGTTTATT TAAAATACTA TATACCTCTT AACAAATAAC 26940

GCTGTTACCC GTGCCCTGTA GGCAGAAGCT CAAGAATGTA ATTCGATAAA TAACGTGTAC 27000

TAGTTTCCAG CGCCACTAGC TTTCTGTAAC AGTGGTTATT TCTCTACTGC TTTTCTGTCA 27060

TTGCTTTGTA TTTAACTTGT ACATGTAGCA TATTCCTTTT CGTTTTTTTT gTCaACACTC 27120

TTkGCTTAAt TTTTkTTACT TTTATAAAAG ATGTCCCTTT TTCACAAAAA TAAAATAACG 27180

AATTCAAAAT AATATTTATT TGTTTTAAAA GCAACTACAG ATAAAAAAAT AACGAAAAAA 27240

TTTAAAAAAT ATTCTTTTAA ATTTTTTTGA CTTTTTTTGk GATTTTCTAT ACTTTTATAA 27300

AATTCCCGAr GAAAAATGAC GAACTTCGGA TCAGAAGTTC GTCaTTTTGT GAAAaaCAGT 27360

TTTAAAGAAT TGGTGAAAAT AATCGTGAAA TTTGTTGTTT AAAAATCAAC CATTTTGACA 27420

TGTCGCGAAC AACTTCTGGA GTCATTGTTG TACATTTTTT TCGATCTTCT AAGAAAATTG 27480

CTTCTAATTG ATCAATGATT TTTTTATCAT ATAACACAGC ATTTGCTTCA AAGTTTAATT 27540

TGTAACTTCG GATATCTTGA TTGGCTGAAC CAACTGTGCA GACTTCATCA TCCATGATCA 27600

TTGTTTTCGC ATGTAAGAAA CCACCGTTAT AAATTAAAAT TTCAATATTT TCTTTCATCA 27660

ATAAGCGGCC GTAATACTGT GTTGCTCGAT AAATAAACGG ATGGTCGGGC TTATCTGGAA 27720

TCATAATTTT AACATCTACT CCTGAAGCCG CAGCAACCTT TAAAGCAGCC AAGACACTAT 27780

CATCAGGAAC TAAATACGGC GTTTGAATCC AGACTCTTTT CTTGGCAGAA GTAATCAATT 27840

TAATAAAGGC CAATTTAATT TGTTCACGGT CACTGTTAGG ACCACTGGCA ATCATCTGAA 27900

TGGATGTATT TGCCTCTGGC ACCAATGCTT CAAGTTTAAA GAAATAATCC AATTGATACG 27960

CCACACGATT TTTCTCGGGG GAAGAGACGT TCCAATCCAT TAAAAAACGC ATTTGCAGTA 28020

ATGAGGCTGC TGGCCCTTGA ATCCGTAAAT GTGTATCCCG CCAATAGCCA AACTTTTTAG 28080

TCGTTCCGGC ATATTGATCG GCAACATTAA AGCCGCCAAT GTAGCCTACT TTTCCGTCAA 28140

TAACAACAAT TTTCCGGTGA TCATGATAAT TCAAACGAAA CTTCAAAAGT GCTTTTTGAG 28200

AAGTAATAAA CGTTTGGACA AAACCACCGT TTTTTTTCAA TTCATTCAAA TGATGAACCT 28260

TGGTGCCCTT TGAGCCAAAG GCATCGTAAA GCAACCGCAC TTCAACCCCT TCAGCCGCCT 28320

TTTCTTCTAA TAAGTTCAAA ATTTTGGTGC CGATATGATC CGTTACAAAG GCATAATATT 28380

CAATATGAAT GGAGTGCTGA GCTTTTTTTA TATCCGCCAT CAACGCATTG AATTTTTCCG 28440

TACCATCCGT AAAAATTTCA ACATCATTTT TCTTAGTCAG AGGCATCCTA TTTAACGAGG 28500

AAAAAAAGTC TGTAAACTGT TGTTGCTCCT CCGTCGGCAT CTTTTGACTA TAAAGTTCAA 28560

AACTTTCTTC TTGGAAATTC TGGAAATTCT CTAATTCCCG TAAATCACTT TGTTGCAAAT 28620

AAAATTTCTT TTkGTCGGkT AAACCTCGAC CAAAGrATAA ATATAAGAAA AAACCAAAAA 28680

CGGGTAGTGG 28690

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAATTATTGA AAAATCACCG AAGCAAACTC ATACAAAATA TACAAAATGG CAAACAGAGT 60

CCATTTATAA ACAAAAAATA AAAAGTCGTT TAGACTTTTT ATTAGAACAA AGTTCTTCAA 120

TTAATGACTT CCTAGAAAAA GCAGAAGCTT TGAATTTATC GGCAGACTTT TCTAATAAGT 180

GGACGACCTA TCGATTGCTT GACGAACCAC AAATAAAAAA TACTCGTAGT CGAAGCTTGT 240

CAAAAAGTGA CCCCACTAGA TATAnTTATG AAAAGATTAT TGAACGATTG AAAGAAAATA 300

AAAACGTTCT AACAGTGGAA GAATGTGTCA AAAGtACGAg AAAAAAATGA ACAAGAAAAA 360

AATAATTTTG ACTATCAaTT TACmATAGAA CCaTGGCAAC TGTCTCACAA AACAGAaAGA 420

GGATATTATA TAAATATCGA TTATGGCTAT GGCAATTCTG GAAAGCTCTT TGTAGGAGGG 480

TATAAGGTTG ATCCATTAGC CAACGGTAAT TACAATATCT ATATTAAAAG AAATGAGTAT 540

TTTTATTTTA TGAGCGACAA GGATGCTACT AAAAGTAAAT ACTTAACAGG GGCTTCGTTG 600

ATTAAACAAT TACGACTGTA TAATGGACAA ACACCACTGA AAAGAGAACC TGTGATGCAA 660

ACCATTGATG AATTAGTTAG TGCCATTAAC TTTTTAGCGG CGAATGAAAT CGAGGACACA 720

AGACAACTAA AATTATTAGA AGAAAAATTA GAAGTTGCTT TTCTTGAAGC AGAAAAAACT 780

TTAGAGACTC TTGACGAGAA GATGTTAGAG CTGCACCAAT TAAGTAACCT CTTATTAGAA 840

AATGAACTGC AGGGAGATCC AGAGTTAATT CAGAAAAAAT TGAAAACATT GTTACCGGAC 900

GCAACGCTTG CGGAATTTTC TTATGAAGAT GTTCGAGGAG AAATAGAAGC AATTAAAACC 960

AGTCAAACTT TGTTAGAGAG TAAACTGGAA CGAACTCGAA ATGAAATTAA TCAGCTTCAT 1020

GAAATTCAAG CCGTACAGGA AAAAGAGCCA GAGAAGCAAA CCGACATTAA GCCCAAACTA 1080

TAAACTATCT ATTGGTGAAC GGAGAGGAGA ATTTTATGTT AGTTTTTAAA CGTATTTTGT 1140

CTGTAATACT ATTTTTACCT TTTTTTATTC TTCATTTACT TTTCCGATAT ATTGGAATTT 1200

TAACATTGCT TACTAGTGGA TTTACCACCA CTTTATTATT GATTATTGCC CGAGTTTTGG 1260

CTTtTCTTTT TTTAATAACA CCAATTGTGA TCTTAGCAAC AGAAGAACTT AGAATCGAAT 1320

GGGCAAGTTG GGTTGGTTGG CTTTTATTTG GATTACTTGT TCTGCTTTTT CATTATCTAG 1380

CTGCCTTGAA TGAAGAATTA GGAGGCTGGT TTTTAGATTT TTCTGATTGG TTAAGCAAGG 1440

TTCCTAGCAA ACTGTGGGCT GAATAATTGC TCCTATGCTA AAACGCCTTA ACTTAAAAAA 1500

GCCAAGGCGT TTTATGGTAT AATATACGAG ATAGTAAAGG TTTATGACGG TGGCTAATCT 1560

CTGAAAAAGG GGTGATTGCC TATGTTGATT TTTGGCTATA CTCCTAGAAA GGACTAGCTT 1620

TGACTATTTT TGAAGCGTTA ATGTTTGCGA TTACTTTTGC GACATTAATT CTAAAAATTA 1680

GTGATAAAAA CAACAaAAAA TAACCGTCAA CTTTAGCCGA GTTTGGTTAT TTTTtGTAAA 1740

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AATATTTAAC TATCGGTCAC CGTCTTAAAC GGTGCTATCA TGAGGGCGTA TGACTAGTAC   1800
GTCCTCTTTA CATGTTTATT ATAACACATT CTCTACAAGA AGAAAGGCGG AAGCCTTTCT   1860
TTTTTTTCAG CGCGCCTTAA CGGCGGTGGC GGTGGGAGTT TGGcGCGCTG AaAAAaACGC   1920
TCtTTTCTTG ATTTCTAATC AAGAAGATAC TCGCTAAAAG CGAGTATCAG GTTTGTCTTA   1980
TATTATGATG ATAAGGCGTG CTGTAAATTC TCTTGCCATT GTCTGACTGC TTGTTTTATC   2040
TTTTCTGGTA CTTsCTGACG GTTACATwtn CCTTGTATTT GTATAACCTG TTGATTTCGA   2100
TATTCTAATG TGAAGTAAGG CATATCTGGC TTTTCTTTTC TTCGGATAAA AACAATCGTT   2160
GTTTTTCCTT GCGTATGCCG TTCGATATAG TGTTGACTGC CCACACAATG GCGTAGAATA   2220
CTTCCTTCTT GAATGATTTC TTGTAATGAA TGTGGTGTGA GAAAAAGCAA ATCGTCAATT   2280
TCAGCTTCTA ACGCTTTAAT TTGGTTTTTC CGTTCTTGAT ACTGCTTTTC TTCAATCTCA   2340
CTTTTCAAAA GGTTTAGCGT GTTCATAGCG TTATCGTGAG CTACTTGTAA GTTTTCAGGA   2400
TACAATACAC TATCGTTATT AAGTGGGGTG TTCAACTCTT CTAACATGTG TAAATAGTCC   2460
ATATAATAGT CAAAACGCTC CCCTTTTCGT ATAAACCATT TTTGAAACTT TGTTAAGTTC   2520
ACTTCTTTCG GTAGTTGCTT AATTTGCGAA TAATGCACGT ACTTTTCTAT TTCGTTTATC   2580
ATAGGCGCAT TTCGCTCTTT TAACGTTTTT TCTAACATGA ATTCATGAAA GGTTGGATTT   2640
CTTGTTTTTA AtTTTTGtTT ATtCGCTTTT AGCCATTTCT TAGTAATTAC TCTCATATCT   2700
ACTTTATGAA AATACAGTCC AAAAACGTTG CGATAGTCGT CAAAAATGAT TTCATTCGCT   2760
AAGGTTGTGG CACCTATCTT TTGTAAAAAC TCAATTTCGT TTCGGTATTT GTAAATATGA   2820
GCTAGTTCTT GACGTTCTAT TTCAGGTAAC TGTAAGTACT TTAATTCCGA TACAGTGGTT   2880
AGTTTTTCTT GCCAGTTATT TGGATAGAAT ACTGTATTTG TATAAGCACT ACTCATAAAA   2940
CCATAATTTG CTAACAAGCC CTCATGCCAA TGTCCGTTCT CATAATGGGC TTTAACATGG   3000
GTATCGTTTG AAAACCGTTC AAGGTTTGAC GGCTCATAGA TAAGGTTTTC TATTCCATCT   3060
GTAATCGTCT GCCAATAACT ATGGGTTTGA ATTTCAATTC GTTTTGCACG AACGAGAATG   3120
ATTCCAAAGG AGTAAAATTT CGTTGGAAAC GATAATCGTG AGTATTTTGT TAATCGTTTT   3180
TTTATGATAG GGcAATTCTT GCGAGAACTC GCAAGAATTG TCTCCTTTTT GTTTTGCCAT   3240
TCATACGTGG GTATTTGTGC AGTACACCAG TTAAAAAAGG CTTTGGGTGG GGTTAATGGT   3300
TTTGGTGTTT TTTTATTCAT ACGCACTCGA ACAAATCAAT TTGTTCGTCC ACCTCTTTTC   3360
TTTCTGATTT TGTTTCTGAT TTTTTGGTTG GTTTCTTTTT TGTTGTGGTC GTTACTTTAC   3420
CAACTGCTTT GGTTTCTGGT AATTTCTCTA ATAAGAAATA CTCTTTTATC CAACTGAAAA   3480
CCACTTCGTC CGCCACCATG GCGCTTGATT GGTTTTTGGC TTGTTCTTGG GCTTTTCCTA   3540
TGCAGTAAGT CATAGCACCT TTTAACGTTC TATCTTyTTT GAGAATACCT AGAAAAAGCG   3600
CTTCGTCTGT TTGTCGGCAT AACCAGTTAT GAACAACTTC TAGTGTACTG TCATGGTCGG   3660
TTTCTAGTTC TTTTArCATT TTCTCAAAAG CTTGTTCTTG CGTGCTTTCT TGAGCTGTAA   3720
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AGAAAAATCG TTCGTAAGAA wkTTTGTCGC TAATCACTAG CCAyTkrTAk TTrTTTCCTT 3780

GGTCTATyGT TTCGTCAATy GTTAGAAAmA GTGAyGArTA GTkwCCGTtG GggTCTTTwA 3840

TCGyAACrAT yGCTTGTTCw GGTAATTTTT CAAGGTAAGy CArTAACGTT TCGACTGGAT 3900

AAAGAGCGAC CTCATAATTA GGATAAAAAC ATAAAAACTG AACGTTTTTT CCGTCTTTTT 3960

CAATGTGTTC TTTTCTGAAA GCGACACTGA TATAGCCTTG TATGTCGTCA AAAATTGTCG 4020

TTGCTAGTGT TGGTTTGTAT TGTTTGAGTG CGTGTGTTAA TTCATTTACA GTTTGTATAT 4080

TTTGAAAGTC CATAACGTTC CCTCGTTTCT TTTAAGCTTC CCCTCTTACA TATGTAAGAG 4140

GGGAGCAAAT TTTCGCTTGT CAAAGGTCAG TCGGTACGTT ATACTTGAAC TACGGTTAGT 4200

AATTCAAGTA AAGTCCTATT AGAAATCTTT TGTCGTTAGC AAAAGGTTTC TTTTTTTGTC 4260

TTTTTTTCGT GGAAATACTT TGATAATGGT TCAAAATCTT TCATATCTCC ATTGCAATTC 4320

ATAGTACTTA CTAGCCACTC TCCAGACTGA CGTTGTGCAT ATAAATAGCC GTTGTTATCA 4380

GAGCCACGAT AAGGTGTAAA GGTTACTTTC CCTTCAACGA GTTCCGTCCA ACCGTCAATT 4440

CGGTCAAGGT CAGTTAGCGT GAGGTATTGT TGTTCTCTTA TTTCTTCTAA TGATTGTGCA 4500

AGATACATTT CTGTTTCTGG TCGAACATAT AGACAAAACT CGTGCCAACC ACAACAAGTT 4560

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CGTTGTTTTA AATGATAAAC TCTGTTGCTT CGTGATTATC TTCTGTCAAG ATAATTTCTT 4860

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AAACAGCTAC CTCTAAGGTT TCAACAATTG TTACACAGTA TTTTTTCTTT TTTTCTGCCA 4980

TATTTATACG TCCTTCCATT CAATGTGATT TAAAAAGAAT GCTAACTGAT TCAAACGATT 5040

ATTGGcATTT TTCAGAcAAC CATAGTTTAG TAACAATGTA GGCGTATCAT TTTCAAGAAT 5100

GGCTTTATTT AACTTCTGAT ATTCTTTACG TGCTTGCTCT AGCTGATTTT TTAGCTGTGG 5160

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CCGACAATTA CAAAAGGTTG AAGTAACTGC CCTACCGTCA TTTTTTCGTC TGAATGAAAA 5340

AGAGTAAATT CTTTTTCtAA AATATTTTCG CCTTGTAACA AACATTCAAT ATACACTTTG 5400

CTAAAGTCGT AAAAACTTTC TATTGAAAAT AATTTTTGAA GATAATATTC TACAGTTTCA 5460

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GTGTTAAATA AATCTAAACA TTCTTCTAAA TCTAGCGATT TTAAATCGTT ATTTAAATAA 5580

CGATTAATGG ATAAGCTATT AATGAAATTT TCTTTTTTGT TCATTGGTTC TCTCCTTTAT 5640

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TGGCTCATGC TAGGACGTGG GACACTATCC TCCTTTCGTT TTTAGATTTG ATTGTTCATT 5760

TTCGCCAGTA TGTTTCGGTC GGTTGCTGTG CCGAGAAAGA ATCATAGACA CCAAGAAAAG 5820

ACAAGGGCGA ACGGAGTGAG TTCATATACC CTTGTCTTTT CGACTGGCTA TGATACTGTA 5880

ACAAACAGCG ACTGACCGGG ACATACGACA ATGAGCGGTC ATAAAACGAT TGAGAGGACA 5940

CACGTCCGTA AAAgCATGAG CCAAAGAGGC GAAATTTTAA TGCACTTAAA AGAACTAGAC 6000

GCAAAGCGGC TAGTTCTTTC TTTTGTTTTG CCTTGCTTTA GCAgGCATTT CTTTCGAGCG 6060

GCGGTGGCGG TTGGAGCGwG ATAGwAATAA ACACTAAAcA aAGTAATnAG GTATGAAAAA 6120

TGGAAAGACG ATTTTTCAGT GAATAG 6146

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTTTGTCAT GATTTGTCAA TACTATGCTT CAGTCGCTTC GCAAGGTTTT GGGACGGAGC 60

TAAGAAATCA ATTAATGAAG AAAATTAATC AGCTTTCACA CAAAGAATTG AATAGTTTTG 120

GTACAGATAC CCTCATCACC CGGATCACAA ACGATATCAA CCAGCTTCAA TTAGCTTTAG 180

CGATGTTTAT TCGGTTGGTC ATTCGGACAC CTTTTTTAAG TATCGGTTCT GTGGTGATGG 240

CTTTTTACAT TGACGTGCAG ATGGGCTTTC TTTTCCTATT ACTTTTACCA ATTTTTAGCC 300

TTATTCTCTT TATTATCATT AAAGTGACTG TGCCTTTATA TCAAAAAGTC CAAGAATATT 360

TGGATCGGTT AAACCGTCAA ATCAGTCAAA ACTTAAGCGG TGTCCGTGTG ATCCGTGCGT 420

TTGCTAGAAA GGAAACAGAG CAACGACATG TTGATAAAGC TTCAGATGAT TTAGGCGATA 480

TTTACATTCG TGTATCGAAT GTsTCTGCTT TATTAACGCC TTTAACCACT TTGATTATGA 540

ATGTTGGAAT TTTATTTTTA CTTTATTTTA GTGGCTTAAA AGTTTCTTTT GGTTCCTTAC 600

AACAAGGGGA AGTTTTAGCA TTGATCAATT ATATGAATCA AATGATGCTC GCTTAA 656

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGGAAGATTG ACAAAAGATC CTGACTTACG TTACACCGCT AGTGGTTCAG CTGTTGCGAC 60

CTTTACACTT GCTGTAAACC GTAACTTTAC GAATCAAAAT GGTGATCGTG AAGCAGACTT 120

TATCAACTGT GTGATTTGGC GTAAACCCGC AGAAACAATG GCTAATTATG CCCGTAAAGG 180

TACATTATTA GGTGTTGTCG GAAGAATTCA AACTCGTAAC TACGAGAACC AACAAGGTCA 240

ACGTGTCTAC GTAACTGAAG TGGTTTGTGA AAACTTCCAA TTGTTAGAAT CTCGTTCTGC 300

TTCAGAACAA AGAGGAACTG GCGGCGGTAG CTTTAATAAC AACGAAAATG GTTATCAATC 360

ACAAAATCGT AGCTTTGGTA ATAACAATGC CAGTTCTGGA TTTAATAACA ACAACAATAG 420

TTTCAATCCA TCATCTTCTC AGTCGCAAAA CAATAACGGT ATGCCTGATT TCgATAAAGA 480

TTCTGATCCA TTTGGTGGCT CAGGTTCATC TATCGACATT TCAGATGATG ATTTACCATT 540

CTAAACGAAT TTGATAGGAG GGAACAAGAA TGGCACAACA AAGAAGAGGC GGACGTAAAC 600

GTCGGAAAGT CGACTATATC GCAGCAAACC ACATCGAATA CATCGACTAT AAAGATACTG 660

AATTGTTAAA ACGATTCATT TCAGAACGTG GCAAAATTTT ACCACGTCGT GTTACAGGTA 720

CTGGCGCTAA AAACCAACGT AAATTAACGA TTGCTATTAA ACGCGCACGT ATCATGGGAT 780

TATTACCATT CGTTAGTGAC GAACAATAAT TTTATGACAA TTTCCnGAAC CAAAGAGCTT 840

GCTCTTTGGT TCTTTTTTAT CTTGACTAGT GTTTCACGTG AAACATAACA AGGTTCGCAG 900

AATGAAGTGT TTTGTGATAA AATAAGGGAT GAAATAACTA GTGAATCACC AGAGCAATAT 960

GCTCGTTGGA ACAAGTCGCC TCAAAGGTCT GCAGAAAGAT TGGAGGCAAA AAAATGCAAA 1020

AGAAGAGAAT TCAAAAAAAC GGTTTCTTAA TTGTTGTGGG TCTTCTCTTA GTAGAATTTC 1080

TCCTCTATTT CTTACTAACA AATAAATGGC TGCTATTGGC GGTAATTATC GCATTAGATA 1140

TCTTTCTCTT AGTGGTTATT CGGCTGTTGA TTAGAGATGT AGAAATTACG AACGTAGAAA 1200

AGATTCAAGA AGCAAGTTCC ATTGCTGAAC AATCGTTGGA TTATGTTGTA AATGAAGTAC 1260

CTGTGGGAAT TATTACGTAT AACGGGGAAA CACGCGCGGT AGAATGGCTT AATCCTTATG 1320

CTGCTTCTAT TTTTAATAAA GACAATCAGC TAACGTTAAC CGCTAGCCAA GTTACGTCTT 1380

ATTTAGAATT AGCAGAACGA AACCAAGATA TTTTTACGAT TGACGAAAAT ACCTATCGCT 1440

TTAGCGTCAA TAAAGAACAA CATACAATTA CTTTTGAAGA TATCACTAAA GAAAGTAATT 1500

TGTATCAAGA AAAAGTCGAA ATGCAAACGG CTATTGGCAT TGTGTCTGTC GATAATTATG 1560

ATGATGTCAC CGATACAATG GATGAGAAAG AAATTTCTTA TTTGAATAGT TTCATTACGA 1620

CGATGGTTTC TGATTGGATG GACCAATACA AAGTTTTTTA TAAGCGAATC AACGCAGAAC 1680

GTTATTTTTT CATTGCCCAA TGGGAAGATA TTCAAAAAAT GATGGACGAA AAATTTTCTA 1740

TTTTGGATAC GATCCGTAAG GAATCAGCTA ACCATGAAGT AGCCATTACG TTAAGTATGG 1800

GGATTGCTTA TGGGGGCCCA ACCTTAGATC AAACCGGGAC CACGGCTCAA ACAAACCTAG 1860

ATACAGCTTT AGTTCGTGGT GGTGATCAAG TGGTTGTAAA AGAAGCCAAA GATGAAGCGA 1920

AgCCGTTATT TTTTGGTGGA AAAACGGCAG TAACGACGAA ACGTTCCCAA GTACGTTCTC 1980

GCGCAATGAG CATGGCAATT AAGGGAATTA TTGCGGAATC TGCTGACATC TATATTATGG 2040

GCCATCGTTA TCCAGATATG GATGCGTTAG GTTCAGCATT TGGTGTTGCT CGTTTAGCCT 2100

CGTTTAATAA TCGAAAAGCG TGGATTGTTT TAGATGAAAA TGAAATCATT CCCGATGTCA 2160

AAAGAGTGTT AGAGGCGATT AAAGAGTACC CAGAATTAGA AGAGCGCATT ATTAGTCCTA 2220

AAGAGGCCAT GAAGCGCAAG AAAGAAAGTA GCTTATTAGT TATGGTAGAT TACCATAAAC 2280

CGTCTCTATC GATCTCACAA GAGCTCTATG AGCGTTTTGA TAAAGTAGTA ATCATTGATC 2340

ACCATCGACG AGGAGACGAA TTTCCAGCAA AACCCTTGCT TTCTTATATT GAATCTTCTG 2400

CCTCTTCTGC TTCAGAATTA GTCACAGAAT TGATCGAATA TCAAAGTAAT AGCGCAAATA 2460

AACTGCAGGC CTTTGAAGCA ACCATGATGT TGGCGGGAAT TGTGGTTGAT ACGAAAAGTT 2520

TCAATACACG AACGACGGCG CGAACATTTG ATGTGGCTAG TTATTTACGA ACTTGTGGAG 2580

CAGACTCATC TTTAGTACAA TATCTATTAA GTTCTGATCT TACAAGCTAT CTGGAAATGA 2640

ACAATTTAAT CTCTAAAAGC GAATATGTCA CAAAAGATAC CGTCGTTGTT GCAGGGAGTG 2700

AAGACAAAGA ATATGATAGT GTCACAGCTG CCAAAACAGC GGACACATTA CTTTCTATGG 2760

CAGGGATTAA TGCAGC 2776

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TCCATTCCAG CTATTTCTTT CTACATCTGT AATATGTCTA ATGTTATCTT GATCATGCGC 60

ATCAAACTCA GATTTAGTTG CCTGCTTTTG ATTTAGTACA TTTCCtwAAC CaACCTGakT 120

AGCTGTTACC GCatGaGGAT TACTTATATT TGATTTATGG GCATTAAAAT CTTCAATATG 180

TGTAGCACTA TCTTGCAATT CTTTTAAAGC TCCGTGGGTT CTGCTAAAGA ACCAATTAAA 240

ATAATCAGCT GGTGGTTTTT GTGAAGCTTT CCAACCATCG CTAGTTAAGC TTTCGGGTGG 300

TTTAATACCT GGTGCTAACC AAACAGGCAA TTCCTTTGTA AATTTCATTT GCATTCTCCT 360

CTCTTTCTAC AGCGGCAGTT TATAATCATT TTCTGGAATA AAGACTCCTC CCAAAGTTCC 420

TCCGATATTA CCATCAATAT CAGCGAATCC TTCTTTACTA ATCTCTATAT CAGTCGTACT 480

TGAAAATGAA AAAGTTCCCT CCAAATTAAC GTAGGCTACT CTAATGCCTC CAGCACTGAT 540

ACTCTCGACA ATTTGTAAAA ATTGACTAAT ACTTAGACCC GAACTATTCA AGTAGTCAAG 600

AGGAGCTTTT TTTATGATTA CACAAGCAGG TTCTTTTTCA TCTACCGTCT CATTAGCTGA 660

TATAATATGG ATATCACTAG GATGACAATT TAAAGATGTC GCAATTGCAT GTAACATTTT 720

GTCGATTGAT CCATCGCTTG TAtTTCTAGC TACCTTTCCA CGAATCAATA CTCTATATAT 780

TTCATCAGTC GTTTTtCCTC TCGCTTGTCC AACATTAGCA CCTAATTCAT CTAGTCCTTT 840

CCCTCGTGCT TCATCTATCG ATCGCCAGTT TGCTACTTTA TTCAGCAAAT CAGTCAAGTC 900

TTTAATTTCA AACTCAATAA TTTCAAGAAG TTTTGAAATA TTTGAATTTT CGCGATTGAA 960

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TAGATCtGGT AAATAATCTC TAAGCTTTTT GGTCACTAGT AATCACCACA TTCTCTGTTT    1020
TACATTCAGC TGACTCATTT GGATTCAGAT TAATGTCTTT GACTTCGGTA GTTTCAGTAG    1080
ATAATCCAAT TTTTACATCA GCGACAACAA CGCCTGGnAT TTGATAAATT AATGGaTAAA    1140
TATAAGAaAA TCTGACTACT TCACCCaTAG tCaGATkGTw AATGTAATTA TTTACTATAA    1200
CTTTTATTtC TTCTTGTCCG kTTTTTTCAA ATTTTGAATC TACTTGAATA GAAATATTCA    1260
CAAAAATAGG AACAGATTTT GCATAATCAA ATTTAACAAT ATGACTAAAT CCTCCTAAGT    1320
CTTTTACTTC AACTTCCTGA TTACCAACAG TGTCAATCCC AGCGGCAACA CTTTTAAAAA    1380
TTGCCTGCCC AATATCGTCT TTCACTCCAC CTAAAATATG CACATGTACC GACTTGGGTG    1440
GATTACCATA CGAATCAGTT TCCATTGTTT TATTTTCAAC AACACTAGCG GTCCGTACCC    1500
CACTAACTTC TAGCAAAGCA GTTAGAATTC CGTTTATTGG CGGTCCAGGA TTCCCACGAA    1560
CAGAAATACC AATTCGGTCG CGATAGGCTT TATCTGTTTC ACGTTCTGCC CCACCCTCAG    1620
CCCTAGCAGG GTTATTAACA GATGATATTT CTTCAGTAGG TTCCACTTGT ACTATAATAG    1680
TATTAGCTGG TACGTTTGAA CTAGCATTCT CTTCTAAAGA AATTGCGCGG CCTTTCCCAA    1740
ATCCATTATC ATCAATTTTG ACTATATCAA TCATCTGAAA CATAACTTTA TTTTCTGTTG    1800
AAAAACGTAC GCCTTCATTA ATGATGTAAC CAGGTTTTCC TGAGAACTCC AGCTCAACCA    1860
TTGCAACTGT AGCTGGATTT CTATAGATAC CACTATTCGC ACCTAAACGA TCCAATGAAA    1920
CCCCTGTAGC TTGACTTATG AAGCCACTAT AATAAACTCT TTCAGTTAGT TCATGAGATA    1980
TAGATAAAAA CCATGCAACG ATACGAATAA TGATACCCAG AACAGAATGT CCTGAAACAT    2040
TAACATCCGA ACCAAACAAG GCTTTTGCCT TTTCAGACAT ATCATAGAGT ATTTCATCAT    2100
ATGTTTTTCT TTTAAATCCA TTTTCATCAA GCACGTATTA CCACCTCCAC TTCATCACCT    2160
AATGTTGATA GCATCTCCAC TGTAATATTC AACTGTCTAT TGTTTCTTAC AATTTCTATA    2220
TTTTCAATAC TATTAATTCT AGGTTCTTGA TCTAAAATCG CTTCTGTAAT ATCTTGTTTC    2280
AAGTAATCTT CATTGTAATT TTTTCCAAAC ATATTATCAC TTTCTAAACC AACGGATGTA    2340
TCTAATTTAA ATTCTTCTAG TCGTATTGAT AAGATCATGA ATACACTTTG TGCAAGTTCT    2400
AAATCTCCTT CAACTAGTAA AATTCCATAG TCAATAAATG ATAAGTCTCC ATTGACTATT    2460
TTCAAATCCC TCATTAAGCA ATCACCCCCA TAATAACAGC GTCATTTTGA CTATGCATTC    2520
TATCAGATGA TAATGAATAA TCAGCAGAAC TTCTATAATT ATCTATGTCA CGATCACAAA    2580
AAACTACTAC TACAACCGCT CCCTGTGAGA TATCAGACTG ACAATGCTTA GTGATCAACG    2640
CGTTTAGTAT TAATGCTCTT TTGCCTCCAT CTGATTTTAA TGCCATTGGC TGAACATCAG    2700
CTCTTGCACC TTTTACAGTG ACAACTCGAC ATAGTTGCAT AACATTAATT TCTTTTAAAA    2760
TTCTATTTTT AAATGATCGA AAAAAAGCTA AGTCAGTTTC TTTCATTAGG TTACCACCTC    2820
ACACGTTGTA ACAAATCGAC TACCATCATA GGAGTGCTGG cCATTTTTTA CATAAAAATT    2880
TCCyTTTACA TTTTTtGAAT CGATATAGAC TGCTGTACCT GTAGTGATTT TATGTTGCAA    2940
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AAGACACTCA ACAGACCAAC CAGTATAATC ATGACTTTCA ACTTTTGTTG GTTGGTTAAT 3000

AAGTCCCGTT TCAGGACTTA ATCTGTATCT CTCTTTATTT CCATCTCGAA AATTTTTAAT 3060

TACAAGTTGA CCTCTTTTAA AATATAGTGA TGTGTCACAA GCTTTGGAAA TCTCTTCTAA 3120

AACCATCATT GCTTGGCCAT CAGCTGTGTA GCCAGACCCA TATATTTTAT TATTTTTTAA 3180

CTTAATTTCT GACAAAGGAA TATTTGCTTC CCTAGCAACT CGATTtATAA TAGTAkGrGC 3240

ATCCGTyCCA TTATTAAAAG TAATATTTAC TTCTTTTkGT yCCGAGTAAc TTTACCTyCT 3300

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CTTCAGATGG ATTAGGTGAG TCAGAAAAAG GTGCTGTAAA GTGAATTTCT AACCGATCCA 3540

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CAAAAGTTAT TTCTTTTGAA GCTCCCGACT CATCCATCGG CACCAAATCT GCTGAAGGTA 3780

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CTATCGGTGT ATGATCTATG TCATATAGAT CTACAGTAAA AAATTTTTCT GTTTGATTAT 3900

AGTCCACCTC AAAAATGTAA TTTGTATTAC CTAAAGGTAT TTCGAATTTT TCAGGTAATG 3960

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CACGAGCGCC TATGGGTATA AATCTATCTG GCCACTTGTT CCAATCTCTT AATTGCTGAA 4080

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CTGTGTCATA CCCTTTACTG ATATCTTGTA TAACTGCATT TTTAAAATAT GATCTGCCTC 4320

GATAAACAAT CCAACGAACA TCTTTTTGCC ATGCAACTAA TGTATTGTAA GCTTGCTCTG 4380

CAGCGTtACC ATTTTTAGCG AGAATCCAGC CACTAATTGT GACTGGACCG CCTGTATACA 4440

TCATATTGTC AGTGATTGGT GCTCCTGaTT CAACAGGATA TTGAGATACA TTAGCAGCAC 4500

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CCAGACACAA CTTTATCCAT AGCTTCACCA AAGGCCTTAC CAAAACTTTT AGCGCCTTCA 6420

ACTGTGCCGT CCCAAATTTC TTTAAATTTC TTTTTGGAAT CCTTTTTAAA GACTTCCCAT 6480

TTAGATAATG TTTGTCCAGT TTCCCAGTCC ACTTGTTCAA GATGACCTTC CGCTTGCtTT 6540

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TCTTCTAAAG CTTTATATCG TTTAGTAACT TCTTCCATTG GTAAGAACTC GTCCTTCAAT 7320

TTTACCTGTA GTGTAnT 7337

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ATAAGGAGGA AATCTGATAT ATGAAAACAA AACGCTTTCA GCGCACGGCG GCGATGCTGC 60

TGTGCATTTT TATCTGCGCG TGGACAATGT TCCCCCTGAT GGGTGCGGCC TTTGCCkCsG 120

AGAATGGGCT GCATGACACC GCTGAACCGG AAATCACCTG CTTCTGTGAT ATTCACTGCA 180

CGGCGGATGC CCTCAATGCA GACTGTCCGG TTTGTACACA GGATGTGAAC GCCTGCACCG 240

GCACGGAACC GGAAGCGCCC ACCGAAACAG AAACACCCAC CGAGCCGGAA ATCACCTGCT 300

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ATGTAGCTGC CTGCACCGGC GCAGAGCCGG AAATTGCCTG TTTCTGCGAT ATTCGCTGCA 420

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TGCCAAACTG GTCTGTATCT GCGCCGCCCA CTGTGAACCC GGCGCGGTCA ACGCCGACTG 660

CCCCGCCTGC CTGTTGAACC TGGCAGACTG TATTGTGGAA GCCCCCACGC CCGTCCCGGT 720

CTGCGTCTGC GAAAACCGCT GTGAACTTGG TGCGGTCAAC GCCGACTGCC CGATcTGCAG 780

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CATCAAAATT ACACCGCCCT CCGGCTGGGC AACCGGCAGT GCTGCCGCCG AGTTTCGCAT 900

TACCGATGAA GCCGGGAACG GCTTTGCGCT GGTGCAGGTG AAAATCGAGA AAAACGGGCA 960

ATGGCGGGAT GTGACGGACA GCTTGAAGCA GAACGAAAAC CGCTGGTATG GGGAAATCGA 1020

CCTTTCGGAG AACTGCACCG TCTATGTCTG CGCcAACGGC CATGATGGGA AgTGTATGAG 1080

AAtCCCGCTA TATTGAGTGT TTCGACCGmA CggcCTGCTT ACGCGcCGGC ATkGAcGGcG 1140

GtTsTcCGTG CGGAACAAGC 1160

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTTACnTGAA CCAATTTCCA ATGTGGATGG GATGATTAnG CCAAACGTTC TGGCCATTnC 60

CCTGGCCATT TTTCAGGACC TTCTACCACA TATTGTGGAT ATTTTGCCAT ATATTCCGCT 120

GCTCCGGGTC TATTTCTTAC ACGCATATTT AAAATTCCTT TCTTTTAAAA ACAGACTGGT 180

GAAATTCGCC AGCCTGTGTG GATGTTAAAT GAATTAGTTT AAATACTAAA CATTCGTTTT 240

AATTGTAAAA TTTCTGCAGT CATTGCTCTT CTTTCGCCCT CTTGGTGATG ACGAACAATC 300

TCTTGTAAAA AGCTAAATAA ACCATACCAA TAAATTCGTT GAACCGTACT TTCATTCGGG 360

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ATGAACACTT yCTCGGTTTC TTkTATTCCC ATGTATGTTT GACCAGTTGC GCCCTTTATC 960

GGCTGCAGAC GCCAGTCTTT ATCCAACTGA AATTCCATGG AAATTATCTC CTATCTCAAC 1020

ACAATTTTAT TGCAATTTTT ACAGCAATTA CCATTTTAGT CGCCAAACCT TGCTTCGTCA 1080

AGCTTCTATG TGGTTCTTTT GTAAATTTTG CTGGGTTTcT CATCTTTATA ACTTATTCAA 1140

GCGCATTGGA ACATACATTT TAGTGAAAAT CACAACTTCT ACAATTAAGG CACCCAGAAT 1200

GATCAAGCTA TTTTGCAAAC TGCCTAAACG AAGGCAGACA ATCCCACCAA AAATAATGGC 1260

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AATTGGATAT AGCTGTGTCA TCACCATATA ATCAAATTGC GTGTACATGG GAATCAACTG 1380

GAACCCGATT AAATAGACAA ACAATAAAGC AACTACCAAC GCAATCCAGA ATTCTTGTAA 1440

AAAGAAGAGT AGCACGCCAC CAACCAAAAT CAAACGAAAC AATAAGCCGC TATATTCGCT 1500

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TGATGGTGGT ACTTTTCCCC GCACCATTCA AGCCAATTAA ACCAACCATT TCACCAGACT 3000

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CAATTGTTAA GCTCATTTCT TTTGCCTCCA ACCTTTTCTC TCTACCATTA TTAAACCCTA 3120

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TGCTTCAGAA GATGATGCCA AAGCTGTCAA GAAAGAAATC ACTGACGGCG GCGATTTCAC 4740

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AAAATCACTT GATTGATTTC CTCGACCATC TCTTCTTTTT TCAAAGGCGC TCGTTCCATA     5940
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TGGGGTTTAT TTTGATAAAC TTCTCGtTTC CCATTCAGTA AAACAACGTT TCCCGCAGTA     6060
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CAGCTAATTG GGCTTTTCTT TGATGATCAT AGTGTAACCA GCCATCATCA ATGATAATTG     6420
GACAAATCAG TTGCTCGCCT TGGACTGCTA AAAAGGCAAA ACGAACAGCC ATCATCAATT     6480
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GTAACTGCTG TTTGAGATAG CCATCTGCTT GATACTCTTG AGCAAAGCGA ACTTTCTCCA     7140
TTTCTTCAGC AAACCCTTCT AAAAAGTGTA ACTTTTCGGA AAGGCTCTTT CCTTGCAAGG     7200
GTAAATGCGT CATCAATGGG AAGATTTGTT CTTCAAATAC TTGGCGTTTT TGTTGATTTT     7260
CCTTCAATTG ACTCATGAGT TCTTCATTTG TTTGAACAAG CAATAAATAG CGCGTAATCA     7320
ATTCCCGCTG ATTCATTAAA GTATCAATTT GTTGCATTTT TCCTAATTGA TGGACTTGGG     7380
CTTGCTCCGC TACTGCTTGT TCAAGTTGTT CCACTTGCAG TTGTGCCTCA CGTTCTTGAT     7440
TCAGCGCCTG TTGGAACTGT TCATTTAAAT AATCTAGTTG CGAAAGTTTT GTCTGCCACT     7500
CTTCTTTCAC TTCATCAGAG GAAGCTTCTT TTCTAGTGGC GTAgcTAAGC ACTTCTTTCG     7560
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CGATAAAACT AACTCCCACG AGAACTAGGC CCCATTTTAA AGGGCTTGGC AAAAAGAAAC    7620
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TTTGGGCACG CGTCGCTTCA CCAAAAAATG CGGCATGCGC TTTTTCAAAA TCTGTTAACT    7740
GGTCTTCCAG ATTTTCAATT TGAGAAGCCA AGAATGCTTT CTGTTCTTGT CCTTTTTGAA    7800
GAGCTTGCGT ATACGCAACT TGTTGTTGGC GCCACTTTTG AACGGTTTCG TTGTCATAAA    7860
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CATAGCGTTG ATTCAACAAT TGTTGAATCA ATGCTTCTTG TTCTAGGTAA AAAGCATATC    8040
CTTCTGGAAC ATCGAGCGCT TCTGACTGAA GAGATAACTC TTTGGTCAAA CGTTGTCGTT    8100
CTTTGTCTAG GTACATATAT TCTTGAAAgG TTTCTTCTAA TTGaACTTGG TCTTCTTTTA    8160
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GTGtCACTCG CTGTTGTTCT GTTTCGCGAA TCGTTTCTTC TAATTGTTGA AAAGTTTGTT    8340
GcTGCGCTTC TTTCTCTTGA ATTTGCTCTT TTAGTTCTTG ATAAGCCGCC AACTTCTGAT    8400
TGAGTAATGG CTGCTGTCCT TTACCTTTAA AGATTTTTTG TGCTTCTTTA AAGTACGCAT    8460
TTCGGTAAGT CAAAAGTTGT TGACTACCAG AAACACCAAT GGCTAACAAG GATGTTTGCA    8520
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CTTGAAATAA CTTTTTCGTT AGCGGATGTA ACATTTGCTG TAAGGTTTTT TCATCCCCCA    8640
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GAACTTCCCC AAACACAGGA TGTGCCAACC ACAAACGACC ACCATACGAG CCACCATTTT    8760
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ATTCAAATGT AATTTTCTGT TGTTGCCATT TTCCAAAGCC CACAATCTCT ACTGCGAGTA    8940
ATTTCATAGT GGGTCCTCCT GAATAGTAAA GTCTTCATTA ATTTGCTCAT GTGCTAGGCG    9000
CAAGCTCTCT AATCGCCACT GCTCATCCAT TGAAAAAATT CCAGCAAATT CTGGATAACG    9060
TAACAATTCC TTGGTGGTAT CTTCAAAAAT AACTGGATCT AAGTATGTTT TTTCTAATGC    9120
CGTTAATAAG TTGGGACTAG CGGCTAAATA GATCGGTTCT TTCGTTGGTT CCTCTGCTTG    9180
CAGTATTAGG CGATAAACAA AAAAATCACC TTGCGTTTTT TGTAAAAGCT GCTGCTGTAA    9240
GTAGCTTAAT AGTTCACCAT TGACAATGGC TTGCACCACG GTCACATCCA AATGTTGCGT    9300
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ACTGGTTTCA AGATAAGACA AAACGCTTTG GGTGTCACGG CATTGCGCAA GAGATACTTC    9420
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AAGTGTGACC ACTGCAACCC CTTGTAAAGA CTGTTCTTTT TTCGTGTGTC CTTGAGGTGT    9540
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GTGTAAGCTG CTTCGTCTGC TTTTACTTCT TCATACGCTG CTTGTAATGC TTTAAATTCG    10620
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ATCCCTCTTT TCTCAATAGT TTCATCTTTA TTGTACCATT TCTCTTAGGT TTTCCCAACT    10740
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CAGAATTTCC AAAGTCTTTC AAGTTATCCC GCCAATTAGA ATTGGCACCA CCAGTTAAAC    10920
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CAATGACAAC TTCTGGTGTA TAACCAATCA CCCACTGATC GTTCGTTTTA CTACTATCGA    11160
AGTTGGTTTC TGTCGTACCT GTTTTACCAG CCATTACGTA GCCTGCTGGT TGTGCGTTGA    11220
CCCCGCTCCC AGAACTAAAG ACCCCTAGTA ACATACTTGT AATCCCGTCT GCAACATCTT    11280
TGGTAATGAC TTGTTCTTTC TTGACTTTAG TATTATCAAC TACAATTGCG CCAGTTGAGT    11340
CGACGATTTT TGTAATTAAA TGCGTTTCAG TTTTATAGCC TTCATTGGCA AAGGCACTAT    11400
AAGCTCCCGC CATAGTTAGT GGCGAAACAC CCGTTTGTAA TCCTCCAAGG GCTAAACCAT    11460
AGTACCGATC TTTTTCTGAT AACGGAATGC CAAATTTCTC TGTTTTTTCA TAGCCTTTAT    11520
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GATACATAGG AACTTCTCCA CTGTACGTGC GGCTATAGTT TTGCGCTGGA TAATAATCTT 11640

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CCACTGTCAC TTGGGACGCA TCCACGCCAA AGTATTTACG AGCTGCATCT TGCACGCCCC 12300

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CTTGCGTTAA GTAAGCATTT TTGGCTAATT GCTGCGTAAT TGTACTTCCG CCACCACCGC 12480

CACCGATTTT CCCGAAGGTC AATTTTCCAA CAACCGCACG GGCAATCCCt TTGATGGAAT 12540

ACCCTTTATG TTGATAAAAC CCGCGATCTT CAGTTGAAAT AACCGCGTCT TGAATATAAG 12600

GAGAAATATT ATCCAGTTCC ACAAAAGTCC CTTTTTGCCC GAATAACTTT CCGACTTCTT 12660

TTCCTGATTC ATCATAAACG CGTGTTGATT CACTTAGCCC TGATTTTAGG GTCTCAACGT 12720

TTGCGGACTT GGCTAAGTAA AATAAATAAA TACTGGCACC TAAAGCGACT ACCAAACCAA 12780

TTAACAAGAA AATTTTATTG ATTTGATACT TTTTCCAAAT CCGCTTTCTG GCTTGATGGA 12840

ATTGTATTAA ATAAGGCTTT 12860

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AACGCTAAAA CCTTTAATAA ATAAAGGTTT TAGCnTTTTA ATAAAGAGCC ACCTGCCGGG 60

CTTGAACCGG CGACCCCCAC CTTACCATGG TGGTGCTCTA CCAACTGAGC TAAGGCGGCA 120

CTTTCAAAGG CTAAACTAAC TCGAGGATTG CAACGAATGA AACCCATAGA GTTCATTTTC 180

AAAGGCTACA CTGCGACGAG TAATCGTCAA AGTTCCTTTT GAAAAATCGT ACAAATCTCG 240

TGCACAAGAA ATAGAATAAC GTATAGACGA AAGTTTGTCA ATTGCTCTTT CGTAAAAAAA 300

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GAAAAATGAT TTTTTTCTAA GAAAAACTGT TGACAATCTC TTTTTTCTCT AGTAAAGTGT     360
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CAAAAGAGAG TCCTGATTGG TGAmAAGGGA CAAGGTTCAG AAAAGTTGAm GATGGCCTCT     480
GAGAATAAAT TGCTGATAAG TAAGCAATTT CGGCTAAGCA CCCGTTACCA TGTGCACCAA     540
GTTAATAAAG ACTTGGATAA GAGATGAGAT ATAAAGAATC AGTTATATTT CAAAAAAAGG     600
TGGTACCGCG AATCATTCGC CCTTTACTAG CAAAACGCTA GTGAAGGGCT TTTTGCTGTG     660
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GATTACTCGA TGCTTGAAGG GGTAGTAACT CTAGTCTGTT TGATTTTGAA AATAAACGAA    1080
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GCCTTGTTAA AAAAGTTAAA TCAAGAACTG AACTTGACGA TTGTCTTAAT CACCCATGAA    2040
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GAATCAAACG ATATTGTTTC GATTTTTAGT CAACCCCAAC AACCTTTAAC CAAAGATTTT    2160
ATCCGGACAG CAACTCATAT TGACCAAGCA TTAACAACAA TTCTTGAACA TCCTAAATTA    2220
GCTGATTTAG ATAAAAATCA AGAATTAATT GAATTTTCTT ATGTGGGAGA TCAAACGAAT    2280
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GAGCCATTAA TTGCACAATT GTATAGCCAA TATCAGGTGT ATACGAATAT CCTTTACGGC 2340

AATGTCGAAA TTGTTCAAAA TGTTCCTATT GGCCATTTAA TTGTGGTGCT TTCTGGTGAT 2400

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GAGTTTCTTC AAAGTACATG GGAAACATTA TACATGGTTT TTTGGACAGC ATTGATTGCT 2640

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TTACTTTTAG ATGAACCCAC CAACTATTTA GATGATACAC ATATTCAATG GCTTGTTCGC 6240

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GCAAGCAGCT AACGTTAACC CTGCTAAAAG TGTTAAAAAA AATAAACTAA ATTTTTTCAT    8160

TCGTTGATTC CTCCATTTCT TTCTCACGGT TTACAAATAC TAGGCCTTTC TTTGGTGAGA    8220
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AAAAGAAAGC CAATAAAAAG AATAAGGCGG CGGTTAAAAC AATCGTCGCA CCAGAAGCTA 8280

AGTTATAAGA ATAACTGAAG AATAGGCCAA TCACTGAACT TAAAATCCCA AaaGTaGAGG 8340

CTAaGCCAaT CATtGTCGGT AAGTGATTTG TTAaTwGATA gCTGTTGCTG CTGGCGTAAT 8400

CAGCtGGCAT GACTAAAATA GTTCCGACGG TTTGTAAmGA AGAAACAGCG ACTAGTGTTA 8460

GTAAAaACAT CAATGCATAG TGGAAAAATT GAaTATTTAA ACCGTAGGCC TGAGCCATTG 8520

TGGGATCAAA AGAAGTGAGT TGCAACTCTT TATAAAACAA TGCCACAAAA ATCAAAACAA 8580

TCACACCGAC GACACAAGTA ATTAAAATAT CGGTATCTGC GACCGCTAAT ACATTTCCAA 8640

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TTCTTGGAGC GTTTCTGCAG TAAATG 9086

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGCGCTTGCA ATAGTGCAAT GTACTAATCG TTTATTTTCC ATGTTCATCT GATAATCAGC 60

CCCCTAACAT TTTGGACACG CTTTCATTAT TACATTAAAG GGGCGTTCCA AAATAAATCT 120

TTTATTTTTG GAACGtCCAT CTCTAAATCA TTCTCTTAAA AACTGTAATA GCTTACGACG 180

ACAAGTCAGA ATTATTCATC CTCATCATCT ACTGCAACAT TTAGCAGCAA TTCGTTGACT 240

TTCACAATAC TTTCTGCTGA TTCCTTAACA TAGTCACCTT CGATCGCTAA TAAACTTGCA 300

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CATGTTAAGT GTTACATCCC CAATACTTGG TGCCCATGAT AGTTTGACAT TAACCATCGT 840

TGCCACTAAA GCGCCAACCA TGAAGACCCC TAGTAAAGTT GCAGCGTCTG TTAAGGCAGT 900

TAAGCGGTGT TGCATAGTTG TTACCAAAGA AATTCCTTCG CGATACGCAA ATTCCAATTG 960

TTTCCAACGG AAGACCATCA CGGCAATTTG AGCAACAATC CAGATAAAGA TACCAGTTGG 1020

GTTACCATTA ATCGCCATGT TGGCaGCTAG CGCCCCAAAA ATAGTTGGAA TTAAAGCTGC 1080

GAAAATTGAA TCCCCAATTG cTGcAAACGG TCCCATTAAA CCAGTTTTCa AACCTGaAAC 1140

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TGTCTAATTG AATCATTAAA CTAGCAACTG GTACTGCAAT AGCAGCGATT GCTTGTTCAG 2040

GGTTCATTCC TAAAGACACA GAAAATGCTG TGGCAAGAAT CGTGCCTGAG TTAGCATCAA 2100

TTTTGGAGGC ACCCCCGAAA GTCCCAACTC CTAATACAGT TAATTGCATG CTTCCACCAA 2160

TAATAAGTCC TGCTTTAATA TCCCCCATCA CTAATCCTGC AAAAAGACCT GCAAACACTG 2220

GCGCACTTAA TGAAGAATAA ATTTGTAATT CATCTAAAAT TTGGTATCCT GCGTATAATG 2280

TTAATAATAA GATCTGCCAC CATAAGATAT TCATTTTTTG TTCCCTCCTA TTTTGTTATC 2340

AAACTCATAA AGTCTTCCGC TTTGTCACTT GGCACCATTT GAGCAATCAG ATGGACACCT 2400

TTAGCATTTA ACTCTTTAAA AACCTCAATA TCTTGATCGA CCACATTGAT TGACTTAGTA 2460

ATCGACCGTG TTTCGTTTGT TTGAGACATG TTCCCAACAT TGATTTCTTT AATCGGCACC 2520

CCAAGTTCTA CTAGTTTTAA TAAACGATCT GGTTTCCGTA CCACAATTAA TAAACGTTGT 2580

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TTCACGCCAG CTGGTGTTGC TAATTTCAAG CCACTTTTTT CAATGGCATT CCCTGCAACT 2700

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TGTCCATGAA TCAAACGTCC ATCAATTCTT ACGCCAATAA TACTCATTGT AATCCCTCTT   2820
TCATTTCTTT ATATAGTGGT TCTTTTACTA ACTGAATTTC TGGTTGGTAC GTTCCTTCCG   2880
TTTCAAAAAT GACGATCTCA TTTTGCCCTT CTTTTAATAA TCCTTTGGGA ATATATAAGG   2940
AAAGCGTCGG ACCAACATTC CAGAAACGAC CAAGATTGGT TTGGTTAACA AAAACAATTC   3000
CTTTGCCAAA TTTAGAAACA TCAATAAATG TATCTTTCAC TTCTGCTAAC TCCACATGAT   3060
ACTGGTAAAA GCTTGGTTGA TCAGGCTGCC ATTCTCTTGA ATAGTCTACC TGTTCACAGC   3120
TTGTCATAGG TAAACAATAT TGTTGCCATT GCGTCATAAA ATGTAAATCT GCCATGACAC   3180
CCGTTCGAAT CCCTTTTTTC TGAGTATCTG CAAATAGTTT ATGCCCGTAA TTGACACGAC   3240
CCATATTTTC CATTAAAATA TCGATTTGAT TATTCTCTTG CGGCAGTGTA ACGTAAATAT   3300
CTTCGCCAAT TTCCGTTTGA TATTGCGTTG CTTGATGTAC CTGATTGACA AATAATTGCA   3360
GACGATCACG ACCGTCAATC ACTCTTAGCT TTTCTTCTGC AGCATCTTTT TCAATGCTTG   3420
tTCGGTAAAG AAGATAGCCg GTATTTTGTC CTAATTGTTC CATGGTTTGC GGATAAACGC   3480
TGACCACTGG CTGACTAATC GTTTCTAAAG TCGCAAACAA ACTCACTTTG TTGGTTAAAG   3540
GAATTGCTGT TTGCGCAAAA GATTCTTTTA CTAATGGTTC AGCTTGTGGT AACGCAGGGT   3600
ACTCTTCGTG AAGCATTTTT TGTAACGCAA AATACTTTTC GGTTGGATTC CCTTGTTCAT   3660
CAAGTGGCGC ATCATAATCA TAGGAAGTGA TTTGTGGTAA ATCAATGGTT CCTCGTGCGG   3720
AGCAGCCATT CATAAACCCA AAATTGGTGC CGCCATGAAA CATATATAAG TTTATACTGC   3780
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GCTCTTTCCA ACGATTAAAC CAGCCATCCC AAAATTCCAT ACACATTAGC GGCCATTTTT   3900
TACCATGTTC TTCAAAAAAG GCTTGCATCA TACCGAAATT TTCTTTGGCT TTTGAGCCAA   3960
AATTTCCGGT TACTAAAATA TCATCTTCAA TCATGCTGCC TGCCCGCAAT GTTGCGCGCC   4020
ATGGCCCGTC AGAAGTAAAA AATGGTGCTG TCACGCCGCG TGCAATCATC AAATCGCGAA   4080
TCGCCCGTAA ATACGCTTTT TCTTCGCCAA ATGAACCATA TTCGTTTTCG ATTTGAATCA   4140
TTAAAATATT GCCACCGTTA GCAAGTTGAT GCGGAACAAT TTTTTCCATT AAAACATCAT   4200
AATATTCCGC AACATGCTTC AGATAGGTTG GATTATTCGA ACGCATCCGT CCTGGTTCAT   4260
TTAATAGCCA GGCTGGAAAA CCGCCAAACT CCCATTCTGC ACAAATATAA GGAGACGGCC   4320
GCACAATCGC ATATAGTCCA AGTTCTTGTG CTAATTTTAA AAAGCGCTCC AAATCTAATA   4380
TTCCCTCAAA ATGAAATGTT CCTTTTTGCG GTTCATGTAA ATTCCATGGT ACATATGTCT   4440
CAACTGTATT GAAGCCTAAA GCTTTCAAGT TATAAAGGGA ATGATGCCAA TCTGAGGGAT   4500
CTACACGAAA ATAATGAATG GCGCCTGATA AAATTTTAAA TGATTGACCA TTTAAAAGAA   4560
ACTCCTCTTT AATTTCAAAT CTGTCCACAT TGTCACCCTT TCTAGTAAAC GCTTTCAATT   4620
GCTGGATAAT TGCTAAATAA AGAAAGCTCT TTATTTAGCA ATTTCGACTA CTTGGATGTT   4680
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CATAAGATGT TTCTTCACGT TCTCTACGTC TACATGCCCA GTCATTCTTT CTTGGGCATT 4740

AGCCATTCCA GCCGCCATGC CCCATTTTAG CAGTTCGGCA GCTGGGGCAT CCTTGGCTAG 4800

TCCATATGCA AGACCAGCAA TGGTTGCATC TCCTGAACCA ACAGGATTTT TwGcTtGAaT 4860

CGTTGGAATT TTTACCACGA TAGAATTGAT CGTGATGTTT GGCAATTGCA CCATCTTTTC 4920

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GTCATCGCAA AACCACCATC ATTGGAACGT GTTGGCATTA AGAATAAAAA GCTGTTTTCT 7320

TCTTTTTGAC TTATTTGTGC TAGTTGTCCT TCTTCGGCAC AAGTAATCGC TAAATGATGA 7380

ATTGTTTCGA CCACTTGATT AGCTACTTCA ACTGCCGCTA AACTTTCAGG ACTATTTCCA 7440

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CCACACTCAA CGTAAATTCA ATAATTTCAT TTTTCATGTT ATATGTCTGG CGTGCTAAAT 7920

GAAGGACTGG CGCTCCTTCC GGaATCaTCA ATAATTTGGc ATCTTCTTTT GACGCAATGC 7980

TAGCGTATAA TTCTTCATCA GCTAAACGAA CGGTTTGCTT AAAATCTTCC GAAAATAGAT 8040

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GAATCATGCA TGTTTCGATT CGTTCCTGCA GCAAATCAAC AAGTTGATGA TACAAAGCTT 8520

TGTTTTTAAA GGCATTTTCC ATAACT 8546

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CGACACATTG TGGGACATTG CTGCACGTTT TGGAACGACA GTTGATAATT TAATGTCACT 60

AAATGGATTA ACATTGGATT CTGTTTTATC GGTGGGTCAA ACCATCCAAA TCGGTTAATT 120

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ACCAACAGAG TCGCCTGTTT TAGAAGGTGG CGAACCAGGT CCACATAAAA TCCAAGGAAT 1020

AGGCGCTGGT TTTGTCCCAG AAGTTTTAGA CACCACCGTT TATCAAAAAG TTGCCGCTGT 1080

TTCTAGTGAA GACGCATTAG AAACTGCTCG TTTAATGGGG CCAAAAGAAG GTATCCTTGT 1140

GGGGATTTCA GCAGGGGCAG CAATTAAAGC TGCCATTGAT TTGGCAGTCG AATTAGGCGC 1200

AGGCAAACGT GTCTTAGCGC TGGTTCCGGA TAACGGTGAA CGTTATCTTT CGACAGCTCT 1260

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AGACAGAGGG AGACGTCACC TCTGCAAAAC AAAGATTGTG AAAGAAGGGA TTTACAACAT 2160

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AGGAACACAA CGCATTGTTG GTGGTCAATT GATGTCTAAA TATGATATCA CACAATCTGC 3360

CAATACTTtA TCATTAGCGG TCCAAAATAA AATGACgTCG AAgATTaGCG ATTTCTGATT 3420

TCTTCTTCCA ACCACATTTT GATCGCCCTg GGAcTACTTA AACTTATagc CCAAGCCGCT 3480

TTAGAAAATA TGT 3493

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1299 base pairs

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

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

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ATTACTCCTT TGTCTTAAAA AGGAGTCTGT AGTGTATTTT ATCAGTTTCT AAAGGAATAC 120

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CCCAAGCACT CTCTCTCGCT TCATTTGGCA CTTTTTGATC AATAAAAACT CTGCTTAATT 240

TTTTCGTAAA CCCTGGTTTT AATGTAATCC GATCACCACT TTGGCGATGA CGAACGGTCA 300

AAGGTGTGGC TGTGGTCAAC GGGATCGCTA ACAACTGACC CGTCCACTGA TTAATCTCTT 360

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AAATCCCCGC ACCAGGTACT AATAAATGTG TAACTTCTTC TCGCAGTGCA GCCTGTTTTT 480

GTTCTAAGCA TAGCCAATCA TAACTTTTAG CTAGTTGCCA TTGCTGTTCT AACATAACCG 540

AGCCTTGCGG TTGCCGTTCA TCATTCAAAA CTTTTAAAAT TTGTGTCATC TGGCGTTGGT 600

TTAACGAAAC CCCTAATGGC ACTAATGTTT TTTGGaAAAA CGCGGTTAAA AAGAAGTGCT 660

GGTACGCAGG CGTTTCTTTT AATAATCTCT TCAAAGGAAT GCGCCAGCCT TGTTTGGTTG 720

GTTCTACGGC TTCAGATAAT TGAGGCTCAA TTTGTTCTTG AATAAATTCT TGGGCAAAAC 780

GTTGTTCATT ACTAAAAGAA GCAATCTGAT CTAAGAATTG CGGATTTTCC TGCTTTAATA 840

GCGGCAAAAC CTGATTACGG AGCCGATTTC TCAAATATTC ATTGGTTTGG TTCGTTTCGT 900

CCTCAAAATA AACGAATGCT TGGCGCTGTG CAAATTGATA CAATTCTTCT TTTGGATAAA 960

TGAGTAACGG ACGAATCAAT TCCCCTGTCG CAAAAGGACG TCTCTCTTTA ATGCCTGCGG 1020

AATGGGAAAA ATTAGTTCCT CGAATCAGCT TCATTAAAAT CGTTTCCGCT TGATCGTCTA 1080

GATGATGTGC CGTCATTAAG ACCGCCGCAC CTTCAATTTC CATGACTTCT TtAAAAAATt 1140

CATAACGAAA TGTGCGCGCT TTGCTTCTAA ATTtCGTTGC TTTcAgGGTC TcCCAACGTG 1200

TTcATAATAC GTaGcgCTCG CTGCTGACAA TAGGTAGCGA GATATTGGCG CTTCCTGTGC 1260

CGACGCTTCT CGCAATTGAA GGATTGACAT GTGGCAAnA 1299

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTACTAGTCT GTTGGAATAC ATTATGATAG TGTAAGATAA ACGGACTATT GGAAAGTCAC 60

AGCAGAGGAG TTTGAACATG TACACATTTA AAATCGGTAT TCCGGCAGAA GTACACGATA 120

CATTTGTTAA AAATCACCCA TTATGTAATT TACTACAGTC ATCTTCATGG GCAAAAGTCA 180

AGGATAACTG GGGTTCTGAA ATTGTTGGGG TTTATGAAAA GGATACATTA GTTGCATCAA 240

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CAGTAATGGA CTATACAAAT GAACGTTTGG TCAGCTACTT TATGGCTGAA TTGAAAAAAT 360

TTGGCAAGAA AAAACGAGCT TTATTTATAA AAATGGATCC AGCGGTTCAT TATCAAGATT 420

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AAGAAGCAGG TGCCAAATAT CAAGGACTGA CAATGGATAT GGGGGCCACC ATCCAGCCTC 540

GCTTCCAAGC GAATATTTAT CGTGAAGATT TTAGTGAGGA ACAATTGTCA AAAAGTACCA 600

AGAAAATGAT TAAAACAGCT GAAAAAAAAG GGGTCGTTGT GCAGCAAGGG CATGTTGACT 660

TTGTTGATGA ATTTGAAAAA GTCATTCAAT CAACCATGGA ACGCCAACAT ATTTCTTTGC 720

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TGGCGCAAGT CAATTTAAAG GAACGCTTAG ATAGCACGCG ACAACGCTAT GACAAAAATC 840

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AAATCGTCAC GGTTGCTGGC GCTTTGGCTG TGACATTTGG TCCAACAAGT GAAATCCTTT 1020

ATGCTGGCTT AGATGATCGT TATAAACGCT ACATGCCAAC ATATGTGACT TGGCGAGATG 1080

CCATTCAAGA ATGTTTTAAC CGTGGcTGCG AAAcTGTAAT ATGGGCGGCT TAGAAGGTAG 1140

TTTAAATGAT GGCyTAATTA AGTTTAAAGC GAACTTCAAC CCmACGATTA ATGAATTTAT 1200

TGGGGAATTC GATTTACCGG TTAATAAATT ATTATTTAAA GCCAGTGAAT ATGCCTATAA 1260

ATTACGAAAA CAAAAAAAAT AAATAAAAAA CACAGGGACT AAAAATCAAA CTTGATTTTT 1320

AGTCCCTGTG TTTTTTTCTA TAGTTTTTGC GTTGCATTCC GTTTCATTAA GCGAACAAAA 1380

CGCTAGCAAT TGCTGAAGCA GCTACACCAG CAACAAGAGC TTCTGGCACA CCAGAACTGA 1440

AAATCGTCGC AATAATAGCT AGGTAAACAG CAGTTCCAGC TTTACCAATA ATTTCAGCAT 1500

AAGCTGAATT AAAAAGAAAA TAAATCATGT TCATGACTAA AATGGTATTC GTTGCTGAGC 1560

CTAAAACACC AGCCACAAAT AAGGAGACAG GTTGCGCTTT TTCCTTCGTT AATTTATTTA 1620

GCCATTTGTA AGCGAAATAA GGAACGACCC CAATTAAAAT CCGCGGAATG AGCACAATTA 1680

AAAGTGCCTT CCAACTACCA TGATCGGTAC CGATCACAGG AATAAATGGA GAAAAAACAA 1740

ACGACAAAGG TGTTGGTGCT GTCGTATTTT TAATTAAGCT AATGATCCCA AACGTGCCGC 1800

CCAACATACT ACCGATTTTT GGCCCTAAAA CAATGGAACC AATAATTACA GGAATATGCA 1860

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GTAAGATAGC TAAGAACATT GCTGTTAACG TAAATTTTTT CGTGTTATTC ATAAATTACT 1980

CCTTGTTATC AGATGCTAAA ATTTTCATCA CTGTTTGAAG AATATCTTCA ACAGTGGCAA 2040

GTGCGCCACG ACCATAATCG CCACAAGCTA ATAGAGCTTC ACGTGGGATT ATTTCTTGAT 2100

AGCCGACTTC TTTTAAAATG CCAATATTTC GTTGGACAAT GGGGTTTTGG TACATATACG 2160

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TTTCCATCAT GACATCCGTA TGCACTGGAT TCTTAGAAAG TGATTGTAAG GTCAGCGGAG 2400

TGATGaACGC TGTGCTACTT TTAGTCATTA AAATTTCCAC ATTGTAGCCA AGCTTAGCTA 2460

GTTGACTTGT AATATCTGCT GCTTTATATG CAGAAATGCT GCCAGAGACG CCTAATAAAA 2520

TAGTTTTCAT TGTTGTTCTC TCCATTTCTT TTCAACATTT TTAACGATCA TTGAACCAAT 2580

CCCTTGTTTT GAATAAGCTT CTTGGACAAT GCCCGTTTCG TTAATTAATA ATCCTTTGTG 2640

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ATCAGCAATC TGATTCAATG TGTTTTGAAC GATAGTTACC AAGGCTTCTT TGGTCTTTGG 2940

CAATGTTTGT TCGCTTAATT GTTGAGCAAA aGAATCAATA AATTGTTCTT CCGTTTGCGC 3000

GGTTTCCGTC GTAAAATCAC TGACTGCCAT TGCGTGAACA ATCGCATCAA ATTGCTTTTC 3060

AGCAAAGAGT TGTTCTAACG TAGTGGCTAA TTCAACCGTT GTTTCTATTT CTTTAATTGA 3120

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TACAATAATG GGGGCTTCTT TGTCGTCGCG TAAGCCaTCG TCTTCTAAAG CTGTGACAGA 3900

TAATCCGGCC GTAAAGCCAG CAGTTCCGAA GATCATTGCT TCTTTGAGAC TCATTTTTTC 3960

AGGAAGTGGA ACTACCCAAT CGCCAGGAAC ACGCACATAT TCAGAATAAC CACCAGTATG 4020

ACTAACCCCT AATTGATAGC CTGTTACGAT CACTTTATCG CCTTCTTTGA AaCGAGGATC 4080

TTCCGATGTG ACAACAGTGC CACTGACATC AATTCCTGGA ATCATTGGAT AATTGCGAAT 4140

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CTTCCAATTA TGTAAAAAAG CAACTCGTCT TATTTTATCA TATTCTGATT TTTTCGTATC 4380

ATTTTTCTTC TTATAAACAG TAAGTTATAC AGAAAAGAAA GATTGTGTGA CAATTAGACT 4440

AGAAAAATAA AGAAAAATGG TTGAAATTTT TCAAAAAGTT CGTATACTAA AAAAGGTAAA 4500

ACT 4503

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GCGTTAGGTC AAGTAAGTCT TGGmTCGTTT TTGATGAcGT CTTTTTAtGG TGTTTTTmaG 60

TACTmGTTTA TCGTATTTTC TATTACGCAA AAATCAATCC AATTTATTTT TATTATTGAT 120

GATTGGCATG ATTTTAGGTA CTTTTTTCAG TAGTATTAGT ACGTTTTTAC AAGTGATTAT 180

GGATCCTAAC GAATACGACT TACTCCAAGG AAAGTTGTTT GCCAGTTTTG GTAACGTCAA 240

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TGCTGTGAGT CAGTTTCAAT TAGTGTTGTT GTGTTTGATC AGTAGTCTGG TCGGCTTATC 420

AACAGCATTA GTGGGACCGA TTACATTTTT AGGTTTTATC GTGGCCAATA TGAGTTATCA 480

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TTTACTGGTG TTTGGTCAAT TGATGGTTGA ACAGGTCTTT CATTTGAATA CCCCGCTCAG 600

TGTGGTGATT CAATTTGTTG GGGGCGTTTA TTTTATATGG AAAATTATTG CAGAAAGGAA 660

GCAACGCACA TGATCCAGAT GAGTGATGTA TCAAAAAAAT ATGGCGATAA ATTTGTCGTT 720

TCAGACATTG ATTTACCTAT TTCTGAAGGC AAATTAACGG CCTTTATTGG ACCAAATGGC 780

GCTGGGAAAA GCACGCTGCT AGCCATGATG AGTCGCTTAA TTCCCAAAGA TACCGGGGAA 840

ATTTATCTGG ACAAGCAAGA AGTAAAAACC TGGAAGCAAT CGGCTTTTTC ACAAAAAATT 900

GCCCTTTTAA AACAAGCCAA CGGTGTACAA CTTAAATTAA CTGTGCGAGA ACTGGTCAAT 960

TTTGGTCGTT TTCCTTATTC CAAAGGTCGC TTAAAAAGCG CTGACCACGA AAAAGTAACA 1020

GAAGCACTGG AACAATTGGG CTTAACTGAA ATGGCGGAAG AATACATTGA TACCCTTTCT 1080

GGGGGCCAAT TACAACGGGC GTATATTGCC ATGATTTTAG CCCAAGATAC CGATTATATT 1140

TTATTGGATG AGCCCTTAAA TAACCTCGAC ATGAATTATG CGGTTCAAAT GATGCAGATT 1200

CTTAAACGCT TAGTGGATGA ACTAGGAAAA ACGATTCTGA TTGTTCTACA TGATATTAAT 1260

TTTGCCGCAA GCTATGCAGA TGAAATTGTC GCCATGAAAG GCGGAAAGCT CTATGCGCAT 1320

GGCGCAACAG AAGAAGTTAT TCAAACAAGT ATTTTAAATG ATCTTTATGA AATGAATATC 1380

CGGATTTGTG AAATTGAAGG AAAACGCTTT TGTCTTTATC ACTAAATCGG GCAATTTAAA 1440

AATAACGTTT TTGGAGGAAA AGAATGAAAA AGAAATTTTT AGCAATGATG GCAGTTTCAA 1500

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GTTTCGGTTT AATTCATGAT ACATTTGGCT TCAAAGCAGC AGACGATAAG ATTGAAGCTT 2160

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CTTAAAAGCT GATAAACGGC GGGAACAAAA GCAACTCCTT CGGAAATAAG CTGAAATTCT 2520

CCAAAAATTA AAGAACAATT TTCGGAAATT TCTTCTTATT TCTCGGAGCT AAACACTTCT 2580

GTCCCGACCT TCTTGATGAA AAACAAAAAA GTTTTAAATT AAAAATGTGG TTGACGGCCT 2640

CGAAAATGTT TGCTAAACTA TCCGTAAATC AGTATGATTG ATGAAACAAA TAAAAGAACA 2700

AAATGTGATG AGAAGGAAAG TACTTTTTAA AATAGCTTGC AGAGAGCCTC GTTTGGTGAG 2760

AAGAGGTAGT GACGTTAAAG GGGAAAATGG CCTTTGAACA GGTTGGTTGA AGCCGTTTGC 2820

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AAGAAGCCTT AACACAAAGT GTCTTAAACG ATGGGTCAAA ACCCCTTAAC GGATTGATTC 4020

CAAGTAAACT TTATGCGAAT CCAGAAACGG ATGAAGATTT CCGAGCTTAC AGTGGCGAAT 4080

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ATTCGGGTTC GTGGACGAGT CTGGCAAACG AGTAGATGCT TCAACAATTG GGTTGACTTA 9600

TGACAAATGG CGTGGGGAGT TGTTAACAAA TAATGTCAAT GACTGGAAAA CAGTCAGTCT 9660

TGAAAAAGGT CAAGTTGCAC CAACCAAAAA CAATTTGAAG GAAATTGCTT ATCCTGCGCA 9720

ATCTCTTGAA ATACTGAGTG ATCGAAGTAC ACAATATAGT GCGGCTAATT TAACCTTTAC 9780

ACTGCCCAAA TACTATGGGA AAATCAGTGT TTATAACAAG AGTGGTACTT TTGATGCAGG 9840

CTACCTGTTT CCAAATATCC AAAATAATAA TAGTTCAGAA CCATCTGTTG AAGGCTTACA 9900

CAAAAATCTT TCTAGCTGGT TTGAACTAAA GAAAAGTGGG AACCAATCGT TTGTTTTTAA 9960

CAAACCGATT CCAGCAGCAC CAATCGATGT TCAGGTGCCT GCTTACTTGC GAGAGATTGT 10020

CTATAATCCC GATCTGATAT CAAATACAGC CGTCTATTAT GTAATAGATA AACCTGTCTA 10080

CTACTATTTA ACCAACCGCA AAGTCACCGA AAACTTCGTA GACACAAGCG GTGCCAAAAT 10140

TACACCACCA ACAGGTTTCA CCCAAGGAAA ACAAACAGCG ATTACCAGTG ACCCATACAC 10200

CTTCAAACAA GCAGGTACCT TACCTGATAC CTACACAACA GGCGGTAAGA CCTACAAGTT 10260

CAAAGGCTGG TACAAAGGGA AAACCAAAAC CGAGCCTTTA ACCACGACGA AAGCACCAAG 10320

TTATGGGGTA ACCTATAATG ATAATGATGA TTTGAATGTG GTGTATGAAG AAGTAACAGC 10380

TATTTATCCA GGGTTCTATG CGCAATTTGT TGATGAACAA GGCAAAGCTT TTACTAATTC 10440

GCTAACTCTT TCTGAAAATT ATACTGAGTT TCTCAGAAAG ACAGGCACTA CTGTTTTTGA 10500

AACGAAGGGC GCCTTTTACC CAATGGTAGG TAAGCGCGAT GCAACAGTGA CAAATAAGTA 10560

TAAGATTGAA ACAACGAGTA GTGTTGCAGT ACCAAATAAT TATTGGACAG CCATGCCTGC 10620

TGACATTGCT AATAGAGGGT ACGCATTAAA TAACTTGGAT ATTACCAATC AAATGAAATA 10680

TGTTGACAAG ATAGAAACTA CTGACACGCA CACTACAATG TACGATTATA CTGGAGTTTC 10740

GGACATTGGG GGCAAACCAA ACAATGCTTC TCAGACAGAA TTAAATCCTA TTGATAAAAC 10800

ATTTGTTAAG CAAACAGATA ACACTTTTGC GATAAAATCA ATTTGGGGAA ATGGaACGTT 10860

TTCGCATATA GTTCCCAAAA TGTTATTGTT AGCAGAAAGT GGCAGTTTTT CAAGATTATT 10920

CGGGTTTGAT GGTACTCCAG ACTACAAGCA AACCGTAAAC TACAAAGTCA CCCGTAAACA 10980

AGTCACCGAA AACTTTGTTG ATGCCAACGG TGCCAAAATC ACCGCACCAA CAGGCTTCAC 11040

CCAAGGCAAC AAAATACCCA TGACTAGCAA CACCTTCAAG TACACAGCCG CAAAAGCCTT 11100

GCCAGCAACT TATACCGCAG GTGGCAAGAC CTATACTTTC CAAGGCTGGT ACAAAGGCAA 11160

AACGAAGCCT AATACTTTAA CAACCAGCAC TACGCCAACA TATAACACAA CTTTTGATGG 11220

CAATGACGAC ATGACGGCGA TTTATAAGGA AGAAGTGCCC AAAGCAAGTG TCGCTTTAAC 11280

GCGCACTACC GCTGAAACCG TGACTAGCGG CGGCAATGTC ACCTGGCGCG CCACAATTAC 11340

CAATACAAGC CAAGCACCAC TAACCACGGC GACCATCAAG AAATCAACCG CTTGGACAAC 11400

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AAAATCTGCC ACGGTTCAGT TCACTACGAA AGCGACGGGG ACAGCGGGGC AAGTCTTGCG 11580

CGCTGGGATT ACCACCAGTG GGAATTACAG TGGTGTTTCT ACTTCGGCCA CCGTACGTGT 11640

GAAAGACAAT GATCAAGCAA TTGTAACACC AACGGCTGAA GGCTTCATCA GTGTTCCAAC 11700

CTTCAATTTT GGTCAAGTTG GGGTAGCGGG AAGCACGCA 11739

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4045 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAATTTCTTC AGTATCCTAA AACAAGAAGT GTATTATGGA AAAATCTATC AAaGTCAAaT 60

GAATTGrTaG AAGCAaTTGA GAACTACATT TATTATTACA ATCATCACCG AATCAAGGAA 120

AAACTTAACT GGAAAAGCCC AGTAGAATTT CGACAATTCA ATCAAAAAAC TGCATAAAAA 180

TAGAGTGGAA AAATCCACTC TATAAAAAGT CTAACTTTTT GGGGTCGCTA CAACAATACG 240

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CTTCTCGCTT TCTTGTTACC CTAAACCAAC ACGTTCAAAA ATCGTGTCAA CATTTTTTAA 360

ATGATAATGG TAATCAAAGG CATCATCTAG CTCTTCTTTT GATAAGACAG ATGTAATTTT 420

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GACACGTTGG CTGTAAATTA GACCATAGGT CGCATCCATG TTACGTTTCA TATTTTCTGG 600

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CGTCGTATCT GGAATAATAA TCCGTTCAGC AGACGAGTGA GAAATATCTC GTTCATGCCA 720

TAAACTCACA TTTTCAAAGG CAGTAATGAC ATGACCACGA ATCACACGTG CCAAACCAGT 780

CATATTTTCA GAACCAATTG GATTCCGTTT ATGCGGCATT GCCGAAGATC CTTTTTGTCC 840

TTTTGCAAAA AATTCTTCTA CTTCACGTGT TTCTGATTTT TGTAGACCAC GAATTTCTGT 900

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ATCACGTGGT AAAACTTGTG TCGAAATCTC TTGAGCACGG ATCCCCAAAT GTTCGCAAAC 1020

ATATTCTTCA ACAAATGGTG rAATATTGGc AAAGGTACCT ACGGCTCCAC TGATTTTACC 1080

CGCTTCGACA CCTTTGGCTG CATGTTCAAA ACGTTCAATG TTGCGTTTCA TTTCAGAATA 1140

CCACAACGCT AATTTCAAAC CAAATGTAGT CGGTTCTGCA TGAACGCCAT GCGTTCTTCC 1200

CATCATGAmC GTATGTTTAT ACTCTTTGGC TTTGGCTCCG ACAATCTCCG TAAATGTTTG 1260

TAAATCTTTC CGTAAAATAT CATTCGCCTG TTTCAATAGA TAACCATAGG CAGTATCCAC 1320

AACATCTGTG CTGGTTAACC CATAGTGTAC CCATTTTCGC TCTTCACCAA GCGTTTCTGA 1380

AACCGCACGA GTAAAAGCGA CAACATCATG ACGTGTTTCT GCTTCAATTT CTAAAATACG 1440

TGCAACATCA AATGATGCAT TTTCTCGGAT TTTTTGTACA TCTTCTTTAG GAATTTCGCC 1500

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TGTCGCAAAT TCGCCACGAC CATTACCAGA AATCAGAACA GATAATTCTT TTTCGTAAGG 2220

AATCCAAGCT TCCAAGACAC AGGTTCCTTC TCTCAGAAGA TTCATGGATG GCGCTAAGTC 2280

TGAAGTACTA TGTAGTACAT AACGACCTTC CCCTCGCGTA TTCTTCAAGA TACACGGATA 2340

ACCAATGCCA TCAATTGCTT CTTGAATATC AGTCGGACTA ACAATCGTTG CATAAGGTGC 2400

AATCACAATA TTATTATCTT CCAAGAAACT TTTTTCCATT AAGCGATCTT GCGTAATCGC 2460

TAAAATGTCT GTTCCTTGCG GTATATTCGC CAAATGTTGA ATCGCTGTTA ACGCATCAAC 2520

ATCTGCATGT TCAAATTCAT ACGTAATCAC TTGGGCACGT TTTGCCAATT TCTCTAACGC 2580

TTCAGGATCA TTATATGCTC CTAATAATTG CCAATCGGCA ACTTGTGCAG CAGGACAATC 2640

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TTTTGCTAAA TGTCCGCCAC CAATGATACC AATCACTTGA CCAGGTAATA GTGGTTTATC 2760

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AAGTGCCAGC AGTGTTTCCA TTAGGTTTTC TCATCAGAAT TTATTAACAT ACTTTAGGaT 2940

AAAACAGCGG TAACTTACTA CTCGTCTCTT TGTAACCAAG CTTTTTTCTC TTTTTCTCTT 3000

CAAATTGATG AAAACATTAA ATTTTTCTAA ACGATGATGA GGTCAAAAAA GTATGAAAGA 3060

AAAGCCACCT GACCTTATCT ATCATACTTT TTTGAAACTA TTCGTTACTT TCTGAGGTTT 3120

CTTTTAAACC ATTGAATAAA AGATTTAAAA TAATTGCGGT AATGCTGCTC ATGACAATTC 3180

CATTACCAGT AAACATGCTA ACAGTTTCTG GTACTTTATT AAAGAGCGTC GGCATAATAT 3240

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AGTCAACTTT TGACAACATG CGCATTCCTT GGACAGCCAC CATTCCAAAC ATAACCAGCA 3360

TTCCGCCGCC TAAAACCGGC TCTGGGATAA TTTGGGCCAT CGCACCAATT TTTGGTAATA 3420

AGCCTAAAAT AATTAAGAAA AAAGCAGAAA AATAAATTGG TCGACGTGTT TTGATCCCAG 3480

ATAATTGAAC TAACCCGACA TTTTGAGAGA AACCTGTATA AGGAAACGTA TTAAAAATCC 3540

CCCCTAAAAT GACGGCTAAA CCTTCTGCAT GATACCCACG ACGTAAATCA TCTTCGCCAA 3600

TTTTCTTCCC TGTAATATCT CCTAAGGCAA AATAAACACC TGTTGATTCA ACCaTACTAA 3660

CAATtGaAAT AATAATCATC AACACAATAG AAGAAAGATC AAACGTTGGT TTGCCAAAAT 3720

AAAATGGCTG TgGAAAaTGa aACCACGTAG CTTGACCAAC AGGAGACAAa TCCACTAATC 3780

CCAGAAACGC AGCTAAAATT GTGCCACCGA CTAGGCCGAT TAACACGGCA ATTGACTTGA 3840

TAAAGCCACG TCCCCAAACT TGCACAACAA TGATTAAGGC AATTGTTACA AATGCGAGGA 3900

GCAAGTTTTT AGGATCACCA AAACTTTTGT CCGTTGCTAA GCCGCCACCC ATTTTTTCAA 3960

CAGCAACAGG AATTAAGGTC AAACCAATAA CTGTAATGAC TGTGCCGGTG ACTAAAGGCG 4020

GAAATAGACG TTTAATTTTT GAGAA 4045

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nAnnAATATA CTATAAAGTC CAAAGAAAGC GCTTTAATTC GATGGAGAAG GTGGTTTAGT 60

GAAAAGATTT TCATTTTTTT TACTAATTTT ACTTGCTTTA ACAGGTTGTA AATCCGGTGA 120

AAAAGAATTT GATGAAGAAT CTCTTCAAAA TCTAAAGGAA ACGkCACAGT CTTAyTCAGA 180

AACAGAATTA CAAAATGGTG ACGTTCGTTT AAATGAATAT ATTTCTTTGA AAGGGGAGAT 240

TGTTGAGAGT GACAGTCGTT CCAGTTTAAT AAAAAAAGGT GATCGTTTTA TTTTGAAAAG 300

TGGTTCTAGT AAATATCAAG TTTyTAATGA GCAAAAGAAA AAATTGAAGA TTGGTGACGA 360

AGTGACAGTT TACGGAGAAT ATTACGGCTT TTTGAAAGGG ACATTAATTG AAAGTGAGGA 420

GAATCATGAT TCAGCCACGA ATTAGACAGA ATCCTTTTGA AACATACGAA GAAGTTGCAG 480

AAGGATTTGA AGATTTATTA GCGCCACTGG AATTGTTTTT TGATCGAGAG TATCAAGGTC 540

ATCTGGATTT AGGGACACAC GGAACGGTTT ATTCTAAAGG GACACGTGAT GCGGAGGCAT 600
TTTTACGACC ATTATGGGGA CTAGGTCCTT ATGTAACGCA AAATGAAAGT GAGTATTTGA 660
ATGACTTTCT AACGGGAATT ATCGAAGGAA CCGATCCTGA GAGTTCATCT TATTGGGGaA 720
AAACAAAAGA TTATGATCAA TTGATTGTTG AGATGGcAGC ATTAAGTACA TTTCTTTTGt 780
TAAACAAAGA AAAAACGTGG GACCAATTAa CAAAAGAACA GCAAAACAAT TTACACAGTT 840
GGCTGATACA AGCCAATGAA AACATTATTC CGCCAAATAA TTGGCATTTC TTTAGAGTGT 900
TGCTGAtTac GtGAAcATgT GAAgCCGTAT cnAAAGAaCA GAtCGCTGTT GATTTGGCTG 960
TAATnGATCG TTTTTAtGtC GGTAATGGTt GGTATTATGA CGGAGTCGAG ACACAAGTTG 1020
ATTATTATGT TTCTTtCGCT ATTCATTATT ATAGTTTATT GTATTGTCGT TTTGCCCCGG 1080
AAGATACCGC AAGAGTGGCT ATTATGAAGG AACGAGCAAC TTTGTTCGCG CAAGAGTTTA 1140
AATATTGGTT TACTCAGCCA GGAGAAGCGA TTCCCTTTGG ACGTAGCTTA ACGTATCGTT 1200
TTGCTCAAGT GTCATTTTTT AGTGCTTTAG TTTTTGCAGA TGTTGAAGCA TTGCCGTGGG 1260
GTGAGATTAA AGGTCTAATC AGCCGACATC TTCATCAATG GATGAACAAA GATATTTTTA 1320
CAACAGATGG ATTATTGTCG GTAGGTTATG ATTATCAAAA TATGGTCTTT GCCGAAGnTA 1380
TaATGGTCCT GGTTCACCTT ATTGGGCCTT tAAAACATTC ATTTtGTTAG CGGTTCCAAA 1440
AGATCATCCT TATTGGCAgC AGAAaCACaG CCtATTAGCT TtCCaGAAAA ACACTTACCT 1500
cACCgAAAGT CGGAACTACT ATCAaGTAAA TGATGCAGGG ACACATGGTT TAATGTTTCC 1560
AGCGGGACAA TTTATTAATT ATCAAGCTCa TGCGCATGAT AAATATAGTA AATTTGTTTA 1620
TTCTTCCCAT TTTGGTTTCA GTACTATAAA GAGTGATTAT TGGTATTACG AAGGTGCTTA 1680
TGATAATTGC TTGGCTTTAG CTGAAGACGA CCACTATTTC CGCACGAAAG GATTAGATGA 1740
TCAGTACGAA ATTCTTGATG ATCGTATCAT TCATCAATGG CATCCTTGGT CCGATGTAGC 1800
AATCAAAACG ACAATTGTAC CATTAGAAGG CCAACATTTA CGGATCCACG AAATTGAGAC 1860
ACAACGTGCA TTAGTGGCTT ATGAAGGTGG CTTCTCAATC CCGCTCTTCG ATGAAAAGGT 1920
CACTTGTGTT TCTGATCAAA TGGCTGAGGT AAAAAATGCA AAAGGTGTGT CAAAAGTAGA 1980
AAATATCAaC GGCTTTTCTG AAGCyGCGAT TATTCGAACA GAACCGAATA CAAATTTACT 2040
TTATCCGTTA ACGGAGTTGC CATATTTGAA AGCAAACTTG TCGAAAGGGA AACATCTTTT 2100
AATTTCATTG GTGACAGGCG TACTACCGAA TGAACAAATT GAGCCAGTTA AAGTTAGGTT 2160
AAAAGAAAAT CAGCTTTTAG TTGAAGAAAA AGTTGTAATT TTGGGGAATT AGGGGGAGAA 2220
ATACACAATG ACAGAAAATG GACAGATTGA GTGGTTGCCG AAGCAAATCA GTTTTGCTTT 2280
AAACAAAGTT AGAGGAAATT TAGAGACATT TAAAGAATTA GTTCCACCCG CGGCAAGTTT 2340
AAATCAAATT TATTATCCTG AAGAAAaTAT TGACTGGACG GCCAGCTTTT GGCCAGGAAT 2400
GTTATTTTTA GCAAAGGAAT TAACAAATTC AACAGAGTTC GATGAGGTGA TTGCCACACA 2460
GATGGCTTCT TTTCAACATC GCTTGGATGA ACAAATTGAG CTGGAAACAC ATGATATAGG 2520

CTTTTTGTAT ATTTTAACAG CCATTGCTGA TTATCAAGTC AATGGTCATG AGGCCTCAAA 2580

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TAGAACTATT ACAAGCATTA GCGGAAAAGT ATACAACGGT TTTACAACCA GAGTCGAACG 3240

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TTTGGTAATT CATGGAGGAA AACTCCTAAA AAATAATAAA TAGCGGAGGT AGTACAAATG 3420

AAATTTTGGA AAAAAGGCTT AACAGCGGCA GCGCTGTTAG CAGTGGCGGC AGTAACTTTA 3480

ACAGCATGTG GTGGTTCAAG TGAAAAGAAA GCAACTGAAA AGAGTGAAGA TGGCAAAACA 3540

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GCTTTTGAAG CGGAAAATCC TGATATCACT ATTGAACCGG TGGACATTGC TTCAGATGAT 3660

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TTTGTTCTTG CCTTGTTTAT TAAAGTGGAG GGAGCGAACG AATGAAGAAA AAAATAATTA 7440

TTTTAAGTAG CTTTTTGATA GGTGCTATTT TTGTGCTCGT TATTTTTACT ACCAGCCAGC 7500

AAAGTATGAT TAATAACgAa GCmATCCAAG TCgArGAATT AATTGTTwAT GGCGATAAAA 7560

ATATGAATCG TATA 7574

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTnTAATGT TCGTGTTTTA TnTTTTAATA ACCTTTTTCG AAAAAATATA CGAACGTTCG 60

GGTTTAAAAA CGAACAAAAA GATGAAAATG TGTTGAAATA TACGTTTTCC TTGCGTATAC 120

TGATGAAGTG AAAAAACGAA CGAGGAGTGT ACGAATGAAC AAGAAAGTTC CTTATTTAAT 180

TGTGGCACCG GGGCTAGTAC TATTATTATT TTTCTTAATG ATTCCATTAA TTACTAGCAT 240

TTTGCCAACC ATTTTTACTG ATCATGGCTT GACACTAAAT CAGTATGTTA CTTTTTTTAA 300

AGATGACTAT AATGTTTCAA TTTTCTGGCG AACGATAAGA GTTTCGTTAA TTGTGACGGG 360

TATTTCAATC GTGTTGGGCA TTCCAACGGC ATACTTTATT GCTGGAGTTT CCAAAAAATG 420

GCGTGGCTTT TTAATGGCTA TGACCTTGTT TCCATTATTA ACCAATTCAG TTATTCGAAG 480

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AGGAGAAATG CTAGAAGCGG CTGAGACGCT AGGCGCCAAT CCAATGACGG CTTTTCGGAA 720

AATTGTTTTA CCTTTATCAA TTCCAGGCAC CATTGTAGGA AGTATATTAG TGTTTACAGG 780

AACTTTAACG GCTTATACGA CGCCACAGCT GTTAGGTGGT AACCAAAAAA TGATGATGTC 840

GACCTTCTTA TATCAAAAGG CTAATACTTT AGGTGATTGG CAATCGGCGA GTGTTCTTGC 900

ATTTATTATG ATTTTAACGA CATTAATTGT GATGAAAGGC CTAGACATGG TCGCTAAGAA 960

AGTAGATCGG AGAGAAGCAA ATsATGCGTA AsAAAAAGGA CTATCTGTTA TTGCAATTCT 1020

AGTTTTTsTG TTTTtATTTT TACCGTTATG TTTGATTGTG GTGcnTCTTT tGGAaCAGCC 1080

GCAGCGATTC AATTTCCGAT TAAAGGATTA CTTTAGATTG GTACGCCAAA GCATTACAAT 1140

CGGAAACGTT TATGGACAGT TTAAGTTAAG CTTGTTGAAT GGGGTATAGC GACTGTTTTA 1200

GCCATTAATA GTAGGGATCC GGCCTCCnA 1229

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CTTGGTTATC TGGTATGGCC ATCCTCTGTG TGAGCAAAAA TTATGGAGAT CTATTnGTAA 60

TATTATTTGT GTGACTCCGT ACCCTCTCCT TGCTGTGGCT GATAAGGGCA TCTATGTGGT 120

TGAAGCACGA AAGrAGGgtT mCGTGTATTg rTaATCCTGT AGcgTATTaA CaATwACCCa 180

cATTTGaTTa CCaATTATTT AATTTAAACA ATTATCGTGT ACTTTCAACT AGAACTCCaA 240

AAAATAATTT TTCAGATCAA aTAGAGTTAG ATATTTATAG TAGAGGAATG GGTGGTATTG 300

GGTTGCCAGG AGATTTATCA TCAGTATCTA GATTTGTAAA AGCAACTTTT ACTAAGTTAA 360

ATTCTGTATC AAGAAGTTCA GAATATGAAA GTATTAGCCA ATTTTTTCAT ATTTTAAGTT 420

CTGTCGAACA ACAAAAAGGA TTGTGTGATG TTGGTGATGA AAAATATGAG TATACGATTT 480

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TAAGTATTTT CGAAATGAGT TTAAATAAAC GGGaATAATA GAaGAGTAGA TTTaAGTTAT 720

TGATAACTAC TAGGTAATTG ATGATAAATT AAmCAAATTA GATGCTTTAA GGAAAGATGA 780

CAAAAAAGTA CAGTATTACA TGAAAAAGTG GATTTTTGAG AAAAAAAGGG TTTAACAATT 840

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AATATCAAAA ACAACTATTC TTATAAAACG AATAGTTGTT TTTTTGTATT CATATTTTCT     900
ATAAAAAAAT GAATAGTAAA CACTTGTAAT TTTTTAATAA GAAgAATAGC TTGTTATAAG     960
AGTAACTACG ATTGTCCGCA TAATTTTTTt GAAGgTGgTA AAAAAAAtAT AGrGkTATAA    1020
ATGtGaTAGG kGtATTAGtA tTTATTTAaa AGrCtAAAAA AtGtGaAGGA GkTTGaATCg    1080
AAaTGaAAAA AGTATGtGCT ATTTTAATGA TTTCTGCGTC AGTTTTAGGA ATGGTGCCCA    1140
GTAATGTACC AATTTTTACA GCAGAAATAA ATTATGCGCA TGAAAATGAA TTACAAATGA    1200
ATCCGTTTGT TATAGCGTTT GTCGATAAAG TGAAGGGTTC TGTTGCAAAG TTTGAAAATC    1260
AAACGCGCCC TCTCTGAACT CCAAATATCT TAGGCTGGTA TTCCCATTAA CCTTGATTTC    1320
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CCGTCGTTTA ATAGGTCGAT GGTCTTGTTC TATTAAATTG TTAAGATACT TCACAGTTCG    1500
GTGCTCTGTC TTAGTATATA AACCCACACT CTGTAACTTT CTAAAGGCGG AGCAAGaGAA    1560
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TAGAGGACTT TGCTGTACTC TTGCACCCAA CGATAAATCG TAGTATGACA AACATTTATT    1800
CCACGATCAT ATAACAATTC CTGaACTTCA CGATAGCTTA GATTGTAACG CaGGTAGTAA    1860
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AACAGAACCT TTTTTTGCAA TAGAATTACT AATGGGAAAA CAAATTAATG CGATAACCAG    2040
ACCGATAGCA ATTTCGTGAA AAATAATTGT TATTAAGAAT AAAACTATAC TAGATATGAA    2100
TAAACTTAAA ACATGTATTT TATCTTCTTT CATAGGATCC TCCCGTTATT GTCATACAAT    2160
AGTTGTTTGA TTTATATTTT AAATTATCAA TAAAAGAAAA GCTAGGAAAA AAGCATTCAA    2220
ACGAAAACCC AGTTAATACA GATACAGGCG TTGTGATTGT CGCAGTTGAA GATAGTAAAC    2280
CGATTATTCA ATTAGCAGAC GGAACAACAA AGAAAGTTGA AGCTAAAGAA ATTGGAGCAG    2340
ACGTTCAAAA AGACGGAACA GTAACGGTTA AAGGTTCAGA CGGAAGAATG AAAGTTTTAC    2400
CAAAAACAGG AGAAACAGAA AATATTGCAT TGTCTGTCCT AGGTTCATTA ATGGTATTAG    2460
GATCAGCATT CATTTTTAAA AAGArAaTCT AATTAAGTAT TTATAAAAGC ATGGTCGCAA    2520
GTTTTACACT CTCCTACTTG AAGTtTCCGA ATGAAAACTC TATAATGAGA AATGTGAAAA    2580
TGTTCACTTA TTATAAATTA AGTtTGGAGG CTTTTATTTA TGAAAATTGC AATTGCAGGG    2640
GCCGGCGCGA TGGGTTCCCG GTTCGGACTG ATGTTGAAAC AAGGTGGTAA CGATGTTTTG    2700
CTAATCGACG GCTGGCAGGA GCATATCAAT GCCATCAAAG AAAACGGATT GAAGGCTAAT    2760
TATAATGGCG AAGAAATTAC TGTTAAAGTC TCAATTGTTA ATCAGAATGA GGTGCCCACT    2820
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CAGGATGTTA AACCATTAAT TGCTGATCAC ACAGAAGTTT TGTGTCTTTT AAACGGTATC 2940

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TTTTAATAAT TTGTGTGCTT AAATGGTAAG GAATATTCCC AACAATTTTA TACCTCTGTT 7560

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TATTCTTTTA GTTTCTTAAA GGCACTTGTA ATAGAGGGGG CTTTATCTGT GACTACAACn 8340

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ATGaTTTTAT CAAaACaAAA GTTTACTCTT TACGACTATA AAATTGTTAC TAATCTATCT 9720

CTTGTATTTT CTTACAAAGA ATTGCAACC 9749

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAAATCAGAT ATCTTATAAn nGnAATCAAG CACGTATTCG CGATAAGGGT AAAAAATTAC 60

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AATGGTACTG TTAAGAAGTA AATTTGTGAA TAGAGGAGGT CGAAGAACAT GGCAACAAAG 180

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GAAGCGAAAC CAGCATTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT 3360

ACTTTTACGA TTCGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT 3420

TTTGAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCCGCA AGCGTATTAC 3480

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TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTCGAAAAA 3660

ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTCACATTA 3720

GAAGGTTGGG ATGGCACGAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT 3780

CAAGCGAATG TTTCGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAGT CAATACTGGG 3840

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ATCAGTGAGT ATGTTCAaGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT 4320

TCACCAGTTC CTTTTAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG 4380

GTTGGTGGCT GGACGCCaGT ATATGCTGAT CCAATCGATT TCTTAAACTT ACTGCAATCA 4440

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CAATTGGTTG CGGAAGAAGC CCCCCTAGTT CCTCTTTATC AATTAACAGA AGCACGCTTA 4620

GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA 4680

GTCTCTATCG GCGACAAGTA AAGGTTGGGA AAAAATGAAA AAAAGTCAAG CTGTTCAATT 4740

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TCTTGAGAAG AAAAATAATC TAAGTGAAGG TCCAGTAGTG CTTTTTGATG CTCATAGTGA 4920

CGAAGTGGGT TTTATGATTC AAGCAATTAA AGAAAACGGC TTGTTGCGTT TTTTTCCGTT 4980

AGGTGGCTGG GTCCCTAATA CGATTTCTGC ACAAAAAGTT CGGATTCGTA ACCGGGAAGG 5040

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TCAGCGACCG TTAACCATTG CTGATTTGAC GATCGACATT GGTGCTACCT CAAAAGAAGA 5160

AGTAATTGAA ACTTACAAAA TCGATCTTGG TGCACCGGTC ATTCCAGATG TGACGTGCTG 5220

TTACAACGAA CAGACAGATC TTTTTTTAGG AAAAGCTTTT GATTGTCGCA TTGGCTGTGC 5280

TTGCTTAGTG GATGTCATGG AGGAGTTGAA AGAAGAGACG CTTCCATTCA AGTTAGTTGC 5340

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CAATCCTGAT TTAGCTATTG TTTTCGAAGG CTGCCCGGCT GATGATACGG CAGAAACGCC 5460

AGAGATGATT CAATCAGCAA TGGGAAAAGG ACCGATGTTA CGTTATTTTG ATGTTTCTAT 5520

GATTACGAAT CCGGAATTTC AAGAGTATGC ACTAGAGATT GCTAAAATAC ACAAAATTCC 5580

TGTTCAAGTT TCTGTTCGAA GTGGTGGTGG AACCAATGGC ATGGCGATTA CACAAGTTCA 5640

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GAAGACACCG TTTTATTCCG AGAATTATAT CACCAACATG TGGCTTGGTT AATTGAAGGG 5940

ATTCAAAAGA GTGCCAAAAA TGAACAAATT ACAGAAATTA CTATTGCCGA TTCGCATAGC 6000

CGTGGATTGA ATTTAGCTTA TGCGCGCTTG GCAGAAATGG ATGAACGAAT TTCCTTAGTG 6060

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AGTAAGAAGC TTACGGAAAA AACGAATGGA CATTTTTTTC TGTAAGCTTC TTGCTATAGT 6720

TATTTCTATT TTTGTTTCTC TAGAATTTCT TTGCTTAAAC GTTGTGCAGT TGGTGTCACC 6780

GCAAGACcGC CTTCAGCGGT TTCCTTGAAA ATTTGTGGCA TTTGGCGTCC CACTTGGTAC 6840

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TTGGTGTAGC ACAAATCAAG CCCATTTTTG CATTAACCTC ATTAACAGCA ATCGCATTTC 7320

GCACGGCTTG TAAAATGGTC TCACCGCTTA AAAAGTTGCC TGAATGTATG TAATCATTTA 7380

AGCGGGTTGC ATCGCCACCA GTTAGCCCTG TTACTGAGGT AACACCAGCG ATTCCTTCAG 7440

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GTTCCGTGAC CACGATAAGT TTTGGCAAAA GACTCATATA AATAAATGTC AACGCTATCA 8160

GGTTGCTGTC CAAAAATACT GCGAACCACT TTTCCAATTC TTGCCGCTCC AGCTGTATGA 8220

GAACTGCTTG GACCAATCAT AACAGGTCCG ATAATATCAA AAACACTATT AAAGCGTAAC 8280

TCTTCCATTT CAGCACCTTC TTCATTAGAA TATGTTTTCA TTGGAAGTCT AACACAAAAA 8340

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GTGGnAATTA GAACGAGAAT TAACGCTTTT AAACGTTGAT CCTGAnGTTT ATGGCGTCCC 9000

TTTCTTCTTn ATCAGGCGGC G 9021

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

ACAATAAACG GGAGGGATCG TTTATGAATA TTGAAAAAAT GACAACCACG CTACAAsAGG 60

CGATTGCTGA AGCTCAAAAA GTTGCGGTGA CACGTCAACA TCAAGAAATT GATATCGCAC 120

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GTTTAGATGT TGACGCATTT GAACGAGAAG TAGATAACGC GTTAGATGAA TATCCAAGTG 240

TGGCAGGCGG TAATGTGCAA TATGGTCAAA ATTTAAGTCA AAATTTGTTC CATTTATTGC 300

AAGAAGCTGa TTCACTTCGA GAAGAtTCCA AGATGaATTT TTATCaaCCG rAATTGtACT 360

TTTAGCTTTA ATGrAATTGa AAAATTATCG TTTaACmAAA TATTTAATGc mACmAGGcAT 420

TACGGaAAAA GAGTTwAGrA AAAATATTGA AGaGATGAGA GGAGGAGATC GTGTGACTTC 480

TCAAAACCAG GAAGAACAAT ATAAAGCACT AGAAAAATAC GGTGTTGACT TAGTACAACA 540

AGTAAAAGCA GGAAAACAAG ATCCAATCAT TGGTCGTGAC GAAGAAATTC GTGACGTTAT 600

TCGGATTTTA TCAAGAAAAA CTAAAAATAA TCCAGTCTTA ATTGGTGAAC CAGGTGTTGG 660

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CAAAATCATT TTATTCATTG ATGAAATTCA TAATATCGTC GGAGCTGGTA AAACAGAAGG 900

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TCGTTTCCAA AAAGTATTAG TCAAAGAACC AACAGTAGAA GATACAATTT CTATTTTGCG 1080

TGGCTTAAAA GAACGATTTG AAATTCACCA CGGCGTGAAT ATTCATGACA ATGCTTTAGT 1140

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TGCTGCCGCT ACTTTATCCG ATCGCTATAT TACTGATCGT TTCTTACCAG ATAAAGCGAT   1200
TGACTTAGTC GATGAAGCAA GCGCAACGAT TCGAGTGGAA ATGAATTCGA TGCCAACAGA   1260
GCTCGATCAA GTAACACGTC GGTTAATGCm ACyAGaAAtT GAAGAAGCGG CCTTGAAAAA   1320
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GCGTGAAGAA GCCAACTCAA TGAAAATGCA ATGGGAAACG GAAAAAGAAG AAGTTAATGC   1440
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TCCaGGCTAT GkTGGTTwTG AAGAAGGTGG CCaGTTAACG GAAGCTGtTC gTCGrAACCC   2040
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ATTACAAGTT TTAGATGATG GTCGTTTGAC AGATTCTAAA GGTCGGGTCG TTGATTTTAA   2160
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ACAAGAAATT GTGTTGGAAA TCACTGATGA AGCTAAAACA TGGATTGCTG AAAATGGGTA   2460
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ATTAGACAAT CAATTAGTTT TTGAAAATGA ACCGATAGAA GAAGTGTAAA AAAGAACGAG   2640
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CCTTGTTGGC GGCTGTCTGT GTAAAGGGCA ACCACCGGGA TTCCTTTGGC ATAAGCAACA   2880
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TCGCTAGCAA GGACGTTTTC TGTATCTGCT AAGGCAATCA TTTTGCTATC GGCATAAGCA   3000
GATTTGTCGT TAATCGCCGC ATTTTCTTGT GGTAAATAAA GATCGATTGT TTTATCCAAT   3060
TGTCGAATTT GTTCGACTAA ATAGGCATTA TAACGTAAGT CAGCTTGCGA AAATAAAGGT   3120
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CCTGCAAAAT AAATTTTTGT CATTTGTCTG TCTCCAATCC AAGGGTTTAG AAATAATCAC 3180

TGAAATAAGC TTCTTGGTCA GGAAAAATCC GTTCCAAAGA ATTTAAAGTT TCTTTATCTG 3240

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GATATTGAGG CTCCTTTAAA GGCTTTGATT TTTGACTCTA TTTACGATAG TTATCGGGGG 5280

GTCGTTTTAA ACATCCGTGT AATTGACGGT GTCGTTCGTC CTGGGGATAA AATCCAAATG 5340

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CAAGAAGCCT TTATGGCGGT TCTGAAAATG GACGACCAAG ATAACGCGAA ATAGCTTGTT 6480

TCCAACGGAA A 6491

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCTACGAAAA ATATGGCACA AAGAAAGTTG GAAAAATGAC AAACTTGTCG ATTTTCCAAC 60

TTTCTTCATC TATTCGTGGT TGGCTTGCTG AACTGCATCC ATCACGGCAT AACGGAAGCC 120

ATTTTTTTCT AGAGCTACGA CACCGCGAAT CGTACTTCCT CCTGGAGAAG TCACTTCATC 180

TTTCAATGCT CCTGGGTGTT TTTTCGTGTC TAAGGCTAAG GTCGCCGTTC CTTTTATCAT 240

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GCCAATTTTC ATAGCATTCC CTCCTTAGTT AAATAArGTG TTtGTGkCAA AAGTCAATTA 900

GCTTTtGACA CnAACACTAA CAGTCGkACt TTTTcCGtAC aGCtGkTTCG TTAaTTaATT 960

gGTAAtcCAT wACGaCkGCT CaAAcGCgCA ATTTTTCaGA AGtCyGaACC AACT 1014

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AAAAATGCAA CTTATTTGCT CAAAAAAGCA AGCGATGATT GACAAACGGT CGTTTTTAAC 120

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CTTTTGTCAC AATTTCAACA TTGCCAAATA CTTCAGCCAT TTTCTTTTCT GCACTAGGTG 16080

CACCTTGTTT CTTTTGAATA ACCACCGTTA GTGTGCCACC AACTTTCAAC AACGGAAGAG 16140

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ACACACGAGA ACCATAATCC ACTGTTCCTC TTGAGAAGAC CCnG 16484

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 8160 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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

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ATCAATGAAG AAAGAATCAA TGTCACGTAT CGAAAGAAGG AAAGCACAAC AAAGAAAGAA 240

AACGCCAGTA CAATGGAAGA AGAGCACTAC TTTATTCAGC TCGGCGTTAA TTGTTTCATC 300

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GCTATCTAAG GCACCAAACT ATAACTTATT TGGGATTAAA GGCAGCTACA ATGGACAATC 900

TGTCTATATG GATACATGGG AATATTTAAA CGGCAAATGG TTAGTGAAAA AAGAACCTTT 960

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(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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ATTTCTTTAG TCGGCTGTTG CAATAAATAA TACATAGAAT GACTACTAAT AATTTCAGTG 180

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CTATTATTCA TAaCGTAAAG ATTCAATTGG ATCTAATTTT GgCTGtCTTC GAGCTGGTAA 4860
AGTTCCTGCT AAAAAAGCaA TAAACATAAT AACTAAGATA ATCGTTAGTG AAGATGGCAA 4920
TGAAAATTGA ATTAATTTAA ATCCTGTTAA AGCCTTTAAA AAAGAATCCG TTGCCAAACG 4980
ATTAACTAAA TTTCCAACCC CAACAGCTCC TAAAATGCCT AATATTGAGC CAAAAAAGCC 5040
AATTAAAGCC GCCTCaACAC TAAAAATTGT AAAgACtTTC CCATTGCTAA GACCCATGGC 5100
TTTCATTAAA CCAATTTCTC GCGTTCTTTC TTGGACAGAC ATATACAGCG TGTTAATAAT 5160
GCCAAAGcTT GCAGCTAACA AGGCAATTGC ACCAAACATG GTTAAGACAC CAGTGATTGC 5220

ATTGATTATA TTACGAATCA TGCCAATTTC ATCTTCGACA GTAGTCGCTA AATAGCCAGC 5280

TTTGTCTAAA TCTTTTTTGA TGTCCTTAAT CTGCTCTGGC GTGCTGTCTT TTTTAACTTC 5340

AGCAATAATC ATCGCGTATT GATTTTTTAA ATGTTCTGGA AGATCTGCTT GATTGATTGA 5400

GACAACTTTA TCAATCAATG CTTTATTCAT CAGCGAGAGC CCATTTTGAA TGACACTGGC 5460

ATTTCTAACG CCAACAATTT TTGCTTCAAT AACTTGCTCT TGTCCTTTCA AGGAACTTGA 5520

GATACCTAAT TGAACTGTTT CCCCCACGGC AGCTTTACTA GATGTATAGC CGAGCGCTTT 5580

TACATATTCT GGTGACAAAT TAATTTCGAA GTCCTGGCTC GTTTGCGAAA CTTTACGGCC 5640

AGCCGCTAAA TCAATGGTCA TCTCATCTAG CGCAGAAGTT GCTGAAAATA CATATTTATG 5700

CTTATCTGCT CCTTTTATAT AATCGATAGC AACGGATTTC ATTGGTTCCA CTGATGTAAC 5760

ATCCGAGATT TTTTTAATCT TCTCAATATC TTTTTCAGCA AGCATACTTT GTTGTTGAAT 5820

CGTACTGGTT TTTTTCTCTG GATTATATTT ACTTGGTTCT GTTCCGTTAC CAACATTCAT 5880

CTCCATTTTT GGCTGAATAA ATAACTGATT TGCACCACCG ACACTGCCGA CTTGTTTGTC 5940

AATATAATCA TTTACACCAA TATTGACTCC TGTAGTTAAA GCTATGGTAA ATGCTCCAAT 6000

AAAGATTGCA ATAATGGTCA ATACGGTTCG ACCTTTATTA CGCATTAAAT TGGTACTAGC 6060

TGATTTTAAA ATATCTCTAA ATTTCATTTA CTCATCTCCT CCTACAATCA AGcCGTCTCG 6120

AACATGAACT TGCCGATCAC AACGTGCTGC TAAGTCTGGA TCATGTGTCA CAATAATtAa 6180

GGTAATcCTT tATTTTTATT TAAAyCAAaT AACAATTCTT CAATTTTCTT CCCAGTGGCA 6240

GAATCTAAAT TCC 6253

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TGTGGCAACT TAAAAAAGAA CAAAATGTTC CCATTTATCG CAGTATTATG GAGATGATTG 60

TTCAAAAGAT TCAAACAGGC GAATTATTAC CAGGCGAAAA AATCCCTTCG GAACGTAAAC 120

TGGCAGAGTA CTTGTCTGnC AATCGTTCAA CCGTTGTTCA TGCATTAGAC GAACTGGTGG 180

ACTTAGGCTG GATTGTGCGA AAAAGAGGGA GTGGAnGTnT GTCAACGAAG GAAAATGGGG 240

GGTAATGATG ACGCCACGAA CGGATTGGCA TCGTTATTTA GAACAAAATG TGTTCAAACA 300

AGTTCATCCC TTGGTGACAG AGATTGAGTT ACGTGCTAAA CAAAATTTGC CGACTGACTT 360

AGATATGTAT ACAGGCGAGT TGCCGTTAGA CTTAATTCCC AGTTTCGATT TTCCAGCATT 420

AAATTGGAAA CAATTTTTAA AAGAGGAAGC ACAAGATGAA TTAGGTTATT TGCCGTTAAG 480

AAAAGAAATC CAAGCCATTA CAGCAACGGA ATATCAGCTT CATTTACCAA GTGAAAGTTT 540

ATTGCTTACT TCAGGTGCGC AACAAGCACT TTTTTTAGTT TTACAAGTTT TATTGAGACA 600

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AGGAGATAGT GTTGCCGTAG AAGATCCATC TTTCTTCTAT GCCTTACCAA TTTTCCAAGC     660
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TCCGACTGGG ACAGTGATGC CTTTGAGAAA AAGAGAACAG CTTGTGAAAG TCTGTCAAAC     840
GTATCAAGTT CCTATTTTAG AAGATGATGT TTTTGGGCAG TTAAGTTTTA TCCCGAAAAC     900
AGAAATTCCT CCTTTAAAAA AATTAGATCC AGATAATGTC TTGTATATCG GTTCGTTGTC     960
AAAAATTTTA GGTTCGACCA CGAAAATTGG TTGGTTAAGT GCGCCCGCCT CCGTGACGAA    1020
ACAAATTGCA GAAGCCAGAA AAATGATGGA TGTTTCGTTG AGTATTTTTC CACAGATGCT    1080
CGCTAAAATG GCGATTGAAG ATCCTTCTTT CTCTGAAAAA ATTACGTTAT TAAATAAACA    1140
AGTGGAACAA CGAGCAACAG CTGTATATCA AGTATTTAAA TCGTTGTCAG AATGGGAAGT    1200
TTCGCCAGTA AAAGGCGGCT TTTATTTATG GGCACATTGG CGTCAAGGGG CACTTAAGCC    1260
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TGAAAAACGT GGAAGTATTC GCTTGAACTG TTCCCGAATT TCACCAGAAG AAATGCCTCT    1380
TTTTTGTGAG CGAATGGTAC GGATTACACG ACAGCTTTCT GAAAATAGAC AAACAAAAAT    1440
AGAACAGTAA GTAAGATTTT TCTTATAAAA ATCATTTGCT GAGAGAAAAC GCTACAACTT    1500
CCCTTTTCTA AACGAATATC CAATGCTATA CTTAAAAAGT AAAAACAAAA AAACAAATGA    1560
GGTGTTTTCC ATGTCTTGGG AACAAGTTTA CCAACAATGG TTAGATGAAG AAAATATTCC    1620
AGAAAATTTA AAAAATGAAT TAAAGGACTT AAATACAGAC CCTGAAAAAT GTGAAGATGC    1680
ATTTTACGCA CCATTAGAAT TTGGGACTGC CGGGATGCGT GGGATTTTAG GCGCCGGTAT    1740
TAATCGGATG AATATCTTTA CGGTTCGTCA AGCAACAGAA GGACTTGCAC GTTTTATGGA    1800
TACGCAAGAT CCTGAAACAA AACGTCGCGG TGTAGCTATT GCCTATGATT CACGTCATAT    1860
GTCTCCAGAA TTTGCAATGG AAGCAGCTAA AACATTAGCT AAACATGATA TTCCTTCTTT    1920
TGTGTTTGAA AGCTTACGAC CAACACCAGA ATTATCTTTT GCGGTCCGCT ACTTTAAAGC    1980
TTTTGCGGGA ATCATGATTA CGGCTTCTCA CAATCCAGCT GCCTATAATG GCTACAAAGT    2040
CTATGGTGAA GACGGTGGTC AAATGCCGCC AGCTGATGCA GATGCATTAA CTAAATATGT    2100
TCGTAGTATC GAAAATCCTT TGAAAATTGA TGTCTTATCA GATGAAGAAG TTGCCCACAG    2160
CGGTTTAATT AACATTGTTG GTGAAGAAGT CGATAACGCG TATTTGAAAG AAATTAAAAC    2220
AGTTACGATT AATCAAGAAT TAATTAACGA AATGGGTAAA GAATTAAAAT TAGTTTACAC    2280
TCCCTTACAT GGAACTGGGA AAATGTTAGG AGAAAAGGCA TTAAAACAAG CCGGTTTTGA    2340
AAAATTTGTT TTAGTACCTG AGCAAGCCGT TGCTGATCCT GACTTTACTA CAGTTAAGTC    2400
ACCAAACCCT GAAGAACATT CAGCTTTTGA ATACGCGATT CGTTTAGGGG AAAAAGAAGG    2460
CGCTGATTTA TTGATTGCAA CAGATCCAGA TGCTGATCGT TTAGGTGCTG CTGTGCGGAT    2520
GCCAAACGGA GACTACCAAG TATTAACAGG AAATCAATTA GGTTCAATTA TGATTCATTA    2580
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TATTTTAGAA GCCCATCAAC AAGCAGGCAC GTTACCTCAA AATGCTGCGG TTCTAAAATC 2640

AATCGTTTCT AGTGAACTTG CTACAGCGAT TGCTGAGAAA TGTAATACGA AGATGTTTAA 2700

TGTTTTAACA GGTTTCAAAT TTATTGCTGA AAAAATTCAA CAATACGAAG AAGACCACAG 2760

TCAAACGTTT ATGTTTGGTT TTGAAGAAAG TTATGGTTAC TTAGTGAAAC CTTTTGTTCG 2820

TGATAAAGAT GCAATTCAAG CGTTAGTTTT ATTAGCAGAA GTAGCGGCTT TCTATAAAAA 2880

ACAAGGAAAA ACATTATACG ATGGTTTACA AGATATCTTT GAAGAATTTG GTTACTTTGA 2940

AGAAAAAACT ATTTCCGTAA CAATGAGCGG AATTGAAGGC AGCGGTAAAA TCAAAGCTTT 3000

AATGGCAAAA TGTCGTGAAC AAGCGCCAAC TGAGTTTGCC GGGATTCAAG TTGCTCAAAC 3060

GGAAGATTTT AAAGAATTAA CACGCACTTT TGCAGATGGT CAAACAGrAC AATTACAAAC 3120

GCCTCCTTCT GATGTGTTGA AATATCATTT AGAAGATGGC AGTTGGATTG CTATCCGACC 3180

ATCAGGAACA GAACCAAAAA TTAAATTCTA TCTAGCGACA AAAGCAACAA GTAGTTCAGA 3240

AGCTTCTGAA AAAATTGCTG CGTTTGAAGC nGTCGTTAAT GAATTAACAA AATAAAATAA 3300

ACGAAACAAG CT 3312

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TATCTTCGTG AAATTCAAGA AGACTTAGCA ACCCTTCCTG AAAATACCTT AGAGATTCAG 60

ATCCATCACG GAAAAATTTC ATTACATACG ACTTCCAATG ATTTTCTTTC CCACTATTTT 120

ktAtTATTTA AtTAtTaCTG kGtCCaTyCT ACTGACTTCa TyCTTTTTCm AGcAATTATC 180

AAAAAAGrAA ACmATTCTGT CTGGAAAGTG AGTCmAGrAA CTAATTTTAG CTCATCTTAC 240

ATTTACAAcG GTTAAaTAAC ATTAATAAAC TATTTGGTTT GTATGGAATT TCCGTCCATT 300

TTTCCCCCTC CGCGAGTAAA GTGATTACAG GTTCTGAATT TCAAGTCCTA TATGCTTTTC 360

TTGATGTCTA CTGGACCATC TTTTTAAATA CCTTAGCCTT ACCACGTTAT ACCTCTACTT 420

ATTTTGAAGA TATACTGACG CAGCATATTA AACCAGAAAT TCTTGAACGC TTGGAACACG 480

CTTCTCTACT AAAATTAAAT TTACTTTTAC ACATCGCAAA ATATCGCTTT CCATATACTT 540

GTGAAGATGA TCTCCAAAAA GAATTTGAAG AACATCCTTA TTTAAGGCTT TTCTCAGACT 600

CAAAACAAAC TATTTTTTGT TCCCAATCAA ATTTTTCAGA AGATCAACAG CGGGTTGTAG 660

ATATCATTGC ACCCATTGCC ATTGATAATT TTGATTCAGC AAAACGAGCC AAAGATTTAC 720

TGGCTGCTCT AAATGaAATT TCTTGCCCAG AATATTTCTA CGTTGATTCT TTATTAACCA 780

ATTTTTGCGA aGTTTTTCAA ATTCCAAAAA TGCGTGAATT TGATCGTCAT TACTTCTTAC 840

TTATTTTATT TAAAAATATT ATCTATAACC AATTATTTAT TTCACAGCAA CCAAATACCG 900

CAATTCTAGA TTTTTTAGTC AATAAAAATA GTACTTATCA AAAAGATTTA CAGAAAAAAA 960

TCTATGCTTT TTATCAAAAC TTTTCAGCGC ATTCCCCTTA TCAGTTAAGA TTTAAGGATC 1020

AGGAGAACCC AATTTGGACA TGTGAATTGT TGTTACGAAT TTATAAGCAC TATAGTCCCC 1080

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TGATGAAAAT CAAGCAACCA TTTAGTGAGG ATATTATTTT TGAACGAACC GATTTTTCTG 1200

GTTGTGATAT TGTGATTACT GACTATCCCt TATTTGATTT ACCAAAAGAA ATAGACCGAA 1260

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GTATCGCCAT TTTTGATTTG CAATATTAAA ACAAACATCA AGCGCCAACC TGTCTCACCA 1380

GCCATAATGA AAACAAGCGA CCTACAAACC ACTTCTGCCA GTTTTAGTCT GACAGAAAAT 1440

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ACGArGATCC AAAGTGTTTT TTGTCTCAGG CTCTTACATT TTTTCCAACA AAGGTATTGc 1620

TaGGCGCTAC TTGAAGCTGA AAACTAGTTT CTCTATCGAG ATTCCTCATC AGTAGACTCA 1680

AATTTAAAAC TTTTTTCTAT AAAAGTGaCT TCTTTTGCGT ATGTTTTTAC AAAAGAAGAA 1740

TAGTCTTTGG GATCTTTGAC CTTTTCCAAT TGGTCAACAG AGACTTCTAA TTCAAATCCT 1800

GTCCCATCTT TAAAGAGATA ATATTTTGAG ATGTCTGTAT ATCCTTGATT CCGTTTTAAA 1860

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CTTGTATCCA AATAATCAGA AAGACTGTTG ACAAGATTGC CAGAAAGGTA CATACCTGCC 1980

GATGTATAAT AGTCTCTTTT TTCATAAAAA CTGATATTGC CTAGATATTT TGTATCTGGA 2040

TACTCCTCTG TAGAAGGTAA AATTAAAAAG TTCTTTCCGC CACTGGTTTC AATATCGGCA 2100

TCGCCGATAA TTTCTATTTG GTAGCCTTGA TTAAATAAAA GTTTATTTTC TTCTATTGTG 2160

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GCATCATATG kATCATAAAA ATTCTTTTGT TTAGCCATTT TTTCTCTCCA CTAATTTTTT 2520

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AGTTTCCAGT AATTGCCATC GCAACTGTTA CAGCAGGATT TAAATGCGCT GGACTCATAT 3840

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GCAATGGATT GAACGACGGC TCGTTCTTTC ACTGTATCTG CTACCACCTc CACGTCAAAC 5640

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TTTCACCAAT CATTTTAAAT TCAATTAATG CCAACACGCT TAAATATTTG ACCAGAGAAA     7980
GTTCATGCAA ACTATCTCCT GGTTGATACG TTTCATCAAA ACAAGCTAAA GCTTTTTCTA     8040
ATAACGTTGT TGAAAAAGAA GCTAATTCCC GACTAGATAA TTGCTGTTCT TTTTCCCAGA     8100
TATGGGCCCG ATCAAAGACT TCCAATTCTC CTTTAAAAAA ATACAGTTTT CCATGAATTT     8160
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ACAAGACCAC ATTTTCCAAG ATAAACGTAT CAGCTAAAGA AACAGCGGAA CGACGTCCCC     8280
GAATTAAGGA ATATTCATCA AAAGCTGATT CTGGTAAGAC CGACATTGTG ATTAGAAAAA     8340
CAAAATGAAT CATGCTTTCT CCTTCGTCTA ATTCTAATGA ATAGCGACTA GAAAAACGGA     8400
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TCAATTGTTG ATATTTTTTT GAAGTGAcCG CTAGGCGCTT TTTCGTAATA CTCAACCAAA     8520
GGCTAACTTT TAACGCATTA TGTTCATTAA AAGTAAAACC TAAGCCAGTC TCAATCCCTT     8580
CAATTATCCG TTTATTTAAC GGCGACATCG TTTTTTTCTG GTGTATTTCA TAGGGAGTAA     8640
TATACCAATA CAACTGAAAG TAAAAGTAAC GAATCTGCAA TTCTTCTCCC TGTAGTTGTC     8700
CATTTTTTAT TTGCAAATCA AAGACGGCTA ACAATTGATT GAGTTCCTTA ATCTTTCGAA     8760
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AATGATTCAA CGAAAAAAAA TCCGATAAGG TGATTGATAG CTGTTGGCCA TCATAAGTAA 8940

GCTGACAATC CTGTCCAAAA GGTTTCAAAA AATAATGTAA ATCCTCTAAG TCTTTTTCAA 9000

AGGAGGcTTT TGTGACCGCT AAAAATGCTG tTAAATCAGA GACTGAGCAG GTGCCGCCTG 9060

CTAAGATGGT TTGTTGTACC GTTAATAATT GTCGCATCGC TTTCTTTTCt AATAATGTCT 9120

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GTCCCATGTT GTAGAGGCGG CGCTGGCTGT CTAACAATTA TGGAAGCAAG TGTTTGCGGA 9420

AAAAATAAAC CTTCCGTTTC GGTTAGACCT GTACTAGCAA GGTAATAGTC CCCCACTTTT 9480

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CTTGTTTCAA GAACAATACC ATTTGCTGTT TCTTCAATTC CTAGGACCGT TTCTTCAAAA 9840

TGGAAAATTA CTGCTTGTTT TTCCAAAGAT TTTTGAACTT CTGCGACCAT TTCTTTATCA 9900

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CTATTTTCCA GTAATGGAAC AGCCGCTAAA GCACCTGATA AAAATTTATA TTTGAGTAGT 10080

TTTTCTGTTT GACTACCACG AATTTGCGTG GAAAACTGGC TCGCGCCTGT CGCTAAAATC 10140

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CTTAAGCCAC CAGATAAATA CCCCACTGTT GCTTGTTTAT CAATTAAAGA AATTTCTGCT 10380

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ATTGAATGAA CGTCTAGAGG AAATGAAAAT TGCCTTTGAA CAATTGACGG ATGACTACAA 10980

TGTTCTATAA TAGAAGAGAA CAATTCGTTG AGAAGGGGTC CTTATGAAGC AAGAAGAAGT 11040

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CGAGGTTCAT GGCTCATCAC ATCACGTTCT GCTGGTTCCA CACCTAACGC AATCGCTGGG 13080

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AAGGTTAACG TACCTGTTTT ATCTGAACAG ATAATGTCTG TACTTCCTAA TGTTTCAACG 14280

GCTGGT 14286

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CAATGCTCAT TTCCACTCnT CCTAAATCTG TTATTGCCAG TAGTTTTGCT CTAACTTTTC 60

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TAAATaATGk GaATAGTAtC CATGCTGTCG aACCTCAAAT TCTTTTAAGT AATCtAATGG    120
AATACTCyTA CGtTCTAAGT TTTTTTGCAT ATTTAAATAA TCATCAACAT CCaCTAAAAA    180
TACTTGATGA CTTTTGTTGA ATTGAATTAA TAAAAATGCT GTTCCACCGC TTAATTTAAA    240
AnCCTTTAAA AAATTTTTTT GGTGATCTTT TAACATTGGT TTATTTCCAA CATAAAATGG    300
AAATGCAGTT TTATTTTCAG TAGATTTGCA ATCGAAGGCG ATTGGCCGTC CCTTCAAATG    360
TCCGATAAAA TCACATCCTG TCTTGTTAGT TGGAATCACT ACGGGTTTTC CACCAACCCT    420
TATAGTTTTA GTTCCATTAG GTATTTTTGC TACTGTGCCT TTTCTGTTAC GACAATACCA    480
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CTCTTAATTT CCCTCTGGAT TTAACCAGTT ATGCATTGTA ACTTTTGGTA TTGAATCGAC    600
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CGTATAAAGT ACGCATACCT TGTAAGAAGT AGCTTTTCGA CCATTACTTT TAAAATCAAT   1080
CAAACCTAGT TGCTTTAACG CGnTTCTATT TTTATTAATT CCTGAGCGTG ACAAACCTGA   1140
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TTAGGCTTTA ATCCTGCTTC TAACATTAAG GAAGAGTTTC CATCTGCAAG TAAATAATTA   1980
TTACCTGCAG ATGAAGAACC TTGTATATTA ATTTCAATCA TTAAAAGCCA CGTCCATCTG   2040
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CCGATATACC TTTAAAATTA TGAATACGGA TTGACTCCAA GCTAATGTTT TTCATACAAT 5580

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AAA 6723

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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AATGGTCCCT AAACCAGATT GTGGGGAAGA CAGCTATGTC GGAAATCACA AATTAGAAAA 360

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TGCTCGTGAA GGCGCAGATA TCGCCTTACA TTTTTTCCCA GGTGAAGAAA AAGACGCCGA 480

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AATGGAACAA GTGATAGACA CTTTCCATGT CAATATTATT GCGATGTTTG GCATTGTCAA 720

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CTTTAATCCC AGTGAGCATT TGTTGGATTA TGCAGCAACG AAGGCATCAA TTGCCAACTT 840

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TGGAGAAGCA ATTAATCTTT AGGAGGGATG TTCCGTGAAT AAAGTTGTTA AAATACTTTT   1140
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CGAAGTCAAT GTCAACGTAG TAGATATCAA AACACAAGCA GAGTACCAAG AAGAAAGTGA   2280
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yGCTGGTTGA AAAATTCGCA ATGTGAGTGT CAGAAAGTAA ACCGGTnGGC nAGAGTTAnC 27360

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11427 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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CGTTAAATTA AGTTCCATAA CTGTTCCTAA AAACTATGCT AATAAGAAAT ATGAAGAAAT 240

TGAATCTATT CCTTTTTCTG AAATGACCAT TTCAGAAAAA TTTGTTCCGA TTGTTTACAA 300

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CATATTAAAA CAAACGATAT CTGAAAAAAA ATTGATAATC AAAGAAGAGA TAATGAGAGG 420

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GACTGATTCA CTTTCCAAAA TTCTATTATA CCAGTTAAAA TCGCTTAAAT AGAAATACAC 720

TTCTAGCAAC ATGTTCCATA GTAAAAGTAG CACTTGTTAA AAATAACTAA TCTGCAACTT 780

ACTATCCTTG AAAATAAAAT TCTCAAACAC TTTACAAACA ATTATTTTTT AGGAAGATGG 840

TTTGTTATTC TTATATTTCG AGAAAAATAA AAATAGCAAA AGATACATTA CGATACAACT 900

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TCCAAGAAAT AATCGACACC TAATTCTTTG TTCAAAATAA TCTCTAACGA CTCAGTCGTC    3780

GGTGTTACAC CGCCAAAGAT CATGCGATCA TTGTGGGTAT ACGTCAAACT GACTTCATTA    3840

GGTACAAATA CTTTTTCAAC TAAAAATTCT TTCCTCAATT CTTCTGTTGA ATAATGACTA    3900

ATATCTTTTG GACTGTGCGT ATATCTCGTA TCCATATTCT GCATGTTTAT TTCCCTCTTT    3960

TACTTAATAT TTAACGAACG ATTCGACCAG AACCTGCTGT CAAAAATTGT TCGATCTCTA    4020

TTTCTGAAAA TTGATTACAA TCCCCGTGAA CAGTATGCTT CAATGCTGAT GCAGCCGTAG    4080

CAAATTCAAC GGTTCTTTGC CCGTCAAAAT CTGAGATCAA TCCATGCAAG ATCCCCGCCG    4140

CAAAAGCATC ACCTCCGCCA ACTCGATCAA CGATTGGATT TATTTTATGA ACTTCAGACT    4200

CATAATACGT ATTCTCCAGC CATAAAGTCC CTACCAACTG ATTGTTGCTA GCCGAAGAAA    4260

CGATCCTTTT CGTTGAATAG AAGCATTTAA TATTGGGAAA CTGCTGCTGC ATTTGTTGAT    4320

AATAATAAAC GAATCCTGAA TTCATCCGGT CTTCTGGAAT CTCCAATAAA TAACGCGCAT    4380

CCAATTCTCC AGCTGAACAA TAATCGACAT AAGGCAAGAT TTCTTTTAAT GCTTTCCCAG    4440

CTGCTGCCTG ACTCCATAGT TTCCCACGAT AATTAATATC AAAGCTGACT AACACACCAA    4500

ATTTCTTTGC GGCTTTCACT AATTCAACCG TCCATTGACA CCATTGCACT GACAAAGCTG    4560

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GAAACTCTGT TACTTCCGCA AAGCTTGACC CCGCTCGATC ATAAGTTACA CTAGCAGCAC    4680

GTTCACCGAT CCCCGTTTCC ATGTAATAAG TTCCTAAACG CGcTCCGCCA AGTTGTACAA    4740

AATCACTCAT CACACCGTTT CGACGCAAAT GTTTCACTGC CGCTTGACCT AGTGAGTTAT    4800

CAGGCACTTT ACTTGCAAAA GAAACCTGAT GACCAAAATT GGCTAATGAA ATAGCTACAT    4860
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TTGCCTCGCC GCCGCCATAG TGACAGATCA ATTGCTGTGT TTCGTTAAGA CGAACACCTA    4920
TATCCGTTGA AAGTCGCAAC ATAATTTCGC CTAAAGTTAG TATGTTTGCC ATAATTAGTT    4980
TTCCTTTATT TCTCTAAATT TGGCCATATA TTGTTTTGCC AAAGCCGTTA CTTTACCAAA    5040
CTCACCAGTT TTAGCGTGAG CTAATAAGTT TCCGCCAACA CCCACTGCCG TCACACCCGC    5100
CTCAAACCAT GACGCCATAT TATCCAGACT AACACCGCCT GTGGGCATAA TATTCAAGTA    5160
CGGCAAAGGT GCTTGGAATG CAGAGATAAT ACTCGGACCA TAGGTACTTC CCGGAAATAA    5220
CTTCACGATA TCTACTCCGC TCTTCAAAGC TGTCTGCATC TCAGTAATTG TCATACATCC    5280
TGGCAAGTAA GGAACTTGAT ACAAGTTACA AATTTCAGCT GTCTCCCGAT TAAAGCTAGG    5340
GCTTACAATA AATTCGGCTC CGGCCATTAT AGCTAGGCGA GCCGTCACAG CATCTAACAC    5400
CGTGCCCGCG CCAATCACGA TATCTTTCTC GTCATGATAT GTTTCAACTA ATGACCGAAT    5460
GACTTCATCT GCTTGAGGGA CTGTAAAAGT CAATTCTAAT CCAATCATTC CGCCCTCTAC    5520
TACTGCATGA CTAATTTTCA AAGCTTCCTC TTTAGAATCT GCTCGCAATA CTGCGATAAC    5580
TCCCGCATTT TCTAAGCGTT TCAATACTTC AACTTTTTTC ATTCGTCTAC GCCTTTCTTA    5640
TAAAGCTTTA TGGAATCAAA TATACGAGCA CCAGATTGAC TATACCGCGC TACTTCTTTT    5700
TAAATTCCTT CTTCTGGCAG TTCTTCTGTT tCATTGTTTT TTTCAAAAaG CmTAATATtG    5760
CTCTTTCCAG CCTGTACGAC TGTTTCAGCA ATTTCAAATG AATCCGTGAC GCTATTTCGC    5820
ATCATCAAGC CTTCTAATAG TATTCCTAAG TTTGTGCCAC TCACAACAAA AACTTGATCT    5880
TTTTCCTCAG AGAATTCAAC ACAGGTTTTA AATGGGGTAC CACCCAACAA ATCTGTGAAA    5940
CAAATAGCTT GATCAAACAT TTGAATTTCT GCCGCTACTT TTTGGCGATA CTCATCTACC    6000
GTCTCCTCGG CTAAAAAGGG AATAATGATC ACATCTTCTA GTTCTCCAGC AATCATCGCT    6060
AAAGCACTCT GCATCCCAAT CGAAAATTCA CTATGCCCAG TAATTAATAA TTTCATCTCA    6120
TTGCTCCTTT ATTTAATCCG AATCTTTGCT TCCTTTTGAT CAATCAAAAC AAGCCGACCA    6180
TAAAAAAATT GGCCATATTC ACTCACTAAT AGTTTATTCC CTTTGACAAT ATCTTCCCGC    6240
ATAACAAAGA GATCAAATTT TTCCGATCCG GCGATTATCC GAAATCCCTT AGCCTGACAG    6300
AATTGCTCAT TTTCTCCTGT TTGACTCACT TTTATTGGCG TAATTTGGAT ATCCTCTAAC    6360
GGAGAAATGA CTGTTGCTTG AATTTCTTTT CCCGTTTTGT AACAAAACTT GTTTGATAAG    6420
CGTGGGTGCT CATTCAGCTG GTTATAAATC TCTGAACCTT TTGCCACTGA TTGCTGTGTT    6480
TGGCCTCCAG CAAAAAGGAG TGTGTACTTA TGCTTGTTCG TAGTTAAAGC AAACCGATGC    6540
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TTCTGTCCTG CAAAGCTATC AATAATAACT ACGGAGTTGA TCGACTTTAA ATAGATGAAG    6660
cTGCGCTCAA AAATCATTGG ATTCTGATCC GCCTTATCCA GCCAGCCGCA TTCTGCAAAA    6720
AAACCGACAG AAAGTTCTTT TATTTGCTGA AATAAGGGTG TCGGTAATTT GTCATAACCC    6780
CACGTATCGG AAACTAAAGT ATGGGGATTT TCTGCGATAA ACATCGTATT GTGCGAAgCG    6840
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AATAAGTCAT CCCCTTGTAG TTGTAGTGTA AATCCACCTG TAGAAGCATG ACCATGTGCG 6960

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CCACTTGATT CGCCACGAAA AAGTTCTTTT GGCTTCATTG TTTCCCAGAT TCTTTCTTCA 7080

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CCCCAATTAC TGAGCCTGTA TTTATCGATA TAGGACCGCT CCAAATAGTC CAGATGGATC 7560

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TACAGTATAC TTCCTCATTC ACTCCGAAAA GTGACAAATA CGGAGACAAG AATAATTTTC 8160

CAAAAATTAA AAATCTTGTT TCTGATTACC CTCGTTTACT ATGCTAAAAT TCCTAGGACA 8220

GACGCTGCTA TCCCAATAGC AAATAGTAAG ATCAATAGTT TATACGTGTT CCAATTTCTC 8280

TTCTTGATCA AATAAAACAC TAAGATAGTT AAAATTACTG GAAGCATTTT AGGCATAATC 8340

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TACATTGCCA ACTGCATACT AGTAATGAAT GGCAGCATTT GAGGGTTGGT ATTATAAAAC 8820

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TCTAAGTTTG CACTCGCCGT TTCTTTCAGC TTCTCTGGTT CATCTTTATA GATTTTCTTC     8880
AGCGCTGGCA TGATCGTGTA TAAATAACTT ACCCCTTGAT AAGATGTATA ATTAAAAGCG     8940
TTCTGTAACA AATACGACCG TAGTGCTGTC TTCATGTAGT CTTTTTGGCT TAATTTTGGT     9000
GTCCTAGATT CCATTACTAA AATCCTCCTC TTCCATCAAG GTGGTTTGGC TTTCGTCTCT     9060
TATGCTCTTT TCTCCAACAA TCGTTTTATC TTTTCCATAA TATTGAATCA ACGCAAAGAC     9120
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TAGTAACACA TAAGGTGTCA GACTCTTTTC GAGCATCACA GACATGATCA TTGCAAAACC     9240
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TGCAACGGCA AAAGCTATAT ATGTTGAATT AGCAATCAGA TTAAAACGTG TATATTTCCC     9420
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ATTGGGTGGT ACGGTTCCGC CTGCTCCAAC ACCAAATCCC ATATAAGCCA ACTCGGCTAA     9660
AGCACCAAAT GTTAAAGCCG TTGGAATGTC ACCCAAAACA ACACCTACAA AAAAGGACAT     9720
AACCAGTGCA CGGTTTGTGT AAATTCCTAA TAGCTGCCCC GaATAACAAA AAGCTGTGAT     9780
CAATCCGATC AATATACCTT GAACTAATGA AATCTCCATC TGCTTCTCCT TCTCCTTCTC     9840
CTTCTAATTT AATTAGATAT TTTTTCCATC AATACATCTA AGTACTGTGA GCCATCATTT     9900
GAAAGTGGTG AAGTCTTGGT GTTGAAAGTT ACACCATAGT TATCTCGCAT CAAGCAGAGA     9960
GCTTGCTTAT CTTCTTTACC TAAATAGATA AATTGAGAGA TTTTCTCCTT GCCTTCGTCA    10020
GCATGAATAT TCCCAATATT TAACTGCTCC ATTGGAAAGC CCAATTTGCA TAGTTCTAAG    10080
GCATCATGCA AGTTTCCAAC GACTACAAAA ATTGTTTGAC TAGGGGCTGC TTTCCAAATA    10140
ACTTTTGCCG TACGTTCGAT CGTCCAAAAA CGAATATTTG TTTCTTTCGG GACTACCGTT    10200
TTCATCAGCG TCTGCTGTAA GCTATCCTCT GCCGCTTTAT CATTGGCACA AATAACTAAG    10260
TTCACTCCTA AACTCTTGAT CCATAGTTGA CCTTGTCCAT GTATCAGACG TTCATCTACA    10320
CGCACCATTT TTACATTGGG TTTTTGCATT TTCTTTCCTC CTGTTTTTAC CAGTACATTT    10380
TCCAATTTTT TTTGAATCGC ACTAAAGCTT CTAGATAGAA ATAATCACCC CAAATATTAC    10440
CTTCATTTAC GCCTTTACCA CTATGCCAAG AATAAACACC CTCATTCAGT AAAGCTGTAA    10500
TTCCGTCTGT TTTGGATTCA GTATAGTTTT CAGATAAGCT TCTTAGCATG GAATGctGCG    10560
CACACTTGTA AACCAACTTA TGACTGTTCG TCTCAGGTAA AAACGCGTCC ATTAGACTCA    10620
TACCACAAAC AGCAATCGcT GTCGCAGAAG TATCTCGGGA CTGTTCGGAA CCATCCATAA    10680
AAATCAGATC CCAATAACTA ACAAAATCCT TCGGcAAGCG ATTCAAGaAA TAATTCGTAA    10740
TCGCCtCAAA AATTTCTGTA TTCTCTTCCT CTGGACAGTA GGAGCGGAAC AATGCCAAAC    10800
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CATaAATCAA CCACGATTGT CCCCTCGCCC AGCTTGAACT ATCGGAATAT CCTTGGCGGG 10860

TTTTTcCATA CAAAGGATCG CCCGTTTCAG CATCGAaGAA AAACGTATGG TAAGCAGATG 10920

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AACGTTTATC TTGAGTCACT GTTGACGCCC AAAATAATAA TGGAATATTA AGTAAGCAGT 11040

CTACGATCAA ACGATAGTTA TCTTGATTGC CCAATTCTCC CCAAGCTTGG ATAAATTCTC 11100

CCTTAGATTG GTAGCGCTGC AATAATTTTT CTGCTGCACT TATCGCGGCA TTCTTAGCAG 11160

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TCCAAAAACC GTTTGTCCAT TCTGTATTAT CCATAGCTAt ATACGTAwTG TCCGTTGkTG 11400

ckGGTGTTGG GAATTaTCTC CCAGTTT 11427

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

CCCTGnGACT ATTTTTCTTA TCTCTTTTAT AAATAGAAGA GAAAGTATTC TGATTTTGTG 60

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ACCCATTTAT TTAGATCATG CGGCAACAAC ACCGCTTCAT CCAACGGTCA TTCAAGCGAT 180

GACTGAAAAT ATGCAAACGA CTTTTGGCAA TCCATCAAGT ATTCATCAGT TTGGACGAAA 240

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AAGTGAAGTC ATTTTACCTC ATGAATTAGG GATCGACTTA TTAAGTATTT CCGCTCATAA 720

AATCAATGGT CCAAAAGGCG TAGGTTTTTT ATTTAAAAGC GATGCAATCC AATTACCACC 780

TCTTTTACAT GGTGGGGAAC AAGAAGAAAA ACGACGTGCG GGCACGGAAA ACTTAGCTGG 840

AATTATTGGC ATGGGTACTG CCGTTTCATT ACTAACTTCT GCAGAAAAGC AAGCAAGAAA 900

AACAGCCTAT CAAAGTTTTC AAACGATTAT TTTAAAAGCG TTAGAAGAAG CCAATATTGA 960

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nGGAATcCCA GTGATTTGCT CTTAATGCAT TTGGACTTAA GAGGTATTGC GATTTCAACA 1080

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GAAAATTCCT CAGCTATTAA AGAATCAATC CGGATTAGTT TTGGCTACGG GAACACACCA 1200

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GGAACCCATG GCATTTACAA CAACGGCTGC TGTTGAAGGC TCAACAGTTT TTTACAAAGT 1380

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GAACTTTCAA TTGATTCGTT CCTTAGATCC AACGCCTCAG AGAAATGAAG GCTTCAAATT 1500

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TTTAAAACCA ATGAATATTT TcAAGAATGA ACAACATGAA ATGAGTAAAG AAAAATACTT 1620

TTTCTTAATG GATGGCTTAA TTAGCCGTGG TGTATTAGAG AAAGTAGAA 1669

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19031 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GGTGAGTGTT CTAGCAGTGC TGTTTGTGGC AGCTGCTTGT TCCTCAAAAC CAGAAGCGAA 60

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CATCTACGAT GATGGCAAAG AAGACGTCTT ACCGAAAGCC TTTGCCCGTG TCAAAGAACT 180

AGGCGATAAA ATCACCGTCA ACCAACCAGG TTCAGAAATT GATGAArTCA ACCAAGAAGC 240

AGGCGTGAAA CCAGTCAAAG TCTCAGATGA CTTGTATCCT TTGTTGAAAA AAGCCTATGA 300

ATACAGCAAA GACTCCCGCG GCGGCTTTGA CATGGCAATT GGCCCAATCA CCTCTATGTG 360

GCACATTGGC TTCGATGATG CCCGCAAACC AAGCCAAGCC GAAATTGATC AAGCCTTGAA 420

ACTTGTCGAT TACACGAAAG TCAAATTCAA CGACAAAGAG CAAACCGTTT ATCTTGAAGA 480

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GAAAGTTCTG AAAGACAACG GCGTTACCAC CGCTATTGTC GATTTAGGTG GGAATGTTTA 600

CGTCTTAGGA CACAGCCCGC GTGGCAAAGA CATGGATTGG ACAGTCGGGA TTCAAGATCC 660

GAATAAAGCC CGCAACACAG TCTTAGGTCA AGTCAAAGAA AGCAACAAAA CCTTAGTCAC 720

ATCAGGAATT TATGAACGCT ACTTAAAAGT CGATGGCAAA ACCTACCACC ATCTCTTTGA 780

TCGTGAAACT GGCTATCCGT TTGATAACGA CATCGCGGGT GTCACCATTA TCACCGACAA 840

ATCCATCGAT GGTGATGGTC TCTCAACAGC CGTCTTCTCA ATGGGCGTCA AAAAAGGACT 900

AGAATATGTC GAAAGTCTGA AAGGAACCGA TGCCATTTTC GTCACAAAAG ATGACAAAGT 960

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CTACATCAGC AAAGATATCG AAGGCAACTT TGAAATCGGC AAAGACTCTG GCTATACGAT    1020
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TTTCAATGAC CTATTTCGGG GAAGTTCAGT GGGGCAACAC GCTGGTTTTC TTCATTGGCA    1200
TGGTGGTCTT TGATATGGCC ACTACCGCCA TTAATAATTA CATGGACTTC AAAAAAGCCA    1260
AATCAGACGT CTATAAATAT GAAGAAAATA TTATCGGACA ATCAGGCGTT TCACCACAAC    1320
TGGTCCGCAA CATGATTTTC GCCATGATTG CCTTCACTGC CGTTGTGGGT GCGTACTTGA    1380
CGGTTCAAAC CGGCTGGCTC TTCCTTGTTT TAGGCGGGAT TTGCTGCTTC ATCGGGATTT    1440
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TCACGATGGG CTTAGGCATC TTCGTCTTAA CCGTTTACTT GAACGTCGTC ACCAATCCGC    1560
CTTTTTACTT AACGGTCGAT TTTGCTAGCG GCGCCTTTCG CTTAGACGGC AATCTCTGGG    1620
CGGTGCTTGC GATTGTCGTG GCGTCCTTGC CCTTGGTCTG TTCGATTGCT AACATCATGC    1680
TCGCCAACAA TTTACGGGAC TTAGACACGG ATATTGAGAA CCACCGTTAT ACATTAGTCT    1740
ATTATATTGG GCGCCCATCG GGGATTGTGC TGTTTCAAGT GTTAGCGCTA sctGGGTATC    1800
TGGTGATTTT ATTCGGCTTC ATTAGTGGTA TTTATCAATG GCCTGTGTTA ATTACATTTG    1860
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TATTCATTAG CGCCTTACTT GGTTAGTCTT GCGAAAAAAT AGCGGGCTGG GCGAAAAAAA    2040
TACTGTTTTT TTTCAGAGGC CTGCGTCAAA ACAATCAAAC AAAGCTCAAA ATGTTAGTAT    2100
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AAAAGCGTTA TTTAATGATT GTGTGTCTAC TATCTTCTCC TAGTTTTTTT ATAAATGTTG    2460
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CCGCTCCTAA AGATCCCCCA CCGAAAACAG ATGCGCCAGC TGCTGATCCC AAGGAACCAG    2580
CTGGTCCTCC GCAAGGAGAT CAACGAAgTG GTGGTTCGAC ACAGACCACC ACAACTGGCT    2640
CAACGCTCCC TCGTACAGGG AGCAAGAGTC AGGCAAATTT GAGCATTCtC nGnTTCGCCT    2700
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ACGGCAGTTG CGGAAACCGT GACGATTGAA AGTAGTCCGA CCGCCGAAAG TAGTGCCAAG    2880
GAAGAGACGC AAGCAAGTAG CGTGAAGGAA GAAACAACGA AAGCCAGTAC GGAAAATAGT    2940
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CAAGTAACAA CTGACACGAG TCAGGAAGAA GCAACGAAAG AAGCGGAGAA AGAAGAACCG 3000

CAAGCAGAAG TGGAACAAGC AGAAACACCA ATCATTCCTA AACCAAAAAA AATCAATATG 3060

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CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAAGG ATCATGGAAG 3180

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ACCTACAAAG TTGGCACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA 3840

ACCGAGCCTT TGGCCACCAC TAAAACACCT AGCTATAAAG TCACGTATGA TGACAATGAT 3900

GATTTGACGG TGGTCTATGA GGAGTTTTCA GGGTACGAGC TGCCTGCTTC GACCAATCAA 3960

TTTGGCTTTG TGGATGAAGC GACGAACAAA TTAATTGCCC CCGACCAAGT GCAGATGAAG 4020

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ACGTTATTTG GGACAGAGTC TGGCATCGAT GACCCAGTCA ATTATTATAC AATGAGTGGC 4440

CCTGTTTACT ATTATTTAGA AAACCGCAAA GTCACCGAGA aCTTCGTAGA CACCAACGGC 4500

GCTAAAATCA CACCGCCAAC AGGTTTCACC CAAGGTAAAA AAACGGTGAT TACAAGCGAC 4560

GCCTACACTT TCAAACAAGC AGGCACCTTA CCAGACACTT ACACAACAGG CGGTAAGACC 4620

TACAAGTTCA AAGGTTGGTA CAAAGGCAAG TCCATACTCA ACACATTGAC AACTACCAAA 4680

GCGCCAAGTT ATCAAGTGAC CTACGATGAC AATGATGATT TGAATGTGGT GTATGAAGAA 4740

GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAACT TTGTGAATGA AAAAGGCGGG 4800

GCTTTCACAC CGGCGTTAAC TTTTAGTGGT AAGTACTATG CGCAAAGTAC GAGTGCGTAC 4860

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AGTATTAATA ATGGTAGTAT GCCATTGTCC CAAGAATTAT TGAAAAAATA TAATAATGGA 4980

CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATTAGC CATCGACCAA 5040

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AAGTACACAG CGGCAAAAGC TTTACCAGCG ACGTATACTA CAGGTGGCAA AGTCTATACG 5520

TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACGT TGAACAAAAC AACAACTCCA 5580

ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAATA 5640

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CCCGCAAGAA GTGAGTGTTG AAATTCCTAA GTATTACCAG ACGATTTCGA TTTCACCAAC 8340

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GTATGACAAG G 19031

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1563 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

GAAAATTTAT CTTTGCCATT AATACGCAAA ATGATTTTTT GGATGATTCT CGTTTCTGCT 60

TTAATGGGGA TTGGGTTGTC ATTTATTGTC GGCTGGCCGT TATTAATggG TCTTTATTGT 120

TACTTAATTG GTATTTTTTA TTCATCAGGA CCGAAACCTT TATCTAGTCT ACCATTAGGG 180

GAAGTTTTCT CAGGATTTAC AATGGGGTTC ATGATTACCC TTATTTGTGT CTACATTAAT 240

ACGTTTGAAG TTTTCAATTG GTCAGCAGCT AATTTATGGG GGATTTTCTT AGTCGCCTTA 300

CCTAACACTT GTTACATTGC TAACTTAATG TTAGCAAATA ATATCTGTGA CTTAGAGGAA 360

GATGAAAATA ACAAGAGATA TACATTAGTT CATTACCTTG GCAAAGCAAG TTCTTTGAAA 420

TTATTCGTCG GATTAAATAC AATAGCAATG TTAGCCATTT TGTTAGCTGT CGGTTTAGGA 480

TTAACCCCGC CAACAATGTT ACTCATGCTT TTAACTTTAC CTTTTGtACG GAAACAAACC 540

CAAGCCTTAC TGAAGGAACA AGTGAAGAGT AAAACATTTG TTTGTGCTGT GAAGATCTTA 600

GCTGTGGGAG CAACTGCACA AGTGCTATTT TTTGCCATAG GTTTGTGGTG GCTGTAAATT 660

TTTTATAGAG TGGAAGGGAA TCAAAATGAA TAAGAAACAT GTTGTTATTT TAGGTGCTGG 720

TTACGCAGGC TTAAAAACAT TACGCGAATT ACAAAAAGGC GCCAAAGACG TCGAAATTAC 780

TTTAGTGGaT CGTAACAACT ATCACTACGA AGCAACGGAT TTGCATGAAG TTGCTGCTGG 840

AACACAACCA GCTGAAAAAA TCACATACAA TATTATGGAT GTTGTCGATG AAAAAATGAC 900

CACCTTTATC CAAGGAACAG TTAAAACAAT TGATGCTGCA ACACAAACAG TTGCTTTAGA 960

AGATGGCCAA ACAATCAATT ATGATTACTT AGTTGTTTCT CTTGGGTTTG AATCAGAATC 1020

ATTTGGTATC CCTGGTGTGC AAGAACATGC TCTACAAATG GTAGATGTGA AAACGGCTTT 1080

AAACGTGTAT GAACATATCC AAGAACAAAT GCGTCAATAT AAAGCAACTC AAAACGAAGA 1140

ATTCTTAAAA ATTGTTGTCT GCGGAgcAGG CTTTACAGGG ATTGAATTAT TAGGTTCTCT 1200

TGTTGAAAAC AAACCAAAAT TTGCTGAAAT CGCAGGTGTC TCAGCAGATC AAATCCAAAT 1260

TTATTGTGTC GAAGCAGTTA CTCGCCTATT GCCGATGTTT AACGAAAAAC TTGCGAACTA 1320

TGGTGTGCAA TTATTAAAAG ATTCAGCTAT TCATTTATTA TTAGGTAAAC CGATTAAAGA 1380

AACAAACCAG GCGCAGTTGT TTATCAAGAT AACGAAGCAG GCGACTTGGC AGAACTTTCT 1440

GCTAAAACAA TTATTTGGAC AACGGGTGTT AGTGGGAGCC ACGTTGTAGG CGATTCTGGC 1500

TTTGAAGCTC GTCGTGGTCG TGTCATGGTT CAACCAGATT TAACAGATGC GAACCATAGC 1560

AAC 1563

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

AAGCGTTGAC ACTCGTGATT TTATTCAAAA CAACTACACA GAGTACAAAG GCGACGACAG 60

TTTCTTAGAA CCAATCGCTC CGAGCACTGA CAAATTATGG ACAAAACTAC AAGAATTATT 120

TGAAATCCAA CATGAAAAAA ATGGCGTTTA TGACATGGAT AGCGATATCC CAGCAACTAT 180

TACGTCACAT GAACCTGGTT ACTTAATCAA AGAAGAAGAA AAAATTGTCG GTTTACAAAC 240

AGATGTACCA TTAAAACAAG CATTTATGCC ATTCGGTGGT ATTAAAATGG CGAACAATGC 300

CTTAGTTTCA AATGGTTATG AAACTGACGA AGAAATGACA AAAATCTTCA CAGAATACAG 360

AAAAACACAT AACCAAGGTG TTTTTGATGC CTACACAGCT GAAATGCGTT TAGCACGTAA 420

AAACAAAATC ATTACTGGTC TTCCAGATGC TTATGGCCGT GGCCGTATTA TCGGTGACTA 480

TCGTCGTATC GCATTATATG GTATCGACTA CTTAATGGAA CAAAAGAAAA AAGATCATGA 540

TAACACTGGT AACAAAGAAA TGACAGACGA TGTTATTCGC TTACGTGAAG AAATTTCTGA 600

ACAATACCGT GCGTTAAATG ACTTAAAACA AATGGCTGCT TCTTATGGTT TCGATATTTC 660

TCGTCCTGCT GCAAATGCGC AAGAAGCAAT CCAATGGTTA TACTTTGGTT ACCTAGGTGC 720

CATTAAATCT CAAAATGGTG CGGCAATGTC AATTGGTCGT ATCTCAGCAT TCTTAGATAT 780

CTATATCCAA CGTGACTTAG AAGCAGGTTT AATCACTGAA TTTGAAGCAC AAGAAATGAT 840

TGACCATTTA ATCATGAAAT TACGTATGGT TAAATTTGCA CGTACACCAG AATACAACCA 900

ATTATTCTCT GGTTATCCAA TTTGGGCAAC ATTATCTATT GCTGGTATGG GTATTGACGG 960

TCGTTCATTA GTTACCAAAA ATGACTTCCG TATCTTACAC ACCTTAACAA ACATGGGACC 1020

ATCTCCAGAA CCTAACTTAA CTGTATTGTA TTCTTCTCAC TTACCAGAAG GTTTCAGAAC 1080

ATATGCAGCT AAAATCGCGA AAGAAAGCTC ATCTATCCAA TTTGAAAACG ATGACTTATT 1140

ACGTGAAAAC TGGGGCTCTG ACGACTGTGC AATCGCATGT TGTGTTTCTG CAACAGTTAT 1200

GGGTAAAGAT ATGCAATTCT TCGGCGCTCG TGCGAACTTA GCGAAAGCTG TTCTTTATGC 1260

AATTAACGGC GGGGTCGACG AAAAAACTAA AATGCAAGTA GCACCAAAAT ATCGTCCAAT 1320

GACTGGTGAC AAATTAGATT ACCATGAATT CATGGaACGC TATAAAGACA TCTTAGACTG 1380

GTTAGCTGAA TTGTACGTTA ACACATTAAA CATTATTCAT TACATGCATG ATAAATATGC 1440

ATATGAAGCA CCACAATTAG CTTTAATGGA TACTGATTTA CAACGGACAT TCGCAACTGG 1500

TATTGCCGGa ATCTCTCATG CGACTGATAG TATCATGGCA ATTAAACACG GTGAAGTAGA 1560

AGTAATCCGT GACGAAGATG GTATGGCAAT TGATTATGTA CCAACAAAAG AATTCCCAAC 1620

ATACGGAAAC GATAACGAAG AAGCCGATGC AATGGCTAAC TGGATTTTAG ATTACTTTAT 1680

GACACAAATT AAACGTCAAC ACACATACCG TAACTCTAAA CCAACGACTT CATTATTAAC 1740

AATCACTTCA AACGTTGTTT ATGGTAAAGC AACAGGGAAC ACGCCTGACG GACGTCGTGC 1800

TGGCAAACCT CTTGCACCAG GTGCGAACCC AAGTTATCAA GACGGTAAAT TCTTAGGTGA 1860

GAAAAATGGC TTATTAGCTT CATTAAACTC AACAGCTCGT TTAGAATATA CAATCGCTTT 1920

AGATGGTATT TCTAATACAC AAACCATCAA CCCTAATGGT TTAGGTAAAG ACGACGACAC 1980

AAGAATTAAC AACTTACGTA ACGTATTAGA TGGCTACTTC GATAAAGGTG GTTACCACTT 2040

AAACGTAAAC GTATTTACAA ACGAATTATT ATTAGATGCA CAAGCACATC CAGAAAAATA 2100

TCCAAACTTA ACTATCCGTG TATCTGGATA TGCCGTGAAA TTCCGTGACT TAACTCCTGA 2160

ACAACAAGCA GACGTTATTT CAAGAACTTC ACACGACAGA CTATAAAAAA CATTTACATT 2220

ATTTAACTGA AAGGGTGACA TTTAACGTGT CATCCTTTTC GTTTGAAAGA AGAGGGATCA 2280

TTATGACAAC ACCAGTTACA GGTAGAATTC ATTCAACAGA AAATTTTGGT ACCGTTGATG 2340

GCCCAGGTGT CCGTTTTATC GTATTTACAC AAGGGTGTCG CATGAGATGT CAATTCTGTC 2400

ATAATCCAGA TACTTGGAAA ATTGGTTCCG GTGGTCGTGT GGTGACGACT GACGAAGTAT 2460

TAGAGGAAGC ATTACGTTTT CGCTCTTATT GGGGCGAAAA GGGTGGTATC ACTGTCAGTG 2520

GTGGTGAGCC GCTATTGCAA ATGGACTTTT TGATCGATTT ATTTAAAAAA GCCAAAGCAC 2580

AAGGCATTCA TACAACCTTA GATACGTGTG GCAAGCCTTT TACTCGGGAA GAACCCTTCA 2640

TTAGTCAATT TGATGAATTG ATGAAGTATA CAGATTTACT CTTATTTGAC ATCAAACATA 2700

TTGATAACGA GCAACATAAA CTGTTAACAA CGCAATCAAA TGATAATATT TTAGAGATGG 2760

CTACCTATTT ATCTGAAATT GACAAACCTG TTTGGATTCG CCACGTATTG GTGCCTCAAC 2820

GTAGTGATTA CGACGAATAT TTAATCCGTC TGGATGCCTT CATAAAAACA TTAAACAATG 2880

TAGATAAAGT TGAAGTGCTT CCTTACCATA CGATGGGCAA GTACAAATGG GAAGAACTAG 2940

GTATTCCTTA TCCATTAGAA GGAATTGAGC CTCCTAAAAA TGATCGTGTT GAAAATGCGA 3000

AAAAACTACT ACATGTCGAG GACTATCAAG GTTATCTAGC ACGTTAACAA ACGAAAAAAT 3060

AGAAAAGAAG ACAATTTTTT TGTTGTTTCT TTTCTATTTT TTGTTATCAT TAAGAGTGAA 3120

TCAAAACCAA GGAGTGTGTA TTATGTCAAA AATTTTAGTT TTTGGACA 3168

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1282 base pairs
(B) TYPE: nucleic acid

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

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

ACCATCTTAA TTTGACAATG AATGACACTG GTTGAGAAGT CGATTCCAAT ATGGAAGGCT 60

CTGTCAGCTA GTTTTTCACT CTACCAACAA AATAATCAAC CAAAATAACA ACGGAAAGCC 120

AAACAAGAAA CATACTAATC ATGCTTCTtC AAAGAAGCAC AAATAAAAAA GTGATGACTC 180

GAGAAGAAAA TCTCTATGGA GTCATCGCTT TTTCTTATAT TTTAGTTAAA AAATTATTTT 240

ACTAAAGGTT GAAGTAACTT GTTCCAGAAA CTAATAAGTG GGCCAGCACC AAATGCACAA 300

ATAATTGTAC CAATCCCAAT TGGACCACCA GCAATAAAGC CAATTAATAG GACCAACAAA 360

TCTTGTGCTT TTCGAACAGA AGCGTAAGGT TTGTTGGTTT GTTGACAGAT GGTTGGCGCA 420

ATCGCATCAT AGGGGGACTC GCCTTGATCT GTAGCCATGT ATAAGGCGCA gcCAAATGTA 480

AAAATCAGGA CTCCGACGAA TAAAGAAAGT AGTTTGCCAA TTGTTGAGCC TCCTAAACTA 540

TTGGCATAAG GTTGAAGCCA AGTAGAAATC TGTTGAATCA AAATTCCTAC TAAAAGCATA 600

TTTAAAATAG TTCCTAGACC AATGGCTTTT TTGTTTTTTA AATAGACATA GAATAAAATA 660

AACGCATTGA CAATAATTTG AAAAATGCCT AATTGCATAC CAAACATCGA AGAAAGTCCG 720

ATATTCATAG CAGTGAAAGG ATCAACTCCT AAACCTGCCA CTCTTAAAGT GGATGCGCCA 780

ATCCCGATAA TAACTAAACC AATTAAAATT AAAAGAACAT TTTTGACTAG TTTCATGGTA 840

AGCCTCCTGA ATAGATTTTG TGTGTGATAG TACAAAGTCT GCAACAAAAA TTCATAGAGA 900

ATTTTGTTGC AGACTACTTT TTAACCAGCT CCGTGTTGGA ACGAAGGATA TAGAGACATC 960

CCGCCATCTA CAAAGAGTGT TGTTCCGGTT ACGTATGAGG ATTCATCAGA AGCTAACCAA 1020

GCGGCCGCAG CAGCTACTTG ATTTGGTTTA CCAATAATAC CCATAGGAAC CATGCTTGTT 1080

GTTTGTTTTA ACTGTTCGGG ATCGGAAAAT TTTTCAGCAT TAATAGGTGT GTTAATCGCT 1140

CCAGGCGCAA TACAGTTGGC ACGAATACCA TATTCCGCAT ATTCCAAAGC GATTGTTTTC 1200

GTGAACATTT CGGTTGCGCC TTTACTTGCC GCATAGTGGG CGAACGTTGG CCAAGGAATC 1260

TTTGGTGTAC GGAGACATAT TA 1282

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

nnAAATAAAG AAATCATAAA ATAACTTTAA AAGTCCTCTT TTAAAGGAAA ATGTCTGTAA 60

AATAGAGAGA AATGGTTTTC TTTCTCGTCA AGTAATGATA AAATAAAACG GATAGATTGT 120

GCTTCTTGTA CAAAAAGGAT ACAAAAATAA AAAGAGGTAA TTGAAAGGAA CACAGATACC 180

AATGGCAAAT TTTTTGAAAA AAATGATCGA AAACGATAAA AAAGAATTAA GACGATTAGA 240

AAAAATCnCC GATAAAATTG ATGCACATgC AAGTGCAATG GAACAACTAA GCGATGAACA 300

ATTACGTGAA AAAACAGATG AATTTAAAGC CCGTTATCAA AAAGGGGAAA CCTTAGACGA 360

ACTATTACCA GAAGCGTTTG CGGTTGTCCG TGAAGCTGCT AAACGAGTAC TAGGTTTATT 420

CCCGTACCGT GTCCAATTAA TGGGTGGGAT TGTGCTTCAT GACGGGAACA TTCCTGAAAT 480

GAGAACAGGT GAAGGGAAAA CCTTGACTGC CACAATGCCT GTATACTTGA ATGCACTATC 540

TGGCGAAGGA GTACACGTTG TTACAGTTAA TGAATACTTA GCAACCCGTG ACTCTAACGA 600

AATGGGAGAA TTATATAATT TCTTAGGCTT AAGCGTTGGC TTAAACATTA ACTCTAAATC 660

TTCTGATGAA AAACGTGAAG CGTATAACTG TGATATCACT TATAGTACAA ATAACGAATT 720

AGGATTTGAC TATTTGCGTG ATAACATGGT TGTTTATCGC AGCCAAATGG TTCAACGTCC 780

ATTAAACTAT GcAATTGTCG ATGAAGTGGA TTCAATCTTA ATTGATGAAG CAAGAACCCC 840

ATTAATTATT TCTGGACAAG CTGAAAAATC GACAGCACTT TATACGCGTG CCGATAATTT 900

TGTCAAACGC TTAAAAGAAG ATGAAGATTA CAAAATTGAT ATTCAGTCTA AAACAATTGG 960

TTTAACAGAA GCAGGTATTG AAAAAGCTGA ACAAACTTTT GGATTGGATA ACCTTTACGA 1020

TATTGAAAAT ACAGCATTAA CGCACCATTT AGATCAAGCG TTACGGGCAA ACTATATCAT 1080

GTTACTAGAC ATTGATTACG TGGTTCAAGA CAATAAAGTC TTAATTGTTG ACCAATTTAC 1140

TGGTCGTATC ATGGATGGTC GTCGTTATTC TGATGGCTTG CATCAAGCGA TTGAAGCAAA 1200

AGAAGGCGTC GAAATTGAAG ATGAAACAAA GACAATGGCG ACGATTACGT TCCAAAACTA 1260

CTTCCGGATG TACAAAAAAC TAGCCGGGAT GACTGGTACT GCTAAAACAG AAGAAGAAGA 1320

ATTCCGTGAA ATTTACAATA TTCAAGTCAT TCAAATCCCA ACCAATCGTC CAATTATCCG 1380

TGACGATCGT CCAGATTTAC TTTATCCAAC CTTAGAAAGT AAATTTAATG CAGTGGTGGA 1440

AGATATTAAA GAACGTTACC ACAAAGGGCA ACCAGTGTTG GTGGGGaCTG TTGCGGTAGA 1500

AaCGTCAGAA TTACTTTCTG ATAAATTAAA CGCAGCTAAA ATTCCTCATG AAGTATTAAA 1560

TGCGAAAAAT CACTTTAAAG AAGCCGAAAT CATTATGAAT GCCGGTCAAA AAGGCGCAGT 1620

TACAATTGCA ACAAATATGG CTGGTCGTGG AACGGATATT AAACTTGGTT TAGGTGTACT 1680

TGAACTAGGT GGTCTAGCAG TTATCGGGAC AGAACGTCAT GAGTCACGTC GTATTGATAA 1740

TCAGTTGCGT GGACGTGCAG GACGTCAAGG GGATCCAGGG GTTTCACAAT TTTATTTATC 1800

TTTAGAAGAT GACTTAATGA AACGCTTTGG TTCAGAACGA ATTAAAACAT TCTTAGAACG 1860

AATGAATGTG CAAGAAGAAG ATGCAGTTAT TCAAAGTAAA ATGTTTACTC GCCAAGTAGA 1920

GTCTGCTCAA AAACGTGTGG AAGGAAATAA CTATGACACA CGTAAAAATG TCTTACAATA 1980

CGATGACGTG ATGCGCGAGC AACGTGAAGT TATTTATGCG CAACGACAAG AAGTAATTAT 2040

GGAAGAAAAT GACTTGTCTG ATGTATTGAT GGGCATGGTA AAACGGACGA TTGGCCGAGT 2100

GGTGGATAGC CATACACAAT TAGAAAAAGA AGAATGGAAT TTAGATGGGA TTGTCGATTT 2160

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TGCAGCCTCA ACACTTGTCC ATGAAGATAC GATTTCTAAA AAAGATTTAG AAAATAAATC    2220
AGCTGAAGAA ATCAAAGACT ACTTAGTGGC ACGTGCGCAA GAAGTATTTG AAGAAAAATC    2280
TCAACAATTG AATGGCCAAG AACAATTGCT AGAATTTGAA AAAGTAGTCA TCTTGCGTGT    2340
TGTCGATACT AAATGGACAG ATCACATTGA TGCAATGGAT CAATTACGCC AATCTGTCGG    2400
GTTACGTGCG TACGGTCAAA ACAACCCATT AGTAGAATAT CAAACAGAAG GTTATTCTAT    2460
GTATAACAAT ATGGTGGGTT CAATCGAATA TGAAGTAACA CGTTTATTCa TGAAATCGGA    2520
AATTCGCCAA AATGTCCAAC GTGAGCAAGT AGCTCAAGGA CAAGCGGAAC ATCCAGAAAC    2580
AGAACAAGAT GCAGCTGCAC AAAGCAACAC AAGTGCGAAg CGTcAACCTG TGCGTGTAGA    2640
TAAAAAAGTG GGCCGTAATG ATTTATGCCC ATGCGGAAGT GGCAAAAAAT TCAAAAATTG    2700
TCATGGAAGA AACGCTTAAT TAAAGAAAAA ACGCAGGGTG GGGCAATTTG TCCCGCCTTT    2760
GCTCTTTTTA CAATAAAAAG AAAGAAGGAA TCATTTTGGA AAACCCAGAA ATTCGTACAT    2820
TATTAGACGA AATGACACAA AAAATTACTA GCTTCAGGAG GTCTCTTTGA CTTAGACCAG    2880
TTAGAAGAAG ACATTGCCGA GGCGGAAAAT CGGATGGGAG AACCTGGTTT TTGGGACAAC    2940
ACAGAAACGG CTCAAAAGCT AATTAATGAA ACCAATAGTT TGAAAGAAAA ATATCAACAA    3000
TTTCATCAGC TCTCTGAGGA AATTGACGAA TTAACGGTGA TGTTTGAATT ACAACAAGAA    3060
GAATATGATG CAGAGATTCA AGAAGAATTG GAAGAAAGAA TTCATCTCTT GCAAGAACGT    3120
TTAACAACGT ATGAGCTATC CTTACTACTA AATGAGCCAT ATGATCATAA TAACGCCCTA    3180
ATTGAATTAC ACCCTGGTGC CGGTGGTACT GAATCACAAG ATTGGGGAAG TATGCTTTTA    3240
CGAATGTACA CACGTTGGGC AGAAAGTCAC GGTTTCCAAG TTGAAACGTT GGATTACCAA    3300
GCTGGAGATG AAGCAGGGAT TAAAAGTGTC ACCTTATTAA TCAAAGGTTA CAATGCTTAT    3360
GGTTACCTAA AATCTGAAAA AGGTGTCCAT CGTCTTGTGC GGATTTCGCC CTTTGATTCC    3420
GCTAAACGCC GTCATACTTC GTTTTGTTCA GTTGATGTAA TGCCTGAATT AGACGACACA    3480
ATAGAAATTG CGATCAATCC AGATGACTTA AAAATTGATA CCTATCGAGC AAGTGGTGCC    3540
GGTGGTCAGC ATATTAATAA AACAGAATCG GCTGTTCGAA TCACACATAT TCCAACAGGT    3600
ACCGTTGTCG CAAGCCAAGC ACAACGTTCT CAATTAAAAA ACCGTGAGCA AGCAATGAGT    3660
ATGTTAAAAG CCAAATTATA TCAATTGGAA ATGGAAAAGA AAGCCCAAGA AGCAGCAAGT    3720
TTACGTGGTG AACAAATGGA AATTGGCTGG GGCTCACAAA TCCGTTCTTA CGTGTTCCAT    3780
CCGTATTCAA TGGTCAAAGA CCATCGGACA AATTACGAAA CCGGCAATGT ACAAGCTGTG    3840
ATGGATGGAG ACCTTGATGG TTTCATTGAT GCCTACTTAA AACAGCGCTT AAGTTAAGCT    3900
CTTCATTAAA TTGAAATAAA AATGTAACTT AATGCAAGAA GTTTGCAATA TTGACATGTT    3960
ATAATGAGTA GGATTGAAGA AAAAAGAGAT GGAGAGAACG CCATGATTGA AATGAAAGAT    4020
GTAATGAAGA AATATTCGAA TGGTACAACA GCGATTCGGA ATATTTCAGT AGAGATTGAC    4080
CAAGGCGAGT TCGTCTATGT GGTTGGTCCC TCAGGTGCAG GGAAATCAAC CTTTATTAGA    4140
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TTAATGTATC GTGAAGAAAA AGCAACAAAA GGTAATTTGA CAGTTGCAGG TCATGATTTA 4200

ATGAAAATAA AAAATAAAGA AGTTCCTTAT TTACGTCGTG AAATCGGCAT CGTTTTCCAA 4260

GACTATAAAC TATTACCAAA GAAAACTGTG TATGAGAACG TGGCCTATGC GATGCAAGTT 4320

ATCGGACGGC GTCCTCGCGA AATCAAAAAA CGCGTGATGG AAGTTTTAGA TTTAGTCGGT 4380

CTAAAACATA AGGTACGTGT TTTTCCAAGC GAACTTTCTG GTGGGGAACA GCAACGGGTA 4440

TCCATTGCAC GAGCAATCGT AAATACACCG AAAGTTTTAA TTGCCGATGA ACCAACTGGG 4500

AACTTAGATC CAGAGAATTC ATGGGAAATC ATGAAATTGT TGGACCGGAT TAATGCACAA 4560

GGAACAACAG TCGTGATGGC AACGCATAAT AGTACAATTG TAAATACGAT TCGTCACCGT 4620

GTTATTGCCA TTGAAAATGG TCGCATTATC CGTGACCAAG TGGAAGGAGA ATACGGCTAC 4680

GATGATTAGA ACATTCTTTT CTCATTTATT TGAAAGTATC AAAAGTTTAA AACGGAACGG 4740

TTGGATGACT GTTGCCTCAG CAAGTGCGGT TACAATTACA TTAGTTTTAG TTGGTATTTT 4800

TATGGGCGTT ATTTTTAATG CAACGAAACT TGCTGATGAT ATCGAAAAAA ACGTGACAGT 4860

GTCTGTCTTT GTCGATATTG GTACAAAACA AAATGAAATG AAAACATTAG AAAAACAACT 4920

TAAAGGATTA GACAATGTTG AAGATATTTC TTATTCAAAC AAAGATCAAC AATTGAAAAA 4980

AATCCAAGAA CAAATGGGGG ATGCCTGGAA TCTTTTCGAA GGCGACAGTA ACCCATTATA 5040

CGACGTGTAT TATGTCCGTG CAAAAACACC AGAAGACACG AAAGATATTG CGAAACAAGC 5100

AGCTAAATTC CCAAGTGTTT TTAAAGCCGA TTACGGTGGT GTAAACTCAG ACAAAATCTT 5160

TAAAATCGCT CAAACCGTTC GAACTTGGGG CTTAGCAGCT GCTGCATTAC TTTTATTCGT 5220

TGCAGTGTTC TTAATTTCCA ACACTATTCG GATTACGATT TTATCTCGTC AAAAAGAAAT 5280

CCAAATTATG CGTCTTGTAG GAGCCAAAAA CAGTTTCATT CGTTGGCCGT TCTTCTTAGA 5340

AGGTGcTTGG aTtGGGtTGA TTGGcGCAAT CGTGCCAGTC ATTATTAkGA CGTTAGGCTA 5400

CCATCAAGTT TATAACATGT TCAACCCGCA GTTATTGCGT TCGAATTATT CATTAATTCG 5460

TCCAGAAGAT TTTATCTGGA AAGTCAATCT ATTAATGATT GCAACAGGAA TGATTATTGG 5520

ATCACTAGGT TCAGTTATTT CAATGCGTCG TTTCTTGAAA ATTTAAACGA AAAAAAGCTC 5580

TCCATTTTGG AGAGCTTTTT TTGTTTTAGT TTTAAAATAC TTGTTATTTA ATTTAAGAGT 5640

TTTCTCAGTT GTACCAACAA ATTGATAACT TATAATTTTC AAGTCCTACA TATAATGGTA 5700

AAATAGAATG GATTGAAATT AATTGGAGGA ATAATGAATC GATGAAAAAA AGATTGCTAT 5760

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GTGAATCCAT CACAGCGGTA GGCTCATCAG CTTTACAACC ATTAGTAGAG ACAGCGAGTG 5880

AGGAATATCA AAGCCAAAAT CCGGGAAGAT TTATTAATGT CCAAGGTGGC GGAAGCGGAA 5940

CAGGTCTGAG TCAAGTCCAA TCTGGCGCGG TAGACATTGG TAATTCTGAT TTATTTGCAG 6000

AAGAGAAAAA GGGCATCAAA GCGGAAGACT TAATTGATCA TAAAGTTGCT GTCGTTGGGA 6060

TTACACCAAT CGTTAACAAA AATGTCGGTG TCAAAGATAT CTCAATGGAA AATTTAAAGA 6120

AAATCTTTTT AGGTGAAGTA ACAAACTGGA AAGAACTTGG CGGGAAAGAC CAAAAAATTG 6180

TTATTTTGAA TAGAGCGGCC GGTAGTGGTA CGCGTGCGAC TTTTGAAAAG TGGGTCTTGG 6240

GAGATAAAAC AGCCATTCGT GCGCAAGAAC AAGATTCCAG CGGCATGGTT CGTTCCATTG 6300

TTTCTGATAC ACCAGGAGCG ATTAGTTATA CCGCATTTTC ATATGTTACT GATGAAGTAG 6360

CTACGTTAAG TATTGATGGT GTTCAGCCAA CAGATGAAAA TGTAATGAAC AATAAATGGA 6420

TTATTTGGTC TTATGAACAC ATGTACACTC GTAAAAATCC AAGTGATTTA ACCAAAGAGT 6480

TTTTAGACTT TATGTTGTCa GATGATATCC AAGAACGTGT GATTGGTCAA TTAGGGTATA 6540

TTCCTGTTTC GAAAATGGAA ATTGAACGGG ATTGGCAAGG AAATGTCATT AAATAATTCT 6600

CTTAACACAA AATTTACAAA CTTAACATAA AATTTACATG TTATTAAAAA CAAATTGATG 6660

TAAAAAAGGT ACACTATTTT TATCTGTAAA AGTTGGATTG TTTGAGGAGG AAATATTCTT 6720

GGAAGATGTA CAGAAAAAAT TATTAACAAA ATCGAAAAGA GCCAAGATGG AGCAACGAGG 6780

GAAATTTATT AGTTTCCTAT GTATTGCCTT AATTGTAGCA GTGGTTGTTT CAATTTTCTA 6840

TTTTGTTGCA AGTAAAGGAC TTGCTACATT CTTTAAAGAT AAGATTAATG TGTTTGATTT 6900

CTTATTTGGA ACAAACTGGA ACCCAAGTGA TATCGGTGCA GACGGTAAAC CCATGGTTGG 6960

GGCTTTACCG ATGATTGCGG GTTCCTTTAT TGTAACGTTT TTGTCAGCGA TTGTTGCGAC 7020

GCCATTTGCG ATTGGAGCGG CTGTTTTTAT GACAGAAATT TCACCTAAAA AAGGAGCAAA 7080

ATTTTTACAA CCAGTTATTG AATTACTTGT AGGGATTCCC TCTGTTGTTT ATGGATTTAT 7140

TGGTTTATCT GtCATTGTTC CTTTTGTCCG TTCAATCTTT GGCGGAACTG GCTTCGGTAT 7200

TTTAGCTGGT ACGTTTGTGC TATTTGTCAT GATTTTACCA ACGGTCACTA CGATGACCGT 7260

AGATGCATTA AAAGCCGTGC CTAGACATTA TCGTGAAGCG TCGTTGGCGC TTGGTGCTAC 7320

GCGTTGGCAA ACGATTTATA AAGTTGTCTT GCGGGCAGCT GTGCCTGGTA TTTTAACTGC 7380

GGTTGTCTTT GGTATGGCTC GTGCGTTTGG TGAAGCCTTA GCAATCCAAA TGGTAATCGG 7440

AAATGCAGCT GTGATGCCAA CTAGTTTGAC AACACCAGCT TCGACACTAA CAAGTATTTT 7500

GACAATGGGG ATTGGGAATA CAATTATGGG AACAGTTGAA AACAACGTTC TTTGGTCTTT 7560

AGCCTTGATT CTATTGTTGA TGTCTTTACT ATTCAACATT GTTATCCGAA TTATCGGTAA 7620

GAGAGGAGCC TTAAAATAAT GAATGCAAAA AAAGCAGATA AAATCGCAAC AGGTATCTTA 7680

TATGCCGTAT CTGGCGTCAT TGTTTTAATT TTGGCGGCCT TACTGATTTA CATTTTAGCT 7740

AGAGGAATTC CACATATTTC GTGGGAATTT TTAACACAAC CATCCAGAGC CTATCAAGTT 7800

GGTGGTGGGA TTGGTATTCA GCTGTTTAAC TCACTATATT TACTATTGAT TACAATGATT 7860

ATTAGTATTC CAATTTCATT AGGTGCTGGA ATTTACTTAT CGGAATATGC GAAAAAGAAT 7920

TGGTTAACTG ATTTAATTCG TACCTCGATT GAAATTTTAA GTTCATTGCC TTCCGTTGTT 7980

GTCGGGCTGT TCGGCTTCTT GATTTTCGTT GTACAAATCG GATATGGCTT TTCAATCTTA 8040

TCAGGTGCGT TAgcATTAAC ATTTTTTAAC TTACCATTAT TGACTAGAAA TGTTGAGGAA 8100

TCTTTGAAAG CCATTCATTA TACACAGCGT GAAGCGGGGT TAGCCTTAGG TCTTTCACGT 8160

TGGGAAACAG TTAAAAAAGT TATTTTGCCA GAAGCATTAC CAGGAATTTT GACAGGTGTT 8220

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AGCGCACCTG CCTTAGATTT CAGTAATTGG AATCCATTGA GCGTTTCAAG TCCAATTAGC 8340

ATTTTCCGTC AAGCGGAAAC GTTGGCTGTG CATATTTGGA AAATTAATAC CGAAGgAACG 8400

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TGGACCTTCT GGTTGCGGTA AATCCACGTA TTTACGTTCG CTAAATCGTA TGAACGATGG 8760

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TGGTTAGTAG TGCCGTCCAT AAATCCgTGA AGGCATATAT TAATCATGAT AAAAAATTGG 10260

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TGrTTATcTA CATGTGGCAC AATACTTGGA AAGAATTGGC GACTATGTCA CAAATATTTG 10740

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AAAGATCGTG AAAACTTAGA AAGAATTCTT GATGAGTTAG CAACAAAAGC CAATCGTGCT 11340

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GAATGGAAAG ACATTAAAAT GAAAGTTCCT GGTGTGGCAA CAACTAAGTT TGAACATGAG 11820

TTTAACTATC CAAATCCACA AGCAAGTTTA ATTGATGTCA AGGTAGCAAA T 11871

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8084 base pairs
(B) TYPE: nucleic acid

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

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

AATGGGTAAC AGATTTAAGA TGGAAGATGG TCTTTGAGCA GAGTAAGTGA GCGAACAGTG 60

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GGCATTAATT GAATTACGTC ATGTAAAAAA AGAGTTTTCC GGTAAAGCGG GTAAAGTCAC 360

GGCTTTAAAA GATATTGATT TAACAGTTGA ATCAGGTGAT ATTTATGGCA TTATTGGcTA 420

TTCAGGTGCA GGAAAAAGTA CGTTGGTTCG CCTATTGAAT GGACTTGAAA CACCTACAGA 480

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CCTAGAAAAT ATCATGCTCC CATTGGAAAT TGCTGGCGTT CCAAAACAAA ATCGGAAAAG 660

CCGCGCAGAA GAGTTAATCA AGTTGGTTGG TTTAGAAGGA CGGGAAACCG CCTACCCAAG 720

TCAACTCTCT GGTGGGCAAA AGCAACGAGT GGGGATTGCC CGTGCCTTAG CTAACAATCC 780

TGACATTTTG CTTTGTGATG AAGCAACGAG TGCTTTGGAT CCGCAGACAA CTGATGAAGT 840

GCTAGAATTA CTACTAAAAA TCAACCAAGA ATTAAATTTA ACGGTTGTAT TAATTACCCA 900

CGAAATGCAC GTGATTCGTA AAATTTGTAA TCGCGTAgcT GTGATGGAAT ATGGTGAAAT 960

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CTTTATCCAA CAAGAAGCGG ATAAAAACAT TGAAGAAACG GAACTGGTTG TTGAAGAAAT 1080

GTTGGAACAA TATCCGAATG GAAAAATTGT TCGCCTGCTT TTCCACGGTG AACAAGCGAA 1140

ATTGCCAATT ATCTCGCATA TTGTCCAAGA ATATCAAGTA GAAGTTAGTA TTATTCAAGG 1200

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GAGCTATAAA CTAGAAGTCA TTCAAGAAGC AAAGCGTTGG GATTATCTCA TCTCACCTAA   5760
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GTAGAAACCT ATTTAGAAGA GGCATTAATG AGTTTGAAAn ACCA 8084

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

TTnCnCCCAA AATGGwTTGk CCGrAGtGCy TAmCTGGaGG AGrATGCyTC CTTtCyTATC 60

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aGCgACTGGG GAAGAGGAAA AAAATAGGAA ACAGCACTGT CATAAGCATA GAGGAAGAAA 180

AGGCCATGCT GCCTATGCAG AACATCTTTA TCAAATAATT GATCATTCGA AATTAACCAT 240

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GAATGCTGTC AATTATTGCT GTCTTAGTAT TAGCAATTGC AGCCGTCGTT TTCCAAATTC 2340

AAACACCAAA AGTATTAGGA CAGGCAACAA CTGAAATTTT TAAAGGCGTC ATGAAAGGCG 2400

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AATTAATTAC CAGTATCGTG ACATTTGTGG GTGTACTTTG GATGATGCTG ACCATTAGCT 2760

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TGGCGCCTCG CTCGCAAAAA CATTTTGCGG CTCAACAAAA AAGCTTAGGA TTATTGAATA 2880

ACCAAGTCGA AGAAACtACG GTGGTCACGT AGTAGTAAAA AGTTTCAACC ACGAAGAAAG 2940

TGATCAAGAA GTATTTGAAA AAGAAAATGA AAAATTATAT CATGCTGGTC GCAAAGCACA 3000

ATTTATTTCA GCGATCATTA TGCCTTTAAT GAACTTTATC AAAAATCTAG GCTACGTGTT 3060

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GAATACAATC CAAGCTACGG TGGCTTCGGC AGAACGTGTC TTTGAAGTAT TAGATGAAGA 3240

AGAAATGGTG GATGAACCTT CTGGCATACC AGTGGAAACA GATAGTCCTT ATCGTGTTTC 3300

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TTTTGAACAT GTTGCTTTTG GCTATTCACC AGAGAAATTA TTAATGAAAG ATTTCAATTT    3360

AAATGTTAAA CCTGGGGAAA TGGTCGCAAT CGTGGGCCCA ACAGGTGCTG GGAAAACAAC    3420

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ATTAAAAACA tTGCCATTCG TGCGAAAAAA GTTGGCGAAA TGGTCGACtT TTATAAAAAA    4320

GTAaTGGGTT TTGTTTTAAA GTCAGAAGAA AATAACCTGT CTATCTGGGG TACACGTGAA    4380

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ATGAAAAAAG GTGTTTTTTC GGGGGCTAGT TTTTGTTTCA TTGAAGGTGA AAAAGAGGAG    5280
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AGCAATTGTT GGGGACTGGC ACAAGTAAAA CCCACCAAAG AACAATTAAC CTCGGCCATG 5340

CTGTTTGATG TGGCTTCTTT AACCAAAGTA GTCGGCACCA CCACCGTTAT TTTGCAATTA 5400

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TTTATGTTAG AAGAAATGTT CCAACAATCA ATGATAGAAA TTTTATCTGA GCGAGTATTG 5700

CTTCCTTTAG GGATGAACGA AAGTACGTTT CTACCAAAGa ATCCTTTAAA CTGTGTGCCA 5760

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ACAATTGATT TGTTACTAGT TAACCAAGTG CCAGCTGCAG ATAAACCACG TTCTCTAGGC 6000

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TTGAAGGTGT GGGTCGATTG ATTACAGAAG ATgCTgCAAA AGCAGATGTG GCTACTTTTG 7140

ATTTGAAAAA aGGCGATAgC TTTATCTTTC CGACAGATAT TCCGAGCTGG CGTTTTGAAG 7200

GTGATCTAAC GATTATAGCT TCAGAACCTG GCAGTCGCTA AAAAAAGAGG AGATCATCAA 7260

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GGACAATTAT GCTGGAGCCA GCAGAAGTAA TTCCACCAAA TAAACAAACT GTTATTAAGG    7500
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ACTGGAAAAG CCTTGGCAGA GCGTAGGATC AATAAAATAA GCAACCGCTA AGGGATCGTT    8100
GATAACACAC CCTAAAATAC GTTCATATTT CCAATGAAAA TCAAAATAAA ATTGAGTAAT    8160
CTCAGCGAGG TAATTCCCCA TTTTGGGGTT GAGTCGTTGA CAATAATTGA GAATTGTTGG    8220
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CTCAAAAACC CAAGCTGCTG CATCAGGATC ACACCAATAA TTAAATTCTG CAACAGGAGA    8340
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TGCTTGGATT TTGCTAGTTC TGGGGAAATA TGTTTCACCT AAACCATCCA TGCCATGTGT    8580
ATCTTGTGCA CTAACAAATG GCCGTTTTAA AGGGCTAGCA GCCCCTTGGT AGACAGGAAT    8640
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GACATTTCCA CAAACAACGG TAATCGCTTG GACATCTAGC TCTGGTGAAG CAAGTGCATA    8760
CAAGAGAGCA AGCGTGTCAT CAATTCCAGG ATCACAATCA ATAATTACTT TTTGCATTTT    8820
TTCCAATCCT CCTTTTTCAT TAACTGCAAA TGATAACTCT TGTTAAAAAA GCTATGACTT    8880
GAGTTAGTAT TGAGAGATAC TTAGTTTTTT ATTCTGGGAA GTTTCCGAAC CAGTCCGAGA    8940
AATTCTCGAT TTTAAATGCA CCTCTTTATC TTACTATATT TTGTAAAGAT GTAAATAGTT    9000
GTCGGATAAA TGAAAAAGAA TCTAGCCCTA TATGTAGGAA CTAGATTCTT CTTTTATTTA    9060
TAAAGCGTTT CAGGAATAGC GATCGGTTCA CCATATTTTT TCTCTAAAGC GGTCCGAATT    9120
AACCGAATCC CTAGATTTTT GTTGCGTGCT AAGATTGGAC CGTGGAAGTA GGAGCCAAAC    9180
ACATTTTTAT AGACAACGCC TTCGCCATTA TCTTGACCGT TATTGCCTTT GCCTTGTTTG    9240
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CCATAATACG TTTCATCAAA TTCTTCATTA TAAATTTCAA TATCACCAAT GAAACGATTG 9360

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GCGGAAAATA TTCGTAAAAA CAAATAATTT TGGTTGAATA TATTTAGTGA CACGGCTTAA 10740

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TTTTAGGGCT AATTTCCCTG GGTAGCTACT GCCGCCTTTA AAAAATGTTT GTAAAACCCA 11040

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AAAGTAGAAT AGTGAAGGAA AAAAGAATAG GGGCTGGGAC AAAAATCACT TTGGATTTTT 11280

GTCccAkGyw TAAAAAAcTG aTaAACGGCG GGAACAGAAG CAACACTCCG CGTTGCTTCG 11340

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AGAGCTACAG CTCTAAGAGT TGCGATGTTT CACTGTGrAA CATGAACAGA TGAAATCATC 11460

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tTCGCAGTTT TCCCCAAATT GACCAGCTAA ACCTTTAGCA ATTTGTGTTA AAAAAGTAAG 12420

TTTTTCGTCG GATAACAT 12438

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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

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GAACTACTTC TAGCGGCTGG CGGGGATATT GATATGTATC GTAAAGACCG ACAATCCGAT 3480

TTnGTCAAAG AAnCTT 3496

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

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AATCTGATTT CCGAACTTTG CGTTTTCATG AAAATTATCT TGAAAAAACC AAAAAATAAA 240

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TATCACGAAC ATTCATTGCT TAAAATGACC AAATTTTCGT AAAACGAGTA ATACAGCTTA 420

GCAAATTCTT TTCTCTTTCA GTAGATTTTA CTAAATCCAT TCCTTGGTAA TTTTAATATA 480

TAAACGTTTA GCTACTTCAA CAGTTAACAT GTACGCAATG ATGATTCCAA AGAACCATGG 540

CCAGTAGTTA GCCGGAAGTT TCACAAAGTC AAAAACCTCT CTTATAGGCG TTGCTACAAT 600

CAAGAAACCG AGTAAGATTG CGCCTAAACT ACTTAGCATC ACAGGCATTG ACGCACGACT 660

TTGAATAAAT GGTATTTTCC GCGTCCGGAC CATATGAACA ACTAACGTTT GACTAACAAG 720

TCCCACCATA AACCAACCTG TTTGGAATAA ATGTTGAGTT GCCAAACTAT TGGCACTAAA 780

CACAAACCAC ATGACAAGAT ACGTTAGAAT ATCGAAAATA CTACTTACCG GGCCAATACA 840

TACCGTAAAT TTCGCTAGTC CGTTCGTTTC CCACCGAACA GGGCTTAATA ACTCTTCTTC 900

AT 902

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

TCTGGTGAAG TCCGTGTGAA TGAATCCTTG TTAACCGGGG AATCTGATGA GATTACCAAA 60

GTAGCAGATA GCCAACTTTT GTCAGGTAGC TTTATTGTGT CAGGTTCTTG TTATGCAAGA 120

ATTGATAAAA TTGGCGCTGA GGCCTATGTT CATCAATTAA CGCTTGAAGC GAAATCAATT 180

AAAAAAGGGG AACAATCAGA GATGGTCGGT TCCATTAACC GTTTGGTGAA ATGGGTAGGG 240

ATTATTATTA TTCCAATCGG CTGTGTTCTA TTTTTCCAAA GTTATTTCAT CAACCATCAA 300

GGGCTTCATG ACAGCATTGT CTCCATGGAA GCTGCCTTGA TTGGGATGAT TCCGGAAGGg 360

TTGTACCTTT TAACAACCGT TGCATTAGCT GCCAGCACAA TGCGCTTAGC GAACCnGGGC 420

GTTTTATTGC ACAACATGAA AAGTATCGAA TCCTTAGCAC GTGTCGATGT GTTATGTGTA 480

GATAAAACAG GAACAATTAC TGAAAACACG ATGGAAGTCC AAGAGTTGGT TCCTGTGGTG 540

AGTATCGAAA ATGATGGTAC AGACTTAACC AATGTCGAAA AATTAATTGG CGATTTTTGC 600

CGAACAATGT CAGCTGACAA CGATACGATG AAAGCGATGA AAGAATTTTT TGTTACTAAT 660

AATCAGAGGG AAGCCGTTAG TTATACCTCG TTTTCGTCTG TCGAAAAATT TAGTAGCGTG 720

ACTTTCCCGG AAGCGACGTA TATTCTTGGG GCGCCAGAGA TGATTTTGAG AGACAATTAT 780

GAAATGTATC AATCTGAAGT GGAACATTAT ACAAGTCAAG GCTATCGCTT ATTGGTGTTC 840

GGAAAGTATT TAGGAGAATT TCAGGAAACG TTGGCAGCAG AGGTTCAACC TCTAGGCTAC 900

ATTCTTCTTT GGAATCCGAT TCGTAAAGAA GCCAAAGCAA CTTTTGAATA TTTCGCTGAA 960

CAAAATGTGG CTATTAAGGT CATTTCTGGC GATAATCCTT TAACAGTATC CAATGTAGCA 1020

CAAGCGGCAG GCATTATTGG TGCTGAAAAT TATGTGGACG CGCGAACATT AACTACAATG 1080

GAAGCCCAGA CAGAgCTTTA GAAAAATACA CCGTTTTTGG TCGTGTCACG CCAGAACAAA 1140

AGAAACAATT TGTATTATTG TTGAAAAAAT TAGATCATAC AGTGGCGATG ACAGGGGATG 1200

GAGTCAATGA TATTTTAGCC ATGAAAGAAG CAGATTGTAG TATTGCCATG GCTTCAGGAA 1260

ATCAAGCTAC AGCACAAGCC TCGCAAGTTG TGTTGTTGGA TTCTGATTTT TCAACGATGC 1320

CGGAGgTTGT CTTTGAAGGC CGCCaAGTAG TTAATAACAT TGAACGCTCT TCAAGTTTAT 1380

TCCTTGTAAA AAATATTTTC TCCTTGCTGA TGTCTGTCTT TGCTATGATT TTTGCCGTGA 1440

CATATCCTTT ACAACCGACA CAAGTCACAT TGATTAGTTT ATTTACAATT GGGATTCCTT 1500

CGACATTTCT AGCTTTGGAA CCAAATCATC GTCGCATTGA AGGGAAATTT CTTTTCAATG 1560

TGTTATCAAA AGCAATTCCT GGTGGGTTAA CGGATATGTT AGTAGTCGGT GCCTTACTAA 1620

TTTGTGGTGA TATTCTTGCA CTTCAAAAAA CGGACATTTC AACGACTGCA ACATTGTTGC 1680

TAGTTTCAGT CGGCTTTATG GTTCTTTATA AAATTAGTTC ACCAATGAAT CGTTACCGCA 1740

AGCGCGTAAT GATTGGCTGT TTAATCGGAA TGGTTATTAC AAGTATTTCC ATGAAAAACT 1800

TGTTCTCGTT AACTTCGGTA TCGCCAACAG CCTTGTTACT TTTAGCCATT CTTTTCTTTG 1860

CAGCAGACTC AACTTTCCAA CATTTATCAA CCATTTCTGA AAAAGTTCAA TTATGGTTTT 1920

ATAAGAAAAG ACATTAGGAG CAAAACACCG AGCCAAAATT ATTTTGGTTC GGTGTTTTTT 1980

GTTTTTTATC GTTGGGAAAA ATAAAAACAC TTGCACCTAG TTAATCCTTG ATAGTATAAA 2040

CCTAACCAAT TATTTTAGAT AGGAAGGATT GaATAAAAAT GaAAAAAAGA AGTTTTGTCT 2100

ATTGGGGaAT GTTTTTCATc TTTTGTCGAC GCTGATAACG CCTTTTCTGA AACTTGAAAC 2160

AGGATATGCG CaAACGGraC CAACTAGTAC CAGTGrAACC AATCAAATTT nCTGtACGCC 2220

AAATGTAGTG CCGCGTAAAC AAGTGGGCAA CATTGTGACA GCGATTCAAC TAACGGACAA 2280

AGAGGGAAAC CCACTTGGGA CCATTAATCA ATATACAGAC ATCTACCTCC GAATTGAGTT 2340

CAACTTACCG GATAATACCG TTAATAGTGG GGATACGAGT GTGATTACTT TACCCGAAGA 2400

GCTACGTCTC GAGAAAAATA TGACCTTTAA TGTAGTAGAT GATACAGGTA CTGTGGTTGC 2460

AATCGCACAG ACCGATGTAG CAAATAAAAC GGTCACGTTA ACGTATACAG ATTACGTAGA 2520

AAACCATGCC AATATTAGTG GGTCTTTATA TTTTACAAGT TTGATTGATT TCGAAAATGT 2580

CGAAAATGAA TCCAAGATTC CTATTTACGT CACGGTTGAA GGGGAAAAAA TATTTGCTGG 2640

CGATCTTGAT TACCAAGGTG AAGGCGATGA TGTTAACGAA AAATTTAGCA AGTATTCGTG 2700

GTTTATCGAA GACGATCCAA CCGAAATTTA CAATGTACTA CGGATTAATC CAACAGGGCA 2760

AACGTATACT GATTTAGAAG TGGAAGATGT GCTAAAAACA GAAAGTTTAA GTTATATGAA 2820

AGACACTATG AAAATTGAAC GAGGACAATG GACACTGGAT GGAAaTGCTA TTTGGCAaTT 2880

CACGCCAGAG GAaGATATAA CTGATCAGTT GGCTGTCCAG TATGGTCCTG ATGACCGTAA 2940

TTTTTCGGTG CATTTTGGCA ATATTGGGAC TAACGAnTAT CGTATCACCT ATAAAACCAA 3000

AATCGATCAT CTTCCCGAAA AAGgTGAAAC CTTCACAAAT TATGCAAAGT TAACAGAAAA 3060

TCAAACGGTG GTGGAAGAAG TCGAAGTGAG TCGTGTCTCA CAAACAGGTG GTGGAGAAGC 3120

TAATGGTGAA CAATATGTTG TTGAAATTCA TAAAGAAGAT GAAGCAGGCC AGCGTTTAGC 3180

AGGTGCAGAA TTTGAACTCA TTCGAAACTC AACCAATCAA ACAGTGGCTA AAATCACAAC 3240

AGATCAAAAC GGAACAGCGA TTGTTAAAGG CTTGTTAAAA GATAACTATA CTTTAGTAGA 3300

AACCAAAGCA CTACCGGTTA CCAACTTTCG CAAAACAAGA TTCCAATAAC ACCTGAAGAC 3360

TTTGGTAAAA ACTTcAGTTG CACTGAAAAC TGTTGTGAAT CATAAGATTT CATATCAaCC 3420

AGTCGCTGCt TCATTTTTAG CTGGAAAAGT TCTTTTAGGA AAACCACTGA AGGATGCTGA 3480

ATTTCAATTT GAATTGTTAG ATGAGAAAGG CACAGTACTA GAAACGGTTA GTAACGATAC 3540

TTTAGGGAAA ATTCAATTTT CACCATTA 3568

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CATGTTTATC TAAAAGTTTT GCCCAGAACA CTTCTACATT TTTTAACATC CTTTGCTCTC 60

CTTTTTATTT TTACTTCACG CAACCTTCTT TCACTAATTA TACATAACTG ATTGCTTTTC 120

TCCTATACTA TTTTTACAAA ATGAAAACTA AAATAATGTC AGTAGTATTT GGACAGAAAA 180

AAAAAGAGAG CGTGGGACAA AAATCACTTT GGATTTTTGC TCCACGCTCA AAAACTTATA 240

AACGGCGGGA ACAGAAGCAA ATCCTTCGGA AATAAGCCGA AATTCTCCAA AAATTACAGA 300

ACAATTTTCG GAAATTCCTT CTTATTTCTC GGAGTTAAAC GCTTCTGTCC CGACCTCATC 360

TTTTTATTTT GCTTGTCGTT CTTTGATTTT CGTGAGTAAA GATTGAACAT GCTGGCGTGC 420

CGAAGCTTCA TCTTCTTGAA GCATCTTTTC CGATAAAATA AAGGAGCCGC CCACTGCTAA 480

TACTTCTTTG GCTTCCACAT ACTCTATAAA GTTTGTTTCA TCAATCCCAC CAGTTGGTAA 540

AAATTGAACA TCATAAAACG GACCGCTTAA ACTTTTAATG GCTTTTAACC CGCCGTAAAT 600

ATCGGCTGGG AAAAATTTAA CCACTCGTAA GCCATACGCC AGCGCTCGCT GAATCTCCCC 660

AGGCGTAgcT GTTCCTGGAA AAATAGGCAC CTCATTTGCC AGACAAAAAT CAATGACTTC 720

TGGAACAATC GCTGGGGAAA CAATGAACTG TGCACCGTTC GCTACTGCCT CTTGGGCTTC 780

TTTCAAGGTT CTAACAGTTC CTGCGCCTAC TATTAAATTC CCTGAAGCAG CAAGTTGTTT 840

GATGGCAGGC AAGGCCAGCT GACTCCGAAA AGTGACTTCA ATAAACGGTA ATTCGTTTTC 900

TACTAAGACT GATTCTACTT GTGGCAAATA GCGTAAATCT GTTGCAGTAT ATAGTGGTAA 960

AAGTTTACAT GTCGCTAATT GTTGATACAG TTGATTTTTT TCAACTTTTG TTTCCATTCT 1020

GTCACTTCCT ATTTTGTTTG GCTTTGGTTG CTTCGTACAG TCCTTGAATA TAGGTCAACC 1080

CCATTGCTCG ATCATATAAA CCATAACCAG GCATCGCTTT TTCATCCCAA ATTGCCCGCC 1140

CATGGTCAGG ACGAATAACG CCTTCATACC CTACGTCTAC CAGTGCTTGC ATTAATTCCG 1200

CCATATCTAA CGAACCAGCG ACACTAGGAT GCGCCGTTTC TTCAAAACGA TGCTCACCTA 1260

AATACTTCAC ATTGCGGAAA TGAACAAAAT TAATTCTGTG ACCTATTTCA CGAATCATAG 1320

TAGGCAAATC ATTCGTCGGG TCCGCACCGA GGGAACCTGT ACAAAATGTA ATCCCATTTG 1380

CTGGTGAGTC CACCAAGGAA AGGATCCGTT TTAAATCCGC TAAATTTTTA GTGATTCTTG 1440

GCAAACCAAA AATTTCCCAA GGTGGATCAT CGGGGTGAAT CCCCATTTTG ATATTTTCTT 1500

CTTCACAGAC AGGAATCACA CGTTCTAAAA AGTAGCGCAA ATTTTCGACC AAATCTTCTT 1560

CCGTTACGCC GGCATACATG GCTTTCAATT CTTGAAATTG TTGCAAACGC TCCTCTTCCC 1620

AACCTGGTAA CCGGAATCCT TTTGACTGAC TGTGAATTAA TTGATACATG TCTTCTGGCT 1680

GCATGTTCTC TACCACAGCT TGATCAAATA ACAACGATAA GCTACCATCT TCATTCTCAT 1740

ACGCCAAGTC CGTTTTAGCC CAACCAAAAA TAGGTTTGAA ACTGTAGCAC ACTAAGGAAA 1800

TTCCACATTT TCCCAAGTTA CGTAACGTTT GGCGATAATT ATCAATATAG TGGTCTCGTT 1860

GATCCGTTCC CGCTTTAATG GCATCATGAA TAGCGACACT TTCAATTCCT AAAAGTGCTA 1920

ATCCTTCTTG TTCCACCGAT TGTTTAAGTG CCTGAATTTC GGCTACTGTC CAAACATCAC 1980

CTGGTAGTTT ATTTAACAAG GTACCGACAA CACCAGTAAT TCCTGGAATC TGTCGAATAT 2040

GTTTTAACGG AATGGCATCG CCTGCCGCTC CGTACCATCT AAATCCCCAT TTCATTGGCT 2100

TTCACCCTTT ACTAACATTC TTAAAAATCA TCGTCCTCAT CCTCTTCGTC CTCAAAGGAA 2160

GTCATAGAAA TATCCCATGC nTGCACACTT TCTTTGCCTT GCGCAA 2206

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1887 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CCATCCATTA ACCAGATTTT TGCCACGAnC TTGnCTGTTA AACGCTCAAG TCGCmtTTTC 60

CCgaATGTGG GTAAAAtGTG TTTTTTCaTA CGTCGTTCAG TAGCTATGAA TGTGGATTCC 120

CTAACTGTTT TTTTGTATTC GTCCAACCAC ATATAATAAA CTTCTTCAAA AGTGGTTAAA 180

CGAGTATGCT CGTTAGCTAG ATTTCCATTA TCAAAATCTA ATTTTTTTTG ATTAAGCTTG 240

AGCTGTGCTT CTTTTTTTGT ATTACAGtTT CTGATAGTGA CATTAATTTG TTTTCCAGTT 300

AAATAATCTA CGCCTAAATA GGCAGTTACT TTCCAGTATT TTTTCCCTTT TTTTGTATAT 360

TGTTTAAAAG TTGCCATTGC TTATCCTTTC CACTTGGGCA AGCGAATAGA AGGAATGACA 420

AATTTCTAGC ACCTCCTTAT TAGATTTTAA AGCCCCTAGC ATGAATCGAA CACGCTAGAA 480

CTCACCAGAG AGGGGGATAA TAAAGCATAT TTTTTTGTTA AGCAGTGCGC GTTACTTTTT 540

ATTCTCTAAT TTTCTAATAG CTTTTTCTAA ATCATTTATT TTTTTTATTA GCATATCTAT 600

TTTTTCATCT TTTTCATCAT TGTTATTAGA TTCATTACTT TTATTAAAAT ATTCAGTAAT 660

AGTAGAAGTT AACATGCCAA CAAACCCAAT TCCCACAATC ATCAAAATGA TTGCAGCAAT 720

TCTTCCTAAT GGAGTAGTTG GaGAAATATC ACCaTACCCG aCAGTTGTTG TTGTTACCAA 780

AGCCCACCAA AACGCATCAA TGTATGGAAC GTTTTCTGCA TATGAGTAAA TCATTGCTGA 840

AATAACAATG AGAACCGAGC TTAAATAAAT CACGTTTAAA AATCCGTTAG TATTTAAAAA 900

TGATTTAGTG TTTCTTGTTA ATTTGCCAAC CACACCTATC GCTCTTGTTA GCTTTGCTAG 960

TCTAGCTATT TTAGCTATTC GAAACAACCT AGCGATTCTA AAGAAAGAAA AAATAGCATC 1020

AAAAGGAATT ATCGCGATCA GATCAAAAAT ATTTTCTTTA AAAAATTTGA TTTTATTTTT 1080

TGAAATAAAA AATCTAACAA TGTAATCAAT TGTAAATGtG aTTAAGaTAA TACTATCAAT 1140

AACGTTAAAT GGTGGATTAC TAATATTAAT AACATTTGAn AAATCAAGAA TAACTAACGC 1200

GATTGAGATT AATGCTAAnA CAACAATAGA GTAATTATAG AATTTTTGAT TTATTTTCAA 1260

TGAAGTTCTC TCACTCTCTA AATGrGGyTT AmGTCCGTGT TCCCAGCACG GACTTTTTTA 1320

TTTCAAATAA ACTTCTTGTC CCATTTTTAA GTtGTAATGA GCTATAACAT TTGAGTAATT 1380

GTATTGTCCT TCATATTTTT CGATTAAGCT TCTAAACATA TATTGTTCTG CTTCAGCTTC 1440

CATCTTAGAA CGAAAAACAG GAATTTTATA CAATGCCATT ATATCCACAT GTTCTTTTAC 1500

ATGCTTTAAT TCGTGATATA TTGCTTCTTC TTGTTCTGAT GGTGTTAAAT TTTGATTTAC 1560

AAATATGATA CCGTAGGTAG GGTCGAAACA TGCGCGTTTG TTCAAAGTAG TAAAAACTAA 1620

CTCCACATTA TATTCTTCTA CCAACTCTTT GATACTTTTC ATATAAGCAC AACCTTTGAC 1680

TTATTTCCCG AATCTACCCT TTAAATATGC ACGGATAACT TCTCTGTCAT GATCATCAAG 1740

CGGTTCACCG TCAAAACTCA TGACGTTATC CAGTACATCA TCTAAATCGT CAGATGGTTT 1800

AGCACCAGCT TGGTTTGGAT TTTCAGTACG ACCTAATAAA TAATCAACAG AAACATTAAA 1860

ATAATkGGCT ACAGCTTCAA GTTTATC 1887

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19024 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TGTAAAAAGG nACnACAGCC ATTGGTACCT TAAACTACCT GGTTAGTTCA ACGATTTTAT 60

CCATAGTTTA AAACATCCAG GATACATGCG tTTCGTkGCG CATTCCaGgC CAGCTGTTTA 120

ATATCGTAGT TTGGATCAGT AGGTTGCGCA TTGACGCCGC GCTTAATTGT GAAAATCAGT 180

TTTGGGAAAA TAGCTGTTCG TTTTTCAATC CCTAAACCAT TAATTCGGAT TTGTAAAATC 240

GCCCGTTGAA TTTCTCGCTC AAACCAGTTG GTACCTAAAC CAAATCCCAG AGAAGTAAAA 300

GGGGTTTGTC CATTGGAAGT AAATAAGGTA TTAATTTCAT ACTCAAGACT TTGCATGGCA 360

TCAAAAATAT CTTTTTTCGT TTTCTTCCGA GCGAATGCTT TTTGGCGTTC TTCTCCTTCA 420

ATCCATTCTT GCGCATCTGC TAAATGTTTT TCATAATTAC GTTCCGCAAA AGGCGCTAAT 480

AATTCATCAA TCCGATCGGC AGAGCAACCA CCATATTGAC TGGAAGCTAC ATTGGCAATA 540

ATTTGAGAAA TTTGTGCAGT GGCCGTTTGA ATTGATTTTG GTGATTCGAC ATCAGCGTTC 600

CCAATTTTAA AGCCATTGTT TAGCATGCCT TTAAAATCAA TTAAACAGCA GTTTGTCATG 660

GGAGTATATG GATGATAATC TAAATCGTGG TAATGAATGT CGCCTTTTTG ATGGGCATTA 720

GCCACGTGTG AAGGCAACAT CTTTAAACCA ATTGATTTTC CAACAATCCC AGCGGTTAGA 780

TCACGTTGCG TATTAAAAAC GTCACTGTCT TTGTTGGCAT TTTCGTTCAC GACAGTCTGA 840

TCTTTATTAA TTAATTTGCC GATAGATACA TTAATATCAG TTGCTTTACT ACGCTCAAAA 900

TCACGTTGGG TTCTGTAATG AATGTATTCT TCGGCTAAGG CATATTCGTT GTTGGATAGC 960

AGAGTATGTT CCACAATATT TTGAATTTCA TAAATTTTTA CGTTATTGGT AAAACGTTCG 1020

GCAATTTCTC GATTGACATC AGCAACAATC GATTGGACTT TTTGATGTGT CAAAGGAGTG 1080

ACTTGGTCAT GTATTTTTTG CTCAGCTTTG ATCAAAGCGT CGTATATTTT TTGATCATCG 1140

AAAGTCACTA AACGACCATC TCGTTTGACG ACTTTAATTG TTGAGAGATT AACATCCTCG 1200

GCTTTTTCAT CAGTAATCTT CATCATTTTA TCCAGCTCCT TATATCTCGT TAGTAACTAT 1260

CCTAATACAA AGGTCGGCTA AATTCAATCG ATATATTGCG TATTTTTAGT AAAATATCAC 1320

TAGACAAACA CTATATATTG TGCTTGCGCT GTTTTGAAAA AATATGAAAA CAAATGAAGA 1380

AAAGGATTGA GCAAATTTTT TTGCGTGAAA AAAATTCTTT GTCCAAATTA AAAAACAGCA 1440

AAGAGTTTTT TGCCAAATTG CTAAAAGCAA CACTAAAAAA TAACAATTAT TAAATAATAA 1500

TTGTTTGCGG ATTTATTCAC GAAATGCCAA TTATTCTTTG ACTACCGAAC GATATTGTAA 1560

GATAAAACGA TGTTCATTCA GATTTTTTCT TGGTAAAATA AGAGTAATAA CAAAACGTTG 1620

GAGCGAGAAA AATGAAAAAA ATTGTAGAAG TAAACCATGT CAGCAAGACA TATGGTCGTT 1680

TAAATAATAA AACAGAAGTA TTAGATAATA TTTCGTTTAC CGTTGATGAA GGCGAATTTG 1740

TGGGGATTAT GGGTCCCAGT GGTGCTGGGa AATCGACACT GTTGAATGTC TTATCCTCGA 1800

TTATTTTGCC AACCGCAGGA ATCGTGCGCA TCGCCGGACA AGATATTTTA AAAATGCGAG 1860

ATAATCAATT AAGTGATTTT CGAAGAAACG AAATGGGGTT TATTTTTCAA TCGTTTAACC 1920

TAATTGATAC GTTAAATGTG AAGGACAATA TTCTGTTGCC TTTAGCTGTA GAAAAAGTTT 1980

CATTAGAAGA AATGGATAAA CGTTTGTTAC ATGTGACTTC GATTTTGGGG ATTCAGGAGC 2040

TTTTATCTGC TTATCCACCA GAGATATCTG TGGGACAAAA ACAACGGGTA GCAGCTGCTC 2100

GTGCTTTGAT TACGAACCCT AAAATTATTT TTGCAGATGA ACCAACTGGC TCGCTGGATT 2160

CAAAATCAGC AACAGAATTG TTGAAATATT TAGCTGAAAT TAATCTACAT GATGATGCCA 2220

CAATTTTGAT GGTGACACAT GACCCGTACA CGGCCAGTTT TTGCAATCGC ATCTTATTCA 2280

TTAAAGACGG TGCGATTTTC TCAGAAGTTG TTCGTCAAGG ATCACGTAAG GAATTTTTTA 2340

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ATCGTGTGAT AGATATGCAA GCAACGATTG GTGGAGGCGG GCGCGCAAAT GATTTTTAAA    2400
CTATCATTAA AAAATTTAAA AGCTCATGTA CCTAATTATC TGGTTTATTA CATTAGTATG    2460
ACTTTTGCAG CGGTCGTTTA TTATTGTTTC CGTGCGATTG CTTACAACCA GCCTCTTGTC    2520
GCAGGTGCAG GCCGTGATAT CGAAATTAAG CGATCTTTAG GACTCGGTAG TACCTTAGTC    2580
ACCATTATTA TTTTGGGCTT TATGTTGGCA GCAAATCGTT TTTTTATAGG AAAACGTAGC    2640
CAAGAAATTG GCTTGTATCG ATTAATTGGC TTGAGAAAGA GCCAAGTTTC ACTAATTTTT    2700
TTAGTAGAAA ATTTAGTTTT AGGCTTTGTT TCACTAATTA ATGGAATTAT TTTAGGAGTG    2760
ATTTTCACCA AGTkGTTTtC AATGATTTTA GCCAAAGTTA TGTTTTTAGA AGTCCCCAGT    2820
TTCTTCTATA TTTCTTGGCG TTCCGTTATT GAAACCGGTG TAGCTTTTGC ATTTATGATT    2880
kTGATTGTCT GCTTAAGAAG TATTTGGATG ATTTATCGTT ATCCATTGTC GCAGCTTATG    2940
CATCAAGAAA AAATTGGTCA AATTAATTAT AGTCGTTTAA CGAAACGGCG GCAGCTTCTA    3000
GGTATTTTAG GACCAATTTG TTTATTAGTA GGTTATTTTA TCGCGTTTGA TTTTCGTAAT    3060
TTAGCGACAG GTATTGTGTA TAAACAATTA AATGATTCAT TGGATATTTC GATTCCAATG    3120
ATTATTACGT TGACGCCTTT TATCATTTTG GGTCTATGTG TGGTGGGAAC TTATTTATTT    3180
TTCCGTTATA CCATGTATTT TATCATTCGC TTATTTAATC ATAGAAAAAA ATGGTATTAC    3240
CAAGATTTAC GCATGATTAC TTTAGGCAAT GCCAAACGCT ACTTATTTAA AAGTAGCAAA    3300
ACACTCACTG GTTTGACCTT ATTAATTGCG ACAGCCTTGA GTGGGATCGG CGTGATGGTT    3360
TTTGTGTATA CGATTAGTAT GCACACGGTC AACAGTGATG GCCCCGTGGA CTTTTTAGTT    3420
TCACAGGAAA GCTATCCTAA ATTGAAGAAA GTTCTCGATG AAGCGAAGGA CACCAAAATA    3480
AAAAATGAAG TGACACTTTC TTATAAAATT ACTGGAATTG AACGCAGTTT GCGAATTGGT    3540
CAAGCGCAAG AGGAACAAGA AACGATTGAA GCAGTTAATG TTTTATCCTT CTCCAACTAC    3600
CGCAACTATC AAAAAATTAA TCCTTATTTA AACGATTTAC ATTTAAAAAA TGACCAAAGT    3660
GTTATCTATA TGGATAGCTT TACCAATATT TTAAGTGGTA TGTCTCGTTA TGAATCGAAA    3720
CTGCAATTTG TTGAAGGGGA GAAGGCACAA CTACAACAAG TGCTGCCTAA CTATCTAGGC    3780
AATTTTTTAT TGCAATATTC CTTACCAACG ATTGTCGTTT CCGATGCCCT TTATCAGAAA    3840
GTGACAAAAA ATTCCATTCA GTATCAGATT AACGCCGTAA ATGTTGACAC GAAAAGCCGT    3900
GAAAAACTTT ATGAAGCCGT AAATAAACAG ATTGCCACAG AATGGCAAGC GCCAATTTTG    3960
TATAAGTATG AAAAAAATAA CCAGCAGTTG AGTGGTTTTG CCAAACAAAT GCCTAACGAA    4020
GAGGTAAAGA ATACGCAAGA TGATGTCACA GAAACTTGGC GGCTAAATAT GAATGATCGc    4080
TACGCCTCTT TACGCTATGA ACGAAAAATT AACGGCTTGA CTTTATATGT CTCCATGTTT    4140
GTGGCAATTT TAGCGTTGTT TATTACGGGC AGTATTTTGA TGTTACGACA ACTGTTTTCA    4200
GCTGTAAGTG AGCGTCAAGA TTACGTGACT TTAAAACGGA TGGGTGTTTC TAGTAAAGCG    4260
ATAACTAAGC AAATTTATCG ACAGAATAGT TTGATTTTCT TTCCGCCGAT GGTCATTGGG    4320
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ATTTTGCATA CCACCTTTGC TATTTATTTG TTAAGCCAAT TTATTAAGAG TCCAGGATAT 4380

TTGTTAGTAT ATCTTTCTTG TGGAATCTTA ATAATTGTTT ATCTAATTTT TTATATTTTA 4440

ACGTCTGCCA TTTATGCGCG GATGATTCGA CACATCCATT TTTAAAAAAC TGTAAAAGCC 4500

GTTGTGAAGC GGTTTTTACA GTTTCTTTAT GCGAAAAAAT TATGAGAGTT CCGTTTATGA 4560

AAATCATGAA AATCTAAGAA GTGACGAAAT TGTTAGTTTT TTTATTAAAT TGTAAGAAAT 4620

TTCAATGGAC TTTGCTGAAA TATAGCATAA AATAATGGAT AGCGATTAAC CTTAGGAGGT 4680

GAATGATAAT GAAAACAACT TTTCAGAAAA TTCTCAATAA CGAAAGTCTT AAATTCATCG 4740

GTAAAACGTT ATTTTATTCT TTCATTGTCA TTGCATTAAT TTATCTTTAT CATTACAAGA 4800

ATATCAATGG AGGAACCTTC ATTTATAACG AGTTTTAAGG AGGCGGCTAT ACATGGAAAA 4860

AGTAATTAAT ATGATTCAAA CGATTGATGA ATGGGCACGT AAAGAACCCC AACGTCCTGT 4920

TTATTTAACC GAAGAAAAAG TCTCTACGTA TGGAGAGTTA AAAGAAAAGT CAGACAATCT 4980

AGCCGCTTAT TTAGCTGAGC TGAAAACGGA CAAGTCAGCG ATTGTCGTAT ACGGAGAATT 5040

AGATTTTGAA ATGATTGTGA GTTTTTTAGG CGCATCGAAA GCTGGTTTTA GCTATATCCC 5100

CATTGATGCA CATACACCAA AAGAACGCAT TGAACTAATT CTAAACGTAG CCAAACCAAC 5160

CGCAGTGATT GCTGTGCATG AATGGCCTGA ATTAGCCACC GAAGTGCCAG TAATTACGGC 5220

GGAAGAATTA ACAGAAATGA TGATGCATGC ACCCCGGCAT GCGCCTGCGT TGATGCCTGT 5280

CACAGGAGCA AGTAATTACT ATATCATTTT CACTTCAGGG ACAACTGGCG TACCAAAGGG 5340

TGTGCAAATC AGCCATGATA ATTTAGTTAG CTTTACGAAT TGGTTGTTGC AAGATTTTGG 5400

TTTAGAAGAA GGGGCCCGCT TTTTAGCACA GGCACCTTAT TCGTTTGATT TATCGGTGAT 5460

GTCTATTTAT CCCGCATTGG CGTTAGGTGG CTCATTAACT CCGTTACCCA ATGAAATCAT 5520

TAACGATTTT AAACAATTAT TTACGCGTTT GCCACAATTA ACAATCGACG TCTGGGTTTC 5580

AACACCGTCC TTTATTGAAT TGTGTCTAAT GGAACCaAGC TTCGATGGTG AACATCTACC 5640

AGCACTGCGC ACGTTTTTAT TCTGCGGAGA AGAATTACCA AAACCAACGG CTGAGAAATT 5700

AGCCGCTCGT TTCCCAACTG CGCATATTTA TAATACGTAT GGGCCGACAG AAGCGACTGT 5760

AGCGATTAGT GCCATTGAAA TCACTCAAGA AGTTTTAAAA AGTGTCCAAC GTTTACCAAT 5820

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GCCTTGGTAC CAAACACTCG TGACACTGGT CTTTCTATAT ATCAGTTTTG GTGGCGAATT 6540

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TCTTTAGGCG AAAAATTGCT GTGCCAGAAT AGCCTTTTTT nTCGGCGAAC TCCAnTACTG 19020

AnGA 19024

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31517 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

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CATATGTAAA AACCAGTCAG CGGATTATTG GCAATCCGTC TAGCCTACAT GACTTAGGCA 120

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CAGCAAATGA AATCTATTTT ACAAGTGGCG GAACTGAAGG AGATAACTGG GTTTTAAAAG 240

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CAGCAGTTAC AGAAACAGCG GAACAATTAG TCGAACTAGG TTTTGAACTT TCTTATGCGC 360

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(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

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ATATTTCnTT TTCAAGTCAG CGACACACTT TTCAAATTCT TCACTCACCG AAACAACTTC 360

CTTCCmAAAT TTAATCkGcT AwTTATwACA aATTTTACCA AAAGTACAAG CAAAATTGCT 420

TTCTTTTTTc AAAAGAAATT CAGACAAAAC TtAACgCGGG AAAAGCTGAT TTATAGGAGC 480

TGAACATGGT TAATCTTCAT TAACAATAAT AcAATTTCTG CCcTTCATTC ATCCGTGTTG 540

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TATCTTTAAA GGCCGTGCCC CGATTGTCAA AAGGATGCGT AATAATACAG TCCTCCGCAA    720

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(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

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TTGGTAAAAA GTTAGATGAA ACACCTTCAA CACCTGTAAC GCCTTCTGCA CCGTCAATGC 360

CTGCAGAACC AGCGAATCAT GATGTTGATA ATGCACAAAC ACGTCAATTT TAACAAGACA 420

ATTTAAGTCA AGTTTTCACG AGGaACAAAA AGCATTTATT AGAATAGCGG ACACTTGTTG 480

TAGTGTGTAA ATTTTTGCTG TTCGTCTAAA CAGATTTGTw ATTTTCGGGT GATCGCGGTT 540

TGCTTTTGCA AGCTGAGGAA AGTCCATGCT CGCACAAGCT GAGATGCTTG TAGTGTTCGT 600

GCTTAGCGAA ATCATAAGCT AAGGTACTCT TTTAGAGTAA CGGCAGGAAA AATGACTAAG 660

GTTTCGACTA TGTCAAAGTA TCCTTGAAAG TGCCACAGTG ACGAAGCGAT GTGGGAAACT 720

CCATCGGTGG AACGCGGTAA ACCCCTCGAG CGAGCAACCC AAACAATGGT AGGGGCGCTC 780

TTCTAAAGGA AATGAACGAG TAGAAGAGGC AGAGTTTACT CTGCAGATAG ATGATGACCG 840

TCACCAATTT TTCCTGAAGA ATTGGTGATA CAGAACATGG CTTATAGAAA ATTACAAGTA 900

ATTCAGGAAG ACCTTCCAAC GTAGTTGTGA AGGCTTTTTT TACGAAAAGA ATAAAAAAAT 960

GTtAAAATAA AGAAACTGAG wTAAAaGTAG TAAgCTGTCT GTTCTAAAGA GGCCGGAACA 1020

GGACCGTTtA GTcAGAGAAA GCGGACAATT wTAAAAAmCA aGCgGAccAG TAGTCsGCAG 1080

GACTGTTAGC TCCAGACmaT wAAAAAGrgT CmAGAAGGAG TTTTaTgaCG AAAGAAAAAm 1140

CaTyCAACyT GTTGCaCGGC TGCTAGTGGC TTAGAAGCAT AGTTGGn 1187

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAATAACTAA AACAGTTAGA AATAATGAAT TTCCTCGTTG CTGTTGGCGT TTTGCtAAAC 60

GaGAACCACC ACCATTTTGA TCAGGTTCAT AAATTGATTG TTCCCATGGC TCACGAGCTT 120

GGTTTTTCTT TTTGTCCTTT TtACTCACTG CTAATTTCCT CCTAAACTTC TCTCGCTTGT 180

TATTATATCA TAGCTTTTGC CAACTGCCGA CTAAAAAAAT GAATTAATCA CGTTCTTTAA 240

ATAATTTTAG AAATTTAGAA CGCCAACCTT CTTCATTTTG ATTGCTGGTC TTGTTCGATT 300

TTACTATTGA ATCTTGGTAA ATGTCAAAGA ATAACGCACA ATTATCACAA CAAGTTTCCG 360

GTGATTGTTT GACAATCGGT TCTTGAAAAT AAGTTTGAAT CAACGTTCTT CGACAGGTTG 420

TGGTTTCAAT ATACGTCAGC ATCCCTCTTA ATTGTGCTTG GCGATCTTTT TCTTTCTCCT 480

CTAAACGATG CTCTAGCTCT TCAAAAGAAT AATCCTTGGC TAAATAGCCT TGGACCCATT 540

TTTGTTGTAA CTCGGTGGCA TTTTCTAGCA AACCTGCTTG TTCTTCTCCT TCAATCAGCG 600

ATTTTAAGGT CGCTCGATTC GCTCTTGTCT CTTCTAAGAA AAACCGATGA ATAAATTCAT 660

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CCCCTTTTTT ATACAATAAT AGCGCCCAAC TTTTTTGACC ATCACGTCCA GCTCGCCCGA      720
TTTCTTGCAG GTAATTTTCT AAGCTATCAG GCAAATCAAA ATGAATCACT CCACGAACAT      780
CAGGTTTGTC GATTCCCATC CCAAAAGCAT TCGTTGCACA AAGAATATCG ATTTGATTAT      840
CAATAAATTG TTCTTGCAAG CGACTACGTT CACTAGCCTC CAAGCCCCCA TGATAATAGG      900
CTACCTTAAA ACTGGTTTTT GCCTGAATAA GTTGACTGAT TTGTTCTGTT TTGTTGCGCG      960
TGGCGCAATA GATAATGATT TTACCAGCCG TTTTAGATAA GTAATCTAGT AACACTTCTT     1020
CTTTTTCTGA CGTTTCCTTC ACGAACAAGC CAATATTTTT TCGATTCACT GAAGAAAGAA     1080
CTTCTTGATA GCTGCCATGA GAAAATAATT GTTTTATAAT TGCGTGCTGT ACAACGGGTG     1140
TCGCTGTGGC AGTTAACGCC AAGGTCAAAG GAAAGTCTAG CTGTTTTTGG ACCAGATCTA     1200
ATTTACTATA TTCAGGGCGA AAATCGACGC CCCACTGATA AACACAATGG GCTTCATCCA     1260
CCACAAATAA TGCAATTTTT TGGCGTTGTA ACACACTAAG TACTTCTTGC TGCAAAAGCA     1320
TTTCTGGGCT TAAAAACAGA TAATCGTATT GGAACATTTT CGCTAAAATA TAACGCTTTT     1380
CTGAATACTG TAACGTACTG TTTAAGGCAA CCGCACCTTT AATTCCTTGT CTTTGTAATT     1440
GACGCATCTG ATCTTCCATT AACGAAAGTA AGGGAGAAAC AATTACCGTT AGTCCCTCTA     1500
ACTTCTGGCC CACAAATTGA TAACACAATG ATTTTCCAGT CCCTGTTGGC AAAACAGCCA     1560
ATGTATTCAT ACCGTCAAGT AAGTTTGTAA TCACTTCTTT TTGACCAGGC TTAAACGCTG     1620
CGTAACCAAA TTGAGTGAAT AATTCTTGTT CTAATGTCAA CAACACTCAC TCCTTTTCTT     1680
GCCAAATTTG TTGGATTTGA TATAACCGAA AATCTAAATA AGAAAGCGTC GCTTCTTGCG     1740
CTCGCCAATC CCGATACACC CACAGCCGCG GATCTTGTTC TGTTTGAGCC AAGTTTTGGA     1800
GCATTGCCTC CTTTTCAAGG TAAACAGACG CCTGCAGCTG CCCTTGAATA GCCAACTCTA     1860
ATAGATGGTC GTGAATGGTA CTCGGTTTTA TTTTTCGCTG CTCAGCAATT TCTTGAAGTG     1920
TCTTACCTTC CGTTAACAAT CGTTGGGTTT CTTGCATACT TTGGTTTAGA TTTTTTTCTA     1980
GATACGGCCA TACAAGCGTT TGTAAAGCAG GATAATTTCC TCCGTACATT ATCAACTGCA     2040
GTAAATGATG AACCGCTTGC GTGTGCCACA AACGCTGTTC AAGAGCTGTC TTATGGCTTG     2100
TTAATTGCTG AGGAACTTTG CCAGTTTGCT GATAACCAGA AAGTTGCGCA ACCAAATAGT     2160
CGCTTTCTGC TTCAGGTAGT AACTCAAACC CTCGCAACAG TTCTTCTTTG ATTGATTGAA     2220
CGCGCTGCTC TTTCTTGTCT TGTTGTAACC ATCGTTTCAA ATATAGTTGC GGAATCGGTG     2280
TTGATAAAAG TGGAATATAC TGTTTTTCCT CAAATGATAA ATATGAAGTC ACTTGCACGG     2340
CAAATTGAAT GAGTTGCCAA CTTTCTCGAT CACTTCTGCC AAAACGATAA AGATCAATTG     2400
CAGGATAATC CAGCAACGAA AAATGGTGCT CCTTTAAAAA TAGTTGCCCT TCTTTTGTTA     2460
GTTGAATCTC ATTTGTCTCT TCGTGATACT GAATTTGTTT CGCCTTCGAA AGTTTTTCAA     2520
GAAATTGAAA ATAGGCTTGT TCGGAAATCG TTGGCCACCA GCCAATGAAC CGTAAACAAT     2580
CATATAAAAA ACCATAAATC AAAACAGAGC TAGTCCGTTT GCCTTTTAAA AGATGATACA     2640
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AAGTTGATGC ACGTACCTTG TATCCATGAG ATAATAACGC TAAAATAAAA GTTGCTTCCA 2700

TAGTAAACCT CTTTTAGATA GGATGTGTCA CTGTTTATGC AATCACGTTT AGTTCCTGAA 2760

AAATGTATTG CTTGTGGACT TTGTCAAGTT TATGCGCCTA ATATATTTGA TTATGATGAT 2820

CATGGGATTG TCCTTTTTAA AGACGAGCCG CATGCTCGAC AACAATTTAT TCCAGAAAAC 2880

GAACGCGAGA ATGTGTTAAA AGCGTACCGC AAATGTCCCA CGCGTGCAAT AGAAATAAGC 2940

AAAAATGAGT GCTAAATAAT TTAGCACTCA TTTTTGCTTA GAGTATCTTT TCGAGCCAAG 3000

CAAGTGTTTG TTCATCTATC GAAACAAACT GTAATTGTCC TTCTTTTAAC GGTTCTTTGA 3060

CTAAATGAAT TTGATCATTT AGGCCATTGA TCCaTTCATA ACGAAGACCA TTTTCTTTTG 3120

CTTTAGAATT TTTGGCTTCT AAATAATAAT TGACATGGTA ATTTTCTTTA CCATCCAATT 3180

GTAGCGTATT AATGGTCACT TCAAAATCTG GTGAACCATC GGTCGATTTC TTTTCACGTA 3240

ATCGTTCAAG TGCTTCTATA AAAGAAGGAA ATTGAGGATT ATTTTCCCCA CCAACGAGAT 3300

ATTTTTTAGC AAATTCTGTA CTATCCGTAT GACTTTTCAC TTGTTTGGCA AATGCTTGAT 3360

AAAAGGTTTC TAGCGCTTTG CGGGCATCAT AGTCGCTAGC TAACGGAAAA TTCAATTGTA 3420

GCGTTGGATT ATCGGAGAGC GCTTCGACAA AATCATTTTC ACCAATCGTT TCTTTTGATG 3480

TTTGAATTTC TTCTCCATTA ATCGTCTTTT TAAGTTGAAT CGTCATCCCT TTGGACCAGA 3540

ACAAAGGGCC AATCGTTTTG CTTCCATTCG TTAGCGTACC AcTTTCCGAT CATTAATATA 3600

AATATCTGCG TCTGGCAGAT TGCTTTCCAC AACAAAATTC ATTCGTTTAA AATCTAAAGG 3660

AATACTAGAA ATATAATTTT CCTCTTCTAA TAAACGGTAC TCTTCTGTGA TAACAGGTTC 3720

GCCGGTGCTA TCTTTCACTG TGGCTGTAAA AGTATATTGT CCTGGCGCTA AGGGGCCCAA 3780

TTCCTTTTGA TAAGTGGTTG AGTCGGAAGT GCCCACTTCC CGCCCGTTCA TTGCCAGCGT 3840

CACACCGCGC TGATTCGTCG TTAACTGAAC AGAAACAGGC GTTAAAATGA ATTGATAACG 3900

GTGAAAGAAA AATGCTGTTT GACTTGTTtC ACGAATAGTT AAACCATGTA ACTTTTTATC 3960

CTTTAATAGC GCTTTTTCTA ATTTTTTTAG CTCAGTTGGA TTTTTTTGAT AATAAGTGAT 4020

TAAAGGCTTA ATGCTTTGCG GATTCACTTG AAATTCAGAC TCGTTCGTCC TCATTTTTTT 4080

ACTTAATTCT TGGGCATCAC CATTCTCAAT CGCTTCAATA AAATAAGAAA TTTGTTGTTC 4140

CTTAGAAAAA TAATGCGTCC CGAGAAAATA GCTACCCG 4178

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

GATTTTAATG GGCGGTATCC TTTTAAGTGC TTCCGCGGTT TTACTTACTG CCTGTGGTGG 60

CGCAGAAAAA ACGAAAGCTG AAAATGAAAG CGGTTCAGCA AATAAAGCAG CTGGTGACGT 120

AAAATTATGG GTTGATACTG AATATATGGG CGTCTTTAAA AAAGTTGTCG CCGATTTTGA 180

AAAAGAAAAC CCCGATATTA AAGTTAACTT AACTGCTGGA AATTCGGCAG ATGCTAAAAA 240

AGACATTGCA AAAGATCCTA AAGCTGCCGC AGaTGTTTTC ATGATGCCAC ATGATCAAAT 300

TGGTCAAATG GCAGAAGCTG GTCTGATTTA CCCTAACACA AAATATGAAA AAGAAGTCAA 360

AGAAAACAAT ATCGACTCGG CAGTCGCAGG AGTCACTTGG AAAGACAAAG TCTATGCCTA 420

CCCTTATGCC GTAGAGTCAC AAGTTCTTTA TTATAACmAA GATACGTATT CTCCAGAGGA 480

AATTAAAACT TGGAAGTCTT TAACTGGAAA AGGcAAAATC GGTACCAATT TTGGCGAAGA 540

TGGCGCAAAT TATATCTTCG GTCCTCTATT TATGAGTAAC GGCGATTACT TATATGGTGA 600

AAATGGCGAA GATCCGAAAG GTACCAACTT TAACAACCAA CAAGGTATAG AAGTATTACA 660

ATGGAtTGCC GATCAAAAAA ATAATCCTGG TGTGATCCAA TCAAATACAG AAGCATTGTC 720

TAATCTAGGT TCTGGCAAAA CGGATGCCTT CCTTTCTGGT CCTTGGTCTA AAAACGATGT 780

AGAAAAAGCT CTTGGCGACA AAATGGGGGC CGCTGCCTAC CCAACCATTG ATTTTGGCAA 840

TGGAGAAAAA CAAATGAAAG CTTTCTTGGG CGTTCGTAGT TTTGCTGTCA ACCAACAAAC 900

ACAAGCACCA TTGGCCGCAA TGACATTAGC AAACTATTTA ACAAGTGAAA AAGCACAAAT 960

GACTTACTTC mAAGAAATCg GTTTTGTCCC tCCAACCAAA AATTACCAAn CAAC 1014

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CGTTCCATGG CCGTTGTTAA TTTATCCATA TCGGACGCAT AACTAATTCG GACGTATCCT 60

TCTGCTTCTG GGCCAAAAGA AATACCTGGA ATCAACGCTA CTGCTTCTTT TTGCGCTAAA 120

TCAATACAAA ATTTCATAGA ATCTTGTTCA TAACCAGTAG GAATCTTAGC AAAAATATAA 180

AAGGCCCCAT TTGGACGCGC AACCTCAAAC CCCAATTGAG TCATCTGTTC ATAAACAAAA 240

TCGCGCCGTT TCCGATACTC TTCTTTCATA ATTTCAGCAT CATGCATTCC TTCGATTAGG 300

GCACGAACAG CCGCTTTTTG AGACACAGTT GCAGCCGCAG TAACTAAATA CTGATGAACT 360

TTAATGATCT CCGCTGTTAA AATCGCTGGT GCAAAAATAA AGCCAATCCG CCAGCCTGTC 420

ATGGcATGTG aTTTCGACAA ACCGkTAATT AAAATCGTTT GGTCACGTAA CATTTCAGCA 480

ATCGAAACAT GACTCTCATC ATAAGTTAAC TCACTATAAA TTTCATCACT AATCACAAAA 540

ATGTCGTATT TTTTTAGAAC ATCAGCAATT GCTTGCAACT CTTGGCGGTT ATAGGTGACA 600

CCAGTTGGGT TGCTAGGATA ATTTAAAATA ATTGCTTTGA CTTGTTCCCC ATGCTCGGCC 660

ATTGCCGCTT CAATCATTTC AGGGGTCAAG ACAAAATCGT TGTCTCGTGT ATCCAAATAT 720

ACCGGTTCCG CCCCCGCCAA TGTAATAATT GGTTCATACC CTGGGTAAAT AGGTGCTGGC 780

AATAGCACTT TGTCACCTTG TTCTAAAATT GCTAATAACG AAGCTGAAAT CGCTTCTGTk 840

GCTCCAACTG TTACTAAAAT TTCTGTCGCA GGCTGGtAAG TCAAATGGtA CTTTtCTTTC 900

ATAAAATAAG CGGCTGCTTC ACGGaCATCT AATAAACCAG ACATCCCTGT AtAATGAGAA 960

AAATTCGCAT CAATTGCTTC TTTGGCTGCT TTTTTGACAT GCTCAGGTGT GTTAAAATCC 1020

GGCTCTCCTA GCGTTAATTT TAAAATACCT TCAATTCCTG AGACTTGTTC GTCAAATTGA 1080

CGAATTAAAG AAACAGCAAT TTTATTTACT TGACGATTAA AACGATtGGT TAAATCCATT 1140

TAGCTTCACT CCTTCAGTTG ACGTTATAGT AGCACAAATT GACCGTAAAA TGAATGATTT 1200

TCTCATTGTT TCGCTAGATT TTTATTATAA ATATCTCAAA AAAACGACAG AAAAGAAAAT 1260

AGGAGAACTT TGTCCTTTTC AACAAAGTTC TCCTATTTAT TTATTTTTCG AAACGCCATG 1320

TCCGAATTTC AAACGGACGT AAtGGTGCAT CAACTTCTAT CGCTGGTGTC AACGGTTCTT 1380

CTAATACATT TGTTAAACAA GTCGCTGGTT GTGTCTCTTT GTGAAGTTCA CAAGGAATAT 1440

TTTGCGCTGT TAGATTAAAG CCACGAACGA CTAAATGATT TGTTTGCTCT TGACGTTTAA 1500

CGGCTGTCCA ACCAATTGGT CCTTCTGCCG TTGTCAAGTA GACATGGTTC GGTGCTAGTT 1560

TACCTTCATG ACGCGCAGTA GTAGCTGCAG TAAAAGGAAT TTGTGCACTA TAGGCTTGTT 1620

GATACGTAGC AAAGCGTTCT TCTGGTTTTC CATGCAATGA CAAACCATAT TTAAAGGTAT 1680

ATTCTCCTTG GCATTGTGCT TCTGGTGTCG CAAAATAGCC CCAATCACCT AGTTCGCCAA 1740

CACAACGAAT TAATGTGACC GCAATGGTTC CATCTGCTAA GACTTCATAC TCATTTAAGC 1800

CTTCATTGAA GATAGTCACG CCTTTGTTTT GGTCATGAAC ATTCACAAAC GCTTGTTGGT 1860

GCTGCGGGTT TGTTGGATTT TCCCATGTGT CGCTTACTTG ATTTGGTCGT GTCACGACTT 1920

CATAAATACT ATCCGCTTCG TGTGTTTCTG TGACCATGCC AGTTGGGAAA AGCACGCGTA 1980

AACGATGATC TTTGATTTGA TTATTAATGG TTGTTTCAAA GAACAATTGG TTACTTTCTT 2040

kGATCATTGT AACCATTGTC GTTATTTCGA ACGGGCGAAg CGTCGTTGAA CGTTGTGCAA 2100

GGCGTTCTCT AAACTCACGA ACAGCCTTTT GTTCTTCTTC TAATCGTTCA TCTGCCGCAA 2160

CTGGTAACAT GACGGTTTGT TTAATTTGAT AACTTGCTTT TACAGGGGAA TTTTCTTTAT 2220

TCGTGATTTC AGCCGTTACA TTTTCGGTTG TAATTCCTTG GTCTTCGGTC GGTTTGAAAA 2280

AGATATATTC ATTCCCAATG TCGCCAGTAT CTTCAAATGT TAACAATTTT GAAAATGTTT 2340

CTCCTGTTTT TTTGTCAGCA ATGGTTAAGC TACCATTGTT TTCAATTTTC ACTTGAATAA 2400

ATTCGTTTTC CATTTCATTT GTTGCTGGTT GAGCCAAAAG ACTTCCTTCA AAAGCTTTCG 2460

TTTCTCCTTG AATCAATGCA AAGCTATCCC AAGAGAATGG CGCCATTTCT TTGACAGATA 2520

ATTCGACCGT TAAGTATTTG GCCATGTACG GTTGACGGAA AGCAtCTTTA GGTAAATCGT 2580

AACCAAAACG AACATCTTCT TTGACAATAC GGCTTGCAAC GGCTTTTCCA GTTgGATCAA 2640

TCACTTGATA AtCTGGGGTG GCTTTTtGTT TTAATTCATG ATAAAGATCT TCAGGTTTcC 2700

TGTATAAAAT GGCAATCGTt CAATCTCCAC TTCCACAGTG ACAACCTCCG TTTTCTGATA 2760

GCCACTAGTA TTAAATAAAA CAAACGGGTG CGCTTTTTCT GGGAAAACAC TTGTATCAAT 2820

TGCTTCTGTT AATTGTCGTG TTGCTTCATC TGCTAAGAAA TGCCCGACAT CATTGGCATT 2880

TTCAAAGCGA GTCATCATGC CTCGGTGAAC CTCGTCGACA GAACAGCCAC AAATACTATC 2940

GTGCGGATGG TTTTGAAGCA ATGTTTTCCA AGCATAATCA AATTGGTCAT GTGGGTAGTC 3000

GCCAGTTACT TCGTAAGCCA TTGCTGCTAA AGGTTCTGCG ATATTTTCTA ATTGGCGTTG 3060

GACTTTTGTG TTCCACTGTT TTAAATAGAC GCGAGCAGAA GAAGTATTGG CTAATGTGTA 3120

CCAGCCATCC GTTTCTTGAC TCGTTAATTC ACCTGTTACT GTTCCTAAAT CTTCTGGTAA 3180

CTCCTCTTGA ACAGCTTTCA AATAGTCATC GAAATTGGAA TGAATAAATT CATATTCTGG 3240

GAATAGTTCA TTGGCTAAAG CGATGGCCTT AGTAATATCT CTTTGTACAG GTTGGTGGTC 3300

GACCCCATTC ATCATCAATA AATGGTTTGT GGAAGCGTAA CGTTCCACAT CAGCCAATTT 3360

TTGTTTCCAA AAAGCGATTG CCGCTTCTTT TTCTGAAGGA ATTTCGTTCC CATTACTATA 3420

CCAGTTAGCA AAAAGCAAGC CGAAAATTTT CGTTTGATCA GGACCTTCCC ACCACATTTC 3480

aGAATATTGT GAGCTATAGT CGCTTTCTAA GACTTGGTTA TCAAAGCCAA TCGGTTTCAC 3540

CCCGCGTCCA AAGGCAGCCG CAGGaGATTT GCTAATTGCA TCATTTGAGG CGTTTGACCC 3600

ATATTCCCAA ATGn 3614

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

CTTACATTCC ACTaAAACgT CAAACCgTAT CCAAAGAAGC GATTTATATT GCCATTGGTA 60

TACGAGAAGA CGGCACTAAA GAAGTACTGA GTTATGCGAT TGCTCCAACT GAATCAACAT 120

ACGTTTGGAA TGAGCTGCTA CAGGATATTA ACTCCAGAGG AGTTCAAGAA GTCTTGCTTT 180

TTATTACGGA CGGCTTAAAA GGCATGAAAG ATACTATCCA TCAAATTTAT CCTAAAGCAA 240

AATATCAGCA TTGTTGTATC CATGTATCTC GTAATATCGC TCATAAAGTA CGTGTCAAAG 300

ACCGAAAAGA AATCTGTGAT GACTTTAAGG CTGTTTATCA AGCTAACTCA AAAGAAGAAG 360

CGAATACCTT CTTATCCGGC ATGATTGAGA AATGGAAGAA AAACTATCCT AAAGTGACGC 420

AGTCAcTCAT AGAAAACCAA GACTTATTAA CTTTTTATGA TTTTCCACCT AGCATTCGTA 480

GAACCATTTA CTCAACCAAT CTAATCGAGT CTTTCAATAA GCAAATTAAA AGATACAGCC 540

GTAGAAAAGA GCAGTTTCAA AATGAAGAAT CACTAGAACG CTTTCTAGTC AGCATTTTTG 600

ATACATACAA TCAAAAATTT CTAAACAGAA GCCATAAAGG TTTTCAACAG GTAACCGATA 660

CATTAGTTTC AATGTTTACT GAGTAACTAA TTATtTTGCA GGAGGACAAT TTATTTACAC 720

AAAATTATTG ACGCTCCCAA GAATGTTTTT AAATAATATa AATAATAGTG TTTTTCAAAG 780

TTTTGTTAAT TTttCATTCG GAATCGCAAT TGAAGAAATC ACGTGGTATA CTTTTAAGAA 840

GArACAATGA CACGAAAGTA GCCATTGGAA AAAGGAGATT ATTTCGTGGG AAAAAAACAT 900

ACATCCTCTT ATGAAGTTGC CTACTATGAC GGCGATTTTA CTGGTGCAAT GAAGATACCG 960

GCTTTGCTAG CGGTTGTCAT TAAAGTATCA GAAGAACAAA CAGAATTACT AGGAAGAGAT 1020

GCGGCTTATG TCGCTCAATT TGGTCTAgGC TGGGTCATCA CCAATTATGA AATAGAGATT 1080

CACCGCTTAC CAAAAGTTGG TGAAAAAGTA GCAATTACAA CGCAAGCTAT GAGTTATAAC 1140

AAATATTTTT GTTATCGTAA CTTTTGGGTT CATGATGAAG AAGGCAAAGA ATGTGTCTTT 1200

GTGAAATCAA CCTTTGTCTT AATGGATCAA AAAAATCGGA AAATCAGTAG TGTGTTACCA 1260

GAAATTATTG CACCTTTTGA TTCTGAAAAA ATCACTAAAA TTTATCGCCA TGAAAAAATT 1320

GAAAAGGTCA CAGAGGGGAA CTTTTTACCT TATCGTGTGC GTTTTTTTGA TATTGATGGC 1380

AATCAACACG TTAATAATGC GATTTACTTT AATTGGTTAT TGGATGTGTT AGGGTATGAC 1440

TTTTTAACAA CGCATCAACC GAAAAAAATT CTTGTGAAAT TTGATAAAGA AGTAGAATAT 1500

GGCCAAGAAG TCGAAAGTCA TTACGAAATT GTCGAACAAG AAAATCAGTT GAAAACACGC 1560

CATGAGATTC GGATTGATGG TCAAACCTAT TGTGAAGCGA ATATCGATTG GACCAACTAA 1620

GTTGAGATGA CGGTTTAGAA AAATAAAAAG TTACGCAGAG GAGGAAGGAC ATGATTCGCT 1680

TAGGATTAAC ATCTTTTAGT GAACACGACT ATTTAACTGG AAAAAAACGG TCCACGCTTT 1740

ATGAATATGC CAGTCATTTA CCGCTAGTTG AAATGGACAC GGCGTATTAC GGGATTCCTC 1800

CCAAAGAACG AGTAGCTGAA TGGGTCAAAG CAGTTCCCGA AAACTTTCGC TTTGTCATGA 1860

AAGTTTATAG TGGAATCAGT TGTCAAGGTG AGTGGCAGAC CTATTATGCA AGTGAAGAAG 1920

AAATGATCAC CGCCTTTTTA GAAAGTATGG CCCCATTAAT TGAAAGTAAA AAATTATTTG 1980

CCTTTCTGGT ACAATTTTCa GGAACATTTG GtTGTACrAA AGAAAATGTC GCTTACTgCA 2040

AAAAATTCGT CACTGGTTAA AGACTACCAT CGCCATTGAA TACAAATAAT CCAGGTATCA 2100

ACCAAACTTG TAAACAATTT GCAATTATAA AAAATCATTC ATGTATGTGA TAACGAAATC 2160

TCATCAnCCT TACTATTACA TCTACCnGTC CCGTCnnGA 2199

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

TnCTCAGGGT TTTTCTTCCC TTCTTGTGAA TGCGGGATTG TACCAATTGT GCATCAATTT 60

GTAAAAAAAG ATGTACCAAC ACATACCGCT TTTGCTTTTA TGTTAACGGC ACCAATCATT 120

AATCCAATTG TGCTATTCTC AACATACGTA GCTTTTAGTG GCGCAACAAA ATTTGTGATT 180

TGGCGAGTTT TAGGTAGTAT GATTGTCGCG TGGGTTATCG GCATTTGGTT AGCTTATTTT 240

CGAAAAGAAT CAATTTTAAC AGAAAAAGAG TTGGCGCAGA TTAAAGAAGA GCAGGTTGCT 300

CATACGCATG AACACGTTGA TGAAGTTCGT TCATTTTGGA AAAACGGCTG GTCAGCGTTA 360

ACCCATAGTA TTGATGAATT TTTTGATACA GGTCGCTATT tAATTTTTGG TtCTTTGTTG 420

GCAGCAATCA TGCAAACGTA TATCCCaACT GGTGCACTtA TGCAATTAGG CCATTCAAAG 480

ATTTtAGCGA TTCTAGTCAT GCTAGTCATC GCTGCCACTC TATCACTTTG TTCAGAAGCG 540

GATGCATTTA TTGGTTCTTC TCTTTTGAGT TTATTTGGCA CAGGACCAAT TGTCGCCTTC 600

TTAGTTTTTG GTCCAATGGT AGATATTAAA AATTTATTGA TGATGAAACG TTATnTTAAG 660

ATGTCATCCA TTGTACAATT TGTTTTGATA GTGGCGCTkG TCGTAmCwAT TTATGCGGCA 720

GTAGTTTAGA AAGGAGGCCT ACAATCGATG ATACGATTTA TTATTTTAAT TGGATATATG 780

GGGTTGATGA TGTATCTTCA AATTTCAGGT GAACTGAACC AATATATCAA TATTCATTAT 840

AATTACTTAG CTGTTTTATC AATGGTTTTA GCTTTTATTA TGGCGATTGT CCAATTGATT 900

TTGTGGAACC AAGCAGATCC ATCAATACAA AAAAAACATG AAGACATGCA CCAACATGGG 960

GGACATGAAC ATCATGGCCA TCAGCATAAT TTGGAAAAAC CCAGCCAAAG AGGGCTTGCC 1020

TATTTACTAC TTTCTTTACC GTTGATTGTT GGCTTATTAT TTCCGACAGT TAGTTTAGAC 1080

ACAACAATTG TTGAAGCAAA AGGATTTAAC TTTCCAGTAA GTAAAGAATC AGTAGGGGAT 1140

CCTGATATGC AAACGCAATA TTTGAAACCT GATACAAGTA TGTATTTCAA TAAGACGGAT 1200

TATGACAAGC AGATGGCAAA AGCCATGAAA CAATATGATG GCCAATCTGT GATTTCAATT 1260

ACGGATGAAA ACTATTTGGA AATTATGGgA ACTAATCTAT AATTATCCAr GTCAATTTGC 1320

aGGGAAAAGG aTTTCTTATA AAGGCTTTGT CTATAATTCC-AAAACGAGAA GAAAGTGTTG 1380

ACCAGTTkGT CtTCCGTTTT GGGaTTATyC ATkGTGtCGC TGATTCtGGt GtTTTTGGCy 1440

TGttGGtTCA TTTyCCTGaA CATACTCAAT TTCAAAACAm TGATTGGGTA ACGATTACCG 1500

GCACGtTGAG TTGTCCTATT ATCCACCGTT TAAACGACAA ATACCAACTG TGCAAGTGGA 1560

GAAAGTCAAA GCAGATcAAG CACCAAAAAA TCAATATGTC TATCGTTCCT TTTAAAAAAA 1620

GTTGGTTGCT TCCTTATCAA ATGGAAGCAA CCAACTTTTT TGCTGTCTAT TTTTTAATTT 1680

TGTTGCGTTT ACGACGAATA AAACCCAAAG ATTCTCTTTT TTCTCGAAAG CTGCGGATAT 1740

TCTGATTGAA AACCTCAGAA GCGACTAAGC CTAACGCAAT TGCCCCAGCA ATCATTACAG 1800

CTTGcACGGT AAAATAGGCA CCTTTTTCAT AATTGCCAAT TACGATATTC CGAACAGCTT 1860

GATAAGCTAA GCCACCAGGT ACCAATGGAA CAATACCAGG rATATTAAAA ATCGTGACAG 1920

GcATTTTCAA TATTTTTGAG AATAGGTAGC TTACTGCCGC AACACCGACA GCACCGATGA 1980

GGGAACCTAA TGCTGCATTT CCACTAAAAA CTTCAACGAT TACCCAATAA AGCATCCAGC 2040

TCACACTACC AGTTAGACCA CAAGCCACCA GTGATCGTCG AGGAACATTA ATAATAATCG 2100

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AAGTCACTCC TTTTAATAGA AAAGTTGAAA GACAAAAGCA ATGCCAAAAC CAATCATTCC 2220

TGAAGTCATT AATGCTTCAG TCCCACGAGA AACACCCGAT AAGTAGTGTC CAGCTAGCAA 2280

ATCGCGAAGA GCATTGGTAA TTTGCACACC AGGCACTAAA GGCATGACAC AACCAATGAT 2340

GATTAAATCT TGTGATTGTC CGAGTCCCAA TTTGACTGAA AGAATAGCGG CTGCACCAAT 2400

GAACAACGAA GCTAAAAATT CAGATAAAAA TTTAATCTTG AGAAACTTTA AACTrAAATA 2460

ATAAAGACTA TAGCCGCAAC CACCAATCAG AGAAGTCAAG AATAAATCGG ACCAGACACC 2520

ACCAAAAAGA ATCATAATTG TAGCGCTGAC AACGGCCGCA CTAACAATGC GTGCGCTAAT 2580

TGGAAAATGT CGGT 2594

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATCCTTTCG CAAGGAGGAC TTACTCAGCA AAATCCGTTC CAATCGAATG TACCAAGGCT 60

TTAACGTTTC AGCAGCCAAT AAAAATGAAG GATGGGGATC AGACCGATGA CAAGAAAAGC 120

CAAAACGGCA GAAGAGATTA AACATATTGC AGAAGAGGAA AACGTACGTT TTTTACGACT 180

AATGTTTACC GACATTATGG GAACAATTAA AAATGTTGAA GTTCCTGTGA GTCAGCTAGA 240

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CGAAGAAAGT GACATGTATT TATACCCTGA CCTATCTACA TGGATGATTT TTCCGTGGGa 360

AAGCGACCAT GGAAAAGTtG CGCGCTTAAT TTGTGATATT TACAATCCTG ATGGTACCCC 420

TTTTgCCGGA GATCCCCGCG GTAATTTAAA ACGCGCCTTA GCAGATATGA AAGAATTAGG 480

CTTTACTTCT TTTAACTTAG GACCAGAACC AGAATTTTTC CTATTTAAAT TAGATGAGAA 540

TGGTGAAATT ACCACTGACT TGAATGATAA AGGTGGCTAT TTTGATTTTG CACCAACCGA 600

TTTAGGTGAA AATTGTCGCC GTGATATTGT TTTAGAGTTA GAAAGTTTAG GCTTTGAAGT 660

GGAAGCTTCA CATCATGAAG TAGCACCTGG TCAACATGAA ATTGACTTTA AATATGCTGA 720

TGTAGTTGAT GCTTGTGACA ATATTCAAAC GTTCAAATTA GTTGTGAAAA CTATTGCGCG 780

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TATGCACTGC AATATGTCAT TATTTAATGA AGAAGGTAAT GTTTTTTATG ACGAGTCAGG 900

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TGCCTATACT GCGGTATGTA ACCCAACAGT GAACTCTTAT AAACGCTTGG TACCAGGTTA 1020

TGAAGCACCT GTTTATGTAG CTTGGAGCGG CAGAAATCGT TCACCACTCa TTCGAGTTCC 1080

TGAATCTCGT GGkTTATCGA CTCGTTTAGA ATTACGTTCT GTCGATCCTT CAGCGAATCC 1140

GTATTTAACA ATGGCTGTCT TATTACAAGC AGGTTTGGAT GGTATTCGTA ATGAACTTAC 1200

ACCACCGCCA GCAGTTGATC GTAACATTTA TGTGATGAAT GAGGAAGAAC GTCAACATGC 1260

ACAAATTGaA GATTTGcCAT CAACCTTACA CAATGcCATC AAAGAATTAC GTAAAGATCA 1320

AGTAATGATT GATGCATTAG GTCGTCATAT TTTTGCCAAT TTTGTAGAAG CGAAACGAAT 1380

GGAATGGGCA GCCTTCCGTC AAACCGTTTC TGAATGGGAA AGAGAACAAT ATTTGGAGTT 1440

GTACTAAAAG CCGTTACTTT TAATAATCTT AATGTTTAGA AAGAGGAAGA TAAGTCGAAA 1500

CGCTTATCTT CCTCTTTCGT TCTTTAGTTT GTGAATGAAT AGATAATTTC TATTTCACAA 1560

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CCGCTATAAT AAACAAGaAT ATGCGTGCAA CTATTCTATT TTTTAGATAT AAAGGATGAG 1740

AAAAACATGC GGAAAATGAA AACAATGGAT GGGAATGCAG CAGCaGCTTA TATTTCCtAT 1800

GCTTTTAcAG AATTAGCAGC CaTTTATCCA ATAAcACCAA GTTCAACGAT GGCTGAACTT 1860

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AAATGCAATC GGAAGCTGGT GCTGCCGGCG TGGTCCATGG CTCTTTAAAA AcAGGCGCGC 1980

TTACCACGAC CTATACGGCT TCACAAGGGT TACTTTTAAT GATTCCTAAT ATGTACAAAA 2040

TAGCTGGAGA ACTATTACCA TCTGTTTTTC ATGTGGCGAG CCGAGCTTTA ACTACGAATG 2100

CTTTAAATAT TTTTGGTGAT CAAGGAGACG TAATGGCCGC ACGCCAAACA GGCTTTGCTA 2160

TGTTGTCAGA AAGCAGTGTG CAAGAAGTGA TGGATTTGGC ACCAGTGGCT CACTTGGCTT 2220

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TAGCCGAATT CCATCGTCGG AGCATGAATC CGAATCACCC TTCCGTTAGT GGAATGAACC 2400

AAAATCCAGA TATTCACTTT CAACAACGAG AAACAATAAA TCCTTATTAT GAAAAATTAC 2460

CTGGTATTGT TCAAAAATAT ATGACAGAAA TTAACCGGTT ACGGGGAACC AATTATGATT 2520

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CGCAAACAAT TGAACAGACT GTTGATTATT TACAACAACA AGGAAGAAAA GTTGGCTTTC 2640

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CTGAAGCGCC AGAAGGATTC ATTGTGCGTG ATTTACGTGG TGCCGACGGC TTGAAGTATC 3960

GTATCCAAGT CTCAGTCAAA GATTGTACTG GCTGTGGTCT TTGTGTTGAA GCCTGTCCAG 4020

CTAAAGGGAA AGCTTTAGTA ATGAAACCTT ATGAAGAAGA AAAAGAGCAG GCTATGAACT 4080

GGGCGTTTGC TATGACGTTA CGTCAAAAGG AAAACCCAGC AAAACCGAAT ACTGTTTTAG 4140

TTCGCAATTT AATAAACCTT ATTAGAGTTT TCTGGT 4176

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CTATATGATA TATCATTTAA AACAAAGGAG CnACTTTCAT GAATATTCAA GCGATTGATA 60

CGCGACACGG AACTGCCAAC CAACATAGTT TTTCAAATGG AAATTGTCTA CCCTATACTG 120

GCGTGCCATT TGGGATGAAC TTTTACGCCC CGCAAACAAC TGACCAAAAA GGCAGCTGGT 180

GGTTTCATCC AGAAGATCGA ACATTTCAAG GCTATCGAGT AACGCATCAA CCAAGTCCTT 240

GGATGGGTGA TTTTAGTCAT TTATTAATGA CCCCTGTCAG TGGTTCATTG TCGGAACTTT 300

CTTTATTCCA TGCCCAAAGT TCTTATCGTC CAGAAGAAAG CCTTTTTTCT CCTGTCGAAA 360

TTAACTTAAC TCAATTACGC TATCAAATAA CTTCTCAATT AATCCCAAGC ATGTATGGTG 420

GTATCTTAAC CATTGATTAT CAACAAAAAG ATAATCACTT ACTACTAACT CTGCCTGGAC 480

GTTATCAAGT AAAACAATTA GATGACCATC AAGTGGCTGT AAAAGTCATC AACTATTCTG 540

GTTGTGAAGA TCCAGATTTT AGTTTTTATT TTGTGCTTCA TTTTGAACAG CCTTTAACCA 600
AATGGTTTGC CCCTTCTTCA GGTGAAGATG GCAAAATCCT TCTTTCTTTT GGAAATATTG 660
CTCAACAAGT TGTTCATTTT AGTAGTTCAT TTATTTCTGA AAAACAAGCG CAGTTAAATT 720
TAGCGCGAGA AATCTCTTTG CGTTCTACTG AGATGCTGCA ACAAGGAATC GCAGATTGGC 780
ATAATTATTT CGATCGCCTT AAAGTAACGC ATGAAAACCC TGAACATACT AAAACGTTTT 840
ATCATACACT GTATCGAACA TTCCTATTTC CGCAAACCTT TTATGAATTG GACGAAAATC 900
AGCAGCCGAT TCATTATGAT ACGTTCTCGC AAACGGTTCG TCCTGGTGTA CTATATACCA 960
ATAATGGCTT TTGGGATACT TATAAAACGG TCTACCCATT GTTCTCACTA ATTGCTCAAG 1020
AAAAATACGA AGAGATGCTA GAAGGCTTTT TAAATAGTTA CAACGAAACA GGTTTCTTGC 1080
CAAAATGGTT ATCTCCAGAT GAGCGTGGTT TAATGCCCGG CACCTTGATT GACGCTGTCA 1140
TTGCTGATGC CGCCGTGAAA AAGATTCGTC CTGACTTGAT GCCTCAGTTC CTAGAAGCGA 1200
TGAAAAAAGG CGCTACACAA CAAAGCGAAC GAGAAAATTA TGGACGTCAA GGAACTCTGG 1260
ATTATCTAAA ATATGGCTAT GTTCCTTCAA CCTATCATGA ATCTGTCAAT CATACCTTAG 1320
ATTATGCGTA CAGCGATTTC TGTATTtCGC AAGTTGCAAA AACATTGAaT GaTTCAGAGA 1380
CCGCAACGTT TTATCGTCAA CAAGCCTTGA ATTATCAACA ACTTTTTAAT CCTGAAACTG 1440
GCTTTATGCA AGCAAaGGAT ACTGAAGGCA ATTTCCGTCC TGACTTTTTA GATATTCGTT 1500
GGGGCAAAGA TTACGCCGAA GGAAGTGCTT GGCAATCAAG TTTTGCGGTT TATCAAGATT 1560
TTGCAGGTTT GATTAAGCTA TATGGTAGCG AGTTAGCTTT CGAAAAAAAA TTAATTCAGC 1620
TATGCAATCA AGCGCCTAAC TTTAACGTTG AAGGCTATGG TTTTGAAATT CATGAAATGA 1680
GTGAAATGGC GGCAATTGAT TTTGGTCAAT TAGCCATCTC AAATCAACCA AGTTTCCATT 1740
ATCCGTTTCT ATTCAGCTAC ATCGGCAAAC CAGAGATGGC TCAACCACTT TTAAAACAAC 1800
TAATGCAAAC ATTTGATGCT TCACCAACTG GCTATCCAGG TGATGAAGAC AATGGCAGCA 1860
TGTCTGCTTG GTATATTTTT AATAGCTTAG GCTTTTATCC CGTCACACCA GGAACTGGTG 1920
AATATGTAAT CGGGATGCCT TTAGTCCAGA CGGCGGAAGT AAAACTATCA AATGGTAAAC 1980
AGTTAACCAT TCAGACATCA CCAAACAAAG TCCAACAACA ATTTATTCAT GAAATTCAGT 2040
TAAACCAAGA AAAACATACT GCGCCTTATT TTACTCATCA AGAACTATTA AATGGCGGGA 2100
CTTTAGATTA TCAATTAGGG ATCGTCCCGA ATCCACAAAA CACAGCAGAA CGACCGTTTT 2160
CATTAAGTAC GGAAAAATAA TAAAAAGAAA GATGTTCATA AAAATTGAAC ATCTTTCTTT 2220
TTATTCTTCG ACACCTGCGT AATTTGATTG GTATTGCTCT CGAAATTCTT TTGGCGTAAT 2280
TCCATTTAAT TTTTTAAACA TTTTTGAAAA ATAGTTGGTA TTGTTAAATC CTACTTTTTC 2340
TGAAATTTCG TTGATTGTAT CATCCGTGTA CAATAATAAT TTCTGGGCAT GCTTGGTACG 2400
CACTTGaTTC AAATATTGAG aAAAACTCCG CTTGGTTTCT TTTTTAAAAA TTTGGCCTAA 2460
ATAACTAGGG TTCAAATGAA GCTCATCCGC CACCGTTTTT AAGTtTAATT CTTCTAAATA 2520

GCCTTGTTCA ATTCTTTCTA CAGCTTGGCT AACACTTTCT GAATATTTTT TTATTyTAGG 2580

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ACGGGAAATA TCTGAAAAAA GTAAGAAGAC TACATAGCGT ACATATTCTG GCGTAGCGTG 2760

TTGTTGACTT AACTGATTGA AAATAGCATC TAATTCCCGT TGAATGGTCT GCATATCCCC 2820

AATCATCAAG GCTTGGTTAA ACGCTAGGAA AGTAAAATCT TCTGCCGAAC GATTCaTTTG 2880

TTCTTTTTGA TTATTTGGCA GAAATTCTTG ATAAAACGTT TCAATTGCTT GCAACTGTTT 2940

TACTTTCTCA TAACTTTCAT AAACCGTTTC CCATTCATTG ACAGATTCCC CTACAAAAAT 3000

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CAGTTGGCCT TTTTTCATAA ATAGTTCCTT GATTGTTTCT AAAAATGACA TCTCAGCTTC 3180

AACCAATAAA ACGGTAAAAT CACCTGGTTT TATAGTCGCA AATTGCTGCA TTAACTCTTC 3240

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GGCTAATAGT TCTTGTTTAT TGACTGGTTT CAAAAGATAA TCTTGGACCT GCAAAGCCAT 3420

GCCTTTTTTG ACGTAATCAA ACTCTTGATA ACcTGATAAA ATTAAACTAA TAAATTGAwG 3480

TCCtTTTkTC TTtGCTtGCT CaATTAATTC gATCCCGCTC ATTcTGGa 3528

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

TGGATCCTAC nAAAGGCCTT TACnTACCCG nTTTCCCAAA TTCCCTTAAC CCATATCnTG 60

ATAGGCTCTA GAGGAAGTAT ATCCCCCAGC CGAGAAAaGt AGtGTTAGTA GAAAGATTCT 120

CGCTAATATA TTTTAAAATT TGATATACAG AACTTACCTC TTGTTCTGGT GTCTTTCCAG 180

TAGTTAAAAT AAGTCTGCCA TAGCTTTCAG ATACTTGCTT AATTTCATCT TCTAGATTTG 240

GATATTCTAC AAAAACATCT TGAATATACT CATAAATAAC AGGAGTGCTA TCTATATATT 300

CAACAAACAT TTTAATGATA GAATTAACTT CACTGTAATG AGCATTAAGA ACTCTAGAAG 360

CTAATTGTCT AAATTTCCTA CTTGCCTTTT TTAAATCTTT TTTATTGATA TTAATCTCCA 420

TCTTGCATCT CCCCACAGAA CGGACAATAT CCGCCTTCCA TTTTTAAGCT TGGACTAATT 480

TTTGCTTCTT TATGACAGCA GTCATAAATT TGAAGTTCCA AGTTATCTAG TTTTGAAATA 540

ATCGGATCAA CAGGATCTTT CTTAATTTTT GAACCTGATT TGAATTTTAC GCTTCCATTC 600

TTTGATGATT TACTCAAATT CTTACCAAAA TCATTAAGTA AATCAGATAC ATGATTATTT 660
ACAATTTTCA TTGCTAATTC TATTACTTCA TCAGTAAACA AACTATCTGG AGTTAGACCA 720
CACTTAGGAC ACCAAACATG CAATTGAGAT TCATCTTCCA AGTCCTTAGG CGTTAGCTTA 780
AAATACTCAC CACACAAAGT GCATTGTAAG AAAATAAATC CATCTGAATC TGATGGGATT 840
GAAATATTAA AAGTAGTGTC AGCTGTCATA GATACATCTC CTTTTGGGAA TACTTAATTT 900
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AAATCATACC CCTTCGGAAC TAAAGGCGTG TAAAACTCAC TAACAACACC CCCACCTGTA 1080
TCTACATAGC CTCGCCCCTT GaTTTGTTTC ATAAAAAAAA TTTTATCAAC CTCACCAAAC 1140
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AGACCAAGAT ACGCATAATT CTCTCCTGTT TTGTAGTTTG GCATTTCTTT CATCAACCTA 1440
CTACGAaCCA TCATACGTTC ATAGAAATCT TCTACACAAG CGGAAATTTG TTCTTTTTGG 1500
GaATATACGT GAGTCATTAT TGTGCCTAAA TCTGCTAGAT CCGCATTTTT GGGaTCAAGG 1560
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TTCCCACCAC CTGTACCACC TGCGATTAAC ATATGAGGCA AGAAATCATA CGCCCATACT 1680
TGATTTTTCA TCAATCGCAA AGCTCCATTT TCTACCACTG CTTCTTCTAT CCCAATTCGA 1740
TTGGCAATCA TATCGTAAAG CAAGGTATAA TCCACATAGG AGTCTTTGAG TTCCTTTTCT 1800
ACTAACTCAC AATACAGTCC GCTTTCTAAC TTCTTTTCTA GCTTTAATAG TTGATCTTGa 1860
TATTTTCCCA GTGAAATTgA ACGCGAATAG ArAGTAAGCC ATCCTTCATc GATAATAAAT 1920
TTgGGGrAGT AACTGATACT TTCTTTGGTC CGACTACCAT cAAATCTTTG AAAAAcCTTC 1980
ACTTTGAGTT TGTTTCACTT CATACCAATG GTTTTCTAGA ATCATCCGAG CTAGCTTTTG 2040
TCGATGCCAT AAACTGCGCC AATGATCCTG AAAAAAGTGA ATATAAAGCA ATATCATACC 2100
TCCTGAAAGA GCAAAACTTC CTAGTAAACA GATTAAATCT TTCGTGGACC AATCAATTTC 2160
ACTAGTGGAG AATGATAGCT TAGAAATCTC AAATTGTCTA AGCTCTTGAA AATAAAAGAC 2220
GCTCATACAA CCAATGAACA AAGCAAGTAG CCAGCCAAGA ACAAAGTGAT AAATTAAATG 2280
CTGATTTCTT GCGCGTATGC GATGTCCTTT GTACATCTGA TGGTTTCCAC CTCCAATCAA 2340
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CGGGAAGCTG TTTCGTTTCA ACCAATTGTT TTAAAAAGCT TTCAATGACA TCCGGCATCT 2460
CCACACCGAT TTCTTCTAAA ATAGACTCAG CTTTTCGACA TAAGTTTTCA TTTATTTCCA 2520
CAATCATAAA GAAGGATTCC TCTTCCCCTA ACCAATCCAG AACATTGAAC TCTTCTTCAC 2580

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TATCGGTATT TCCCCCAAGT AGCCCCTGAT GCATAATCAG AAACATTTTC TCATCATCGG    2640
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ACTCTACTTC TGTATCGTAG GCAAACTCTC GTAATGGCAC ATTTGCTGGA ATACTGACTT    2940
GAATCATTCG ACCTTGTGCT GAGGATTTCA AATTATAGGT TCGTTCTTTG ACCTCATTAC    3000
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CCTATGCTTT CACTAAATCA TCGACATACA ACACATAATC GGTAAAACCG CGGTTTTCAA    3180
TCGCATACCC TTTGGCAACT AAATGGGGAT TCACAGcTTT CAGCGGTTGA TCTTGGTCAA    3240
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TGGAATATAG ATGATAGCTA CGACCAATCA CCACAGTATT tCGGCCATAT CCTTCTGTTA    3360
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CAAATTTCAA TTCCATATTC TTTTCCTCTT TTCATTGTTA GTTTTGGATA CAAAAATAGC    3480
GCGACCACTT TTTTAGGAGG CGGTCGCACA AGTCGGTTCC TACTATTCAC TTGTTTCATC    3540
TCATCACCTT AATTGCGGCG ATTCCAGAAA TAATACCCAG CAGTCGAAAA AATCAAGATA    3600
AAGCCAACTA ACAGTAGAAC GTTGGAATTT TTCTCCCCAG TTTGCGGGAA TGTCTTCACT    3660
GTGGGACTAG ATTCTTGAGA ATTACTTGGA ACAGCTGGTG TTTCCGGTTG TTTTGGCGTA    3720
CTCGGTATGG TTGGCACTTC TTTTGGTGTT AAGGTTTGAG ATTTTTCTTT CAAATCTTCA    3780
TTGTGTTTTC CATTCACGTT TCCATCTTTT TCGTAATTGA TTTCCGTAAA AGTAAACTTA    3840
GTTCCTTCTG GATACTTTCC GGTATCTACT TTTTCCGCAA GTACGGTTTT GGTAAATTCT    3900
TTATCATTCA CTTCATGCTC AATTTTGCCA GATTTCCAAA TTTCTTTGTT CGTACCATCT    3960
GGTAGTAAAG CATACAGAAT TGTTTCGAAA GCTTCTTTTG AGCCATCCAG TACATCATGG    4020
GTAACCGACA CATCATCAAA CATATCCATC ACGTCACCAT GAGTAAAAGT TTGCGAACCA    4080
TCTTCTAGGT GGGCTTTTGT TTGGATGGAA ACATGGCGTT CAATCGTACA ATTGACGGTT    4140
TGTGCTTGAT TGTTCAAGCT AGCATCCTTC GCTACTGGCT CATTGCCTGC TTCAAAGGCT    4200
ACCTTGTTTT CATACACATA ATTGAACAAG ACGATGCTTT TATCCAAAAC TTGTTCAGCG    4260
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GTTTCGGCAA TCACCACCGG TTTGGCTTTT TCGTCTTTTT CTTGGGCAGC TTTTGTGGCT    4380
TCCACATCAA TGGCTTGAGC TACGACATAC CAGTCTTCTT TGATTTCATG CAAGTTATAT    4440
CTCAATTTAT CAACTAGCTC GGTAAAATCA AGGGTATTCA ATTTTTATT TCCGTCTTTC     4500
CAAGTCGCAA GAGAAGTCAA ACTATCTTCT TTCTCGGGCA AATCATAAAG CATCAAACGG    4560
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TTCAGACTAA CAGAAAACTC GTTGTTAGTT AGTTTCTCGT AAGGAACGGT CACCATCTTA      4620
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TCTTTGTTTT CCTTAAATGT AGAACGGATT TCTAGTGGTG TAATCTTTTG AAATCCTTCT      4740
GGAGCCTCTA TTTCTTCAAG TAAATAATCC CCATAAGGAA GATTTTCAAA CTTACCATAG      4800
CCATCAAAAC CTAATTGCTC GTTACAAGCT GTGGTCGCTT TATCTTCAGC ACCTGTGATT      4860
TCmTTGGTCC CTTCCaATGG CGACACTTTA AAAGATAAGT CGTTAAATCC aGTTTCGGCA      4920
GTGCCATCAG CCGATCCAGC AAATTTAAAG AAATCAAAGC CAAAGCGAAT AACTTGTTCT      4980
TTTGCCGTAA CATCTCGAGT AATTACGGCA TTTTTTTCGT TATTATCAAC TTTTTTGATG      5040
GATACAGGAT ACTtCGTTTC ATCCAAAGTA TATCCTTcAG GTGCTTTGGT TTCTTGCCAG      5100
AAATACTCGT TAATTGCTAG GTGTTTAACG GCAACTTGGT TCTTTTCATC TAAAGCCAAA      5160
GTCACTGTTT CATCAGAAGC TTTCGTTCCC TTCACTAATT CTGTTTTAAA AGCTTCACTC      5220
CATTTAACAG CTTGACCATC TTTTGCAGTA AAGAGAGTAT ATTCAGCTCC TTTAAACTCA      5280
GCTTTCCCTT GACTCTCATT ACCGGTATCT TTGTCTTCTT TTGTCAAAGT GGTTTCCCCA      5340
GTAATTTCTT GGTTTTGCCC TTTTACGTTA CTGGTAACAA GAGCCACGGT TTGATTGGCA      5400
TATTTTAACT CGACTTTTGT TGGTTTGAAG GTATTCACGA AACCATTACT AGATTTAGTT      5460
TCTGTCACGT AATAGGTTCC CAGTTCCAAA GCATTAGCAA GCTCTTTTGG TGTTTCCGCA      5520
CGACCTTTTT CATCCGTTGT TATTTCTTGG ACAATTTCAC CAGCTGGGCT GTCTTTACGA      5580
ATGGCAAATG TATTTCCAGC TAGAGAATAA TTGTCATTCC AAAGATCaGT ACCTGTTTCT      5640
ACCCCAGTCT TCTCTAAAAG AATTTGACCT TTTTGTCGCA TATTTTTCGA AGTCATGGAA      5700
ATGGTCTCGC CCGCTTTAAT GGTGGCAGCC ATGGGTGTGG TATCAATCAT ATAAGGATCT      5760
GGCACCGATT TTTCAGTAAT AGTTACCTTT GTACCATGGG GAATTCCATC CAAAATAGAA      5820
ATCCCATCTT TATCTGTTGT CACATCTTTT GAAGGTAAAG CTTTCCCAAA ATCTAAATGG      5880
AAAACCGTTT CTGGTACAAT ATCACCTGAT TCTTTATCGA TTTTTTTGAT CTTTAAAGAA      5940
CCCTTAGTTT CCACATTAAT TTTAATAGCG TAGGTATTGG GCTTATCAAG CGCACCAGCC      6000
ATCACAGTTT GAAGTCCTGC TTTTTTATAA GCGACTGGAG TTCCAGTACC AGCTGATTTT      6060
TtCAATGTTA ATGTTCCTGA TTTGGAATTA GAGTTTGGAG TAAGCACTAA TTGATTCCCA      6120
ATTACACGGT AATCTATATT CGCCGTATTT TGGACGACTT TATCAAACTC AGATAAATTT      6180
AATTCATTTT TATCTATTAA AGTTGTCGAT TGACCTAAAA TTGTTTTTAC AGTGGTATTA      6240
TGAAAACTTG GTTTTTTTTG ATACTCCTCA ATTGCCTTAT TAATTTTTCC TTCAATAGAT      6300
TTTATATCAA CTGAAGCACC ACCTAATCTT TTTATGGAAT GGAGTTTATA ACCGTTCACT      6360
TCTTCCCAAA TCATCTTTTG TGCAACCATA TTTGTATCAA TATCTGTTCC AGCCTTTTCC      6420
CAAAGAACCG ATACTAGTTT CGCTTTATCA GACATTGATG GCAAAGGGTT TTTCTGATAA      6480
CCGTGCGTCA CTTCTGTTGG AATACTAACA CCTGGTTCAA TACAAAATAC TGTTTGTTTT      6540
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GCACCATTGT ATTCTGCATA TAATGACGTA GTACGTTCTG AGAGCGTGCT GCCATCGCTA 6600

AAAGTTCCGT CAACTTCATA CAGTTTACTT ACGTCATAAT GAATTGTTAC CTCTTGAGGG 6660

TGAGTAATTT CATCGGCAAA AGCAATCGTA GGACCAATCG TTCCGCCAAT TGTTTGACTT 6720

AATAGAGCCA AAGTCGCAAA TAACGACCAA TTTTTAAATG TTGTTTTTTT CATATAATTA 6780

ATCCCCTTTC GTTTTTGAGT AATAAAAAAG AGACATTCAC CTCTGaATGT CTCAAATGTT 6840

TAAAACTATT TTTTTCAAAG ATTATCAGAT ACCATATATC AAAAACTCCA AAGAGACTTT 6900

TCCTATATGG GCATACTGAA TAATGCGAGC CGTATTCGGA ATATCTTTTC CGtCTTCGTA 6960

TTTATCCaTC TTACATTTAT TCATAAAGCC CGCCTTTCTT TTTGAACATA AAAAAAGACC 7020

CTCAATTTTT GACGGTCTCA TCGTAAAAAT TTACGTTATT CATTCACCCA AGCTTCCACT 7080

AAATCCaCAG TATCACTTTG TGGACGTAAA GTTTTATCAC TTATAAAATC AACATTCACA 7140

ATCATTGGTA AGGACAAAGC TGTCCCAGTG ATAATACAGA TACCTTGTGA TAAACCTGGA 7200

AGCATTGATT TAGAAACTCT ATCTAGAGTT GATAATGAAT TATCAATTAT TTGAAGATCT 7260

CGCTCATTCA CTAGCTTGTG TAGAAAGAAA TTATGAACTT GTGAGAGAAG TGTGGGTGAA 7320

ATATCCGCTG GTCTTTGACT TGATAAAGTA AGGAAAAAAC CAAATTTCCG ACCTTCTTTA 7380

ATGATTTCCT CAAAAGTAGA AAGTCTATAA TCCTTCCATG ACGTATTGTC GTTTCTTGAT 7440

TGATCAGACA AAATATTATG TGCTTCATCG ATAATAAGAT GGAAACTAAC CTTATCTTTA 7500

CTCGTCTTCT GCTCATCGAA AAACATTTTT GAAGTTAACA TCGCTACAAT TTGTTTAGCT 7560

TCTTGATTCA AATCACGTAA AGAAATTATC TCAAGAAATT TGACATTGTC GATCTGTCCC 7620

ACTATCTCTA TATACTTCTG GAAATCTTCA ATACGGCTAT CGATTCGCTT TAGAAGCGGG 7680

TCTATATGAT CCGATATGAC ATTTCGATAT AGTAAGTCTT TGACTAATTG TAATTTACAT 7740

CTAAGTTCAA ACTCTTTGAA TATATTTAAT TTTTCCGTTA GAATCACATT TTCAACTTGT 7800

TCAAGATTAA CTGCCTGCAT ATGTTTAGAT TCCCAATTTC CATCAAAAAA AGTACCGTTT 7860

ACAATAAATT TTGCAGGGTC ATCCtTACTG TATATCTGTG CCTGTTTGAT TGGCTCCAAA 7920

GCTTCACTAG AATCATAAAA TTCACCCAGG ATACTTACAA ATCTATTTTT TAAATCCATA 7980

TTGGGAAAAG TCGTAAATAT CTCTCTAAGT ATAGAACTTA TCCATCTTTG CAGTGACTCT 8040

TCACCAAAAC CAAACTTATT TATCCCTTTA AGAACACGTT CCAAAAAAGG TTTTTGAGTT 8100

kGTkGAGTCG CTGrAAAAAG rATwGaCmAG aTCTCAGAAC TAAAAAAGAT ATCCCTTTTA 8160

ATCTGTAACC TCTTATTTGA AACGGTTCTA GTGGATAATT CATATATATT TTTTTCGCTC 8220

TTAGGTACAC CAAATGAGTT ATCATGCACA TACTCACCGT TAAAGTCTAT GACAACAAAT 8280

CTACTTTTCT CTCTTAGCAA TGGGAACGAT TGTTTAAATA GCTCAAAATA CAATTTATGA 8340

AGTGTATTTG ACTTGCCACT ACCAGTATTT CCAAAAATAC CAATATGTGA CGCAAAAAAA 8400

GAACTTATTG GTAAGTTAAC CTCAATTTGC TCATTTAAGC TTTTCCCGAT TTTAATAGTT 8460

TGATCTCCAT TAAAATGATC GAAGCTATTT ACATAGATAG TTTGTGTCTC TTCAGTTGTC 8520

GGTATTGAAC AAATATTTCC AATCATTGGA ATATATGTTG TACCAGTAGT GAAACAGCCT 8580

TCTGAAATAT ATCCAATAAT TTGGATATCA AGAATTCTTT TTATGGTATT CTTACTGAAT 8640

CTGTTATCCA ACTGATAGTT CTGCTTATTA TTTTGAGTAT CCCAAATTGA TTCAGAATTG 8700

ATTCTGCCTA TTATTTTAAT AAAGTTCTGA CGAATAACTA CAAAACTATT TACACTTAAG 8760

TTTTTTATCA CTTCACCATT ATTAATATAT GTCGCTTGGT TCATATCATC AAAAGTGATA 8820

GCTTTACACC TGATTCCGTT CACTTCAACA ACTAAAGCAA CCTCTATATT AGAATTATTC 8880

GTCATCATCT ACTACCTCCG TATATTGACT ATCAATATAC TTTTCAGAAA GATTTCCTTC 8940

GATAATCCTG TTAAAAGCTT CAAAATCTAT AACCGCATCT TTATTATCGT AAACTGATAC 9000

TTCCTCAGAA TAAGTGACAA TAGTACTATC ATTTGATCTA ATCkGATTTG TTTCTAACGG 9060

TAGGGGCGTC TCTTCTTCGT TTTCAGCTTG TTCCATAATA AAATCTGAAG GTGTTATAAA 9120

CACAATATTG GATGGAACTG CATTGGCTCC AAAACTAAAT TGATTTATTA TTTCACCTTT 9180

AGTACCATCT TTATAACAGA AAATGAATAC CAATAAATTT GGATTATTTA AAGATCTTTG 9240

GACAATATCT GTTATATGCT CATCTAAAAA TGAAAAACCA AATGCTATTA AAACCGATTG 9300

TTCCTTCTCA AGCTCGTAAG ACAAGAATCT AAGCATATTA AAATACTGCT CTTCAATTAA 9360

GGTAGACTGA AATTTCCTTT TTGTGGGTAA AACAATCTGT ATTTCACTAA TTTTCTCACT 9420

TATGCCTTGT AATTGATTAT AATACTTTTT ACCAAAATAA TTGATTACTT CAGTAGGACT 9480

ATCAATAAAT CCATCAACAG GTTTGCCTAG TATGACATCT TTCAATATCT CAATGGTAAA 9540

TGACCGTTGA AAATTTGTAT CATGAACTAT ATCGTTTTGG AGTTCTGACC AAACTTCTTC 9600

TGCTTTTTCA GCAGTTTTAA TAGTGTCCAA AAGGCTGTTA TCAACAAGCA CTCTATCTCT 9660

CCCGATAAAG TTTTGCTCAT TCAGCCaATT CACAGATCCA TGACATTTCA CCAAATTAAT 9720

TGTTGGTAAT TCGTTGGCAT AATTATCAAA GGCCCCGGCA TACAACATTG TCTTATTAAA 9780

ATTTTCAGTG CTGAGATATC TTTTCATATA ACCATTCGTC CCGTCATTAA AGAAAATTTT 9840

GGGATTTGAT TCTATATTTT TTTCgACAGC TATTTCaAGA AACAAATCAT AATTCGTAGT 9900

AAAGATATTA GTTCTTCTTG GGGAAACACG ACTATTTCTC AGTTTAGGA ACTCCACGCA 9960

ATTAAAAATA AATCTAGAAT ATTGATTCAT CACAGAAGAC CCAGAATCCA AGTGGTTTTC 10020

CGATTCACCT TTTTTTATAT ATTCAACCAA TATTGAATTA TCTTTGATTG CTATATAATA 10080

AAAAGCAAAC ATAACTAGTC TTTTACCTTC TTCAGTTATA TCTTTGCTAG TCATATATTC 10140

CTCAATTTTT CCTAAGCTTG AAAAAAATGG TACCGAAGCA CCTGCTCCAA ATaAGAATGT 10200

CGTTCtTTTC TCTgAAAGAA CAGCTCTAAG AGCTTTTACC TTTGAAATTG TCATAATAGT 10260

TCCCTCCAAA ATTGGAATTC ACTGTTATTT TACCACAATT TAATAACAAA CGATGATTCT 10320

CCTCAAAATT GTTTTTAAGA TATTTTTTTT TAAACTAATT AACGCCATAT ATCAAAAAAT 10380

TCAAAGAGAC TTTTCCTATA TAGGCATACT GAATAATACG ATCCGTATTT GGGATATCTT 10440

TTCCGTTCTC GTATTTGTCC ATTGACCATT TTGTAATAGG CGGTGAAAAA AACTTTCCAA 10500

AGTCTTCTCT TTCTAAGCGA TAATCCCTTC GAATCTTCCG AAGTCTTAGC CCCATTCGGA 10560

AGGAATCTAA CTTTTCAAAC TTGCTAATCC TACTTCCCTT CTTCAACATC TTACTAAAAG 10620

TCTCTCCATA CAAAATATAA GGGACGGCCA CTTTCCCAAG ATAGGCAACA TTCATTAATC 10680

TTTCGATATC AGGAATATTC GTACCCTTTT CCCATCTATT CACAACATTC TTACCCGCTG 10740

GTCGAGTAAA GTTCTTACCA AATTTTTCCA GTGTCTCACC TCGATTTTTC CGAATCTCTT 10800

GGATTCGTTT TCCCATCGCT ATTTTATCGA TGATGGGTAA TTTAAACGAA CCATCCTCTT 10860

GTTTTATATC CATCAAAATT TCTTTACCCT CGTTAGACAA TAACTGAGTG ATTTTCACAA 10920

TTGCATTTTT TGATAATGGT CGACTTTGAT TTAAGAATTT ATTTAGAAGA GATATTTCGA 10980

TTCCTAACTT CTTAGATAAA TCCTCACGAG AAAAAATATT TTTAGTTTGA TATTTTTCTA 11040

AATCAATCAA GACTTGTTGT TTTCTTTGAA TCATATCTTT AATAAATGAT TCAGCGCCGA 11100

GAACGTCACT CAAAATTCTA TCGtTCTTTT TAGATATGCT GCGTAATCCA TTTTCATATT 11160

TTACGATTGT AGCTTGTGAT ATATTTGATA ACCTTGCCAG TTCTTCTTGA GTTAATTGcT 11220

TAGATAACCT AGCTTCTTTT AAATGATTTC CCATTTTGaT TAACTCATCT TTaTTTaTTT 11280

GCATGAAAAA AGCACCTCCy TATGaGAGrT GcTTTcATCA TACGCTGACA AGTAAAAATC 11340

CTCAAGGAAA TTATTCCTTT TTTGTCCTTT TTTGTTAAGT TGTGACAACC GTATGACAGT 11400

TGAAACTTTT 11410

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AATTAAATTT AGATTGTTAT CGATCATTCT AAACTCATTG TTTTCTAATG TCAATAAAAT 60

AATGAGATTT AGATTAAAAT AAAATGAATT TCGAATTTTA TGAGCTTTTT TAATAAATCA 120

GTAAATTCCA TGACATGTGA GATACTTCTC ATTTACAAAC ATTCTTAAAA AAGGTATGAT 180

AGTAAAGAGG CAACTTGCAA AGGAGTAGAA GACGAATGAG TGAACAACCT CAACAACGTT 240

CAACCGAAGA AGTTGAAGCA ATTAAAGAAG ATATTTTAAC TGCATTAGAA ACAGTGATTG 300

ACCCTGAATT AGGCATCGAT ATTGTTAATT TAGGACTAAT TTATGAAGTT GAATTTGCAG 360

AAGAAACTGG TGATACTGTC ATCAAAATGA CCTTAACCAC AATGGGTTGT CCGTTAGCAG 420

ATGTTTTAAC aGAACAAATC CATGGTGTTT TAAAAGATAT TCCTGAAGTG AATAATATCG 480

AaGTAAAATT AGTCTGGTAC CCTGCTTGGA CAACGGATAA AATGAGCCGT TACGCACGAA 540

TTGCTTTGGG TATTCGCTAG TTATTTCGAG ACTAATGATA AAAAACATAT GAAAGAACCG 600

ATTGGTCCGT TCTTTCATAT GTTTTTTTGT TTGTTTAATT TACTTATTTG AAAAAAACTA 660

CCTGATGCCA TCAATACTTG GCTTTTTCCA AATTTTTGCT ACTGGATGGA AGTCTAATAA 720

AAACTGTAGC TGCGTTCCAC CGAAGCCTGA CGCTCCAGCA AACATGATAT GAAAAGTGAG 780

CCCTCTATCC ATAATCAGAT ACCCTGTATC CAGCACGCCA TTTCTTTCAT AAAACTGATA 840

ACGTTTTcTC TTTGGGCTTC ATcGCTGCAT TTTTGcCAAT TTCTTCACTC TCCAAAAGAA 900

CCCCCTTAGG aTAACGTGTC TTcAATAACG cTAACACGGg TGAACCTAAa TCGnTTGtTC 960

GGTGGTGCTG ATCAATTGCA AAGAAAAaGA CATAGGnTGC tTCAGGkGCA AtTGGACTAT 1020

TTAACAAAAT CCCCACGTTC TCATCCGCCT CyTGaATAAC mAACmAATGA AaTTTtCCTG 1080

sCTtGAGAAG ACATCAATAA TTGATCAAAC GGCAGTCTCT CTTCTTCTGG AAAAGCTTCT 1140

ATGTAGGTTG CTTCCCAATA GGGCTTGATT TTCTTGATTT AATAATGTGA ATTGCATAAA 1200

AGCTCCTTTC TAAAATTGAT GCTCGTACTA ATAACTTTTG GTACTTACAT AAGACCTAAA 1260

AGTATTAAAC ATGCGACTGG GnTATCCTAT ACGCAATTAT nTTTGGATAC TAAATC 1316

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2001 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

TTATGGnGGA TnAAATAGGT TCTTACTGGT TATGGCTAAT ATATAATAAT TTTACTTTAC 60

TAATTTTCAA ATTTCAACAn AAAACGACCA CCTTATCGGG AAAAGGTAGT CTGCATGAAA 120

AATAAGAATT TTAATATGTA TCAATATTAC AATATCTGTT TTkTGAGTTC ATTAATTTTT 180

ATGTAAAAAG ATGCCGCCTC ATTGGGGAAA GGCGGCAAGA TGTACTAAAA ATGAAAAATA 240

AAAATTAATT GGTAAAGACA TTTACCGCCT TCTTTATTAA AATACAAGTT TTCATTTTAC 300

AAAATAATTG TATTTTATTT AAATTCAAAT ATACAATTAT ATTAAAATAC TCCTATCTTG 360

GACTTGGGAT AAGATAGGAG CnCTCTTCTC GAAAGAAGAT CATATATGAG TGTATTAAAA 420

AGGTAACTAT ATTTTAAATC ATCTTTTTTT ATATTTCAAC TATTTTTATA AAAAATCCCT 480

ACTyCTCATT TCATTGCGAG AGGTAGGGAT TTACTAGTAC mTaATGTAGC TAAAGTTTGA 540

TAAGTCATAC TAATTTAAAC AGATAGTTCT AGGGTAACCA GATGaAACAT TTACCCATAG 600

ATTAATTTCC CAACACTTTC TGTGTACAAC CAAATAAATT CATCTGGGAA TTGAACATGC 660

GAGATTGTTT TCCCATTTAA AGAGTATTGT TCGGTAATGA TCCCTACAGA AGATGGTTGA 720

AAAGCAAAAT AGTCTCCGAC TTTTAATTCT TGATCTGGCA TATTCTCTCC TGTTGCCGGA 780

TCGATCTTAT CAATATAAGC AACATTAATT CCGTTTTCTG TCCAATCAAA GTCCGGCTGC 840

CCCAATACAT CATTTCTTAC TTGCCAAATA CCGTTTACAA ATTGTAAATC GTCTACTCTA 900

TATCCGTAAC GGCGCTTAGG TTTAGGAGGA ACTGGAGGAG CGGGTGTTGG ATTACTTTTG 960

GGATTAGCGT ATTTGTCCCA CATGCTTCTA TCACCAAAGA ATACGTTTAA ATCTAATCGA 1020

CCATTCCAGC CAGGCAATTG ACCATTTGAC GTATATTGAT ACATTGAAAT AAAATTCCAA 1080

TAAGGGACTG GTGGCGGAGT AGGTTGGGAA TATCCTTGTG GATTATTTGC TCCGTAATCA 1140

GCTAACCACA AACCATAATC AGCTTTTGCA ATAGAGCTAA AATTATATGA TTGTAAAACA 1200

TTGGTATAAG TATAAAACAT AGGTTTTACC CCTGTTTTAC CTTGAACATA ATCTAACCAA 1260

CGTTTAGCCC AAGCAACGTC TCCTTTATTA GTACTTTCCC AGTCTAAAAC CAAGACGGCC 1320

TTACCGATAT AACCTTTAAT ATTTTTTAAA AAGAACTCAG CTTCTTGTTC CGCTGTCCCT 1380

TCAAGTCCTA CCTCATTCGC AAAATGATAT ACAGCTACTT TTTTCCCACT GCTAATGGCT 1440

TGTTGGAATG CTCTATCACA GTCAGGATTT ATATATCCTG TTCCTCCTGT AGCTTTAACT 1500

ATAACAAAAT CTGCAGGGAC ACCTTCTTTA CCTACGTTAA TATTTGATTG CCAACTAGAA 1560

ATATCAATTC CGTTCAATGT CATTTTTATC ATCTCCTATA AAATTTTTAA AAGATTGATG 1620

TAAGCCAGTG CTTGCTAATC CACTTAAAGC CCCATATATT GTATTTtCAG GTGTGATTTT 1680

ACCTTGTATC CACCATGAGA TTAATATACC TAAAATGAAT ACAATTAAAG GAATAAACTG 1740

ATTATATTTA TCTTTTAATA TATTAGTAwt TTyAATAACA AACCCGACAG CTAAACACCC 1800

TAGCACCACT AATGGCATCA ATTCAATTTT AGAAAAGTCC ATTATTTGCC CCTCCGTTCT 1860

AAATCTCGTA TTCTTTCGTT ATTTTCTTTT AAATTGTTCC ATAAAGATTT TATTTGTTCA 1920

TTTAATTnTA TTACTTCATC CTCTACTAAG CCTTGTTTTT CnTTAGTTTG ATCAATTAAT 1980

AAATTAAGCT TATnTACTGT G 2001

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

AATGATTGTA CGCTTCTTTA AAGGTTACTG TTGTGTCTTC TTTTCGATAA AGGATATATT 60

CGTCATCTAG CATATCCATT TGCAGCTCCT GTTTAAATCC ATTTCTGGCA ACAATAGCAG 120

AAACTAGATG AGCAACAGTC AAGCCATCTA ACGGAATATC CACTCCATTC ATTGCTAATG 180

TGTAGACGGT ATCTTCCACT AAACCACAGG CGTTGCAACC ACCACTGGTT AAATCTACTG 240

TACTTGTTAT AATTGCCTCT TGCATCGTTT CTTCCCCCAT ATTGTTTTTT AAAGTTATTC 300

TTTCATTTGT TATTTACGAA CGTAATTCAC ATCATAATCG TCAACTTCAA TATAGATATA 360

GATTTTTTTA TCAGGCATTT TACTTCGAAT GTCTCGTTCA ATCGCATTCA CAACATCAGG 420

TGCATCTTCT TCCATTGGTT CTACCACATC AATTTTTGCC GCTACTAAAA TTTCAGTTGG 480

ACCTAAATGA ACGGTCTTTA CATCAATTAG TTTTTCAACA TCCGCCCGAT CAAATGCGGT 540

TTTAATTTTT GCTAAATCTG TAGCGGTCAC ACTTTCTCCT ATAATCAAAC TATAAAATTC 600

TTTCGCTAAG AAAATGGCTG CACACATTAA TAGTAAACCA ATCAGTAAAC CACTGATAGC 660

ATCAAaTGCA GCAATCCCAG TTACCATTGT TAAAAGGGTT CCCACCAAAG CTAAACACAA 720

ACCAATAACC GCACAAAAGT CTTCCGTAAA AATAATTAAA ATTTCACTGT GACGACTTTC 780

TCGCAAAAAT TTTAAGAGCG ATAACTTCTC TGTATTCAAT TCTTTGATTT CTTTCATCGC 840

TACACGCAAC GAGCTACCTT CCACAAGCAA ACCAAAAATT AAAATACCAA TGACAATAGC 900

CACATTTTCT ACTTCATGAG AGGGATGCAG TAACTTCTGA ATAGCCTCCA TTACGCCTAA 960

CGCGCCCCCA CCAAAAAAGA GCATCGTTGC AACAATTGTA CTAAAAAAGT ATTTTGCACG 1020

GCCTTCTCCA AATTGATGTA ACGCACTTTG TCCACGAGAA GCGCGCTTAT TCCCAAAAAG 1080

TAATAACACC TGATTACTAC AGTCCACGAC ACTGTGGATA CTTTCATTCA TCATAGCGGT 1140

ACTACCACTT AAAGCAAAAC CAACAAATTT ACTAATCGCT ACTAAAATAT TCGCAATCAG 1200

TGCGGCAATA ACTGCAAACA TGCCACTCGA TTTTTTTGTC TCCATAATTA CCTCCTATAT 1260

GTAACGTAAA ACTAAGATAA ACCACCCGTT TATTCATCCA TCATTTTACC ACTTCTGAGG 1320

TATTTGTAAA AAAGAGTTCT CTTAAAATTC AAAAAGAAAT GTACTGACTG TTTTAGTTGG 1380

CCCTCATTTA TCGGTGTCCA TCCCACTCTT GATAAAATTC CTCCAGATAA AGTTCCATAA 1440

ATTGATGACG CTTTTCCGCC AATAAGCGAC CATAATTTGT ATTCATTTGT TCCTTTAACT 1500

TTAAAAGTTT CTCATAAAAA TGCATAATAG CAGTATCTTC CCCATTCCGG TATTCTTCTT 1560

GGGTTAACTG TTCACGAGGT TGTTTGTGAG GATCGTGAAT TAAACGGCCT TTATTTCCCG 1620

AATAAGCCAT CACCCGTGCA ATTCCAATCG CACCGATGGC ATCTAATCGA TCCGCATCCT 1680

GGACCACTTT TCCTTCTAAT GTAGTGACTG TTTTCCCAGT ATTTCCTCCT TTAAAGGACA 1740

TATTAGCAAT AATGGAAAGG ATGTGATTCG TTTGCTCTGT TGATACGTTA TTTGCTTCCA 1800

ACCATTGTTG CACCTTTAGC AAgCCAGCCT CTTCACTTTC GTTAAATTTT TCATCGCCAA 1860

TATCATGTAA CAATGCTGTT AATATACATA AAAATAAATT TGCTTGTTCT TTCTCTGCAA 1920

TTGTTTTTGC TAATTGTGTC ACCCGATAAA TATGCCACCA GTCATGGCCA CTTGCTTCGT 1980

TGGCTAATTC TTGTTGAACA TAACGCTCTG CTGCTTGAAT AATTGTTTGT TCTTCAAAAC 2040

TAAGAGATTC ATTTTCAAAC ATCCTAACAC TCCTTTATTC TGGATTTAAA ATTTCCACTT 2100

GGATAATCCC GCTAGCTTTC AGAAACATAT TGGTGACAAT CGGACCTACA AAAGAAAATC 2160

CTCTTTTTTT TAAGTCTTTT GCTACGTTAT CTGATAAAAG CTGTGTGCGT GGGACTTGGT 2220

ATGCTTCTTC ATAAATAGAT AAAACGGGGA CGTTTTTTAC AAATTGCCAT AGATAATTGG 2280

CAAAACTGCC AAATTCTTCT TGTACTTTTA AAATTGCTTG CGCATTTTTA ATGGTTGCTT 2340

CAATTTTGCG CCGATTGCGA ATCATATCTG GATCAGCTAC TATTCGATCG ACTTCGTCAG 2400

GCAACAGCGC GGCAACTTTT TCCGGCTTCA TTTGGCAAAA ATTTTTCATG AATGCTACTT 2460

TTTTCCCTGC TGCTGCTTTC CAACTTAAAC CAACTTGAAA AACACCCACC GTCAACAATA 2520

AAAACAGCAA ATCATCCTCT CTTGTAGGTT TTCCCCATTG TTCTGTATAC CATTGATAGT 2580

TGTTCATCGC CGCCTCCTTT TAAGACTGTT CAAATGTTAA TAATGCTTGT TTCATTGCTA 2640

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AACCACCACG GTAACCGGTT AATTGTCCCT TGCTGCCGAT GACTCGATGG CAAGGAATGA   2700
CCATTAATAA AGGATTTTTC CCAATCGCTG TGCCAACTGC TCGAACCGCA CGTGGACGCC   2760
CAATTTTTTC TGAAATTTCC TGATAGGTCA TTGTCACACC ATAAGGGATT TCTTGCAACG   2820
CTTGCCAAAC TTCTTTTTGA AAGGGCGTTC CTTCGATGTC TATGGGGCAA GCAAACGTTG   2880
TCGAGTGTTG GTTAAGATAA CTTATTAGTG CTTCTTTATA AGGCGCAGTT TTCTTTTCAG   2940
AAGCTTCTAA TTGTGCTTGA GGGTACCAGT TTTTCAGCTC TTCTATCGAT TGATTGGCTG   3000
AACCTACAAA AGCTAGTCCA GCATCTGTCA CACCAAGATA ATAGTGATCG TTCTGCCATT   3060
CTTGTTGCGC ATAATAAATT TTTTTTGCCA TATTTCTACA CTTCTTTCTC GTATTTTCTT   3120
ATCTTCATTA TAATTCTTTT GGCTTTCAAA ATCTTGCGCT CCCATCACTT TTTACTTGTT   3180
TTTATTAGGG ATTCTTTTAC AATGAAGAAA ATGGGAGGTG TGCTTACAAT GAAAATAACG   3240
TATCGACTTA CTCAGAAACG TTGGGAAGCC ATTCAAAATA ATAATACGCA ATTTGATGGT   3300
GATTTTTTTT ATGGTGTGAC CACAACTAAA ATTTTTTGTC GTCCTTCGTG CCCTTCCCGT   3360
GTGCCCAATA AGAACCACGT TCTGATTTTC AAAACGGCTC AGGAAGCTTT AACACTTGGT   3420
TTTCGTCCAT GTAAAAGATG TCAACCAACC GGGCAAGTCG TTCCTAACGA GGAATGGGTT   3480
GCTCAAATTA AGCAATTTAT TGATCGGCAT TCAGCGGAAC CATTAAGTTT AGACTATTTA   3540
GCGCAAgcCT GCCACGGTAG TCCCTTTCAT TTGCAGCGAA CCTTTAAGGA ACAGACAAAA   3600
CAAACCCCGT CAGCTTATTT AACAAGTGTC CGAATTAGGC AAGCCCAAGA ATTGCTTCTC   3660
CATTCACCCC TTACGATTCA ACAAATCGCG AAAAAAGTTG GCTTCCAAAC CGCAGCATAT   3720
TTTGCCACCA CTTTTAAAAA AGAAACAGGC GTAACCCCCT CTGTTTATCG CAGTAAAAAT   3780
GAGCCGAAAA AATAACATTT CGGCTCATCG GATTATTTAT TGGGGCGTGA TTGTAGCCAT   3840
GCTACAATCA ATTGACTGAT TTCTGTTTGC TGTTGCTCAT TAGAAATTGT CGCTTTGCTA   3900
TCTCCTTTTT GGACACCGTA ATTACCAAAC CCTGCATGAT TCCCACCTTC GATAGATACA   3960
TACTGCGTAT CTTTTGGCAA AAACTGTTTG GCTTTTTGGT AGCTAGTCCA ATTTAAAACA   4020
CCATCGTTTG TGGCTGTTAT TGACAGAACC GGCAGATTTT TCTTGTTTAG TGCACCTTTT   4080
TCGTCAGGAT AGCTAGCTAA ATAAATCATG CCTTTGATTC GTTGCTCATT TTCCGCTACA   4140
AAACGGCTAG CCATCACACC ACCCAGAGAA TGTCCAGCCA AAACGAAGTT TTGTTGTGGA   4200
TGATCCTTTA TAATTTGTTC TGCAGCATTT GGTGCAAGAA CCGCTAAATT CAAAGGAAAA   4260
TGAACAACAT AGACATCATA ACCTTTCGTA GCAACTTCTT GCGCCCATTC ACTATAACTA   4320
GCGGGCGCAA CCAATGCACC TGGATAAAAA ATCAGTGCTG TATCATTTTT TTGCCCGTTT   4380
GTATAATAAT CATAGTTTTT TTCTTGCGTG GCACTTTGGC TTATTTTTAA GGCTGAATCG   4440
GTTGCTTGAT ACGTACTATT TTTAATAAAA ATAGTCAGAC CGATGACTAA TACCGCTAAA   4500
AAAAGCCCGA TTCCTAGGAC AATTTTTTTC CAACGTGATT TkGTtCTATT TTTCATCTCA   4560
TTTCCTCCCA ATGAAAAAAT TCTTCTTTCT GATTCTACCT TTAATAAAAA AAGrACACAA   4620
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CAATaGGaGT yGGTGAAGCa ACCCGTCTGT TGCTCCACCA ACTCCTAACT AGACCGTTTC 4680

TCG 4683

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

CGCATTGAAA TTTGTTGCTC TCTTGATCGT GATnGGTnGC CTTAATAGTG ACGGCTTTTA 60

CTGTCGGGCT TGGTTTGACA TCAATGCTAG AAACACTAGG AACAACCTTT GTGAATAATC 120

GAGGCATGGC TATCTTTATT ATTATyATGT TAGCAACAGG AACGTTAGAA AGAAATGGCT 180

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TTTGGTTTAG ATCAAGAGCG CTATGTCCCA GTAATGATTT TATCTGTGGG TAAGGGCATG 5400

GAAACTGGTT ATGAATCTGT TCGTTTAGCA CCAGAAAAAA TCACGACATT TGAATAGGCA 5460

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(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

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CCCGCTGGAA GCTGCCTGCC ATTGTTGGGA AATGAACACC CATGAATACA GTTTCCCGAT 780

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GGTTTTTTTG TTCCTATCCA ACCAATCACA ATAAATTTAT GGAGGTAATT TATGGAATTT 3840

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AGCCGATATG TGAAGCAAAA TTCAGTGAGA ACTCCAACGG GTTCCGCCCG AACCGTTCCG   5160
CTGAGACTGC TATTGCACAA TGCATGAGGC TGATACAGGT ACAGCATCTG TACCATGTGG   5220
TTGACCTCGA TATTAAAGGC TTCTTTGACA ATATCAGCCA TACAAAGCTG ATTCGTCAGA   5280
TATGGGCATT GGGAATCCGG GACAAAAAGC TGTTATGCAT TATAAAAGAG ATGCTGAAAG   5340
CACCTGTTGT TCTGCCAAAT GGAGAGAAAA CATATCCCGC ACGGGGTACC CCGCAAGGCG   5400
GTATTTTGTC GCCATTGCTT GCAAACATCG TATTGAATGA ACTGGATTGG TGGATTGCCT   5460
CACAATGGGA GGAGATGCCA ACAAAAACAA AATTCAAAAC AAGGAGCAAT GCGCAGGGAA   5520
CAGAGATTAA GAGCCACGCC TACAGGGCTC TGCGCCGGAG CAGATTAAAA GAGATGCATG   5580
CAGTTCGGTA CGCAGATGAT TTTAAAATTT TCTGCGCAAC ACATGAGGAT GCTGTCAGAG   5640
CATATAAGGC AACAGAGTTA TGGCTAAAGG ACAGGCTGGG GCTGGAAATC AGCCCTGACA   5700
AATCCAAAGT AGTTAATCTC AAAAGACAGT ATTCTGATTT TCTCGGGTTC AAGCTGAAAG   5760
TCCGTAAAAA GGGTAAGAAA TATGTGGTTC GGTCTCATAT GAGCGATAAA GCATACAAAA   5820
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AGGCGCATGA AAAAGTCTCG GAAGAAGTAA AGAAACTGGC TTATTCGTCA GATGATAATG    5880
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GTATTTCTAC AGAAGTATCT CATGACTTCA GCAGACTTGC CTTCAGTATC AACAAACAGC    6000
TCAGAAACAG ACTGAAAGGC GACTTATCCA AAAAGGGACA GCTCAGAAAT GGGTTCATTA    6060
AAGAAAAGTA TGGAGCAAGC AGACAGATGA GGTTCCTTCA TGGACGTCCg GTGGTTCCAC    6120
TGGGATATGT CCAGTCAAAG AATGCCCAGC ATAAAAGGAA ATCCATCAAT AAATATACGG    6180
TCAAAGGTCG GGAACAGATT CATAAGAATC TTGCAATCGA CACAGCTACA ATGTTATGGC    6240
TGATGAGAAA TCCTGTAAAG GGCAGAACCA TTGAATATGC GGATAACCGT ATTTCTTTGT    6300
ATGCGGCACA GTATGGTAAA TGTGCAGTGA CAGGAATTCC GATGAATTCC CACGATATTC    6360
ACTGCCACCA TAAAGTACCG GTAAGCAATG GCGGTTCGGA TGAATACGCA AATCTTATTC    6420
TTGTCAGCAA AGCGGTTCAT ATCCTTATCC ATGCTTCTTC AGAACCTACG ATTGAGAAGT    6480
ACCTGAAATC CTTAAATCTT GACAATAAAC AAATAGAAAA GCTTAACAAA CTTCGTTCTA    6540
TGGCAGAAAT GCCACCTATT ATTCTTTGAA TTTAATGCTG TAACGAAGTG TGTAAGTTGT    6600
GTTTAAAAGC CCTGGACGGC TGAATTCGAT GGAGCGCCGT GTGCGGTGAA AGTCGCATGC    6660
ACGGTGTGGA GCGGGGGAAA ATCCGGAGAT AACTTCAAAG GATTACCTAT CGCTATCTGG    6720
CGCGAAATCG CAGGGAATGA AACAACTTAT GGCCGGCGGC GGAGTTGCCC TGATTGGGAT    6780
GCAGCTTATC CCTCTGCTGG CAAACCTGTT CGGTTAAGGC GGGATAGCCT ATGCTGAACA    6840
TCCTCGACAT AATCACAGAC TGGATCAAGG AAATCCTGCG GGACTGCATC ATGGGCAACC    6900
TGGACGGGAT GTTTGACCAG ATTAACAATG AAGTCGGGGA GGTTGCGGCG AATGTGGGGA    6960
CGACCCCGGC GGCATGGAAC GCCGGGGTCT TTTCCATGAT CCGCAATCTG AGCGATACAG    7020
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TGAAGGTGTT TATCGCAGTC TATCTGGTCA CACACACCTT TGACATCACA ATGGCGATTT    7200
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AACTTTTCGG CCTGCTGGTG GAAACCATGC TGCTGAAAAT CACCATGCCG GTGCTGTCGT    7380
TCTGCGTCAT GCTGGTTCTG GTGGGGCGCA TGATTGAAAT TTATATCTAC TGCTCGGTGG    7440
GCGCAATCCC CTTTGCGACG ATGGCAAACC GGGATTGGGG GCAGATGGGA AATAACTATC    7500
TGCGTGGTCT TGTGGCTCTT GGGCTGCAAG GCTTTTTCAT TATGATCTGT GTTTCGATTT    7560
ACGCTGTGCT GGTGGGGCAG ATTGGGAGCG CCGACAACAT CCACATAGCC ATCTGGCAGT    7620
GTGCGGGCTA TACCGTTCTG CTGTGCTTCT CCCTGTTCAA AACCGGCGCG GTCAGTAAAT    7680
CAATTTTTAA CGCCCATTAA GGAGGTGGAA CCCATTTGAA ACAATATGAA ATCATTCTGG    7740
CCGACCCTCC GTGGAGATAC TCACAAAAGG GGGGTGCAGG GAGCGGCAGA ACGTCACTAC    7800
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TCCTGCCGCT GGCTTCCCAG CACGATATGA ACCGGCTATT TGAGAAAGTG CGCGACCAGG 9420

TAGGGCAGAC GGTGTATATC ACTCCGCCGG ACGATACCCA CAAGCGGTAT TTTGTCATGC 9480

GGCGGGArGA ACGCGCACAG GAGCAGCCAG AACGCAAGCC CTCTATCAAG GCCCAGCTTT 9540

CTGCAAAGCC CGTCCCCGGC GATAAGCCCG CCACAAAAAC CAAAGACCGG GAGGTGAGAT 9600

AAATGCCCTT TGTACCCGTA CCCAAAGACC TTGCCAAAGT AAAAACAAAA GTGGCGTTCA 9660

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(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

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GAGTCTTTTA TCACGGTTGA GAAAATAACT TCTCAGCGTA TGTATGAAAA AAGATCAGTA 240

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CCTTCACTCA ATCAAACGAT TGAATGGTAG TGCCGTAAAT ATCGCAGCCA TTGAGGCAAA 1140

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CACCGGAACA CcTGTCsCCT ATaAAAAGG 1409

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

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CTTTTCGCGA TTGGTCAGGA CAAGCCCCTT CTGAAGTAAT GAAAACACAA ATCCAAAAAA 900

CGTTTCCTAA ATTCTCTTyC TATATTGATA TTAAAGGAGG ACAATCAATG GATGTTAAAT 960

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AAATGCATAC ATTTGATGAC ATATATCCTC ATCAAGTAGT AAATGCTTCT TTTGACTTTC 1140

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AATGGTTGCC TTCATCTGGT TACCAAGTCG TTGCAGCACC AGAAATTTCG TTTACGCAAT 1380

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GAATGGTACC AAAACAACAA ACCCTTGTTC AGCATAATGA CTATAGTTTT AGAGTCATGT 1680

TGTTTGGAAT GGTACCAAAA CAAACTTTTT TGATTTGGCT TTTTCTCCCC TGTTTTATAG 1740

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GAATTTTTAT CATCAAAGAC GAGCTGCTTC AATTTTCGAA AACTAATCAA GTGATAAGTC 1860

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AGTTTTCCAC TTTTTCTTCG TACCGTTTTC AATAGGATTA GCACTTGTTG TAGCAATTAT 2280

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GGCGGTAGAA GCGCTCTTAG CTTTCTTCTT AGAGTCAACA TTCTTAGGTT TGTGGATCTT 2520

TACTTGGGAT AAAATGAATC CAAAaGTtCA CGTAACCTTT ATCTGGTTAG TCGTATTCGG 2580

TTCAATGATG TCTGCTTTCT GGATTTTAGT TGCGAATAGT TTTATGCAAC ATCCAGTAGG 2640

TTATGTCATC AATAATGGCC GTGCTGAAAT GGTGGACTTT GTAGCTGTCA TCAGCAATCC 2700

AAAAGTTTGG TATGAATTTT CACATGTTAT CATGGGCGCC TTTACATTGG GCGGCATGGC 2760

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CAAATTATCA GGTTCGGTTG ATGGAATGGA TACAGTCAAC AAGCGTTTGG TAGAAAAAtA    3120
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CGCACCATTC CTTGCCAATA CAACAGGTTG GTTAGTCACT GAATTAGGTC GTTATCCGTG    3360
GACTGTCTAT GGATTATTTA CGATTGAACA AAGTGTTTCA CCAAATGTAT CGGTTGCTTC    3420
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AGAAAATGAA CCAGCGTTGG ATCCATTTGA TAAGGGGGTA TTTGGCGAAT GAGTACACTA    3600
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CATAACATGC CGGAAGGTAA ACGTCGTCGG ATGTGGAACT GGACACTATC AATTGGTAGT    3960
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GATGCAAACG GCAATATGCA TGCGCAATTT ACGGATTATT TTAATCTGTT TTCAATTGTT    4080
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GTACTAGTTG CTCTCTTGTT CAGTGGCTTG TTCCCACGTG TTATGATTGG TAGTGAAGGT    4440
TTTGATTTGT TGATTAAAGA TGCAACAAGC ACACCATATA CACTAAAAAT TATGACGTGG    4500
ATTTCTTTAA GCATTTTACC ATTCGTGTTA GCTTATACTG CTTGGTCCTA TTATATTTTC    4560
AGAAAACGTA TTTCACAGAC AGCCGTACCA GAGGGGTATT AAATCTATGA TTGATAAAGA    4620
CATCTTACAG ATGCCTAAAA TCAAAAAAAT TCTTGTCTTG CTTGCAGGTT TTTCTTTCCT    4680
GCAAGCAGTC TTTATAATTG GGCAAGCTTT TTTTCTTTCA AAAGCCATTG TCGGCCTTTG    4740
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TCTTTGCCAT TAATACGCAA AATGATnTTT TGGGATGATC CCGGTTTCTG CTTTAATGGG 9600

GATTGGGGTT GCCATTnAA 9619

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

GCTCGCTTCC AATAGAATAT TTAAAAAAAT TTAAAAAGTC TACATAATTC CAAACAAGAT 60

TACCCTTTCA TTTTACACGT GATAAAATAT TTTTGCAAGA ATTGTCCTCA TTCTGAAGCA 120

AAAAAATTCT CTTCTCTCAA ACTAATGTAT CCGCTATCAC CAAGAATAAT ATGATCCAAC 180

AATTGAATCC CCATCATTTC GCCACATTCT TCCATTCGTT TGGTAAATTG GATATCTTGT 240

GGAGACGGTG TCGGATTGCC AGATGGATGA TTATGAGCTA ATAGTATGCG AGCAGAAGAA 300

TATTTAACCG CTTCCCGAAA AATTTCGCGT GGATGAGCAA TACTTTGATT CAGTGATCCT 360

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GTGGCTTGCT GCAAATAAGA AAGTTGCTTA AACTGTTTTA ACAGCGTTGC GGCAACAGTC 660

ATCACGTCTG CTTCTTTTGA GCCAGTACGT AACAGAATCG CCAACAACTC TTGATTCGAT 720

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GGTTTTCGGG GCTTCTGTTC CTAAAAGTTG ACGAGCTTTT TGAAAAATTT CTGGGTCCGG 1080

TTTTGCTCGT TTAACATCCT CTGCTGAAAC AATACCTACA AAACGATCCT GAATTCCAGC 1140

ATGGCTTAAT AACATTTCAA TTGCTGGACG GACGTTACTT GAAGCAACTA ATCGAGGAAT 1200

TTTTTGATCA TCTAAAAAGT CGAGGAATTC CACCACCCCT GGTTTTAAAG GGACGTTACC 1260

AGATCGAAAC TCTTGCAAGG TATCATCATA AGAACGGCGG ATAAATTCTT CCACTGTGTC 1320

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AACATAGTCT AAATAGACTT CTTTACTATA TGGTAACCCC ATTGCATCTG CTACTTTTTG 1440

AGTAGATGTA TAGTAAATCA ACTCCGTATC AAAAAGCAAC CCATCCATAT CAAAAATTAC 1500

GCCAnCAATT nCTnCATCAT T 1521

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TCACCTAACT TATTACAAAG AAATAATAGT CTTTTAAGTA ACTCTTTGTC AAGACATAAG 60

CAGAAGTCAA AACAGTTCTA TTTACAAATG AATGCGACGA ACCATTTCTT CTGTTATTTG 120

TTCTACAATA TCAATGGTTG TTTTTGGCGA ACGTTGATTT CTGGGGATAT CGATTGAGTA 180

AATTTTGGCA ATACGACCAG GATTTGCATC CATTAATACA ACCCGATCAG AAAGTTGAAC 240

TGCTTGTTGA ACATCATGCG TGATCATCAC AATTGATTTA GTCGCAATTT GATTGTTTAG 300

CCAAATTTCT AATAAATCGT TAGATAATTG GCTGGCTGTA ATGATATCTA AAGCTGAAAA 360

AGGTTCGTCT AAGAGCAATA AGCTAGGTTC GATGGCTAAA GCACGAGCAA AGCCTACACG 420

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TGATTGTCCG ATAATACTTA AAAATTCATT CGTTTTAACT GTTAAATCAA TATTTTCAAG 780

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TAATAATTCT TTATTTTCCA TCGTCTTATT AGATAGGTCA AGGGAAATCA CCTATCGTTC 900

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ATTATAGGGT AATCACAATA ATTGAGCTTT GGCTTTCTGA GACGTAAGAA AAAAATTCTA 2820

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CTATCCCAAA AGCAAAAGAA GAACAAGCTG GATTGGGG 5738

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

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AAATTATCGT TGTTCTTCGC AGCACTAGAT TGTCCTTGGG CATCTGTTTG TACTTCAATA 120

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TTGTCAATAA TAGTAGATAC TTCTTTGGCA TCATAAGTTG TCATGCTTTG CATTAGTTAG 240

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TGACGTCCCA AAGCAGTCAC ACTATAATTT CCAACACCAG TTTCATCTAC AATATCTACA 420

ATTCCGTTAT TAAATGCAGT TTCCAAAACA TTTGCAACAG TTGTATCCAA TAAAGCAATC 480

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ATGTTTGATT TAACCCAGTG ATCCCCATGC AGGGCATCGA TAAATTCGCC ACTCATTGTT 600

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CGGAATTTCC AAGTAACACT TCCGACTGTT AAGCTTGCAG TATTACCAAT TAATGCAGCA    780
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TGATAAGATG ATCCGtGAAA CACATAAATC GCTGAGTCAT CTCTCAtTGC GTTAGAATAG 12360

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CGCCTAGCCG AATCCACACk GAATAACAAT ACTAGGTTGC TCGCCTTTTC CTGTTTCCGC 13800

AGGCAGGCAC TTTGAAAGGA AGGAGTGAAA ATCGTGTGTC ACAGTAGTAG AAACATTTAT 13860

TGACA 13865

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

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TTCGGTAGGG ATCcAACTAA AagCTTCCGC GGCCCaTTTT TCCGcAAGTc TTTATAAGAT 180

CCTTTTTTAT CATGGTTTTG CATTTTTTCG TCTGCTTTCA AAATTGCATA GGACACATAT 240

ACATTTCGTT TACCAGCGCT AGCAAATTGT AACGATAAAT CGACACCCAT CCATTCTTTT 300

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TATTCTCTGT ATCATTCGTA ATAATCAATG ATACCATCGG CACATGATCA TAAAGATAGT 840

TAATTTTATA GGAACCATAA AATTCGGCAA TCTCTACTTG TGCTTTTAAG cCACGGCGTT 900

CCGTCGCCGC TTGAACCGCT TTTTGACCAG CCACATAGGC GTAACCTTTG CTTTCAGGGT 960

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TGTAATTATG ATTTAAAATC AGTTCTGGAT TCCAGTCCGA TTTGTAAAAC GCGTTGAAGC 1200

GACGACCATT TTCTGTAATT TTATCTTCAT CAGTATAAAG AAAATCAATC GTTGGGTCTG 1260

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GAACCATGTT TGGACGCTCC ACCACGTATT GAACCTTCTG GCCTGATTTG GTGTCAATGT 1800

TTAACGTGTA GGCTGGTAAA TCTTCTGGAT CTTTAATCGT AATTACAAAA CCATAATCTT 1860

GATCGCCTTC TAATTCAAAC ATATCAATAA CATCACGACG GTATTCTGTT TCCACCGTAT 1920

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GCATAGGGGC AGTCTCCGTC TGTTTATTCA TTTCTTCTAA AAATTGATTT CTTTCATCTA 2160

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CCATCTCTTC TCGGGAAAAA CCCAAGACCA TTCCATTTAA GAAAATATTT TCATATCCTG 4140

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ACCAATACGT CAAAACAGTT ACTAATGGCG TTAAAAACGC CCAGACAATT CCTA 5154

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10996 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

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TCTTTAGGAA CAGATACAAT TAGTTTTACG GCACTGAATA ATGCGTATGA AGGAATTTAT 120

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GATGATGGTC TGACGTACAC AGTGAAACTA AGAGAAGAAG CAAAATGGTC CAATGGTGAT 240

CCTGTCACAG CTGCCGATTA TGTTTTTAGT TGGCAACGTA CAGCAGATCC TCAGACTGGC 300

GCTGAGTATG CTTATTTTCT AGAAATGATT GAAAACGGTG CAGACATTGT AGCTGGTAAG 360

AAACCAGTCT CTGAATTAGG CATTAAAGCA AACGGAGATT ACGAGCTAGA AATTAAACTG 420

GCAAAACCAA CACCATATTT TGATTATTTA CTGGCCTTTC CACTATTTTT CCCGCAACAT 480

CAAGCAACCG TAGAGAAATA TGGCAAAGAT TACGCTGCTT CCAGTGAAAA AGCAGTCTAT 540

AATGGTCCGT TTGTCTTAGC TAACTTTGAA GGGGCTGGCT CAGATACCAA TTGGACTTTG 600

GAAAAAAATG AAAACTATTG GGATAAAGAC AATGTCAAAT TAGATAAAAT CAATTTTGAT 660

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GCCTAAATCG ATTCGATCAG GATATAAAGC TGCTAACGTT TTAAACGTTT CTGCGACTTT    2580
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TATCTAGATA AAACGTTTGA TCAAAAGAAA ACAGCAGAAT TTCCTGAATA TCAAAATGCG 7320

CTAGTCAAAT CGATTGAAAC GATTAATACC AATTGGCGAA GTGCGGCAGG TGCCTTTAAG 7380

CATGACGGGA TTGTTCCGTC CATGTCTTAT AAATGGTTTA TTGGTATGTG GCTTGGGAT 7440

TCGTGGAAAG CGGATGTAGC AACGGCTGAT TTTAATCCTG AGTTAGCTAA AAATAATATG 7500

CGGGCCTTGT TTGATTATCA AATTCAAAAA GATGATACCG TACGTCCACA AGATGCAGGA 7560

GCGATCATTG ATGCTGTCTT TTACAATCAA GACAGTGCGC GTGGTGGTGA AGGTGGCAAC 7620

TGGAATGAAC GAAATTCTAA ACCACCATTG GCTGCATGGG CAGTTTGGCA TATTTATCAA 7680

GAAACCAAAG ATAAGGAATT TTTAAAAGAA ATGTATCCCA AACTTGTGGC TTATCATAAT 7740

TGGTGGTATA CCAACAGAGA CCACAATAAA AATGGGATaG CAGAATATGG AAGCATGGTC 7800

AGTGATGCTC ACTGGCAAAA AGACGACAAG GATCAAATCA TTAAAGATAA AAATGGCCAC 7860

CTAAAGTGGA TGATGATGCT GTTATTGAAG CAGCCGCGTG GGAAAGTGGC ATGGATAACG 7920

CTACACGGTT TGACAAAGAA GGTGTGGGCA AAGGCGACGT TGGAGTTAAA GTTTTTGAAA 7980

ACAAAAATAA AGGAAAAGTA GTGGGGTATT CGATTAATCA AGAATCAGTG GATTTGAATG 8040

CGTATCTCTA CGCTGAAAAG GGCTATTTAG CTTCGATAGC AGAAGAACTA GGCAAAAAAG 8100

AGGACTATAA GAACTATCAA AAAGAAGCGA AGAAACTAAA AAAATATATT CAAGAAAATA 8160

TGTTTGATGA AAAAACAGGC TTCTTCTATG ACTTACAAAT AAATGAAGAC GGCTCGAAAA 8220

CAAAATTGTT AGTCAATCGT GGCAAAGGAA CAGAAGGCTG GTTGCCGCTC TGGGCAAAAG 8280

TAGCGACCAA AGAACAGGCG GCGGCAGTTA AGAAAAACAT GATGAATCAA GAAATGTTCA 8340

ATACCTTTAT GCCATTCCCA ACGGCATCCA AAGACAATGA AAAATTTGCT GCAACGAAAT 8400

ATTGGCGGGG ACCAGTTTGG CTTGATCAAG CCTTGTTTGG TGTAGAAGCT CTTCAAAACT 8460

ATGACTATAC AAAAGAAGCG AAAGAAATGA CACAAAAACT CTTCTTACAT GCCGAAGGAT 8520

TGATGGGAGA AGGCCCTATT CATGAAAATT ATGATCCACT GACAGGGAAG GGCTTAAGTA 8580

CGAAAAACTT TAGTTGGTCA GCAGCAGCGT ACTATTTATT GTATAAAAAC ACCTTATTAA 8640

GTAATAACCC CACAACGCAA ACTGCTTTTG AGATAAAATA GAAAAACAGC TCTTGAGAAA 8700

ATATCTCTCA AGAGCTGTTT TTTTCTTCAC TTGCTACAAT CTGTTTCCCT CTGATTTAAT 8760

TAAATGTAAT TTATTTGTTT AAATAAATAT ATTTCATATA ATTAAATAAA ATATCTGAAA 8820

ATAAACGATA TGTACTTTTA TTAAAAATGT TATTTAATAA AAATGAAATA GATATTCAAT 8880

GAAATTGATT GTACAATGGT TAATGAAGAG TGGGTTTAAC GGAATAGTGT AATAAGGAAT 8940

AAGCTGATAT CAAAGCCAAA CATATGCAAA ACCTCCTTCT CTGTTAGCTA TATTGACTTC 9000

TATTATAGAA CATTTCTTTT GGTTTTTTCA AGGGAAGTTA AGTATATAAG TTTTTATGAT 9060

TATCAAAATA TTACAATATT ATAATTACGG AAATAATAAA AATGAATATT TTgAAATATT 9120

TATTAATGTT TTCGCTGATT TTGTTTAATT TGTACAGGTA TTGTTGGATC TTTAAGTTAA 9180

TAAAAAAATA ATATTTAATA TTATTTTTAT TATmAAAGGG GGATATTATG GATGTGCTAG 9240

GTGCTCTAAA ATATTTTAGA AAAAAGAAAA AAATTGCTCA GAAAGATGTT TTGCCAAAAA 9300

AGGGGAAACA AACCTATCGA AGAATCGAAA TTGGTGAAGC CAAGCTAAGT TACGAGGATT 9360

TAATGACGGC ATTACAGTCA TTGGGGATTA CTTTTAATGA ATTTTTTTTT ATGGTATCTG 9420

ATACGAGAAT CATGGCTTCT TCAGAAGTCA AACATCAAAT TGAATGTTGT CAAATGGGGT 9480

TGAACAATAC AAGTGAAAAA AAGAATCTGA TTCATTATTT TTATCAATTA GAGCGCAATC 9540

CTCATAAAAA TGCGTTGGAA ATGTCTATTT ACACAGATAT TAAATTAACG TTTAGTAATG 9600

ATTGGGAGGA AATTCCAGAA TTTGATGAAA CCGATCGAAT GGTAATTCTC GCGCTTATCT 9660

CTAGCAAAAG CTACTATACA TACTACGATT ATCAAATGGT GACTAATCCT GCCGCCTTGT 9720

TTTCTGAAAA TGAAGTCCTT CAGATTCTTG AGCAGATGTT TCCTGTCAAA GATGCTGAAT 9780

TACGTGATAC CCAAACACTA AATGTTGCCT ATGGTTTTTA CCTAAATATC ATTACTGGGG 9840

AACTTTATAA GAAAAATTAT GCGAAAGCTC GGGAATATTT AGCGCTAGTG AGTGTTACCA 9900

CGATTCCTGC TGAAATCTAC TATATTCATT TTAACTTACG TTACTTAAAA AACCTTACGT 9960

ATTATCTGTA CACTGGCAAA ATGAGATATT ATAAAGAAGT AATCGCCGTT ATTGATATGA 10020

TTGAAAGCTT TGGGGATGCA CGTTTGGCGG AAGGCATGAA AAAAGAAATG CTTCAGCTGA 10080

CGGCTGGTCG GACATTTAAT TTAGAAAAAG GTCAGTTTCC ATTGAATATT GTCACTGAAA 10140

AATAAAAAGC CCCCCcCCCC CGCAAGGTCA AACTTGCGGG GGGTGCTGAT GTTAAACAAT 10200

AATGTTATCT CTAATCATAT CTAAATCTTT AATCAAAATT TTGCGGTTAC GTAGTTCAAT 10260

TGCCCCTAAC TCTTTTAGTT GCTGCATCAT CCGGTTAACG CTACTAGCAG AAGTTATCCC 10320

ACAAAAATGC GCAATTTCTT CATTGGTCAC CACGAAATCA ATTAAAATAC CTTCCTCTGT 10380

TTCTACGCCA AATGAATCGT ACATTTCATA GATTTGTGTA CAAACGGCCC CAAATTTGCC 10440

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TTTGACATAC ATTTGCAAGT CTTTACTATT ATTGATATCC CGCCAAAATT GAACACGGTC 10560

GATTTGGTAA AGTTCTGCTT GTGGAGATTC GATGCGAATA TTAAAAGGTG CATCAATAAA 10620

TTCTGAATAT TCATCACGTA GCAATGAAAC AATTTCCAAA TTGTTGATAT AACGTAAATT 10680

AAATTCACGA CCGTCTTTGG AAATAACGCT AGTTTTGATG ATGCCACTTT TTAAAATATA 10740

GGCATAACGA TCTTGCAGTC CTTCATAAGT TAAATAATTT TTCTTCTTTT TTACAACGAC 10800

TCGAAAGGAA TGTTCATCTA AGTAGTCTTG TAAAACATTT CTCATTGGCG GTAACTCCTC 10860

AATTATCTCT AAATATTTTT GTTTTTGCCT GTTGGGCTTC TTTCTTATTT AAGCGAATTG 10920

GaCATCATAT GTCAATAACa AATGTTGAtA AAAAAgGTCa ATTAAACgCT ATTTTGAAAA 10980

ATAAAATCAG CnTTTA 10996

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CGGCCCAnTT TTTTAAATGC nTnCATTCTT TTAAGGCTTT CCAATCCCAT CATTATCATT 60

TGnATCTGTG ACCATCGTGG CCACTTTTTG AATGGAgGAC TCGCATTGCC CaTTGCGACG 120

CCAATCCCTG CATGGCTTAA CATTTCTCGG TCATTTTCGC CGTCCCCAAA GGCAATGATA 180

TTTTTTGCAT CAATACCCAC ACGTTTAGCT AAATACGTTA ACGTAGCTGA TTTTGAGCCA 240

TCTTTAGGCA CAACATCTAC GCTATGTTGA TGCCAGCGAA TAAAGCGAAA TTCTGGGTAT 300

TCTTCTTCAA ACGTACACTG ATCTTCTGCG TCATAAAAAG CCAGCGCTTG GTAAATATCA 360

TTTTGACGAT AAAAGTGTTC ATCATAAGCA GGTGAATGAA AATGAAAAGA GTTCATCGCA 420

ATTTCCATTT TTTCAGCACG GTGCTGGkTG CTCTTCTTAA TATCATCTAA GCCCACACAA 480

GCAAATCCTA AGCCGCGTTG ATCACTGTCT TGTGCCAAAC GTTCCAACGC TTCAGCGTGC 540

AATAAATTTT GATAATATTG CTCATGATCC ACAAAAGCCG CGGCGCCATT ACATAATACG 600

TAATTGGTAA AATCTAAATC CCAAATCACC TCTTGCGCCA TATAACGACT TCTGCCAGTT 660

GCCAGCGTAA CTAAGTGTCC TTGCTCCCGC AATTTTGCTA GCGCTTCTCT CGTGCTATCC 720

AATGCTTTCT TCTCCGAATT TAACAACGTC CCATCAATAT CAAATGCAAA AAGTTTTCTT 780

TCCATCATTT CTCCtTATTC GCTCGCTTTC GCTAAATATT TACTGCCTTC TCGTTGTGCT 840

AAAGGACTCA ACACTAATTC TTTCATCAAT TCCTCGACCC ATTGCGGATT CGTTTTACTA 900

TATTGGGCGT AATGGACCAG CCAATCGCTT TTTGAATGAA GACTCCTCTG nAGTCnA 957

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

AGTCATTnGT AATCTTTTAA ACTATCGATT AGTCGGGATT GTGTTAGGTA GTTTACTTGG 60
TTTTGCCGGC GCTTATGTTT TCACAACTGC GCTACGTTTC TATAATCGGG CCTACTCAAT 120
TGATGAAACC TTTGAAAATC AACAAGAAGA AAGAGGCGTT TTATGAAAAT AACTTATCCC 180
TTGCCACCAA ATCTACCAGA ACAACTTCCT CTATTAACGA ACTGTCAATT AGAAGATGAG 240
GCAATCTTAG AAAATCATTT GTATCAGCaG ATTGATTTAC CGAAtCAAGA AGTTCGTAAC 300
TTAGTCTTTC GGGATGCTGT TTTCGATCAT CTTTCATTAG CAAATGGCCA GTTTGCTTCT 360
TTTGATTGTA GTAATGTGCG TTTTGAAGCT TGCGATTTTT CTAACGTCGA ATGGCTGTCT 420
GGCAGTTTTC ATCGAGTGAC TTTCCTTCGT TGCAATTTGA CAGGAACGAA TTTTGCAGAT 480
AGCTATTTAA AAGATTGTCT ATTTGAGGAT TGCAAAGCCG ATTATGCTTC TTTTCGTTTT 540
GCAAATTTTA ATCTTGTTCA CTTTAATCAG ACTCGTTTAG TCGAAAGTGA ATTTTTCGAG 600
GTCACCTGGA AGAAACTCCT TCTAGAAGCT TGCGATTTAA CCGAAAGTAA TTGGCTAAAT 660
ACTTCTTTAA AAGGATTGGA TTTTTCCCAA AACACCTTTG AACGCTTGAC TTTCTCACCA 720
AACTATTTAT CAGGTCTTAA AGTCACCCCT GAACAAGCCA TTTATTTGGC AAGTGCCCTT 780
GGTTTGGTGA TTACCTAAGA AAATTTTAAA AAAATAGCCG AATAACTGGT TCTGTCGGTT 840
CTTTCTTATT AAATTGTTAT TAATTTTTTG GAAAAACCAA CGGAACCATT TTACTTGTGC 900
CTTATTTTTA GGkAAACTAT CyTAGGTTAA GCAATCTCTT TTTTTGGAAC AAGAGAAACT 960
TTTGGAATCA TTTCCTATAA ATCATGAAGA GATTATGACA AACGTTCTTC TAATCCAAGA 1020
ACGTCTTTTG TCCTATACTC GATTCTACTC AAAAGGAATG TCAGTGAATG AATATAAAAA 1080
AACAAGGCCT CGGTCAAGCG ACGGGAAAAA TCATTTTAAT GGGAGAACAC GCCGTTGTTT 1140
ACGGCGAACC AGCAATCGCC TTTCCTTTTC AAGCGACAGA AATCACAGCC GTCTTTACCC 1200
TAGCAAAAAC TATGCAGATT GATTGTGCAT ATTTTACAGG ATTGCTTGAA GACGTGCCCC 1260
AAGAGCTAGC AAATATCAAG GAAGTTGTTC AGCAAACCTT ACACTTTTTA AAGGAAGATA 1320
CGTTTAAAGG CACTTTGACC TTAACAAGTA CGATTCCCGC TGAACGAGGA ATGGGCTCAA 1380
GCGCAsAACC GCTGTGGCCA TCGTTCGAAG CCTTTTTGAT TATTTTGATT ACGCTTATAC 1440
ATATCAAGAA TTGTTTGAGC TTGTTTCCTT AAGTGAGAAA ATTGCTCATG GCAATCCTAG 1500
TGGTATCGAT GCCGCAGCAA CAAGCGGCGC TGATCCCTTA TTTTTTACTA GAGGATTTCC 1560
GCCCACACAT TTCTCGATGA ATTTATCTAA TGCCTACTTA GTAGTAGCTG ATACGGGAAT 1620
TAAAGGTCAA ACACGTGAAG CCGTGAAAGA CATTGCGCAg cTAGCTCAAA ATAATCCCAC 1680
CGCAATCGCT GAAACAATGA AACAATTAGG TTCTTTTACT AAAGAAGCAA AGCAAGCGAT 1740
TTTACAAGAT GATAAACAAA AATTAGGTCA GCTAATGACG TTAGCGCAAG AGCAACTCCA 1800
GCAATTATCC GTCAGCAACG ATATGCTGGA TCGACTAGTG GCTCTCTCTT TAGAACATGG 1860

CGCTCTAGGA GCAAAATTAA CCGGCGGCGG TCGCGGTGGC TGTATGATTG CCTTAACAGA 1920

TAATAAAAAG ACCGCACAAA CCATTGCACA GACTTTAGAA GAAAATGGAG CTGTTGCTAC 1980

ATGGATTCAA TCATTAGAGG TGAAAAAGTA ATGCTTTCAG GAAAAGCACG AGCGCATACA 2040

AATATTGCTC TGATTAAATA TTGGGGAAAA GCCAATGAAG AATACATTTT ACCAATGAAT 2100

AGTAGTTTAT CATTAACATT AGATGCCTTT TACACAGAAA CAACTGTGAT ATTTGATGCC 2160

CATTATTCAG AAGATGTATT TATTTTAGAT GGTATCTTGC AAAACGAAAA ACAAACAAAA 2220

AAAGTCAAAG AATTTTTGAA CCTTGTTCGT CAACAAGCCG ATTGTACTTG GTTtGCAAAA 2280

GTGGAAAGTC AAAATTTTGT GCCTACTGCA GCTGGTTTGG CTTCTTCAGC GAGTGGTCTA 2340

GCTGCTTTAG CAGGGGCCTG TAACGTAGCC TTAGGATTAA ATCTTTCAGC AAAAGACTTA 2400

TCACGTTTAG CGCGACGTGG TTCAGGTTCT GCTTGTCGCA GCATTTTTGG TGGTTTTGCT 2460

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AGCCGTGATG GAATGAAACG AACAGTAGAA ACTTCTAGCT TTTATCAAGG TTGGTTGGAC 2640

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CGGGCCAAAG GAATTCCTTG TTACTTTACA ATGGATGCAG GTCCGAATGT CAAGGTCTTA 2880

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CAGTTAGTCC CAGCTTTTGC TGGTCCCGGA ATTGAATTGT TTGAAACGAA AGGAATGGAT 3000

AAATAAGCAT GATTGAAGTT ACTACGCCAG GAAAGTTATT TATTGCAGGA GAATATGCCG 3060

TTGTTGAACC TGGCCACCCT GCCATTATCG TTGCTGTGGA TCAATTCGTA ACTGTAACTG 3120

TCGAAGAAAC AACAGATGAA GGCAGTATTC AATCTGCACA ATACAGCTCT TTACCTATTC 3180

GTTGGACACG CCGAAATGGT GAGCTTGTAT TAGATATTCG CGAAAATCCT TTTCATTATG 3240

TTTTAGCGGC GATTCATCTA ACTGAAAAAT ATGCGCAAGA GCAAAACAAA GAATTGTCAT 3300

TTTATCATTT AAAAGTGACG AGTGAATTAG ATAGTTCAAA TGGACGAAAA TATGGTCTTG 3360

GTTCAAGCGG TGCGGTAACC GTTGGAACTG TCAAAGCCTT GAATATTTTT TATGACTTAG 3420

GTTTGGAAAA TGAGGAAATT TTCAAATTAT CAGCATTAGC TCACTTAGCC GTTCAAGGAA 3480

ATGGTTCTTG CGGAGATATC GCCGcCAGCT GTTACGGGGG CTGGATTGCC TTTTCAACCT 3540

TCGATCATGA TTGGGtCAAT CAAAAAGTAG CCACTGAAAC ATTAACTGAT TTGTTAGCAA 3600

TGGACTGGCC TGAATTAATG ATTTTTCCGT TAAAAGTACC GAAACAaCTA CGTTTACTAA 3660

TTGGTTGGAC AGGTAGTCCT GCGTCCACTT CAGACTTAGT TGATCGAGTC CATCAATCAA 3720

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GCGGGGGCGA TTGTGGGATT GTAATTTTCC GCCAAAAATC TGGGATTTTA CCATTAATGA 4020

CTGCTTGGGA AAAAGACGGA ATTACCCCAC TGCCACTTCA CGTCTATACC TATGGTCAAA 4080

AGGAGTGTAA GGAGAAGCAT GAATCGAAAA GATGAACATC TATCATTAGC TAAAGCGTTC 4140

CACAAAGAAA AAAGTAATGA CTTTGATCGT GTGCGTTTTG TTCACCAATC GTTTGCTGAA 4200

TCCGCTGTTA ACGAAGTGGA TATTTCCACT TCGTTTCTTT CTTTTCAGCT TCCCCAACCT 4260

TTTTATGTCA ATGCAATGAC AGGTGGTAGT CAGCGTGCAA AAGAAATTAA TCAGCAATTA 4320

GGCATTATTg CCAAAGAAAC TGGCCTTTTA GTTGCGACAG GATCTGTCTC GGCAGCGTTA 4380

AAAGATGCTA GTTTAGCGGA TACGTATCAA ATTATGCGAA AAGAAAACCC AGATGGACTC 4440

ATTTTTGCCA ATATTGGTGC AGGCTTGGGT GTGGAAGAAG CAAAGCGAGC GCTTGATTTA 4500

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GTGCCTGTCA TTGTCAAAGA GGTTGGCTTT GGCATGAGCC ArGAAACCTT AGAAAAACTT 4680

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AGTTCACTAA TTAATGGTTC TTTCGGATTT GCAGTTGTAC ATTGGTCTTC ATATGCAAGT 5280

TCTGCCATAC GATCAACCGT TGTGTCTAAT GTTTCTTGTG AGACACCTTG GGCTTTCAAG 5340

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AGTTCTGCGG TAGTATTTCC TTTTAAGCCT AAGAATTTTG CAATGTCTGC ATAATCAGTA 5460

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GAATTTTCTA AATGATCGAA AACTAACTTG ATTGCTTGTA AACTTAAACC ACGTGTGTAA 5760

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ACATCATTTT TACGTTTTTG TAGCTCTTTA CGTACGATAT CTGCATAGCC AAATTGAACC 6300

ATACCTGGGT CACAAACTAA CATGACACGT TCAACATTTT CCATTTTTTG TAGATATgTA 6360

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GTTTCGCTAC CGTTTTAATA TTAATTAAGT TAATGGcTGa TACGTTTTTA GAAACAGAGT 6480

TTTTCCCgTA TGgAACCaCA ACCAAGTGTT AAGGATGGAA TCATTTCGTT ATAAATGTTA 6540

CCGATACCGC CTTCTGCTGA TGGAGTATTC ACTAAAATAC GACAAGCTTT CATACGTAAA 6600

CCAAAAGCAA CTTGTAACTC TTCATCTTCT GTATGAATTA CTGCTGTATG TCCTAAACCA 6660

CCTAAGTTTA ACATCGCTTC ACATAGTTCA AAAGCATGCT CTGCATTGTT TGATTTCATC 6720

ATTGCTAAAA CTGGCGATAA TTTTTCTCTT GATAATGGAT ATTCTGGACC TGCACCTTCT 6780

AATTCAGCGA CTAAAATTTT TGTGCCTTTT GGTACACTAA TTCCTGCTAA TTCAG 6835

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3977 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

AGTACCAAGC ACTTGACCGC TTTTTTCCTT AGGTGTGCCT TGTAGCAACT nACGCAGTCG 60

CATTACTGAT nTAACCAGAA AAAACACCTT GTAATAAGCG TAAGCCAATC AATTGATAAA 120

CACTTGTGAc TGCGCCCATT AAACTAATGA CGATAGCCAT CCCTAATGAA GCGCGTAATA 180

ACATTAACTT GCGTCCTTTT CGGTCGGCTA AACGGCCCCA CCAAGGTGAA ACAATGGTTG 240

TGACTAAAAA AGTGGAAGAG AACGTGATTC CGCTCCAAAA ATTCAATTGT TGGTGGGTAA 300

AAGTACCTAA TGTGTTGATA TAAAGAGGCA TAAATGGCAT CACTAAGCTA AAGCCAATAC 360

CAGCCATAAA TGTGCCAAAC CATAAAACGA GCAGATTTTT TTCCCAAGGT TGTCTTGGAC 420

GGAAAATTTT ACTTTTAATT AATTCATACA TTCTATTTCC TCACTTTCTA GTAAAGAAAT 480

TCAAATTTGG CTTTGGCGAG TAGTTGATCA TTCAATGCTT GATGCAATTC ATTCGCAAAA 540

AAGCCTTCTT TTAAATTTAG TGGATTTTTT GTAGTGTACA CATATAACGT ATAGGTGTGC 600

ACACCAGAGC GAGGGCTTAA CCCCAGATAA CGTTCGGTTA ACTCAGGTAA CGTTTCAGTG 660

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GCAAGCGCAG GAATCATCTG TTTCCCCAAA GGAGAAGCAA GACTATTTTT TCCTTGAATG      720
GTAGGCTTGA GTGCTGTTCG ACTAAAGTCT TCAGGAATCT CATTGGTTAC AGGAACATTG      780
GCAGCTAACC AATGAATAAA AGGGAAACCG ATTAGAGGAA TCGTGTCATA ATCAATTAAT      840
TCCCAGGATA AATAACGGGC TTCTTTAGGA ATGGCCGCTA AAGAAATAGG AAAAGATAAA      900
ATAGGACGTT CGTGTAATAA AAATTCTGCA CTGGTTCGTT TGCCATAACG ATCGGCCAAA      960
TGAGAACGGT TGGTAATATG CATGCCAAAC AGCCTTCTTT CAAAAATGAT GTTTACAAAT     1020
TATTATTATA AACTATAATT TATAGTTTAA AAAGAGTCAA TAGATATGAT AAACTAATAC     1080
TTGTCCAAAA TTTAAGAATT GGAGGCGTCA GAAAGATGGC AAAAAAACGG AATTTAACGA     1140
AAGCCAAAAT CCTTGAAAGT GCCCGCAATC TAGCGGAAGA ATTGGGCGTT CAACAATTAA     1200
CCTTTCAAAA TTTAGCCGTT GATTTAGGCA TCAAGTATCC TTCACTCTAT AATCACTTTA     1260
AAAATATTGC TGAAGTAAAA AATGCTCTAG TGGACTTGTT AATTCAAGAA TTAAATGATG     1320
CATTGCGAAG AGCCTTAGTG GGTAAGAGTG GCGCAGAAGC AATTCGGaTA TATGCkGAAA     1380
CGTACCAACA ATTTGCyTTT GAAAATTCTG CAGTCTATGA ATTACTTATC AGTGTGCCGA     1440
AAACGCAAAA CCAACAATTA ATTGAAGGCA TCCATGAAAC CAATCAAATT ATCTTACAAC     1500
TTTTAGCTTT TTATCCATTT AATAATGAAG AACGACTGCA TAAAAGTCGA GAATTACGTA     1560
GCTTAATCCA TGGTTATATT ACCTTACGTT TTTtAGGTTA TTTTCAACGC GAAGAAGCCA     1620
CGCCGGAAGa AAGTTATCGT CGCATGATTG aAGaTTTTAT TGTTTCTTTA gAAGTGGcAG     1680
GaTAAAATAA ATTTCAAAAA TTTCTCAGTC CGAAACCAAA TCCTTGcAAC TTTTTcaGAA     1740
AGTGaCTATG ATACCTACAG TAGCaAAAAA AgGAGCGGTT CAATGTATCm AGtAATTACA     1800
ATGtATGGcG aCmATGAACC TTGGTGGTTT TTTGATGATT GGCAAGAGGA CATTGTTCAA     1860
GAAAAAACCT TCGATAACTT GACCGATGCA GAGACATATT ATGTGGAAGT TTGGCAAAAA     1920
CTTTCTCAGA ATTATACATA CGTCAACACA AAGCCTAATT ATTTAACGGC TTTCTGGAAT     1980
GATGGGGAAG AACGCTGGTG TGAAGAATGC GATGAAGATT TACAACAATA CTTCGGTTTA     2040
GCATTACTAG AAAATCATCA TGCGGTTACT TTTGAAAATA AAGCTGAGTT TACCACAATA     2100
TCCAATCATT TTGGCAAAAC AAAATTCTGC AAACGGAAAG TTATTTGAAA CGCATGAGTT     2160
TAAAGAAAAA CCTCAGGGAA TTTTCTTTAA ACTCTTTTTC TATTCTCGGA ATTTAGAGAA     2220
AATCGAACCA ATATTTGGTA TAATACGAAA AGATAGCACT CAAAAAGGAG CGAAACTAGT     2280
GGTTGCAAAA CAATTAATTA TTGCTGAAAA ACCTAGCGTA gCAAAAGATT TAAGCCGCGT     2340
TTTAGGAGCA AATCAAAAAA ATAAGAATTA TTATGAAGGA CCCAACGTGA TTGTCACATG     2400
GGCTTTAGGC CATCTCTTAG GACTAAAAAT GCCAGAAGAT TTAAACAAAG AATGGCAAAC     2460
GTGGCAAATG GAAACTTTAC CGATGATTCC TAAGAATTTA GGGATTAAGC CGTTACCGAA     2520
AACGGGACAT CAATTAAAAG CGATTAAACA ATTAGCCAAT CGTAAAGATG TTTCTGAAGC     2580
CGTGATTGCC ACTGATGCTG GTCGTGAAGG TGAATTGGTG GCCCGCTGGA TTTTAGAATA     2640
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TGTCCGTTTT AACAAACCAG TCAAACGCTT ATGGATTTCA TCTCAAACAG ACAAAGCCAT 2700

TAAAGACGGG TTTAAGAAAA TTCGCCCAGC GAAAGACTAC GATAATTTGT ATTACTCTGC 2760

CTTGGCGCGC GCAAAAGCTG ACTGGTTAGT GGGGCTAAAC GTCACACGGG CCTTGACAGT 2820

GAAATATCAA GATAACTTAT CCGCAGGTCG TGTTCAAACA CCAACTTTAG CAATGGTACG 2880

CCAACAAGAA AAAACGATTG AACAATTTAA GCCTCAAACT TATTTTACTA TCTCGTTATC 2940

TGTTGAATCA GAAAAAGCAA AGATGACCCA AAAAAATCCA TACGCTTTAA AAGAACGGCA 3000

GGAAGCAGAA CAATTAGTCA AaGAACTCTC AAAACAAAAG GGCTTAGTTA CCGATATCCA 3060

AGAAAAAGTT AAAaCAGAAA ACGCGCCGTT ACCGTATGAT TTAACCGAAA TCCAGCGTGA 3120

AgCCAACCAG CGATTCCAAT TTTCTGCAAA GAaACGTTGT CTCTTGTACA AAGTTTATAC 3180

GAAACCCATA AAATTGTTTC CTATCCTCGA ACTGACAGCA AATATCTAAC GACGGATATG 3240

AAAGGAACGA TGAAAGAGCG CCTTCAAGCT ATTGCTGATT TTTCACCAGA AGTGAAAGGC 3300

TACCTTAAAA ATGGGGCTGT TGTTAAACAA CAAAAAGTTT TCCAAAATGC AAAAGTCACG 3360

GATCACCATG GGTTGATTCC AACTGAACAA CGTCCTCGTT ATGAAAAGCT AAGTAATGAT 3420

GAACAAAAAA TCTATCAAAT GATTGTTCAA CGATTCTTAG GTTTGTTTGC TGAGCCAAAT 3480

CAAACCAAAC AAACAAAAGT TACAGTCGCT TTTGGAAAAG AAACATTTGT CTTTCATCAA 3540

AATAAAGTAG TTGTTGCTGG CTGGAAAACA ACAGCCGAAC AGCCGCTATC CACTGTCCAA 3600

TGGCAAAAAG GCATGACCGT TGCGCCAAAC TTTACCATTA ACAAAGAATT AACGTCGCCG 3660

CCAAAACCAT TAACCGAAGG AACGTTGTTA GGAAAAATGG AGAAACACAG TTTAGGCACA 3720

CCGGCAACGC GAGCTGAAAT CATTGAAAAA CTGATTAAAT CAGAATTGAT GGaACGAACC 3780

AATAGCGGTT TAAGTGTCTC TGCCAAAGGa AAGCmACTAT TAGACTTGGT GaATCCATCA 3840

CTTGTGaCAC CTGGAACTtA ACGGGAAAAA TGGGGaAAAG TcGcTcGaaG CaATcGCTTT 3900

CGGGGTTCCA ACAAAAGAGT TCAACTTTTT CnTTTAAAGG GATATTTGGA AGAGGGnTAC 3960

GGAAAAATTT AGTTCCG 3977

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

nnTATTTTTC AATGTATCCG CGTAATTCTT CTTCAGTGAC ACTTTCGTCA AAGATATACT 60

CACCAATGAT GATCGTTGGT ACAAATTGAA TGTGCGCCGC ATTGGCTTCA GCAATCACTG 120

CGGAAACAAG CGTTGCATCT TTTTGTTCTT TTAAGCCCAG ATTTTTTTCA GCATACGTCG 180

CTACTTCTTC TAAGGTTAAG TTTCCCCATT CATCTTGCGT ACAAACATTT TATGCAATGC 240

TGACAGCGCT TGTTCAGGCG CTGAATAGTC AATGTAGTGA TGCATCACAT TGCCGCGTTG 300

TAAACTTTCT TTTTCTTTAT CAAACAACTT AATGATACGT TCAACTTTAC CACTTTTGAC 360

AGATTGTGCT AACAGTTCCT CAGACTCTTC AAACCATTTT CTGCAATAAG GACAGCGAAC 420

ATTGATAAAT TCTATCATTT TGACAGGGGC ATTACTCTCA CCAATGTGAA GCCCTGTTTC 480

TGTGTTAACT TTTGTTGCAT CAATTACTGA AATATCCATA AAAAACCTCA TCCTTTCAAA 540

CCTTTATTTC TCTTTTAGTA TACCGTTTTT CAATAAAAAA ATCATAAGAC ACGAATTCAA 600

ATTTTCTGAA TTCGTGCCTC TGTTCACTTT TTTAACGATT AATCGAACGA GCCATTCTAG 660

CAACAGTATG tCTTTTCCCA CGTATCGCAT CAGAAAGCTC TTTAATAwTT TCAATACCAA 720

CTAAGCCCAT ATtGGCATCG CCAaTATGTT GAATATCTAC GCCTAAAATT TTATTTCTAA 780

TGCCGATTGC TTGGgATAAC TTCAGGTTGA GCACTTTCTT GTGAAGTTCC AATGGCACTC 840

aTAACTAATT TTCCTTTTGA ATGTGCAAAA TCCACAACTT CTTtGACTTG TTGATCATCA 900

ATGCCCCAAA CCGTGCCGAC TGCTGGGACT AAGACAATAT CAGCGCCCGC TTCAATAAAT 960

TGTTCAGCTG ATTTTAAACT GACCACTGGT TCATCTACGC CTGaACTGTG CATTTTTCCG 1020

GCAATAATGA TGCCGTCAAA ATGTTTTTTG GCTAAGGCCA CGTTCTTAGC AATCAAGTCG 1080

TTGGTCACGC CAGTTCCTGG ATTACCTGTC AATAAGATAA AATCCAAACC CAGTTCATTG 1140

GCTTTTTTGA AAGTAGCTGC TGATGCTTTT CTACCTGGTT CAATCGAAAC TCTCGTTGAA 1200

GCTAAGTCTA AATTTTCATC AACAGGTTCG ACATTCATGC CaATCGGTAA ACCGACTAGT 1260

TCTTTCAAAC GATGAACAAC CTCATCATTA GGGACACATG TTTCCGCAGT ATATTGCCCT 1320

TCATAAGCGG CTACTACAAT GGGTTGATTA ACATCGAAAA CATTCAATAA AATCATGTCT 1380

GCGCCATATG CTTTTGACAT TTCCGCACAA GTGATATCAC CTGCTACGGA TGGATGAACT 1440

ACCACATTTT CCGATAATAT TACGCGCCCT TCGCTCGCTT TAATACTCTG AAACAGCTCT 1500

TCTTTTGACA TCCGTTTGAT TTCTGATGCA TTTGCACTAA TTAATCGTkG AACCATTTTG 1560

ACCCCTCCAA TAGTTTTTAA TGTTTTAGTT AAAAACAGCA ATAAGTAATC GTTTGCATTT 1620

TATTACATGC AACATTCGTG cCAACGTCGT TTCTTTAAAc CACAGGTCAA CACTACATTT 1680

CAGtGCTACA CACTTTTTGc ACACTTTAAT TTTTTTTACA CGCTTAAAGA AAAAGTGAAG 1740

GATAGCACTT CAAACGGAAA TGTTATTCTT CACTTCTGGA GCAGAAAAGT TACGCACTTT 1800

TTTCTCGTAA TTTTTCTGCA AATTCATTAA TTTTTCGAAT ACGATGATTA ATACCTGACT 1860

TAGAAATAGC TCCTGAAGGA ATCATTTCCC CTAGTTCTTT GAGACTAACT TCCGGATACT 1920

CTAACCGTAA TTCTGCGATT TCCTGAAGTT TCTCCGGTAA TGACGTCAGC CCTACTGTAC 1980

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TCGCTGTTTC GCAATTCACT AAACGATTTA CTGAATTCCG CATATCACGG ACAATCCGGA 2100

CATCTTCAAA TTTCAACATA GAGTTCGTGG CACCAATTAA TGTTAAAAAG TCGGCAATTT 2160

TTTCAGCACC TTTTAAATAA CAAATATACC CATTTCGGCG TCCCAATGTT CGAGCGTTTA 2220

AGTCATAGTA ATTCAACATC TTACAAATAT CATTATTGTG TTCTTCATAA ATTGAAAAAA 2280

TTTCTAAATG ATAGCGACTT GTTTCCGGAT TATTAACTGA GCCAGAAGCC ATAAAGGCCC 2340

CGCGTAAATA GGAACGCATT TTTTGCGCGT TACCCATGAT TTCATTTGAC ACATTGCCAT 2400

TAAAAACGAC CCCATCCATA ATATCCAAAT CAGCTAGAAT TTTTTGTGTA TCTTGTTTTA 2460

GACGCACAAT GTAAACATTA TTTTTCTTTA GTTTCATTTT TTTACGAACT AATAATTCTG 2520

CTTGTGCATG GTAATGATCT TTCAGCAATG AATACATTCG ACGAGCAATT GCAGCATTTT 2580

CCGTTTGTAC ATTCAAGACA AACTGTTGAT TAACTAAGCT AAGCGAGCCG TTCATCCGAA 2640

TTAATGCTGC TAATTCTGcT TTCGCGTGTT CTCGATGGAC TTCTAAACCA GTTAACTCTT 2700

TTTTGACATC CGAGGCAAAA GACATCTAAG CTCCTCCTCT CTTGATTCTT TTGATTAATT 2760

AATATTTCGT TCCAAATACG ATACGGAAAA GTTCTTCAAC AACTTTTTCC CCATCATGAA 2820

AAACTCCGCC ATCTCTTAAT TCTAAAAAGT CTGTCGAAAT GACTCGGCAA CCTTCTTCAC 2880

GTAATCCTTG AAAATCATGC TTTACTTGAA CTAAATATTC ATCATAAATT TCAGGATCCA 2940

TATAATTTTC TGGTACTTTT TCTGTGTTAA CCAGCACCGT ATCAACAAAC TGCGCTTGTA 3000

GATGCTCGTT TAAGACACGA ACATGATCTG CATCCGTAAA ATGTTCCGTT TCCCCTTTTT 3060

GGGTCATGAT GTTACAAATA TAGACTACTT CGGCTGCCGT TTGTTTGATG GCTTCACCAA 3120

TTTCTGTAAT AACTAAATTA GGCAAAATAC TTGTAAAAAG ACTCCCTGGC CCTAACACGA 3180

CCATGTCTGC TTCTTCAATT GCTTTGACGA CTTTACGCGC AgcTCTTGGC TGCTCTTCTC 3240

CGTGTGTATT TGTTACAAAC ACATGGTCAA TCGTCTTGCG ATCCAGTGCA ATTTTTGATT 3300

CTCCCACCGC CACTGAGCCA TCTTTAAATA CAGCATGTAA CGTTAATGGC CGTTCTGATG 3360

ATGGATAAAT CCGTCCATCA ACATGCATCA TTTTTGAAAG CAATTGAATC GCTTCATACG 3420

TACTTCCTCT CATTTCTGAG ACAGCAGCAA TGATTAAATT ACCGATTGCA TGATTGGCAA 3480

AATGACTATC TGATTTATCA AAACGATATT GAAAAATATC TTCATATAAT TGTGGCATAT 3540

CTGACAATGC CACTAAAACA TTTCTTAAAT CTCCCGGAGG TGTCATGTTA TTAATAGAGG 3600

AACGAAGCTC GCCACTACTA CCGCCATCAT CAGCGACCGT TACGACGGCA GTAATATCAA 3660

CACTTTGATT TCTTAAACTT TTCAAAATTA CTGGCAAGCC TGTTCCACCA CCAACAACCA 3720

CGATCTTCGG TTTACGAATT CGATAGGTTT TCATTAAGAG CGATTAACCG TTTCTTTTCT 3780

TTTTAAGCGG TCGCGGTGGG TAATATTTAC ATGGTAATCT TCCTCTTTTA ATTCAGCGCC 3840

AACACGTTCT GTCAATGCAA CAGAGCGATG TTGTCCGCCA GTACAGCCAA TTGCAATGGT 3900

GACGCTACTT TTACCTTCTT TTTTATATCC AGGTAAGACT GTTCGCAGTA AATCGATAAA 3960

TTTTGTATAA AATTCATCTG TTTCTGGGAA GCCCATCACA TAATCATAAA CAGGTTGATC 4020

CATTCCAGTT AACGGTCGTA GTTCATCAAT ATAATGGGGG TTAGGTAAAA AGCGAACATC 4080

CATAACGATA TCTGCATCAA TCGGCAAGCC ATATTTAAAG CCGAAGGACA CCATTTCCAC 4140

TCGAAATTCG TGTGTCTCTC TCGTTGCTAG TTCTTTATTC AAACGTTCCC GCAATTGACG 4200

AGGGGACAAG TCCGTAGTGT CAATAACCAA CTGAGCATCC GCCTTGATTT CTTCCAGCAT 4260

TGCACGTTCT TTACGAATAC CTTCTGTCAC TAAACCATCC ATCGCCATTG GATGCGCACG 4320

CCGTGTCTCT TTATAACGAG AAACCAACTC TTCATCGGTG GCATCTAAAA ATAAAATCGT 4380

TGTATCAATA AAATTAGTAT TTTCAAGTTC GACTAACATA TCCTGAATTT CTCTAAAGAA 4440

GGTCCGTGAA CGTAAATCAA TCACTAACGC AATCTTGGTA ACTTTTCCAG ATTCTTTAAT 4500

TAATTCCCAA AATTTTGGGA TTAAGCTTGG TGGTAAATTG TCGATACAGA AATAGCCCAT 4560

GTCTTCAAAG CTTTGAACAG CGACTGTTTT TCCAGCGCCA CTCATTCCTG TAATAATAAC 4620

CAGTTGTAAA TTTTCTGGCA TATTCAACAC TCCCTTCACT TGCATCACTA TATTATAACA 4680

CCCCGGGCGT ATCAAAGAAA GCTTTTCAAT CATTCTTATA AAGATTTCTA TTCTTTCATA 4740

GAAAAACAGC ATTGACATTT TTGTCAATGC TGTTTTAATT GCTGAATTAT ACTATATAAC 4800

TCTGTGTTAT TTTAATACAA ACTCAATTTC TGTTTTATCA GTAAAATTAG CTTCAAACTC 4860

AAATTGTTTT ACTTGTTCAT TCACGGCTAA CTTTTTCGTA ATGTGTTCTT TAATTTGTTC 4920

ATTTGTAGCT GTTTTGATTG ACAATCCATC TAAAAGAGTC ATGATTTTGT CTTGTGCTGC 4980

CTTACCTTCT AATTCTAAAT CAGCAGATTC ATCTTCATAC GTTGCTTCAA TTGTTCAGTT 5040

CGATTTTATT TCATAGGTGA ACTCAATTTC ATTTTCGTCG TATTCAATTT CTACGTCAAT 5100

CTCTTGAAGA CTGGCAACAG TCGGTGTCGG TGTGGTTAGT TCATTGTCTG CTGTTTCATG 5160

GTCCCCACCA ACTTCAGGAG TTACAGTTTC CCACTTAAAG GTACCAATTT TAGCTGTTGC 5220

TAGATAGGGA TTATTAATGG TTATGACTTT CAATTGAAGG TCTGAATGGT TGGCGATATC 5280

TGTTAAAATC CCCAGAGCCT GATATGTATT TTGTGTAAAA CGTGTCGCAA TATTTTGCGC 5340

ATCAATTGTG GAATAGCCTA ATGTTTCCCA GGTGATTTGT TGCTTTAATT CCTGATGAAC 5400

GGCTGTACTG TCGCCGGCTC CAATTGAATG CCCGTTGcTt CTtTTAAGnC TTCCTGGnAA 5460

AACTCATTAC TTTTTCATGG GCTGATTGTG AAATTAAnGT CGCTGCTCCA TGGGGTACnA 5520

ATGACAAAAG 5530

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTTAGGGG ATGAGATGTA TCATGGAAAG ATGGATCAAG GAATTGAGCG GCAAGCGTTG 60

CATTGCATGG AACTAATTTT TACTCATCCT TTTACCAAAG AAACGGTTCA TCTGATTTCC 120

CCACTnGCGG AGGATATGAA AAGTGTAGAT GATACGTTAT AATAATAAAG AGGCAGGAGG 180

GGAAAGTGTA AGATGAATGA AGGCCAAGAA ATGGAAGAGC AATTTGCCCT TCTTTTAGAA 240

ACGCTAAAAA ATCAACAAAT GAACGAATTT CGTGAGCTAT TTTTAGCGTT ACACATTTAT 300

GAACAAGGAC AATTTTACCA ATCGTTAGAT GAAAAAGACC GACAACATTT ATACAATTAC 360

CTATCTCCGA AAGAACTAGC GGATATGTTT GATGTTATCG AAGAAGATAA TGAGAATATG 420

AAAGATTATT TAGCTGAAAT GCGCCCaAGT TATGCAGCCG ATATGTTAGC TGAGATGTAT 480

ACCGATAATG CGGTGGATTT ACTAAATATG TTAGATAAGA GTCAAAAGGC GAAATATCTT 540

AGTTTGTTAA GTAGTGAAGA AGCAGGCGAA ATTAAAGAGT TACTTCATTA CGAAGATGAA 600

ACTGCTGGGG CGATTATGAC CACCGAATTT GTTTCGATTG TGGCGAATCA AACAGTGCGT 660

TCTGCGATGT ACGTCTTAAA GAATCAAGCG GACATGGCGG AAACAATCTA TTACGTTTAC 720

GTAGTCGACC AAGAAAATCA TTTAGTCGGC GTTATTTCGT TGCGGGATTT AATTGTTAAT 780

GATGATGATA CCTTGATTGC TGATATTTTG AATGAACGGG TTATTTCAGT TCATGTTGGC 840

GATGACCAAG AAGATGTCGC GCAAACAATT CGTGACTATG ACTTCTTAGC TGTGCCAGTT 900

ACAGATTATG ATGATCATTT GTTGGGGATT GTAACAGTTG ATGATATTAT TGATGTTATC 960

GATGATGAAG CCGCTAGCGA CTACTCTGGT TTAGCCGGGG TCGACGTTGA AGAAGTTAGT 1020

GAGAACCCTT TAAAAGCCGC TTCTAAACGA TTACCTTGGT TAATTACGCT GCTGTTTTTA 1080

GGGATGTCTA CGGCCTCGTT AATCAGTAAT TATGAGTCGT TAGTTAGCGA AgCGAGTATT 1140

TTAGCCGTTT TTATTTCTTT AATTACCGGA ACAGCCGGCA ATGCCGGGAC ACAATCATTG 1200

GCGGTCGCGG TACGCCGTTT GGCTATGAAA GATGAAAAGG ATAGTAATTT TGGTCGCTTA 1260

ATCTTAAGTG AAGTGCTCAC GGGACTAGTG ACGGGGGCTG TGACAGGTTT AACCATTATG 1320

ATTGTGGTTG GCGTGTGGCA ACATAATCTT CCGCtTGGAT TTGTGATTGG GATGGCAATG 1380

CTCTGTGCAA TTACTGTGGC GAATTTAGCA GGGAGTTTAA TCCCAATGTT AATGGATAAA 1440

TTAGGGTTTG ATCCCGCAGT TGCCAGTGGC CCGTTTATTA CTACCTTAAG TGATTTAACC 1500

AGTGTATTAA TTTATTTCAA TATTGCCAGC ATGTTTATGC GTTATTTTGT TTAAAAAATT 1560

GCACTTATTT ATCATGAGAC TGAGGTAAAA GGATTCGTTG GTTTGCTTGA AATCAAAAAA 1620

GTGAGATAGC CGTTAATACG ACGGCTrCCT CACTTTTTTA GATACAAGAA ATTAAACAAT 1680

TTTTGTGCCA TGGACTTCTG TGACkTTTAA AgTGTCCATC ACAGTTTGAA CGTTTTCTGT 1740

GGAAATACCG CCACCTGGkA AAATAAGAAT CCGkTGaTCT GCGTAGACaA TTAAwTCTTT 1800

TAAAkGATCA AAGTwGtCTy CGATAGGGGk ACCAGCyGGc CCGCCATGAG TTAAAATACG 1860

sGkCACACCA CGCTCAGCTA ACCaGTCGAT CGCCTTAAAT TGaTTTTCTT TCGaCAAGGC 1920

aTCAAAaGCC aTATGGAAAG TGATTTGCaA GCCTTCaGCC gTTtCAATGA ATAAGTcCAA 1980

AgCTTCTTCa TCTAACCaAC CGTCCTCAGT TAAAaCAGCC cAATAACcAA TGCCCGTCGG 2040

TTCCCTAATT TCTTTGCCTC GATTAAATCG GTATGCATAA TTTTTAATTC AATATCATTA 2100

TAGACAAAAT TGCCGCCACG AGGACGAATG ATTGTCAtCA CTGGTACAGA ATGTtCGCCa 2160

GCGtATGCTA AGaCTTCTTC AATAACACCA GTACTTGGCG TCGTTCCACC CACGGCTAAG 2220

TTATCGCATA ATTCGATGCG ATTCGCACCT TTTTGAATGG CTTGGGGAAT CTTAGTGAAA 2280

TTTTCGGCAC AGAATTCTTT AATCATTTCT TATCGCTCCT TGCTTTTTCT TCACAGGCAT 2340

TGTACCATAA TTCTGCTTAC TACCATAGCC CTGAAAAAAA GAGTGCAACT TTTTATAAGA 2400

GAAAATGTTC ATTTAATGAA CGTAAGGAGT TTTAAATGTT AAAGAAAATT GAACGAGCAC 2460

AACAATTATT GAAAAAAGAA GCAGCCGTTT TTCGCTGTCC AACTTGTCAT GAACCAATGC 2520

ATTTAGAAGG GGTTGGTCTG ATTTGTCAAC AGAGGCATCA ATTTGATTTA T 2571

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2988 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

AAAGTTGTTG ACAAATAACA AACGAGATGn TAAGATATAG AAGTTGTCAC nACAGACAAC 60

AACAACCAAG CAAAACAACT TAAAAAAACT TTTTyAAAAA AgTTCTTGAC ATTCAAACGr 120

AAGTTTGTTm TGATATAAAA GTTGCTGCGA GGTAACGTAG ACCTTTGAAA ACTGAACAAA 180

GAATAGACGA ACCAAATGTG TAGGGCGTCT TGATTCAATT CAAGACAACA AACATTTTTA 240

ACAAGCAAGC AATATGCTAG CAAACAAATT GAGCTTAACA ATCGTAAGAT TGTTCTAACT 300

TTTATTATGA GAGTTTGATC CTGGCTCAGG ACGAACGCTG GCGGCGTGCC TAATACATGC 360

AAGTCGAACG CTTCTTTCCT CCCGAGTGCT TGCACTCAAT TGGAAAGAGG AGTGGCGGGG 420

CGATGCCAAA AAGCAAACGC TTGTTAAAGT AACACTGAAA GGGCAATTAA AAGAAGTCAC 480

GTTTCCAGAA ACAATTAAGG TCTTTAATAA TtGTAAAACT GGGACATTGT TTGGCGATTG 540

GGCTGACGTA AAACCTTTTT TAGAAGCAAA CAAAGAAAAA ATTGAGGATT ATGTTGTAGA 600

AAACGATGCA CGTAACTCAG CAATTCCTTT TCTTGATCTG AAAGACATTA ATGCTCGGAT 660

TGAACCAGGT GCTTTGATTC GCGAAAAAGT TGAAATTGGC GATCAAGCGG TGATTATGAT 720

GGGGGCTATT CTAAATATTG GCGCCGTCGT TGGTGCAGGG ACTATGATTG ATATGGGCGC 780

TGTTTTGGGC GGTCGTGCAA CTGTAGGGAA GCATTGTCAT ATTGGCGCAG GAACGGTTTT 840

AGCTGGTGTC ATTGAACCAC CAAGTGCCGC ACCTGTGGTT ATTGAAAACG AGGTTGTCAT 900

TGGAGCGAAT GCGGTCGTAC TAGAAGGGGT TCGTGTTGGT GAAGGTGCCG TTGTGGCTGC 960

TGGGGCGGTA GTTGTGGAAG ACGTTCCAGC GCATACCGTT GTTGCAGGCG TGCCAGCAAA 1020

AGTAATTAAA CAAATTGATG ATAAAACCAA GAGTAAAACA GAGATTTTAG AAGAATTACG 1080

TAAACTCTAA AAATAAATTA GTCAGTCGCG ATGAAGAAAC TTCTTCATGG CGGCTTTCGA 1140

TTACCCAAAA AATGAAGGAG TGGCTTTTGT GGAGCAAGAA GAATTAATTG CGATTAGACG 1200

GCAACTACAT CAAATACCtG AAATCGGTTT AGaAGAAAAG GAAACACAAG CCTTTTTACT 1260

TAATGAAATT GATAAAATGA AGCAACCTTA TCTGCAAGTT CGAACATGGC AAACGGGGAT 1320

TTTAGTCTTC ATAGAAGGCA AAAATCCTCA GAAAACCATC GGCTGGCGTG CTGATATTGA 1380

TGGTTTACCT ATTCAAGAGG AAGTGGTTTC TGCTTTTCAA TCAAAACGAC CAGGGTTTAT 1440

GCATGCCTGT GGGCACGATT TTCACATGAC AATCGGTTTA GGGGTTTTGA AAGAATTAAG 1500

TCAACAGCAA CCAGACAATA ACTTTTTATT TTTATTTCAA CCTGCTGAAG AAAATGAAGC 1560

AGGGGGGATG TTGATGTATG AAGACCATGC GTTTGGTGAG TGGTTACCTG ATGAATTTTA 1620

TGCGCTTCAT GTTAATCCTG ATTTGCCAGT CGGAACTATT AGTACCAGAG TAGGGACATT 1680

GTTTGCTGCC ACTTGTGAAG TGAACATTAC CTTAAAAGGA AAAGGTGGAC ATGCGGCTTT 1740

TCCGCATCAA GCGAATGATA TGGTCTTAGC GGCCACAAAT TTAATTCAGC AAGCGCAAAC 1800

GATCGTTAGT CGAAATGTTG ATCCTGTGGT TGGGGCAGTC GTTACCTTTG GAACTTTTCA 1860

TGCAGGGACT GCCTGcAATG TGATTGCCGA AGAAGCAACT TTATCTGGTA CAATTCGCAC 1920

ATTGACAGCA GAAACGAATG AACAAACGCA GCGAAGAATT CGCGAAATTA GTGAAGGTAT 1980

TGCGCAATCT TTTCAATGTG AAGTAACTGT TCATCTTGAT CAGAAAGGGT ATTTACCTGT 2040

AGTGAATGAG CCAGCATGTA CCACGAATTT TATTGAATAC ATGAGCAAAC AAGCAACAGT 2100

TCAATTTCAA CAAGCACCGG TTGCAATGAC AGGTGAAGAT TTTGGCTATC TATTGTCTAA 2160

AGTCCCAGGC ACGATGTTTT GGTTAGGCGT GGCAAGTCCC TACAGCCTTC ATTCTGCTAA 2220

GTTTGAACCG AACGAAGAGG CGTTATTGTT TGGAGTGGAG GCAGTTAGTG GCTTTTTAAA 2280

ATCATTGGAC AATTAGAAAA ACAGCCACCA GATAACTAAT AAATATCTGG TGGCTGTTTT 2340

TTATTTTGCA ATAATGGGCG TATTGGGAAT CGTAAAACCG GCCTCTGTTA ATGCTTTGAT 2400

ATATTGGGCT AGAAATTCTT CTTTGACCGC AAATTGTTTG CCGTTTAGTA CATACATGGT 2460

CGTTCGCACC GCAAAGTTGC CATTGCCTAA ATCGACCATa CCAAAAATAT CTGGCTCAGT 2520

TTGAATACTT TCGATATACT TTTCTTTTAA TGTTTCATTG ACTTCTGTAA TCACTTCACA 2580

AATTTTTTCA TAACCTTCTT CAGGATTGAT GCGGACATCA ATTAACACTT GCATATTGGC 2640

ACGAGACAGG TTACTGATTG TGGTGATGTT TCGGTTTGGA ATAAAATGAA CAGTTCCATC 2700

AACCGCTTTA ATTTGAGTGG TTCGTAATCC GACAGAAGTA ACAGTTCCTT CAATATTTAA 2760

CGCCAATAAG CGAATATAAT CGCCTACATC CATTTGTTGT TCCAAAATAA TGAAAAATCC 2820

GGTAATTAAG TCATTCATGA ATCCTTGAGC CCCTAAACCA ATGGCAACAC CGGCAATTCC 2880

AGCTCCGGCT AATAATGAGC CAACAGGCAC ACCGACAATG GTCAAAAGAG AATAGATGAA 2940

GAnAAAGAAC AGCGTATATG GAAATGCATT AATGGnTTAn AnTGGGTA 2988

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

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CnTATAGACA TATTCTCnCC AACTTATTTT TTGGTGGGAG TTCCCGGTTA TTCnTCCATA      60
TTGTTTTCnG GTAATTCGTT GGTAACTAAC AAATGTTTCC ATATTGGTCA TCTGTCAATC     120
CAAGTAAGCC GTATTCAGCT TTAATATCTG CATATTTAGG ATAATCTAAA ATAACTTTGC     180
CGATTAGTGG TATATAAGAC AATGCCCAAG AAATAACCGC AAAGTTCAAC ATTACATTCC     240
CAACAAAAGA AGTTGTTCTA TTATTTGTTA GGCCATTTAA ATCATCAGGA TAATGAACTA     300
ATTTGCCATT GCGTAAACCC CAGTTCAAAT AATCTTTTGG CTCTTCATTT ACTTCAATTT     360
CAATATAGTT TTTCTTAGCA ATAAACGAAT AGTCCGTAAG CATTTGATTT TCGTCCATTG     420
TAATCCATAT TTTTATCTTA TCCATGTTGC ACTCCCTCCA AATTCTACAT CATCATTTTG     480
AAGTCCATAA ACTCGAATCA TAATTCGACC AGATGTTTCT ATTTGTATTG CTGCATATTT     540
ATTTGTTTGA ATCGTATTGC CTATATTTAA GGTTAACGGT ATTTTAATAA TCATATTTTG     600
AGGTCTATAG CTAGCTTGAA TATAGGTATC CACACCATGC CAACCATTGG CTTTtCCTTT     660
TTTAAAAATT CCTTCAACAT TACATGTAAT AATTGTATTT GATCTTTGAA TGTGAATAGT     720
AATTCCATTG TAAGAAATAT GTTGACCAAC AGCATTAAAT GCCGTTTTGT CAATCTTTTT     780
ATTTAAATCA TTTGTATACT GTGTTTTAGT AACTAAATTG CTTATATCAG GCGTATCACC     840
TTTAGGTCCT TGCTCTCCTT TTGCGCCTGG AACACCATCG TTTCCTTTTT CACCTTTTGG     900
ACCTTGTGGA CCAGTATCCC CCTTGTCACC TTTAGGTCCT TTTAAACCAA TCGGACCTTG     960
CGAGCCTGTT TCTCCTTTTT CTCCTTGTGG TCCAATGTCT CCTTGTAAAC CTTCTGGGCC    1020
TCTAGGGCCT ATATCCCCCT TATCTCCTTT TGGACCTTGT GGACCAATAT CGCCTTTGTC    1080
TCCTTTTCGA CCTTTAAAAT CTGTAAAACT TTTTTTATCA AAGGATAAAA CATGAGCACT    1140
ATTGTTTGGC AATATATACG CAACACATTC TTCAGCAGCT TCTATAGCTG GTAGTTCATC    1200
TACACGTTCA AATGAACAAA TACTTACATC TGATTCACAT GGACTAAATC CTATATTGCC    1260
ACAATCAGAA CAAAAGCTTC TAACCCTCAT CATCAATAGC CCCTTTCATC ATATCGCTAA    1320
AGCAAGAAGC ACATTCGGTA ATGGGTACTC CTGTAAATTG AGTGATTTTT TTGATGAAAT    1380
AAGCATTTTT TTCAATACAT ATTTGATAAA GTAAACGATC GTTATCACTG GcTTGCCAAG    1440
CTTCAAAAGC TGTATACATT GCCATTGCAG CGTGTTtAAC TATACACCAT TGTCCCTTAT    1500
CACCTTTACC                                                           1510
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(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

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ATTGAAGTTG CTGCAAATGC yTCGkTGATT TCATACAGAT CAATTTCTTC CGTAGTAAGT      60
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TGATTGCGCG CTAACAGTTT TTGAATGGCT TTaATCGGCG AAATTCCCAT ATAGGCTGGA    120
TCAATACCGA CTTCCACACT GTCTCGAATA ATAGCTAAAT AAGGAAGACC GTGTGCTTCG    180
GCATATTCTT GTGAAGCAAT AATCAAAGCA GAAGCCCCAT CATTAATGGT TGATGCATTC    240
CCTGCTGTTA CAGTACCGTC TTCTTTAAAA ACTGTTTTAA GCGTTCCTAG CTTCTCAACG    300
CTCGAATTAG GGCGAATCCC TTCATCTTTC TCCACAAGCG TTCCTGATAC TTCTAATGGG    360
GCTATTTCGT CAGCGAATAT CCCTTCTGCT TGTGCTTGAG CTGCTTTTAA TTGTGAATGT    420
ACAGAAAATT GATCTTGCTC TTCTCTAGTT ACATGATACT TTTCGGCCAC ATTTTCAGCA    480
GTTAAGCCCA TTGCCTGACC ACTAAAGGCA TCCGTTAATC CATCATACAT CATACTAGAA    540
AAAGGCGCAT CGTAGCTTTC TGTTTCGTAA TTAAAACGTT GTAATTTAGG TGCTTGGGAC    600
ATATTCTCAA TCCCGCCAGC AATTAAAACT TCCgCTTCTC CTAATTGAAT CAATTGTTTC    660
GCCAAAATAA CGGCCTTCAT TCCTGATCCG CAGACCTCAT TAACCGTCAT TGCGGGAATT    720
TCATGAGACA AACCGCTGTT TATTGCTATT TGTCGTGCGG GATTTTGGCC ATTTCCAGCT    780
TGTAAAACAT TTCCAAAGAT TACTTGATCA ATTTCTTCAG AAATAGTGGA ATGTCTTTTT    840
AAAAGTTGTG TTGTAACATG TGTTCCTAAG TCTACGGCAC TTACTTGACT TAAGCTGCCT    900
TTATATTTTC CAATTGGTGT TCGTAATGCA TCAATAATAA CTACTGTTTT CAACTAAATG    960
CACCTCCATC TTGaAATATA TCATAAAATC CCAGAATCAC AAGTGCCAAT TACTGAATGT   1020
TAACAGACTT ATAAGATATT TTTTAATAAT CTATGAAGTT AATACAAAAA TTCCCCATTT   1080
TGGTTCATTT CGTGCTATTT TATATAATGA ATCTATTTAT CGTAAAGGAG TTAAAGAAAT   1140
GACAATTGGG ATTGATAAAA TTAGTTTTTT TGTGCCCCCT TATTATATTG ATATGACGGC   1200
ACTGGCTGaA GCCAGAAATG TAGACCCTGG AAAATTTCAT ATTGGTATTG GGCAAGACCA   1260
AATGGCGGTG AACCCAATCA GCCAAGATAT TGTGACATTT GCAGCCAATG CCGCAGAAGC   1320
GATCTTGACC AAAGAAGATA AAGAGGCCAT TGATATGGTG ATTGTCGGGA CTGAGTCCAG   1380
TATCGATGAG TCAAAAGCGG CCGCAGTTGT CTTACATCGT TTAATGGGGA TTCAACCTTT   1440
CGCTCGCTCT TTCGAAATCA AGGAAGCTTG TTACGGAGCA ACAGCAGGCT TACAGTTAGC   1500
TAAGAATCAC GTAGCCTTAC ATCCAGATAA AAAAGTCTTG GTCGTAGCGG CAGATATTGC   1560
AAAATATGGC TTAAATTCTG GCGGTGAGCC TACACAAGGA GCTGGGGCGG TTGCAATGTT   1620
AGTTGCTAGT GAACCGCGCA TTTTGGCTTT AAAAGAGGAT AATGTGATGC TGACGCAAGA   1680
TATCTATGAC TTTTGGCGTC CAACAGGCCA CCCGTATCCT ATGGTCGATG GTCCTTTGTC   1740
AAACGAAACC TACATCCAAT CTTTTGCCCA AGTCTGGGAT GAACATAAAA AACGAACCGG   1800
TCTTGATTTT GCAGATTATG ATGCTTTAGC GTTCCATATT CCTTACACAA AAATGGGCAA   1860
AAAAGCCTTA TTAGCAAAAA TCTCCGACCA AACTGAAGCA GAACAGGAmC GAATTTTAGC   1920
CCGTTATGAA GAAAGTATCG TCTATAgTCG TCGCGTAGGa AACTTGTATA CgGGTTCaCT   1980
TTATCTGGGA CTCaTTTCCC tTTTAGAAAA TGCAACGACT TTAACCGCAG GCAATCAAAT   2040
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TGGTTTATTC AGTTATGGTT CTGGTGctGT CGCTGAATTT TTCACTGGTG AATTAGTAGC 2100

TGGTTATCAA AATCATTTAC AAAAAGAAAC TCATTTAGCA CTGCTGGATA ATCGGACAGA 2160

ACTTTCTATC GCTGAATATG AAGCCATGTT TGCAGAAACT TTAGACACAG ACATTGATCA 2220

AACGTTAGAA GATGAATTAA AATATAGTAT TTCTGCTATT AATAATACCG TTCGTTCTTA 2280

TCGAAACTAA GTATTTAAAT CCCCCGATTC AATCAACAAA AGAGCTAGAC ATTCAAGCAA 2340

AAACTTGAAT GTCTAGCTCT TTTTATGAAA GCCAAACTTC TTTGACCCCG TCTGTCACGG 2400

CGATACCATC TGTCAAAGCT AAACGTTGTG AATAAGAAAC GTAGCCATAA TAAACATCAA 2460

CACCGCCGCC ATTGTTCCAA GTAACAGTGA TTTTAACATT TGGAGTAATC GATTTTGTAG 2520

CTGGTTGGGT CGTCGGGCGA TAACTAGTCG TATCATAACT TAAAATAGTG CCCGAAGCTC 2580

CACTTATTTC GGCTTTTCCT GTGTAAATTT CGCCATTCGT ATTCGTCTGC GTGACCGCTC 2640

CATTCGCTTC AATGATTAAA CCCGCTTGCT TTTGATCTCC TCGTGGATAA TAAAAAAGAT 2700

ACGTGGTTGC CCATTTAGCA AATTCATCTG GAATTGGTTT AAGTGATCCC GTTGGTGCCG 2760

GACTCGACTT CGTTTGCTTT TCAACCGCGA CTTCTTCTTG TCTTTTTAAG CCTTCACTAT 2820

TTTGATTATT TAGTTTCTCA ACCGTTTCTT TAACGATCGA ATAATGAGGT TTCCCTAAAT 2880

CGCTAACAGG GATCGTAGCT AATTTTTCTT CTGATTCTTT ATATTGCCCC TCTGCCGTTA 2940

ACTTTTTAGC TTCTGTAATA ATGGCATCAT ACTTGGTTTG GTCTACGGAA GAGGATGTGC 3000

TTTGTCCCGT AGCTTCGACT TGTTTTGTGA CACTGGTTTT TTCTGTGGTC ACGTCTGATG 3060

AATTTCCACA AGCACTTACA AACATTGAGC TAACGATTAA TAAACATCCC ACAATCACAT 3120

GCTTTTTCAT TTTTAAATCC CCCATTTGTC TATCTTTGTT ATTTTTTGTT ACTTAAATTA 3180

TCCCATAGAT GAACAAAAGA AACCATTATT TATAAAAAAG CTTAGCAAGC GCTTCAAGAG 3240

AGGCACTTGC TAAACTTTTT TCTCACTGTT ATTGATTGAT TACTTTGACT AGTTCTTCAA 3300

ATAATAATGC ACTAGATGCT GCTCCTGGAT CAATATGACC AATTGCTCGT TCCCCTAAAT 3360

AAGAGGCACG TCCTTTTTTC GCCACCCAAT CTTTTGTTGC TTCAGCAAAT TGTTCAATTT 3420

TTTCTTCATT AAATTGTTCC GTTCCAATTA CTTCAGCAAC AGGTGCCCAG ACATCAACCA 3480

TCGTTTTATC TCCTGGTTCA GCTTTGCCAC GCATCTGAAT CCCAGCTAGA CCTTGCTGAA 3540

CAATTTCTTT TAATTGCTCT GGCGAACTGA TGGTTTCCAA ATCTTTTGTC GCTTTAGTCA 3600

TATTCATAAA CGCAGTACCA TATAAAGGAC CAGAAGCTCC GCCAACTTTT GAAATCAAAG 3660

CCATGGATAG GACTTTAAAT GTCTCCGTGA TTGTTGTTGG TACTTTTTTG TCAAACGCAA 3720

TTTTGTATTC AGCCATACCA CGAGCCATGT TGTTACCGTG ATCCCCATCA CCAATCGGCG 3780

TGTCTAATTC ACTTAGATAG TCTTTTTTTT CTTCAATAAC TTTTGAATAA TTGTCTAACC 3840

ATGTTTGAAT GTCTTTTACT GTTAATTCCA TCTTTTATCA CCCTTACCAA GAAATTGTTG 3900

TTACATTGCT TTCTAGCGCT GTTTGCCAGT CTTTTGTCGC CAAGTCAATC ATCGTTAAAG 3960

ATAATCCTTG CATGTCAATA GACGTCATAT AGTTACCCAC TTTATGGAAG GTCACTTGAA 4020

CACCTTTATC TTCTAACAAT GTTAGCACGT CGTTCATAAA TACAAATTGT TCCATTAATG 4080

GCGTGCCACC CATGCCATTG ACAAGTACCC CTACTGTTTG TGGTTGTTGC TCATAGCTAC 4140

TTAATGTTTT TTCAACTAAT TCTTTCGCTA ACTCTTTCGA TGGTTGGATT TTTTCACGAC 4200

GATAGCCTGG TTCTCCGTGA ATCCCTACGC CAAATTCAAT TTCATCTTCT GGTAAAGTAA 4260

AACCTGGTTT GCCAACTTCA GGCACAGTGG CTGCTTTTAA AGCCACTCCA ATTGTTTTCG 4320

TGGCTGATAC AATCTTTTCT CCTAAAGAAA CGAGCTCTTC TAAAGAAGCA CCTTGGCGGG 4380

CATGATGTCC TAAAATTTTA TGGACAAGAA CAGTCCCGGC AACGCCGCGT TTTCCAGCGG 4440

TATAGGTGCT ATCTTCGACA GCAATATCAT CATCGACAAC GACCATTTCT ACATGAATGT 4500

CTTCCATATC AGCCATATCT TTGGCCATTT CAAAGTTCAA AATATCGCCT GTATAATTTT 4560

TTACGATTAA CAGAACACCG GCCCCTTGGT CTGCCGCTTG GATCCCTGTT AAAATTTGAT 4620

CTGGTGTTGG TGAAGTAAAG ACATCACCTA AAACTGCGGC ATTTAACATT CCATCACCAA 4680

CAAACCCAGC ATGTGCAGGC TCATGACCAC TTCCGCCACC AGATACTAAC CCAACTTGTT 4740

TGTTTGAGTC GTTGCGAGCA ATCACGCGAG AATCTTCGAC TTGATGAACA AGGTTTCCAT 4800

AGCTTTTCAC AATTCCTTGG AGCATTTCTT CGACAATTTT ACCAGGTTCA TTAATAATTT 4860

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AATCATCTGA GACACCTGCA GTAATTGctG ACGCAAAGGC ACCTTCAACC AATGGTGCAT 4980

CGACTAAATG ATAATGTTTC TGTTGGTCTT CTTCTAGCAT ATCAAAAGCT AATTCTGAAC 5040

TTAAAACGGC ACTGCCTAAA TCGGCAAAAA TTAAAAATTC TCGGTCAGAG TCCGCTTCGT 5100

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GTGAATGAAT TGTAATTTCT tCACTGGCGT TCATCTGTTC AATCATCTCT TTAATACCAT 5220

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TCGCTACTTC TTCAACGACA ATTGGGAATG GCATTGAATG AATTGATTCT TCTGGAATGC 5400

AAGCAATTTT GGCTACTTCC AACGCTTCTT CATAAGTGAT TTCATCGACa CCAATGTCTG 5460

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TTGCTGCATC TTCTAATACA AGTTGTGCAA TCGTTGCAAA AGCTACTTTT TCACCATGTA 5580

AATAACTGTG CGCACCAGGT AAGACTGTCA TACCGTTATG AATCGCATGC GCTGCAGCTA 5640

AACCGCCACT TTCAAAACCT AAGCCTGAAA GTAAGATATT TGTTTCGATA ATCTTATTCA 5700

ATGATTCAGT AACCACATTT GCATCACAAG CTAATTTCGC TTTTAACCCA TCTTCCTGGA 5760

GGTTTTCCCA GCAAAGTTTT GCCATGGCCA AAGCTGCATA TGTGCCGCTA GCAGCAGGCG 5820

TTAAGCCTTC TCTTGAACCC ATTGGCAAAC TAGCATTAAC CCGAGAATAT GAATTGTGTG 5880

TTGCGCGTGC TTCAAAATAT GTGGATAAGG CATCCCCCAT TCCAGCAACT AAAAATCTAG 5940

TTGGCGCTTT GGCAACCACT TTTGTATCAA CCATAACGAC GCTTGGACTT TGTTTAAAGT 6000

AAGCATAATC ATCAAATGAG CCATCTTCAT GATATAGTAC AGCTGAATGC GAAGTTGGTG 6060

CATCTTGAGC CGCAATCGTT GGTACAATAA TTAAGTTTTC ACCTTCTGCT ACGACTTTTG 6120

AAGCATCGAT TGCTTTACCG CCACCTAAAC CAATGATACA GTCTGCTTGT TCTTTTTGTC 6180

CAACGTTTTG CAAGCGCTTT GTTTCTTCAC GCGTTACTTC TCCACTAAAG CCACCCTCTA 6240

CGAAGGTAAT GTCAAACTTT TTCGCTGTTT CTTCCAATkG TGrACGwACA CGATCAACGT 6300

CAGCAGGATT TGCaATTAGT AACGCTTTTT TTCCaAAAGT TGAAACGAAG TAACCTAAGT 6360

TTAGTAATTC ATCTTCCCCT TGAACATATT TCGTTGGTAA AATCAATGCT TTTCTCATGT 6420

TGATAGCCTC CTATATTTTG TTnACATCCA TAGTATAAAA CGCTTTCATC TAAAAAGCAT 6480

TGAACTTTTG GTAtCGTTTy CTTGCAAAAA ATGATAGAAT TATTTTGTGA AATAATAAAA 6540

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TTTTAGATTT AGAAAAGTGG GAAAAATTGC AAGAATCATT GGCCTTAAGC ACTCGTTTAG 6660

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TTTGCCAACT GGTACGTCAC TCCCCTGAGC TCTCGAAACT TTGTGAAAAA TGTGATGCTC 6780

GTGGTGGCTT GGAAGCTGTT CGCACTGGTC AGCCTTTTAT CTACCGTTGT CACTTTAACA 6840

TCGTTGATAT GGCCATCCCC ATTATTGTTG ATGACCAGTA TGTAGGAGCC ATTATGGCTG 6900

GTGAAGTTTT GCTCGAAGAT CACCAAGAAG AGTTAGAACA GGTTTTAACC ATGAATGATG 6960

CCTTCATTCA AGAATTTTTA GTAACACACC AAGAGCTGTA TCAACAATAC CCTGTTTTAG 7020

AACTAGCAGA CTTAGAAAAG AGCGCGACAT TAATCGCTGA TCTAAGCCAA TATATTATTT 7080

CTGAAGCCAT CAAAAAAGAT TATTTAATCA ATACGTACAA ACAATCCTTA CAGATTAGTT 7140

CGCGAAAAGA AGAGCTGGAG CCATTGAATA TGATCCAAAA AGATATTCmA CAAmCTTTAT 7200

TAACTGCTCA ATTAACTCCT TCAAGkGCCT tCCAAmCTAA AAwTAAGCAa TaCCAcCGGG 7260

TTTAGATGnC CCTTGGGGAA ACCAATn 7287

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GTATGCCAAT CGTTTTAATT ACTTGTTGGT CACCGCTAAC GATGCCCACA TCAATCAACT 60

TGCCAACTAA TTTAGGGACG CCAAGGGTTC CTGCGATTTG CAAACAGATG GTTAAAGTTG 120

TCGCAAGAAC AATCCATTTA TTTTCTTTAA TAAACTCTTT CATTAATTTC ATGAAATTTC 180

CTCCTTAAAC AATACCGTTT TAGCTGTTAC AAAGAGTCAT TGTACACGTc AAGTAACTTG 240

AATGTCAACA GTAGAAATGC TAAACTTTTT GATGGAGGGA ACAGTATGGA AAAAAATTAC 300

ACAtAAAAGa TGTTTCTGAG TTGTTAAATA TCCCTAAGTC CACGATTCGT TATTGGGACG 360

AGCAAGGGTT GATTAGTACA ACACGCAATG AAGAAAACGG ATATCGAACC TTTGATTTAG 420

AAGATTTGTT CAAAATATAT GATATTGATT TTTATCGAAA AATGGGGATT CCTATCAAAG 480

ATATGTTGAA TTTATATAAA AAGACACCTA CCGATCTCTA TGCCACCATG GAAGCAACAG 540

AAGAACAACT GGGGCAAGAA ATAAAAAGGC TTCAACATAA ATACAAAGAA ATCAAGAAAA 600

GAAAATTACA TTTACATGCG TTAATTGATT TAGAAACATT GGTTTTTTCA GATGAACCAA 660

TTCCTTTTGA TAAAATTGTT GTTGTTGATA TTGAGGATCC AGAAGAGATG AAAGTTTACA 720

TGGAACACAT TTCAACTTTA GGTATTTACG GGGATTTAAG TGAATCCAAT GAACTGACGT 780

ATGGGATTTG TTTGGCAAAT CATGTGAATA AAAAAAGTTT AGATAAAGTG ATTTGGCTCA 840

AAGAATCAAG TAGCCAATAC AAAGGCTTTA TTTTAAAAGT CAATACACAA GATACCCGTT 900

TGAATAATAT CGAAGAAGTA AAAAAGCGTT TAGCAAAACA AGGATTTGAA ACAGGCATCG 960

TTGTCGGAGA GCATATCTTG ACACAACTAG AAGAGGAAAA CCAATATATT GAATATTATT 1020

ATGGTTGGAT TGAAATTTTa GGGGAAAaGT AAAACAATTA AaAAAAGGAA CTAGCAATAG 1080

CAAATGTAGC TAAGCTAGTT TCTTTTTTTG GTAAATGTAA TGAAAATTAC ATGAAAAAAG 1140

TTTTAGTTTT TAAAACAATT TAGAACGAAT GTTATTAAAG GGAAAACAAT AAAAAAATTA 1200

CTCTTAAAGC TAGAACTTAC CTATGTTTGT AATTTTTTAG GGAAAGTCAA TATATTTGCT 1260

TCATATAAAA CGTGTTATTT AATTCACGAT TTTTTGTTGA AATATCGGGT TTTTTCTTTT 1320

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TGGATGTTGA GAAACAATTA GTAATTGTAA AAGTTGTTTG AAGATGATTT GTTTAAGTAA 1500

ATGAAAAGAA CGAAGGAGAA TGTAAATGAA TAAAGCAGTT AAAAATTTTG TGAGTTACCT 1560

TATGATTACC ATGCTGTTTA TTTTAAATTT GTTACCAATG ATGAACGCAT TTGCTCAAGA 1620

AGTAACAAGT GATGCTGAGA AGACTGTTGA AAAAGACGGG CTCAAAGTAA TAGGGAAAAT 1680

AGAAGATACA TCGTCTCAAG AAGATATTAA AACGGTCACT TACGAAtAAC AAATACGCGA 1740

GATGTACCAA TCAAAGATCT CATTTTAAAA CAAAAAAATA CCAATGATAG TCCAATCAAA 1800

TTTGTTTTAG ATACTTTAAG TGAAGAGCGA GGACCTACGT CTTTAGAAGA ACAAGCAAAG 1860

GTTGAAACAA ATGAGAAAGA TCAAACAACC GATATTAAAC TGCTTAACCT TCAACCAAAT 1920

TCGACAAGAA AGATTACCAT AAATGGGCAA ATAACTACAA AAGCGTCGAA CAAGTTATTG 1980

GTCAGCGTAC TAATAGAAGA TAATGAAAAA GGAACACTAG TAATTGATTT ACCTAGTAAA 2040

GATATACTAG CAGATAAAGA GTCGGTTTCG AAGGAAAAAC AGGAAACTTC AGAAACAAAA 2100

GTAGAAAATC AGGCAAACGA AACAGCCTCT TCTACAAATG AAATGACCGC AACTACTAGT 2160

AACGAAACAA AGCCTGAAGC AGGAAAGGCG ATAGAAAGTA TTCAAGAGAC AGCACTAACG 2220

CAGGCTACCG AAAGTCCTGA GCAACCTCCA TTAAAGGCGC AACCTACTGG TCCGTTAGTG 2280

CCACCAACAC CTGGTCGGGG GTTTAATACA CCGATTTATC AAAGCGTTCA TAAAGGAGAA 2340

CTTTTTTCAA CGGGAAATAC CAACTTAAAA ATTGCGAATG AAAATACGGC GGCTGCACAA 2400

ACATTTTTAA ACACACGAGG AGCAAGTAGT GGTTATGCAA TTAACAATTT TCCTTTAGAA 2460

TTTGCAGATG TTGACAATGA TCCAAATACG TATAACTCTA GTCGGGCTTA TATTGATTTA 2520

AATGGTGCAA AAGAGATTGC TTGGGCGGGC TTATTTTGGA GTGCATCTAG ATATAAAGGC 2580

CCTGCTTACG GAACAAATCT TTCTGATGAA GAAATTAGTG CACCAGTTCA ATTTACTACA 2640

CCAAATGGAA CCGTACAGCG TGTTTCGCCC CAAAGGTACC ATCGTATCGA TCAAGATGCA 2700

ACAAACCCAG GACAACGTTT CGGGTACAAT AACACTGGAT TTTCTAATTA TGCAGATGTA 2760

ACTTCAATTT TACAAGGGGA TAAAAGTGCG ACAGGGAGTT ATACGTTGGC AGATATTCCT 2820

ATGACAAGTA GTTTAAATGG TCAATATCAA TATTATAACT TTAGTGGTTG GAGTTTGTTT 2880

GTTGTTACAA AGGATCAGGC AAGTAAGTCA AGAGCTTTTA GTATTTACTA TGGAGCACGT 2940

GGTAATGCTG CTGGAACCAA TAATGAATTT ACTATGAGCA ACTTTTTAAC AGCAAAACAA 3000

GGAAATCTTG ATCCAATTGT GACCTGGTTT ACTGTTCAAG GAGATAAATA CTGGACTGGA 3060

GACAACGCAC AAATTAAAAA TAGCGCAGGA ACTTGGGTAA ATATTTCGAA CACGCTCAAT 3120

CCAGTTAACA ATGCTATGAA CGCAACTGTG ACAGATAACG ATGAACATAT GGTAGACAAG 3180

TATCCAGGGA AATTTGCGCC GGATCATCCT AATTTTTTAG ATATTGATAT CGATCGTATG 3240

GCAATTCCCG AAGGTGTTTT AAATGCTGGA CAAAACCAAA TTAATTTTAG AACAACAAGT 3300

AGTGGTGACG ATTATTCTAC GAATGCGATT GGTTTTGCTG TAAACGCAGA AACGCCTGAA 3360

TTTGAAATTA AGAAAGAAAT TGTGGAACCA AAAGAAACTT ACAAAGTTGG TGAAACAATC 3420

ACGTATCGTG TCTCACTAAA AAATACAAAA GCTGATTCTG AAGCGATAAA TTCAGTCTCG 3480

AAGGATGCAC TAGATGGTCG CTTAAATTAT TTGCCAGGCT CTTTAAAAAT TATTAGTGGA 3540

CCAAATTCTG GTGAAAAAAC GGATGCTTCA GGCGATGATC AAGCTGAATA TGATGAAACC 3600

AATAAACAAA TTATAGTCCG TGTCGGCAAT GGTGCAACTG CTACACAAGG AGGTAGCTAC 3660

AAAGCTGATA CAGCTGAAAC AATTTACGAA TTTAAAGCGC GGATAAATGA ACGAGCAAAA 3720

GCAAATGAAT TAGTGCCTAA TAGCGCACCG TTGAGG 3756

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1046 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ATAGAAAAGC ATTATGtGTC CCCaGCGGTT TcCaTGAGGC CaCAAAAGGT TCCATACCGA 60

CTTTAATaTG TTGAGGATCA GATAACCATT TAGCAAAAAA CTCATGCCAA ATTCGTTCTC 120

TTCCTGTAAA TAAATCAACA GTATCCGATT CCGCACATAA GTAAAATAAC AATGGTCCCA 180

ATGCAGCTAC TCCGACAAAA CCAAATAGCC AAACTTTCGA ACGTTGCAAG AAACGTTTTG 240

GTAAAAGATT ATCCACCAGA ATAAAACCAA CTAAAATGGC AAAAGAGGTT TTTGATTGAC 300

TGACCCATGT ACCTAAAACA CCACCAATGT ATACAGGTAA AAGCAGCAGG TTAAAAACCT 360

TATTTCTATA TGCTTTGATC AAACTACTGG CCATCATTGT TGAaAACATC AACGTTGCAC 420

CAATCGTATT GGTATTAATC CAAATACTTT CTAGTTTATT TGATTCTTTA AAAATTTCGT 480

CTGCTGGAAT CAACTGAGGC AACTCCACGG ACATCCGATA CAAAGTCGCA CTCAAAGCAA 540

CTAAAGAGAC AATTAATAAA AGCGTTTGAT CCAAACGATC AAAGACACAA ACTTTAAAAC 600

AAAGAACCAA CAAAATAATT AAAGGAATCA TTGTATCTGT TTGCATCGTG CTATGACGGA 660

TTGATTCCGT AAAGTGAAaC AAGAGCCAGG TGGCTAGCGC CAACGCTACG GTCAGCCAGT 720

CAATAAATTT TAATTTCGTA CAATTTAATA GCAGTACAAG TATTACTGCT ATTAATAATA 780

AAATTGAACT ATTGGCATAC ATATATTTTG TGACTGGCGC ATCAATTCCT ACGACCCACA 840

TCGTATACGA GCCGATCATT GTAACTAATA AAATAAGTCG ACCGATTCTA TTCAATACTT 900

TTCCCATATT CmAACCTCAT TCCATGAATG AATCACTAGT CGTTTATTCG ATAAATATAT 960

GCCCCGTTCT GATCAGGTCC ATATAATTTT TCAAAATGAA TCGTTGGTGT GTCTAACGGT 1020

TCTAATGGTT TATAAACGAC CGCATA 1046

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TAAGTCGGAT TATTGTCGCC TATAATGACC AAAGAGAGCC GGTGACGGTT AAAGATTTAA 60

ACGTGGCAGG TGCGCTGACT TTATTATTAA AAGACGCCTT AAAACCTAAT TTAGTTCAAA 120

CGATTGAAGG AACTCCAGCT TTTGTTCACG GTGGTCCTTT TGCCAATATC GCTCATGGAT 180

GTAACAGTAT TTTAGCGACA AAAACGGCTT TGCATCTAGG GGATTATGTC GTAACAGAAG 240

CAGGTTTTGG TGGCGACTTA GGTGGCGAAA AATTTTTAGA TATTAAAGTA CCTTCTTTAG 300

GAAAAGCACC CGATGCCGTT GTGATTGTGG CAACGATTCG CGCGTTGAAA ATGCATGGCG 360

GTTTGGCGAA AGATCAGTTA GCAGAAGAAA ATTTACCAGC GTTACAAAAA GGCTTTGCCA 420

ACTTAGAAAA ACATATTCAA AACATGCAAC GTTATGATGT ACCAGTAGTT GTTGCAATTA 480

ATGAGTTTAC ACAGGATACA GAGAAGGAAA TTCAACTGTT GAAAGAAGCC TGCCAAGCGT 540

TAGGCGTGCC CGTCGAGTTA ACAAGTGTTT GGGCGCAAGG TGGCGCAGGT GGCACGAATC 600

TAGCGAAAAC AGTAGTAGCA GAGATTGAAG CCGATACAAA ACAGTTTCAA CCTTTATATA 660

ATCCTCGCCA AACTATTGAA GAAAAAATTC AAGCCATTGT ACAAACGATT TACGGCGGGG 720

AACAGGCGAT TTTTTCTCCG AAAGCGCAAA AACAAATCGC AGACTTTACA AAAAATGGTT 780

GGGATCAATT ACCAATCTGC ATGGCGAAGA CACAGTATTC ACTTTCTGAC GATCCTcAAA 840

AATTAGGACG GCCAGAAGGA TTTACGATTA CAATTCGTGA ACTAGTTCCA AAAATCGGTG 900

CAGGGTTTAT CGTGGCGTTA ACGGGTGACA TTTtAACGAT GCCTGGCTTG CCGAAGgTTC 960

CTGCTGCGTT AAAtATGGgA tGTGGACGAA ACGGGTCAAG CGAGCGGTCT CTTTTAAAGC 1020

CGCTCTTTCC TGAGACCTAT TTTTAGTATA TACTTGAAAG TAGCTCAATA AAAAATAATG 1080

ACGGAAATTT ATTGCGTAGT TTATTATAAG GAGCAACGAC TATGGGGGAA CGAGCAGATA 1140

CATTTTTAGC ACACTTTAAT CGCATTGAAA AGTGGATGAG AGAGAGACTG AACAATCCTG 1200

TCAACATGGG ATTCAGTGAA ATGACAAGAC GTCTTTCCCG AAAAGAAAAA GGACAGATTG 1260

CTCAATTTGA AGAGGATTTG CTTCAAATGG CTCAGTTAAG AAATGCCATC GTTCATGAGC 1320

GAATTGCTGA TGATTTTGTA ATTGCAGAGC CAAACGAATG GGCAGTTCAA CGAATTGAAA 1380

CGATTGAACA AGCTTTAACA AAACCAGAAA AAGTAGTGCC TAAATTTGCG AAACGTGTTA 1440

CAGCTTTTGA AATCACCACT TCTTTAGAAA CGTTATTAAC GATTATTGCA AAAAAACAAT 1500

ATTCTCAATT TCCGATTTAT GAAAAAGGTG TATTTAAAGG ATTAATCACG GTTCGAGGGA 1560

TTGGTGTATG GTTTGCCATT GAGAGCACCA AAGGCGAAGT TCACATTGCC AACCGAACGG 1620

TGCGAGAATT GTTGGCATCA AATTATAAAC GCAGCAACTA TCAATTTGTT TCAATTGAAG 1680

CAACCGTTTT TGAAGTTGAA CAAATGTTTC GGGAGCAGCC ACGCTTAGAA GCTGTGCTTA 1740

TTAGTAAAAG TGGCCATCCT AATGGTGAGT TAGTAGGCAT TGTTCGACCA AGAGATTTAG 1800

CAAGTATTCA TAGAGAAAAG GAATGACGCG ATTGTTAGTA GTATATTTTT TAAyCaGTGC 1860

CTTATTAGTA GGGCTTGACC AATGGAGCAA ATATTTGACG GTCCAAAACA TTTCTTTGGG 1920

tGAAACAAAA GAATTCATTC CTGGATTTTT GTCGCTGACC CATTTAAGAA ATACCGGAGC 1980

TGCTTGGAGC TTATTAGAAG GAAAGATGAT ATTCTTTTAT GTCATCACAG TAATTGTTAG 2040

TGTCGTGATT ATTTATTTAT TAATTAAGAA TTATAAAAAA AGTATCTGGT ATTCTGTAGG 2100

TTTATCTTTT GTCTTAGCAG GTGCCATTGG GAATTTTATT GATCGTGTAC GTTTAGGCTA 2160

CGTAGTGGAC ATGCTCCAAA CGGATTTTAT GAATTTTCCT ATTTTTAATG TTGCAGATAG 2220

TACGTTAGTG GTCGGCGTTA TTTGTATATT TATTTATTTG ATTTTAGATG AAAAAGCAGC 2280

AAAGGAAGGC AAAAATGGAA CAAATTAACG TAACGATTCA AACAGAAAAA GGCCGGATTG 2340

ATAAAGTATT AAGTGAACAT TTACCCAATC ATTCCCGCTC GCAAATTCAA CAATGGTTAA 2400

AAGAAAAACA CGTAACAGTT AATGGTGAAA CGGTCCGCGC AAATTACAAA GTTACAGCAG 2460

GCGATGAAAT TGTTGTAACA ATTCCTGAAC CAGAAGTTCT AGATATGGTA GCAGAGGATA 2520

TTCCTTTGAC CATTGTTTAT GAAGACAATG ATGTGATTGT TGTCAACAAA CCTCAAGGCA 2580

TGGTCGTTCA TCCTTCGGCA GGGCATCCCA AGGGTACATT AGTGAACGCG TTACTTCATC 2640

ATGCGGATCA CTTATCGGCG ATTAATGATG TGGTGCGACC GGGAATTGTT CATCGAATTG 2700

ATAAAGATAC TTCGGGGCTA TTGATGGTGG CTAAAAATGA TCAAGCCCAT GAATCATTAG 2760

CGAAACAGCT AAAAGAAAAA ACATCGTTAC GTAAATACGT TGCCTTGGTC CACGGTGTTA 2820

TTCCTCACGA TAAGGGAGAG ATAAATGCGC CTATTGGTCG TTCCAAGGTT GACCGCAAAA 2880

TGCAAGCGGT CATTGAAGGC GGTAAAGAAG CAGTCACGCA TTTTACTGTT TTAGAGCGTT 2940

TTGATGCATT TACCTTAGTT GAATTACAAC TAGAAACAGG CCGGACACAT CAAATCCGTG 3000

TTCACATGAA ATATATCGGT TATCCATTAG CTGGAGATCC GTTATATGGA CCGAAAAAAA 3060

CATTGCCTGG CAATGGACAA TTTTTACATG CGAAGTTATT AGGCTTTACA CATCCTACTA 3120

CAGGTGAACA ATTAGTCTTT GAAGCACCTT TACCAGAAGT TTTTGAAAAA ACTTTACACC 3180

AATTAAGAAA TAATCATTGA TTTTTTTCTG AAGAAGAGGT AAACTCTTTT TTAAGAAGAA 3240

AAATAACTAA ATAACTGTAA CCTTTAAGTT TAGTCCCGTG AGGCTAAGAA GGAATCATGC 3300

AAAAGAACAC TAGGTGCGCT TAGTTAGTAA GTTGTGTGGG CTACATGGTA CCCTTGTACC 3360

TTTTTAAACT GTAACCAACA TCCTCCTATC CTCATACGGG TAGGAGGATT TTTTGTTGGA 3420

AAAAATAACA GGACAATTTC AATAAAAACC CACTTATTTT TCAGCTGCTC AATTGAAGGA 3480

AGAATCGCTG ACCCCAAGAC AGCGAGGACG TAGATAAAAA AGAAATGAGG AGGAAATTAT 3540

TATGCCAAAG AAAGAAGTTG TTGACGCAgT CACAATGAAA CGAGCGCTTA CTCGAATCTC 3600

GTATGAAATT ATTGAAAGAA ACAAAGGAAT TCAAGACATT GTTTTAGTAG GAATTAAAAC 3660

GCGTGGGATA TACATTGCAC AACGTCTAGC CGAACGCTTA AAACAATTAG AAGATATTGA 3720

CGTGCCAGTT GGTGAATTAG ATATTACTTT GTATCGTGAT GATGTGAAAG ATATGGAGGA 3780

ACCTGaATTA CATTCTTCTG ACGTACCAGT CTCAATTGAA GGTAAAGAAG TTATTTTAGT 3840

GGATGATGTC TTGTACACGG GCCGGACCAT TCGTGCTGCG ATGGACGCTG TTATGGATTT 3900

AGGTCGTCCG AGAAAAATCT CTTTAGCAGT CTTAGTAGAT CGTGGACATC GGGAACTACC 3960

GATTCGTGCC GATTATGTAG GAAAAAATAT TCCAACATCA AAAACTGAGG AAATTATTGT 4020

GGAAATGGAA GAGCGTGACG GCGCAGATCG TATTATGATC AGTAAAGGAA ACGAATAAAA 4080

AGGAGTGAAC AACGTTGTCA GAAAAAGAAT TTCGAAATGA GGATGCAGTC TTAGATATTA 4140

AAGACAGACC GCAAGCTTTT CACTGGGTTG GCCTAAGTTT ACAACATTTA TTTACGATGT 4200

TTGGTGCAAC GGTTTTAGTA CCAATCTTAG TGGGAATTGA CCCAGGGATT GCTTTAGTCA 4260

GTTCAGGATT AGGAACAATG GTCTATCTGA TTACTACAAA AGGAAAAATC CCCGCTTATC 4320

TTGGCaGTAG CTTTGCTTTT aTTGCAGCGA TGCAGATGTT AATGAAGAGT GATGGTTATC 4380

CAGCCATTGC CCAAGGTGCT ATGACAACCG GCTTGGTATA CCTAATCGTT TCATTAATCA 4440

TTAAAAAAAT TGGTTCCGAC TGGTTGGATA AAATTTTACC GCCTATCGTT GTAGGACCTG 4500

TCGTGATGGT TATCGGTTTA GGCTTGGCGG CTAATGCCGC AAATAACGCA ATGTATAACA 4560

ACAACGTTTA TGATTTTAAA TATATTGCCG TAGCCTTAAT TACTTTAGGC TTAACCATTT 4620

TTTACAACAT GTTTTTCAAA GGCTTCCTAG GATTAATTCC AATTCTTTTG GGAATTGTCA 4680

GTGGGTACCT AGTCGCTTTA GCTTTCGGAA TTATTGATTT AACCCCTATT AAAGAAGCTG 4740

CGTGGTTTGC TTTACCGAAT TTTGAAGTAC CTTTTGTTCA ATATGAACCG AAATTGTATT 4800

TAAATGCCAT TACAACAATG GCACCAATTG CTTTTGTAAC AATGACAGAA CATATTGGTC 4860

ATTTAATGGT CTTGaATAAA TTAACCAAGC GCAACTTTTT CCAAGACCCA GGCTTATCTA 4920

AAACTTTAAT GGGAGATGGC TTAGCGCAAA TTGTAGCAGG TTTTGTTGGT GGACCACCAG 4980

TTACAAGTTA TGGTGAAAAT ATCGGCGTGC TAGCAATTAC AAGAGTACAC AGTGTCTTCG 5040

TGATTGGTGG AGCCGCGGTG TTCGCTGTAG CTTTAGGCTT TGTTGGAAAA TTAAGTGCCT 5100

TGaTTCTAAG TATCCCAGGA CCAGTTaTTT nCAGGAATTA GTTTCGTCTT GkTTCGGTGT 5160

GaTTGCCGCA ATgGTTTGaA AATCtTAATC GATAATAAGA nTAATTTGGA TAAGAAAAAG 5220

AATTnTTGAT TGC 5233

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TnATAGTATA TTTTTTTAGT CAAAAAATCA ATAGTTTTTG CTAAAAAAAA GTAAAAAAAG 60

CTTTTTCTTG CtTTTTTTTA CTAAAAAGAA ATATACTATA TGCTATAATA GTACTTGAGA 120

AGGAGGCATT TAGAATGGCA ACTATCACAG ATATCGCAAA AGTCGCGAAT GTTTCAATTT 180

CAACTGTATC GCGAGTTCTG AACTATGATC CAAACTTATC CGTTACAGAG GAAACCAAGC 240

GAAAAATTTT TGAAGCAGCA GAAACCCTGA ATTATACGAA ATATAAAACT AAAAATAAAA 300

ACAAACAGCA GGAGCAACTG ACACCTAACC TTTCCGTACA AACAGCTCCG CAAGAGCCTT 360

CGATTGCCGT CGTTCAGTGG CGTTCAGATG ACGAAGAACT AACGGATATT TACTATATGT 420

CGATTCGTTT AGGCGCTGAA AAGCGGGCCG AAGAGTTAGG TTACAATATT CTAAAAGTTT 480

CTCAATTGGA ACAACATAAC CTTCAAGGGA TTGATGGCAT TTTGGCAATT GGCAAATTCA 540

CTCAAAAGAC GTTACAAGAG TTGCAGCAAC TGCATCCCAA TCTTTGTGTA ATTGGCAGTA 600

ATTTCCCATT GGAAGAATTT GATTCTGTAA ATACTGATTT TTATCAAGCA ACCGAGATTG 660

CCTTAACCCA TCTTTTGGAA TTGGGCCACG AAAAAATTGC CTTTATTGGT GCCGAAGAAA 720

GCGAAAATAT GTATGGTTTC CGTCGCTATA AAACACCGAC AACCAACGCT TATCTTGACA 780

TTATGCAGCA TTATCACTTG TTTAACGAAG ATTATTTTAT CTTAAAAGAA AATGGCATGT 840

TGGATGTCAA AACGGGGGAA CAATTGACAG AAGAAGCGTT AGAAAAATGG GGAAATGATT 900

TACCTACTGC GATTCTTGCT TATAATGACG CCTTTGCAAT CGGTGTGATA CATACGTTAG 960

CCGCACACGG TATAAAgGTT CCtGAAGAAA TTAGTGTCAT GGGGATCAAT GATATCTCTA 1020

TTTCTCAATA TGTCTCACCG CCGCTATCCT CTGTCCATGC CTTTACTGAA GAAATGGGCG 1080

AGACAGGCAT TAATTTATTG CACAAACGAA TTCAAATGCC TAGCATTCCT CGTAGAGTCC 1140

TGTTAAACAC AGAATTGGTT GTCCGCCAAT CGACAACTAG CCCACGCCAG AAATAAAAAA 1200

TAAGGACCGC TCCTATAAAG GAACCGTCCT TATTTTTTAT TTGTTTTGAC CAAATAATTC 1260

AATTTGTGTT AATGCTGGAA ATGGTGATGG TTCATCTGCT TGAATTAACT CTGTTAGTAT 1320

CACCCACTCC GCTGCCCGTT TCGCAAAGGT AAAGCTCTGG CGTTGCTCAG TCTTAACAGT 1380

TTTAAAAACT TCATGTGTAC CGTCGGAAAA TTTTAAAGTC ACTTGTTGCC AATAATTATC 1440

ATGGGGAAAG TCCGCTCGTA ATGTTAAGAT CACTTTATCC AACAAGACTT CACGCCCAAA 1500

TTCAATTTTT AATGCGGCAT CTAACTGCTG ATTAATCCCC CATGATTGAT AAGGATACGG 1560

CCCATGATAA AGATTAGCGA AGGTACCATC AATCGCATTA CAAGCAAAAA AAGTGGCATC 1620

ATTTCGCGTT TCCACGTTGG CAGATGCATG AGGATACGCA CCAGTAAAAT GTTGTAAATC 1680

ATGTGGATTT AACGCCCAAT TACGATAACT CTTAATTTCT TCTTTAGTGG CAATACGCAC 1740

ACTTATATAA GGTTTCTTGG TTTCAAAACG ATACGCTGCT CGCGCTTCGA TAGCGTTTTC 1800

ATTTTTTATG ATTGGAAACG TCCATTTTTG TTCTGGAACA TAAATCAAAC TGCTGTCAAG 1860

CGTAgcATcT AACTTCACCA TTAAATAAGT ATTGGGCGTA TCTAAACAAA CTTGAATCAC 1920

ATCGCCGTCT TGTAATTGAC AATCCCGAGC AGCTAAACAA ACAAAATCTT TTCCTGTAAT 1980

AGTTAACTCT TTCAAAGrAT CTGAATCATC TATCTTAGCT TTTCTAACTT CTTGtTCTTG 2040

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AATAAATTTA TGATTTTTTC TGATCATCTT CATCCATTTT CGATTCCGAC AACTGGCCTC 2400

TAAAGCCCGG TATATCAACA TCGAAAATTA AAAAATCGTC TAAAAACAGC TTGTGACAGC 2460

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GGAATGCCCC AAACGCTTTG AAACAGCATA GATATTGTTG TTATGCTCAA TCAAAAAAGC 2640

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AAAACCTAAG TCATCCCCGA TCGTTTTTTG GGTCTCTTTC CATTCCCTCA AGTCTACTAT 2820

CGTTTGCTTA TCTAGAGTAA TCGTTCGGAT ACTTGAAGCA TTTTTTGTAT CTGAGAAATC 2880

ATAATCTGTT CTTGTTCGAA TATAGAGTGA TTTATTCACG CAGCAAGTAC CTTTATGAAA 2940

ATCAATATCT GGCCATTGTA GCGCAAAAAG TTCTTCACTT CTTAGTCCAG TTACGAACAA 3000

AAAGCGCATC ATTCGTTTAT AAAATGCTTC TTGGAAATCA CAGCGATATG AACAATTATA 3060

TACTTTCTTG AATTCATCAA CAGTCCAAAA TGCCACAACC GATCGTTGAG TTCTGATTTT 3120

CCCAATAGTA TCTACTGGAT TCTCATCAAT GACTTCCAAA ACCATCGCAC GTTTAAAAAT 3180

AATCCGTAAC TTATTAAAAA TCTGCTTAAT ATAATTATTC GATAGCGGAC GTATTTTcCC 3240

TTCTTTATTC GTGACAAAGC ATTCTTGAAC AAGAAATTGT TGAAmCTCTT GAATATGAAT 3300

CGGTCTAATT TTyTCCATTT GCATTTTCCC GAAATAAGtA ACGCGCGTTT TAAAGTCTTA 3360

TCAGTTTTTA CATAAGTTTT CTCAATCGTC CCAAGCTTAT ACCAAGGGAA AAAATACTTC 3420

TTATAAAATT CTCGAAAArT AaTTCCTTGT AAATAAATCT CTTGaGAGTC AGAGTAATTC 3480

TTTTTTAATT CTTCCATCGC ATCTTTTGCT TCTTTTTGCG TTTTAAATCC TCTTCTAGTA 3540

GGTTGTATTC TCTTTCCGAA ACGATCATAG CCCAGAGTTA AAGAAAAATA CCAAGTCCCC 3600

CTCTTTTCAT CCTTATACAC ATTTGCAATT CTTCTCATCA GTATTATTCC TCCCAAGAAA 3660

TGTGTAAGAC TTCTTCAATG ATACTGACGG GTATTCGTTT TATTTTTTTA TTTTTGTAAA 3720

AAGAGTACCC TTTAGTAATT AAAAGTGTCT TACATTCCTT GAAGATTTTA TCAGCGTAAT 3780

ACTGTGAAAA ACCCAACTTT ATTATATCTT GCCGAGTGGC TGTCTTCATT CTACCACCTT 3840

CTTTTTCAGC TGTCAGCTCT TATAAAAAAT GTATTCATCT ACCAACTGCT CTTGTCAGAA 3900

AGCACATAGG ATTTTCACCT CTCCCCAGTA ATGGCGAGCC AATTTAGTTA CGGAAGTATC 3960

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AAAAAAGCAA CTTCGTGTGT AAGAAAGTCA CTTCTTTCAG TAACTGATAT CcAAGCTTAC 4200

AGCATCTTGC CTTTCTTGTT TTGAAATATT TCCATtGCTC AwGGrCAACA GATTTGACCA 4260

ATGTTACTTG ATTCTTCGCA TTCTCTCTTG CGTAGCTATC ACAATAAAGA TAGTCTTtGA 4320

ATCcGCyACA AAGAaCTTCA GTGCTtAGGA AaCTTACGAT TtGGCtAATT AyCGaTGrAG 4380

TtACATCTAA GTGGTTCATG GGGAAGTAGT AAAATCGCAG AAAACTTCTT TTTATTCTGA 4440

CGTTTCTCTA CTTAAAAAAA CGGTCTTCTA GGC 4473

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CAATTGTATG TGCCATCTGC ATACGTGCTG CGGCAATTGC CACTCTCAAC GTAATAGATA 60

ATATTTCGGC ATAATCAAAT TGATTTTGAT CGAGTGGATT AATTAAATTT CGCATTTTTT 120

TCAATGCACT ACGATAACAA CCTTGAAACA ATGTCCCTGA CCCAAATTTA ATTTTAGGGA 180

TTTTTTCAGC CCCTTTTGTC TTTGTCACAT AGTTCATAAT TTGGTAAATA TCGTATTCTG 240

TAAGTTCTTT TTGAGTGATA AATTCCATCA GTAAGCGTAC ATTGCTTTCT TCACCACTGA 300

TTGTAAACCC TTGCCGCGCT TGGCGAATTA AGGTTAAATC ATATGCTTGC AGCAACCGTT 360

CGACCTGTTC CAAATCACTG ACAATTGTGT TTCGACTCAC TAATAATTCA TCTGCTAGCT 420

GCTGTGCCGT TAAGTACCCT TTGACTGACA ATAACTGAAA AATCAATACA TTGACTCGTC 480

TTTTTTGATC AGGATAGGTT TCAAATCGAT CGACATCGAT AATTTCATTT TTTAACAGTA 540

AGCGTTTAGA GTCAGGTAAA TCTAGCCAGA TTCCCTTATT TCGTTTTGAA TAAAGTGTCT 600

CATCGTGCTG TTCAAACCAA GCACGAATAT CTTCTAAATC ATACTTAATT GTTCGAACGC 660

TGACAGTAAA GCTCTCAGCT AATTCTTGCG TGGTAATACT CCCTTCCAAA TCCAAAAGCA 720

TCAATAAAAT ATTTATCGCT CTTTTGGACA ACAACACGGT CATGCCTTGT CACCTCTTTT 780

CTTTTCCCTT TACACTTAAA ACTATAGCGT TATTTTATCT GTTCCACAAC ACAAAAAAGT 840

TGCACTTATA AAAGTGCAAC ACTTCTCTTT TCATACAAAA AAAATCCCTT AACAGTAGTA 900

ACTGTTAAGG GATACCACAC TATTTATTTG CATAAATAGA CAGAAACCTT CTCCACAAAA 960

GTATTCTGTC CGACACGTTA CAAATCCGGT AACTGATAGC CGTACTATCT GGTGTCGTTG 1020

TGTTTGACAA TCACTAGCCG TCAAAACGGA ATAGCCGAAG CTATCTGATT GAGTCAACTC 1080

GTCGCATAAA ACACACTTTA ACACAGAATA GTTTGGATAG CAAGTGATGG TAATTATTCG 1140

TTATCGAACC ATTCTTGATA AAAACTTTCA ACAATTTTAA CGGTTGCTAT CGTTAATTCT 1200

TTCGTCATTA CTGGGCTAGT TAACTTTTTG TCTTGTAAAC ATTGATTCAC ATGATTGATT 1260

TCATACGTAA ATTCACTAGT GAATTGTTCA GACCATTTGA CAGTGTTGCC TTGAGCATCT 1320

GTATAATAAG CACAATCTGT TTTCCAGAAA TTAGGAATAA CGATTTGCCC TTTCGTCCCA 1380

CAAATGGTCA TTTCaCTAGG TATCTTTAAA CCAACATTAA TAAAAATATT GCCCAGCGTC 1440

CCTTCAGCAA ATTTCAAAGC TAAATTACAT TGACTATCCG TCGCCCCTTG CTGATACGTT 1500

GCGGTTCCCG TAACCTCTTG AATCTCTTTC CCTAATACGT ATTGTAAGTA TTGTAATGGA 1560

TAACTTCCTG AGCCATGAAG CGCTCCACCA CCCGCTTCTC TCGAGTAAAA CCAGGGAATA 1620

TGATCCACAT TGGGATAGGC AGTAACTGAC TGAACCCATA AAATCTCTCC CAATCCCCCT 1680

TCTTGAATCG TTGCCTTTAC TTTTTGGGTA ATTGGTAAAA AGACAGACTT CTGAGCTTCC 1740

ATTAGAAAAA CCCCTTGCTC CTGTGCGATT GCAAAGAGTT CTTCTGCTTC AGCAGCATTT 1800

AATGTAAATG GTTTTTCCAG TAGGACGGGT TTTCCTTGTG ATAACGCAAG CTTAGCTGCT 1860

GAGTAATGTC CTTGATTGTA GGTGGGAATA TAAATAATAT CAATTGTTTC ATCCTTACAT 1920

AACTCTTCAT AACTGCCATA AGCCACCGGA ATCGCTAATT CTTTAGCCAT TTTTTGAGCA 1980

TTCTCTAAAC GCCTTGATGC AATCCCGCGC ACTTcAGcTT GCGCGCTTTC TCGAAGCCCT 2040

GCTACAAATC TTGGGACAAT TTGGGCAGTA CTCATAATTC CATAACGAAT TTTATCCATG 2100

TGATCGCCTC CTCTTTCACT ATACGAGAAA AACGAATATT TGGAAACCAT TTCAACAAAA 2160

AAAGAAACCG TTTCCCCAAA ACGATTTCTT TATATGTAAA TTAACGGATA CCAACGCTAA 2220

CTTTTAAAGC TTGATTGACC TGTTCCATCT CTTCACGAGA AAGTTGACAA ACCTTGTGTA 2280

GCATTCGTTC TTTATCCAAT GTTCGAATTT GTTCTAACAA AATAAGTGAT GGCGTCCTGC 2340

ACTCGTTATG GGGAATTTCG ATAAGGACTT GCGTTGGTTG CAGCCGCTTG CTTACGTTAC 2400

GGGTAATCGG TGCAACAATC AACGTTGGAC TAAATAAGTT ACCTTTGTTA TtTTGAATAA 2460

TCaGGACAGG TCGAATCcCA CCTTGTTCAG AACCAACAAC TGGTGAGAGA TTCGCATAAA 2520

AAACCTCACC TCTTTTTATC ATTCAGATTC CCTTCCCTCC TTTTCCTTTA AAAAATTATA 2580

GCATATTGTT TCTTGCAATA TTTTCAACTT TTTAGCTATC CCtTAAAATA TTTGATAAAA 2640

CCACCCTTTA AAAGTCAAAA AAAGCTTAAA CAGTCGACTC TGATATAGAG ACGGCTATTT 2700

AAGCTGACTA TTACATTTTT GTTAAAATAC TATCCACTTT TGTATTAATT AAATCAATAG 2760

CGACGTGGTT TTCGCCACCT TCTGGCACAA TGATATCTGC ATAACGTTTC GTAGGTTCAA 2820

TAAATTGGTG ATACATGGGC TTGACGACTG TCAAATATTG TTCAATCACA GAATCCAACG 2880

TACGGCCACG TTCTTCCATA TCACGCTTGA TTCGACGAAT AATACGGATG TCATCATCTG 2940

TATCCACATA CACTTTAATA TCCATTAAAT CCCTTAAGCG GCGATCTTCT AAAATTAAAA 3000

TCCCTTCAAG AATAATTACT TCTTTCGGTT CTTGTATCAC CGTTTCTGTA CTTCTTGTAT 3060

GCGCAACGTA GTCATAAACT GGCTTTTCAA TGGCTTGATA ATTTAACAGT TGTTCAACAT 3120

GTTGAATCAA TAAATCTGTA TCAAACGCAA AAGGATGATC ATAATTGGTA TTTAAACGTT 3180

CTTCAAAACT CAAATGGCTC TGATCTTTAT AATAAGAATC CTGTTCTAAC ATCATAATTG 3240

AATGATCGGG AAAATTATTA AAAATCGCAC GGCTAACACT GGTTTTTCCG CTTCCTGATC 3300

CGCCAGTAAC ACCAATGATA ATTGGCTGAC TATCTTTCAT GTATAAACCT CTTTCTTTTC 3360

AAAAACTTCA TTGTCTTTTA CTATTATAAT GAAAACTCTG AAGAATGCCA GACCTTTTCC 3420

AAGACTTTTC ATGTGATTTT TATCTTCTTA TGAAAAATCT GCCCACACTT CTTTCAATTA 3480

CAGTATACTT ATCAATAAAA GGAGAATCCT ACCTATGATT AAAAAAGTCA AAAAAGAAGC 3540

ACTTACAACG GCGCATTACG CTCkTCcTkT ATGAGGgCAG ATyCCTCAAA AAAAATGGGG 3600

GGCAGATTAC CATACCCGCG GGnATTTGGC TTTGGACTAT CCGACTGGAA GAACTTTCCA 3660

nG 3662

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

TGAnTATGAA CGACGTTATG ATGAGCACCA AGGACTAATT TTGGGTTCAG TGACAACAGC 60

CATTCCTTTA TCAAAAGAAC AACATCAAGC AATGGAAGAA AAAGCTGCCC AATTATTAGG 120

GTATGAACAA GCGCATTTAG TCAATTTAAT TGACCCGTCA ATTGTCGGCG GAGTGGTTAT 180

TGAAGCAAAC CATCAAGTAA TCGATGGCAG CATCCGCAAA CAATTAGAAC ATATGCAGCA 240

GAAGTTATTA AAATAATCTT TAGGACTACA AAGAGGTGAA TTGAATGGCT ATCAAAGCAG 300

AAGAAATCAG TGCCTTGATT AAAGAACAAA TCGAAAACTA TCAACAACAG CTTGCTGTTG 360

AAGAAGTTGG AACAGTCACT TACGTCGGTG ACGGAATTGC CCGCGCCCAC GGTTTAGAAA 420

ATGCCATGAG TGGAGAACTT GTTGAGTTTT CAAACGGTTC ATACGGAATG GCACAAAACT 480

TAGAAACAAA TGATGTAGGG ATTATTATCC TTGGCGATTT TGAAACCATT CGTGAAGGAG 540

ATAAAGTACA ACGCACAGGC AAAATCATGG AAGTACCCGT TGGGGAAGCT TTGATTGGCC 600

GTGTTGTTAA TCCATTAGGT CAACCATTAG ATGGTTTAGG CGAAATTAAA ACAGACAAAA 660

CACGTCCTGT GGAAGCAACA GCTCCCGGTG TTATGCAACG TCAATCTGTT GCTGAACCAA 720

TGCAAACTGG CTTAAAAGCC ATTGATGCCC TCGTACCAAT TGGTCGTGGA CAACGGGAAT 780

TAGTTATTGG AGACCGTAAA ACAGGGAAAA CATCGATTGC AATTGATACA ATTATTAACC 840

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GTAACCAAGT AGAAACACTT CGTAAATTTG GTGCCTTAGA TTATACAATC GTTGTGACTG 960

CAGGGGCTTC ACAACCAGCA CCATTACTTT ACATTGCACC ATATGCAGGA ACTGCAATGG 1020

GTGAAGAATT CATGTATAAC GGCAAACATG TCTTAATTAT TTTTGATGAC TTATCAAAAC 1080

AAGCCGTGGC TTATCGTGAA CTTTCTCTAC TATTACGCCG TCCACCAGGT CGTGAAGCTT 1140

ATCCAGGGGA TGTCTTCTAT TTACACTCAC GTTTATTAGA ACGTGCAGCT AAATTAAGTG 1200

ATGAATTAGG TGGCGGTTCA ATGACAGCCT TACCATTCGT TGAAACACAA GCAGGCGATA 1260

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GCGACTTGTT CTATGCAGGC ACTCGTCCAG CCGTTGATGC TGGGTTATCT GTTTCTCGGG 1380

TCGGAGGATC AGCGCAAATC AAAGCAATGA AAAAAGTTGC CGGAACGCTT CGTTTAGACT 1440

TAGCTAGTTA CCGTGAGTTA GAAGCCTTTA CACAATTTGG CTCTGATTTA GATGCGGCAA 1500

CACAAGCTAA ATTAAACCGT GGTCGTCGTA CGGTAGAAAT TTTAAAACAA AAACTACATG 1560

CGCCACTGCC TGTAGAAAAA CAAGTCTTAA TTTTATATGC GTTAACACAC GGCTTTTTAG 1620

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GCAAACATGC AGACTTATTG GAAACCATTC GTACAACGAA AGACTTACCA GATACTGATG 1740

CATTAGATGC AGCGATTACA GAGTTTTCTG AAATGTTTGC AGCGGCAAAC AATAGCGGAG 1800

ATTCAGCCAA AGAAGCTTTA GAAAAAATCG ATAACGCATA AGAGAGGTGA GCGACATTGG 1860

GTGCTTCATT AAACGAAATC AAACAACGCA TTGCATCAAC AAAAAAGACA AGCCAAATTA 1920

CCAAAGCGAT GCAAATGGTT TCTGCAGCCA AATTGACCAA GTCAGAAGGC GCCTCTAAAA 1980

GCTTTCAAGA ATATTCTTCA AAAATTCGTA GTGTCGTTAC GCATTTAGTA GCTGCTCAGT 2040

TAAGTGAATT ACGTGAAACA GAACAATCTT CTCTTAGTGA AGGGAACTAT CATGTGATGT 2100

TAGCACAACG ACCTGTCAAA AAAACAGGCT ATATCGTTAT CACTTCTGAC AAAGGGTTAG 2160

TTGGTGGCTA CAATAGCTCA ATCTTAAAAC AAACCATGAG TATGATTCAA GAAGACCATG 2220

ATTCTAATAA AGAATATGCC TTAATCGCTA TTGGTGGTAC AGGGGCGGAT TTCTTTAAAG 2280

CACGCGGAAT CGATGTTTCC TATGAGCTAA GAGGCTTAAC GGATCAACCA ACGTTTGAAG 2340

AAGTCCGTAA GATTGTGACA ACGGCAACGA CTATGTACCA AAACGAAGTG tTnGATGAAT 2400

TGTATGTTTG TTATAATCAC CACGTTAACT CACTAACGAG TCAGTTTCGT GTGGAAAAAA 2460

TGTTGCCAAT TACTGATTTA GATCCATCAG AGGCGACCTC TTACGAACAA GAATATCTTT 2520

TAGAGCCTTC ACCTGAAGCA ATCTTGGATC AATTATTACC ACAATATGCA GAAAGCTTAA 2580

TTTATGGGGC GATCATTGAT GCGAAAACAG CAGAACATGC TGCTGGGATG ACCGCCATGA 2640

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GACGTGGAAT TTTCATTAGA TCAATCCTTA CCCGATATTA ACAACGCTTT AGTCGTTTAT 2940

AAAAATGGCG AACAAAACAA AAAGTAGTAC TTGAAGTCGC TTTAGAACTA GGTGATGGAG 3000

TGATTCGTTC TATCGCTATG GAATCGACAG ATGGTTTACA ACGTGGAATG GAAGTTATCG 3060

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GTGGTGCCGG TGTTGGTAAA ACCGTCTTAA TTCAAGAATT AATTCATAAT ATTGCCCAAG 3360

AACATGGAGG GATTTCCGTC TTTACTGGTG TTGGTGAACG GACACGTGAA GGGAACGACC 3420

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TGCAAATGGC ATTACACGTG TCTCTAATTT GAAATATTTA GATCGTGGCT ATTATGAGTT 6420

CCATAAAAAA CTTCAAAAAT TAGGCGCGAA CGTTGAACGT GTCAATGATG AAAAAATTGA 6480

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ACTGCTACCG ATACCTTGAA GCAACATGCA GTTATTCAAT CATTCCCAGA AAAAGACCAA 6960

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GAAAGTTTCT TATTTATTTA AGCCCGTCTG GCAGTTTTTC GGCGTTGTCG GCTTACCAGT 7380

AATTATGGCG GGGATTTTAT ATTATTTATT AAATCCAATT GTCGATTATT TAGAGAAAAA 7440

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TACCATCATT AAAAACGTCT CAACGTyCAC AGTACmAGGA ATTGGTAATT tCnTTGGGGC 7740

GGTGGCTACG 7750

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GCCCCCAGAA TGTTCCAAAA GAAATTTTGT ATGCATTTTT AATTGTGCTG GCGATTGATA 60

GGGCTGGTGA CTTACTGAGT TGATATAATC AGCCAAACTT TCCGCTTTCG TTAACAGTTC 120

TCGATTTTGT TCATTCCAAT TATTGCCAAA GTCTTTAAAC GGATAAAGTA AACCTAGCTG 180

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GCAGTTACTG GAAAAAAATC TATGCCGCTT GCACTCATCG AGAAAGAAGG AATTGAATTA 1020

TCTTTTGGAA TCGCACCGCG AATCCCTTAT CTCGACGCAg TGGAACAATA TATTCAGACA 1080

CACTAGATTC ATAAAGTTTT GAAAGTATAA CAAAGGAGTT GCTATTTATG CCAACCGCAA 1140

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GCTTAGTGCC ATTAAAAGCC AGTGATGACA ATCGAAAAGT CGTAGATAAT TACGTCAAAG 2040

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CTTCGATTTA ACTAGAATCT TACGTGTGAT TCGACCATAC AAAGGAGGCA TTGCC 8395

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

AAACTATATC ACTGGAaTCC mAAAGGCGGT ACCAGCACTT GGTCATTGGA TAAGAAAATG 60

CAAGGAAAAA CGAATTTACA TTTATATGAA TTAACAGATC AAGGGCGTAT TGACAAAGGC 120

GCAATTGCCA CTACAAATAA CCAAGTGACC ATCCAAGCCG AGGCTAATAC ACCGTATGTC 180

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GAGGTTAAAA AAGATGCCAA TGGTGATTAT GTCTTTAGTT CAGAAAAAGA AAGAACCGAA 360

ATCAAACAAG ATATCAATCT TCCTAAACCA GGAAAATATA GTTTGTATCT AAACACAGAA 420

ACACATGATC GTAAAGCCAC AGTAACTGTT AAAATTGGTG GTAAGaAATA TACGCGGACA 480

GTGAATAATT CGGTTGCCCA AAACTACATT CAGGCAGATA TTAACCATAC AAGCAGGAAA 540

AATCCGCAGT ATATGCAAAA TATGCGAATT GATTTTGAAA TCCCAGATAA TGCCAAAAAA 600

GGCTCGGTGA CATTAGCGGT TGATAAAGGC AATTCCGTTA CAAAATTTGA TGATTTACGA 660

ATTGTTGAGC GTCAAACGGA TATCATGAAC CCAGACAAAC AAACAGTTAT TAAGCAAGAT 720

TTTGAAGACA CACAAGCAGT TGGGTTATAT CCGTTTGTTA AAGGCTCAGC TGGTGGTGTA 780

GAAGATCCAC GGATTCATTT ATCAGAAAGA AATGAACCTT ACACACAATA TGGTTGGAAT 840

GGAAACCTTG TTTCAGATGT ATTAGAAGGC AACTGGTCCT TGAAAGCCCA TAAACAAGGA 900

GCAGGATTGA TGCTTCAAAC AATTCCGCAA AATATTAAAT TTGAACCGAA CAAGAAATAT 960

ACGGTCCAAT TTGaTTATCA AACTGATGGT GAAAATGTCT TTACTGCTGG GACCATTAAT 1020

GGGGAGTTGA AAAATAACAA TGACTTTAAG CCAGTCGGTG AGTTAACTTC GACAGCAGCA 1080

GATGGTCAAA CCAAGCATTA TGAAGCAGAA ATAATTGGGG ATGCTTCAGG AAACACTACG 1140

TTTGGTATTT TTACAACAGG TGCCGATAAA GATTTCATTA TGGATAACTT TACGGTCACA 1200

GTGGAATCAA AAAAATAAAT TTAGTCTATC TAAGCAACTt GGTCTACAAG TTAAACGTAC 1260

TTGTAGCCCA AGTTGCTTCT TTTATGAAAA GAAGCAAGGT CTAGTGCCTC ATTTTTATAC 1320

TGCaGAATAA ACCGACACAT TTTTTAAAGT GTCAGGCTTC TTTGTGTATT TCATCAAGAA 1380

CGAATGGACA AACTTGCCTT TTGCCACAAA TCGTTTaCmA TTACmATGAT AGGCATAATT 1440

TATTTAGAGG TGAAGTGATT GAAGAAATAC AATGTTGATT GGAAyTACTG GGTTGTCCGC 1500

TTTTTATtTG TAATGGCGCT GATTGTTGGC TATTTATTAA TCACGAATTA TCAGCACTTT 1560

GTCCATAGTG TTTCGGGTTT ATTAGGCATC TTATCCCCAT TCATTACTGG GTTTGTGATT 1620

GCTTATTTAT TGAGTGGAaG TCAGAAAAAA ATCGAGGGAT TACTAGAAAG AGTTCCTTTA 1680

CCAGTCGTTA AAAAAGCGAA ACACGGCTTG AGCGTACTCC TTTTGTACCT GATTATTTTG 1740

TTTATTTTTG TTTTGACATT AAACTATATC GTTCCGCTAC TCATTAGTAA TTTAGTAGAT 1800

TTAGCAAACT CTTTACCCAC TTTTTATGAT CACATGGTTC AGTTTGTAAT GAGTTTAGAA 1860

GATAAAGGGA TTTTAAAAAC AGCCGCGATT GAAAAATATT TAAATAGTGT CCTTAAAGAT 1920

TTGTCGCCAG AACGTTTTTT AAATcAATGG ACACAAGCGT TGTTTTCATT AGGAACGTTG 1980

ACTAAAAATG TTTCATCATT CTTTTTAAAT GCATTTTTGA CGTTGATTAT CTCAATATAT 2040

GCGCTGGTAT TTAAGCAATC TATTTTGACA TTTGTTGAAA AGGCTGCCCA CAAATTGCTG 2100

TCTGAAAAAG TGTACAAGCA AACACAAACT TGGTTAAATA CAACGAATAA AATTTTCTAT 2160

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TTAAGTATTT TGAATGTGAA ATTTGCTGTG ACTTTGGGGA TTTTATTAGG TATTTGTAAT 2280

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ACAGGTGGTG TTACTCAAGC AATTACGGTG TTACTAGTTT TATTAATTTT ACAACAAATT 2400

GACGGCAATA TTATTGGTCC TCGAATTATG GGAGATGCCC TAAATGTCAA TCCGATTTTA 2460

ATTATTGTTT CAATCACGAT TGGGGGAGCG TACTTCGGCG TCTTAGGGAT GTTTTTAGCA 2520

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AATGATAAGA TTGTAGATTC TATTGAATCC TAAAGTAAAA CTTTTCGTCG CGCGTTGACG 2640

AAAAGTTTTT TAGTGGAAAA GAAAGTTTAA TTATTTGGAA TTTTTGaTAT GCTATACTTA 2700

AAGTAAATAA AAAATCAAAA TTGAGGTGAA TAGATGCAGT TTTTAAAAAA ATATGGCGGC 2760

TATTTTTTAG TTTTAGGGGT CTTACTTGAT TTTTTTACAC CTTATTATGT CGGATTCAAA 2820

GATCAAGGTT ACAATCAATT GACAGAAGTA ATTAGCTTAT TAGGTGATGT GAATAGTCCA 2880

GTTAGGGAAA ACTTTAATCG GTTAACTATC ATTGCGGGAA TGTTGATGTT AGCAAGTTTA 2940

CCTAGGATAT ATGCTATTTT TTCCAGAAAA ACGAAAAAAG GTGCTTGGTT AGTAGTGGCA 3000

ATGATTGGCG CTTATGGTTT ATTTGATTGT ATTTTCAGTG GGCTCTTCAG CGTAGACACT 3060

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TCAAGCGCTG GCACAGTTGC TGCCGCGCTT CATAACGGAG GATCAGCAGT CGGTTATACA    3120
GGCTTTTTGT TGTTATCAGG CGTCTTAACC ATTATCTACA GTAAATACGG TTCGCAAAAA    3180
AATAAAAACC TTTTTGGCTT TTTGTTTATT TTATGTATGC TTGCAGCCGG CTTATATGGC    3240
TTAGCAAGGA TTCCACAGTT GCAACAGGTA AAACCATTTA ATTATTTAGG CTTATGGCAA    3300
AGAGTGAGTT CaTTTTGTAA TTATCTACCA ATGCTGGCAC TGTGtTTACA AACTAAAACC    3360
AATGACAAAT TTGATTGAAC ATTTGTCATT GGTTTTTTAC TAGTTAAAAT TGTCTGGTAA    3420
TAACTTAATT ATTGGCTACG GTGACTTCAC CAGTAACAGT GGCACCATCT TTTTCTAAGT    3480
CAGCAGAATC TTTGTATtCT TGTTTATCAA AAGTAATATT GCCATTAACT TTGGTACCAT    3540
TTAAAGTAAA GCCATTTGCT TTCACCTCAA TATCACCTTT GACAGTCCCG TGAACGATGT    3600
TGAAATTTTC AGAAGAAACG ATTAGCTTAG GAACCGTGAT TTCATATTCA GCAGTTACTT    3660
TTTTATTATC ATCTTGGGAA TAAAGTGCTA ATTTACGATA GACATCGTTG GAATCTTTCC    3720
CCTTATCATG GAAAGTACCA GCAACTGTTA CCTCTTTATC AAAAGTGACA TTGTCAGTAG    3780
CTGCGACAAT CCAATTTCCT TTATCACTTA ACGCCATTtC GAGCTCTTCA GGCTTGGCAC    3840
TAATTGAAGC ACCAGAGACT ACTTCTGTAC TTGAATTAGC TGTTTCTTTG CTACTAGAAC    3900
TACTATCTGT TTTTTTATCA GATGAACAAG CACTAAGCAA CACAAGAGCA GCAGTTGCCG    3960
TCAAAACAGT GGTGAGTACT TTAGACATTT TCATGAAAAT CCCTCCAAAA AATTTATTTA    4020
TTTCTTCCTT TATCATAACT GATTCAAAGG GAAATGAGTA ATCATACACT CAAAGATTGA    4080
GAAGTTTGGC TAATGGGAAA TTAGGCTTAT TCTCTCAAGA AGGTTCAGGA AATATTCAAA    4140
GTAATCATTT CTTTTTCAAA TGTTCCTTTT CTGTAGTAAG CTAGTAATAG ACAGAATTTA    4200
AGGAGGAGAT TTTGATGCCT TGGAATATGA ATGATTATCC TACATCAATG AAAAATTTAG    4260
CACCTTTGAT TCGGAAAAAA GCGATAGATA TTGGCAATGC GTTGCTTGCG GATGGCTACC    4320
CTGATGATCG CGCCATTCCA ATTGCGATTA GTCAAGCGGA GAAATGGTAT CAAGAGGCAA    4380
GTGCAGCAGA CAAAAAGGCA TTTGAACAAG AAGCAAATCC TACGAAACAA GATTCGCATA    4440
AACAGGATAA ACATGCGGGA AAATTATTAA CGGCGGCTGT CAACGTTwmA TmTAAAGACG    4500
GCCAATGGTT GGTGATTTCA GACaGCGCTG AAAAAGCAaG TAATACATTT CCCCACAAAC    4560
mAGAGGCGAT TGAACGAGCC CaAGAAATTG CTCGGAATAA GCAAACAAAG CTGAAAATCT    4620
ATAAGCAAGA TGGTACGTTA CAAGAAACCA AAGAGTATAC TGAATAATTT TTCGAAACCT    4680
TGATATTCCG TTGCAATTCA AGAAACGGTT ATCAAGGTTT TTTTGCGAGG GAGAAATGGA    4740
CAAGTAAGAA AAAATAACAA AAGTTAAGAA TGAGAATAAG ACTTGCTTTT CTAGTTTTTG    4800
GTGGGTACAA TTACACTAAT TAAGATAAAA AATCAAAATA ATTGAGGTGC TACGACAATG    4860
GAAAAAGCCA ATCTTGATTG GAATAATTTA GGATTTTCTT ACATTAAAAC GCCCTTTCGT    4920
TATATTAGTT ATTGGCGAGA TGGCAAGTGG GAAGAAGGCA CGCTAACAGA TAACAATCAG    4980
TTAACGATTA GTGAAGGTTC GCCTGCTCTA CATTATGGCC AACAATGTTT TGAAGGATTA    5040
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AAAGCGTATC AATGTGCAGA TGGTTCTGTC AATTTGTTTC GTCCAGATGA AAATGCCAAA 5100

CGGCTACAAA AAAGTTGTGC GCGTCTACTG ATGCCACAAG TGCCAGTAGA AACCTTTGTT 5160

TCTGCATGCC AAGAAGTGGT GAAAGCCAAC CTTGCTTATT TACCGCCATA TGGAACGGGC 5220

GGTACGTTGT ATCTTCGCCC TTATATGATT GGTGTCGGCG ATAATATTGG CGTAnACCTG 5280

CCAAAGAATA CATTTTTTCC AATGATTGCG TGCCGGnTGG TTCGATTTTA AAAATGGGTT 5340

AGCACCAACC AACTTTATCG 5360

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

TGGCCATGCT TATCTATTAA TTCCCGCTGT GTTTATCGGC ATTTGCCTTT ACTTTATTTT 60

TAACTCACGT ACGATGCAAC GAAAGAAGGC AAAAGTGTCA CGGCTAAATT GTCGGCGGGC 120

TTAGGGCTGA ACTTATTAAT TGCTTTACCA GCCTTTCTAT ATTTATTATC aGTTGGCACA 180

GCGCAAATAC CTTATGTGCT TTTTCTGTTC TTACTTTTTC TATTGTTAAT GGATCTTTTG 240

CTGACCTTTC TATTTGCTGC TTACGTCTTG TATTCATGGA TGTACCAAAT GATTCCTTTA 300

AAAAAAGCGG TTGATTATAT CATTGTTTTA GGTTCGGGAA TTCGTAGCGA GGAAGTACCT 360

CCACTTTTGA AGAGTCGGTT AGATAAAGGG ATTGAATATT ATGAAAAAAA TCCCACTGCT 420

AAATTTGTAG TCAGCGGTGG TCAAGGTCCT GACGAACCTG TGGCCGAAGC TTTCGCAATG 480

AAAAAATATT tGCTTTCACA AAATATTCCT GCAGAAGCAA TTTTGATGGA GGACCAATCC 540

ACAACCACTT ATGAAAATAT GgTtGTTTTC TAAAGCAATA ATTCAGGCAG ATTGGCAAAA 600

GATGCCgtCt GAtTCTAAAc AACCCTCTGT tATTTTTtCA ACAAATAACT ATCATGTCTT 660

ACGAGGAGCT ATGTATGCCC aTCGTGTCGG CTTAAAAGCT GAAGGTGTCG GGGCGCCAAC 720

TGCCTTATAT TTTTTACCAA CTGCTCTAAT CCGAGAATAC ATTGCCTTAC TGGTTCATGA 780

TrAGCGAATT GTGCTTTTTG TTTTTCTACT TGTCACTCTT CTTTTAGGAA TCAGTATCTT 840

ACCCATCTAA AAAAACArcG ACtCACATTT TTGTGAGTCG CTGTTTTTAT TCTTTTAATA 900

TAAAAAGGTT TAATGAACGT AATTGGCTAT CAATGCAATC AGCCATAAAT GGAGCGGATA 960

GAATCCGTAA AATAAATATT TGAAAAATGG TGCTTTGCTC CCTCTCTCAC CATTGTAAAG 1020

CGATATAAAG GGTAACACAG TGATAAACAT AAAATCAGAA TTATAAGCTA ACATTTCAAT 1080

TGTCGTTGGC CAATCTCCCA ACCATTGAAA ACTTGTAACT AAGAAAAAGA GCGCTAATGC 1140

ACCATATAAA CAGTTCCGTA AGACAAGTCT CTTTCTGGcT AAATACGTAA tCAACATAAA 1200

AGGTAACATC ACAATGCCAC CTTCAGCAAA CATTGCTCCT ATTCCTAAAA TTGCTAGTAT 1260

ACTAATCAAT AAAACAATTT TTAAACTGAT TTTTGGcATC TCTAGCATCG CTTTTGTCAC 1320

AATTAmCATA CTGACACCAA GGGCTAAGGT GAAGAAAATA TTGTTGTGAA CAGCGACAGy 1380

GGaTTATTCA CTAAATGATT TAGAAGCGTA TTTCCAACAA ACATGATTGC TGCCCAAATA 1440

TACAAACGAC CATTGTAACG aTAAACATTC CGTGTATAGT TGAAaCCTTC TACAGCCATG 1500

TAACCmAAAA ACACACCGAC ACmACGAGTA ATTACATGAA AAATCAGTGC CCATTCTGGG 1560

CGGAACAAAA TAACTAATAT GGGCCAGGAC CATTAACCCC ATCATCAATA ACTTTAAGCG 1620

ATTTGCGTCC AGGAATCGCC CCTT 1644

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5926 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

nCCnCGTcAC TArGAAtCAG CTACgTCACG AAGGGAAAGT aCCTGCCATT GTTTACGGTT 60

ACCAAATTGA AAGTACACCA ATCTATTTTG AAGAAAAAGA CTTATCAAAA ATTTTACGCG 120

AACATGGTGC TAACACCGTT ATTAAAATGA CAGTTGATGG CAAAAACATC AACACATTAA 180

TGTCGAAAGC ACAGTTAGAT ACCTTTACTG GTCAAATGCT TCATGTTGAA TTCTTATCTG 240

TAAATATGAA AGAAACAACA GAAGTCGAAG CAGAAGTTCA ATTAATTGGT GAATCTGCAG 300

GTGTGAAAGC TGGGGGTACC TTAGCTCAAA ACTTGTACAC TGTTTTAGTG GCAGCCACAC 360

CAGACAAATT GCCAGAATCA ATTGAAGTAG ATATTACAAA CTTAGAAATT GGTGATGCTC 420

TTACAATCGC TGATTTACCT GAACACAAAG ACTATGAAAT TTTAACTGAT CCAGAAGAAC 480

AACTAGTTGC TATTGTTGAA GCACAAACTG CTCCTGAAGA AGAAGAAGGA ACAGCTGCTG 540

AAACGACTGA ACCAGAATTA GCCGAATAAA GAGTACACTT TGTTCAGCT GATTCTCTTA 600

AGTTTTAGAA ATGGGATGTA CGTTGAAACA ACGTACGTCC CATTTTCTTT TTACTGCATG 660

TCGTGATTTC TTCACATAAA TGATGACACC TGCAAAGCTA GGAAGCTACA GAGGAATATT 720

AAATTTTTGC TAATCTACGC AATATTTTCA AACGAAACAA TTTCTTTTTT TTAAATTTGC 780

AGTATACTAA AAGTAAGTAA ACAAAAAGGA GGTCATCCAT ATGTTTGAAC GTTTTGATAG 840

TGACCGTAGC CGCTATGCTT CATTAGGTGT TGTTTCTAGC TTACCTAGTG GCTTAATTGA 900

TAGTATTTGG TTGATTATTG ACTTAAATCT AAAAGGGGTT ATCCCTTTAA ACGACTTACT 960

TCACTTTGAT TTGTTGAACA ATAATGGCAA AGTGACTGTC CATTTTTCTC AAGAAAATAG 1020

TTCAGTAGAA ATGGCCATCG ACTTACCATT TAGTTATTCT ACGGCATATC CGTCGCGAAT 1080

TTTTGCTTTT GATGATGGCC ATCGTGAAAC GATTTTATTA CCTGCAGAAA TGTTAGAATC 1140

TTAAATAATT TCAACAAAGT AGCCTCAAAT TCCGATTAAA CTGGAATTTG AGGCTACTTT 1200

AATTTCTTTT AGTTATTCTA CAATAATTTG TTTACTACTT CCTGCAGCAT TTTCAAAATT 1260

AATAGTAAAG GTTTCTGTTG CATCATCATA AGTGATTCCG TCACTTTGAC TAATTACTGT 1320

GCTGTAATCT TTTGGTATTT TTAAAGTCAG TGTCTTAGTT GTTTGTGTGG GATCAGArAA 1380

AGTATACGTT TTTTGGTGTT GTTGTGTCTT TCTCATTAAA GAAATAGCTT TATTTGAGGT 1440

AATCCCTGCT ATTGTACCGC CAGTTTCTGA CCAAATGTTA ACTCCAAGAT AGCCTTCTTC 1500

TTCTTGCTTA ACTGCTTGAA TTTCTTCTGT ATTTGAGAGA ACTTCTACTG TTTTTTTGGC 1560

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ATCACTTGGA AATGCTTCAT TAATTGCTTT ATAGGTTCCT TTTCTAGTTT CACTTTTAAC 1740

ATTTACCGTT GTTTCTTCTG GAAAATAATA ACCCATATTA GCATTGGAAT GATCCGACTT 1800

TAGTAATAAC CATTGTTTTT TACTCGTTTC ATTTTTCTCA TGAATCTCCC CAATATTTGA 1860

TAGCACTTGA TACTGATACG CATCATTTAA CAAACGATTA TCAACAACTG TCTCAATCGA 1920

AGCTTCTGTA TCCCCTTTAA TTCCTGCGCC TAATGCGATA ATTTGCCCAT TTAATACAAA 1980

CCAAGATTTT TTAGCTTGTA GGTTCATAGG TAAAAGTTTC CCATTATTTT TGGTCCCGTC 2040

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CTCTTTCGAT GTGATTGTTG TAAATGCTGA AACTTCATCT GCCAAAGAAA TGGTATCTAC 2160

CGTTGTTCCT GGTAGTCGAT AGGGATCTAC AGTTGGCCAA TAGCTGGAAT TAAATTGAAC 2220

CTCGTCATCA TTATATACGT ACATCATTCC GTCACCAGTG TGCCAGCCAC GTTTATTTTC 2280

TTTATTCCCT GCTTCAAAAG ATGCAGTGCG CTTTGAATAC AAGCCTAGCC CAAACATATA 2340

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CAAAATTTGT CCAACCCCTT TCACCAAAAC ATTGCCATAC GAACCTGTAT AAGGAATGTT 2820

ATTGTGCTGG ATAAAAGAAC CATCTTGGTA AAAACCATCA CCTTTTGTGA CTAATTTAAA 2880

TACATCGACG ATACTACTGG ATGCTTGGTT AATTTTCCCG CTATCCTTTT GTAAAATTCC 2940

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TGGGACATAA CTGCTCAGCG CATTTGTATA GATTTGTTGC TTTTCTGGAG AAACTTTATC 3120

CTCTAAAATC ATTAGAATAT TAAGAAACTT CTGTGGCACA CCAATTTGCC AGTCCCACCA 3180

ATTTCCATGG TACTTTTTCC CATCATATCC TTTTTGCGTT ACCATAAAAT CTAAGCCATC 3240

AATAATGGTT GCTGCCAATT TGTCATCTTG GTAAAGCGTA CTCCCCTTCG TTCCATAGGn 3300

TAACGCTAAT TTTTGCAATT TGGTAAATTG AGTCGTTAAA TCAGCCGATG GCGTATTGCC 3360

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ATCAGGATAA TGAACCTCTT CATTTTCATA AAATAATTGA TCATTCAGGA ATGTTTGAAT 3720

TTTTTTCCCA TCATAGCGAA CTAGCAGTTT ATATTGTTGA CCACTTAGTA ATGTTGGTCC 3780

CGGAATATTA GTTAGCCATT TACCGCCTGG TTGTCCTAAC TGCCAGCGAC CGTCACGATT 3840

ATAAGCAAAA GATTGCCATT GACTCGTCTT TTGTTTATCT CCGCGAAAAA CCAATCCGAA 3900

GTTACTTTGC CCTTCATATA AAAAGGTTAG TTCAAGATCT CCTGAAGATT GTTCGCGTGC 3960

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ACCAGCAGAA TCATTCTTTT TTTCTGCTGT TCCTACCAAA TCTTGCCAAT GCCCAACTTG 4080

ATTGGGGAAA TCTGAAATGT AAGAGGGTTG CTCAATCGTT TGGCTCGCTT CGTTTTCTTC 4140

TGCAAAAGTA AGGGTGGTTC CCATAAATCC ATTCGTCAAA GCAGTAAACA GTCCGACCAG 4200

CATTACCCAT ATTTTCCTGT TTTTCATTCT TTCTCCTCCT AAAAAATTAT CGTAAAACGC 4260

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AATTAAAATA ATCCAAATCA CTCGTGTGGA ATTTAGTTTC TTTTGACCTA ACATCCAATA 4440

AGTCAAAAGA ACAAGTAAGA TTGGAACTAA GGAAGGCAAA ATCGCATCTA ACGTATCTTG 4500

AATAACTAAT TCGACCCCGT TCTTTTTATA AACAAAAGGA ACTGTCGCCT TGATAACTGA 4560

AGGAATTAAG GCACCAATCA CAGTcACACC AAGAACAGTT GCTGCATTCG TAAAGGCAGA 4620

TAACTTGTCT TTTAAGGTCG TCACTAGTTT GACCCCTTGC TTATAACCAA GTGGTAAGAG 4680

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GAATAAAGAG TCCCCAACGC CTGcCAAAGA ACCCATCAGA GCTGTTTTTA GCGCAATAAT 4860

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CAAAATCACC ATTTCCTGTT GTTGCTTGTG TCGTGCTTTT TGCCCCATCA CGTTTAAATA 5220

CAAGCATCGC TGCTACCATC CCAACTATCG AAACACCTAA CATTGGAaCT TTTAAATAAG 5280

CCGCTAAGAA AAAGCCTAAT AGTAAATAGG GGATATATTG CTTCGTTGGC AAGTAACGTA 5340

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GAATCCGTTT TACTTGCATC TTATCAATCG CTTTATCGAC ACTATGAAGT AAAAAGACAT 5580

TACAAAAACG GGCGACTACA TCTAGTTGCA ACATCAACAG AGmAACAGGA ACAGCTAAAC 5640

CAATGCCATA CTCCGCTCCT TTTCCAGAGA TTACAGCGAA AGCGGTTCCT AAAACAGCCC 5700

CTGTGAAATA ATCAGGTACC GATGCTCCAC CAAAAGCAGC AATTCCTAAA CGCATTAATT 5760

GAAGAGTGCC GCCAACCATT AAACCAGTTT TTAAATCTCC CATAATACAT TCCAGAAATC 5820

ATTCCAGCAA TAGCTGGTTG CGTCAACGTA TTTGAAATAA GTGGTCATTA ATAGCnATAA 5880

ACGCTTAATA GTAATTAAGA TAATTTGATA CGGCTGCTAA ATGCTT 5926

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GGATATaGAA aCCCAACGGT TnCAAACAGC AAAAAAAATG GCaAAAATAT TACAAGTTCC 60

GTGGACAATT TTTTTTGATG AAGAAGTACT CGAAACGTAT GATTTTTGAT aGGrGGATAA 120

AAtGACaACC AAAGAAAAAA TTGAATTTAT CAAACAAGTA ACACyTCATT CAGATTCAGA 180

AGTAGAGAAA ATTATTAAAG GAATGAGCGA TACCAGTATT AACCGCTGGT ATGAAATAGA 240

GAAATATCGC ATTGATCAAG AATTAGAAGA AGCGGTGTTA ACTATCTATT GTTAAAAGAA 300

TACACCTATA TCAGTCGGAT AGAAATAACA AATTATACGA AATGAGGTAA AAATGACGAA 360

ATCTATAAAA CTAAACAAAC AATTAAGAAA AGCAGCTTTT AAAAAAGGAT TAAGCCAAAA 420

ACAAGTGGCC CAATTAGTAT ATTTTGCACA TACTACAACA AATGGTCACT TTAATGGCTA 480

CCCAGTACCG CCAGAAAGTG CTATAGCCTA TAACGAATTA TTTAACGATA GTGAGTTGGC 540

ATTTGCATTA GGCCAAGAGT TATTGGGCCT AATAGGGCTA GCAACTGGAG TGAAAGTAAA 600

AAAAGAGCCA TTAGCGCTTT CGGTACTAAA GGAAAAAGAG GAACGAGAAA GAGAAAAAAT 660

CGAAGTGGAA AACGAAATCG ATTATTTAAT GGCGATTCCA GTTGAAGAAT TGACCGAAAA 720

ACAAAAACAG GCAATATTAC AGTATTGTAG CGAATATTCA GATGAATTGT TGTTTGAAGT 780

TTCTCTTATT TGTAAGCAAT TAGAACTAAT AGGGATGTCC TTTATGGATT TAATGATATT 840

AAGAACACCT TATTGGAAAA ATAAAGAATG GATTGaATAA AGGAGGGAAG TAATTTGGAG 900

TCAAACATTA GTATGCAAGA TGTGTCTAAG AGACTTTCTA GGAATCTATA TATGATGATG 960

GGAACTCCTA GAGAGGATAC CAAAAAAATT TGGAAGGTAT CTGAGCTTTC AAAAGCAAGC 1020

GGAGTTACAC CATGTGTTaT TAGTCGGATT AAAAATGACA CTGAAGGAAA AGAAAAACCG 1080

ACTATTGAAA CAGTTGTTAA GCTTGCTAAA gCATTAAATG TTGATCCTGC AGAATTATTG 1140

AAATAAGAGG TGAAAATAAA TGGAAAAAGA AAATATCCAA GAAAATTATC ACGAATCATT 1200

AAAAGAGCGG AAAATCAAAG ACACTTTACA AGAAATTAAA GAGAGATTAA ATGGCGTAAA 1260

ACTAACCTAA AATGAAAGGA AGTTArAAAT GAATAAGAGG AAACCACGTa GTTTATATGA 1320

AGCAAGAATT TTAGGGACTT TGTTAGTATT CTTCATACTT GGTCTAGTAA TAAAGAACAG 1380

TATTCCGTTT AACTACTTAC TTTTAATACT TGGACCTATT ATTGCAATTT GGTTTATGAA 1440

ATATGACGAT GCTAAaTATC rAGAAAaTTT AAATAAAAAT GAAAAGGAAG TGTATTAATT 1500

GAATAGAAAA ATCAGAAGTC TAATAAAAGA ATTAACAGAG GAATGTGACA AAGAAAAAGT 1560

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GTAATCTTCG AAGGAGATGA ATTTGAGATA GGATCGGAGG ATGGTAGAAC CGTCGTTACA 2940

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GAGACAAAAA AACAGCGGAG CTAATCGCTT ATTATTCAAA AAATGTTAGT CTTGCTACTC     4860
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CGACGGTAgC TTGCTTTAGG AGGrGTAATk GTgCtATCTA TTCTAAGAGG TTATAAAGAA 9120

G 9121

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

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TTGGCGATTG GGCTGACGTA AAACCTTTTT TAGAaGCAAm CAAaGAaAAA TTGAGaTTAT 11580

GTTGTAGAAA ACGATGC 11597

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

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TCCAACCAGG AGAAATCGTT GGGATTGTTG GGAAAAGTGG CTCTGGCAAG TCCACGTTGT 240

TACGTTTGTT GAATTTAATG GAACAACCGA GTGAAGGGGA GATTCGTATT GATGGCAGAA 300

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CTCTCTACTT TTAAAGTATT AAATGTAACT ATTTTAGTTC TATTTAAAAA TGAAAGGATG 23940

ATTTACATGA AAGTAGCAGT ATTAGGAGCA ACAGGAAAAG AAGGACAATT ACTTTTAGCA 24000

GAAGCTAAAC GTCGCGGGAT GGACGTGACA GCCATCGTTC GTAATGCCTC AAAAATAACA 24060

GATGGCACAC CGACCATTGA AAAAGATGTT TATCAATTAA CAACAGAAGA TATTCAAGCG 24120

TTTGATGTAT TAATTAGTGC CTTAGGATTC CCTGATGTGC AAGATTTCCC AAAATCTACC 24180

CAGCATTTGA TTGAGATTTT AACCAATCAA AAAACGCGCT TGTTTGTCGT TGGGGGCGCT 24240

GGAACCTTGT ATGTGGACCC AGAACACACA ACTCAATTAA AAGATACACC ATCATTCCCA 24300

GCAGAAATTC AGCCATTAGC TTCGGCGATG GGCGAAgCTT TAAACTTATT GAAAGAAGCT 24360

CAAAACATCC ACTGGACCTA TATTAGTCCT GCAGCCATGT TTGATGCTGA TGGTCCTGCG 24420

ACAGGCCATT ATGAAGTCGC TGGCGAAGAA TTAACAACCA ATAGTCAAGG TGACAGCTAC 24480

ATTAGTTACG CAGACTACGC CGTTGCCATG TTAGATGAAG TGGAAAGTAA TGCACACCCA 24540

AATCAACGAA TTAGTGTGTA TCAATAAaAG AAmCAAGAnA AATGGGGCTC CGTTAAACAA 24600

C 24601

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

CTTCCATTTT GGCACACAAA TTTTTmCAAa GrATTgAGCT TCAGGAAaTA ATTTTTTTAT 60

CAGGAAATTa TTAATTATTA CGAAAAAAAT GTTCATTTTC TCACAATwCa TTGgTATAAT 120

AACGTTATAT CGAAAGGAGA GAAATGAATG AGTGTAGTAT TAGTACTTTT GGGTCTATTA 180

GGGTTACTTG TCAGCGGGGG ACTGACTATC AAAGCATTAA TTAAGAAACA ACCGAAAAAA 240

CAATATGGCT ATGCCGCGTT AGCAAGTGCC GCTCTATTTA TTGGTGGGGT TGCCACGACA 300

GATTCTTCCC CGACACTTTC ACTTGATGCA GAGAGTGTTG AAACCGATGC CAATGGCTCA 360

GCCACCATCA AAGGCGAATA CGACGGCAAC AGCAAACTAA CGGCCAATGG CAAGGAAGTA 420

AAAACGAAAG ACAAAACGTT TGCTTACAAA GTAAAACTGT CCGATGAAAA AACGCAAAAA 480

ATCACTTTTG TTGCTGAGAA GAAAGATACC AAAGTTGAAA AATCAGTCGA AGTCACACCG 540

TCAAAAGAAT TTATTGCGAG CATCACAGAT TCTGAGCAAG AATTGGCCAA AACAGAAAAA 600

GCCTTAGCTT ACGCTGAAAA ACAACCTTCT CAGAAAAACT ATGATGAAGC CGCAACCTTA 660

GTATCTTCAT TAAGTCAAGA ATACGAGGAA TACAATGATC GCCTTGAAAA AATCAAAGAA 720

GCAGTACCTG TTGATGAAGC AGTTACAACT GCTGAAAAAT CTAAAAGTAA AAGCGATTAT 780

CAAGCAGCTG AAAAATTAGT AGCTGCTGCC CCAGTTGGCA AAGAAGGATT TCAACAACGA 840

TTAACGACTG TTCAAACCGC TATCGCTGAA AAAGAAAAAA ATGAACAATT AGTCGCCAGT 900

GCAAcTGCCG CTGTTGAAAA AGCTGAACAA GAACCAACCA ATGAAGCTTA CTATAATGAA 960

GCGGTCAAAC AAATTGACGC TTTAAACTCC CCAAATCAAG CTTTAACAAA ACGGGTAGCC 1020

GTTGTTAAAA CTCAATTAGA TGCCCACAAA GAAAAACAAC GAAAAGAAGC AGAAGCTCAG 1080

AAACTAGCCG CTGAAAAAGC GCAAAAAGAA CAAGCCGAAG CGGCAGCAAA AGCGCAAgCT 1140

GAAGCAGAGG CGCAACAAGC CGCACAGGCG CCGGCGGAAG TCGAGACGGC TGCTGCGGAA 1200

GCACCAAGCG GTAACGCCTT AATTAAAGGG TCACGTAATG GAATTTATCA TGTACCTGGA 1260

AGTAGaTATT ATAATAGAAC TACGAATcCA GTAGCTTGGT TCTCTACTGT TGAAGAAGCA 1320

GAAGCAGCAG GATACCGAGC ACCCAAACAG TwAATACtTA GCAATAATTA ATCAAmCAgn 1380

AAATGGGcTC CGTTGTTTAg GAGGC 1405

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TATTGGATTA CAACAGTACT TTTTGTTGCA ATTGGTGGAT TTTTACGTTT TTTTACAATA 60

TTTGATGCTT CAAACGAATT ATATCTAAAC GTCCAGAATT TTTTAGAAGG CTCAGAAAAC 120

TCAATTAGTT TTGACCACAA TTTATTGATT ATCTTGTATA TTATAGTTCT AACAGTCATC 180

GCGCTGACTA TTGCAAGGGT AAATAATAAA CGTTGGCTAA GACTAGGAGT ATAAACGACA 240

CCCACTTCGC AGATAGGATT CATCTACTTA TTCGAGACAA TAGATTAAAT CAAATAAAAT 300

ACAACTAGTT GAAACTAAAA AAGCATCAAT TTTGATACGC CCCAAACTGA TATTTTtCTA 360

AACTTTGGGG CGTGTAATCA AAATACGAGC TTCTTAGTGT GGCACTGGAT ATTTCAACGC 420

ATTTTTCTTC AACTTTTCTT CGATAATTTC GTCCAAATCA AACCCTAAAT TATCAGCCAT 480

CATGTAGGAG TAAATGAGAA CATCAGCCAA TTCTTCTTTG ATTCGTTCTT CTTGTTTGAT 540

GCCTTCTTCT GCTGTTTTCC ATTGAAAAAG TTCTAACAAT TCTGCTGCTT CTAAACAAAT 600

TGAGAGCGCC AAATCTTTTT CATTATGGTG GGGGCGCCAA TTTCTTTCAT CACGAAATTG 660

ATTAATTTTT GCCATTGTAT CCATTTGTTC CCCTGCTTTC TTATTCATTT GATGGCAACT 720

GAAACCCAyC GAACGTTTCA CCATCATAGT ATTTTAATAA CTGTTCTGTA GACAATAATG 780

AGGAGGTTAT TTCTTCCTCT TCAACAACTG CTTGATTCTC TTCTCTATAC AACAAATAAG 840

CCTGTAAAAG CTGTTGGTAA AGTTTTTTTC GTGAAGAGGC TTCCGCTGAA AGAAACGtTA 900

ATTCTTTTAA GTGTCCGCGA TAGACAGGCA AATCATCAAC GAATTCGATT GGTAATTCTA 960

CTACAGTTAA CTGAAATTCT TCAAAGACTT sTTCGTACAT CTGCCATTCC CTCTTTCTGT 1020

CGATATTGTT TTGGGGTCAT GCCCATTTCT TCTTTAAAAC GTTTATAAAA AAAGGCTTTG 1080

TCTTGATAGC CGATTCGTTC aACAATCGTT TGAATCGATA AATCtGTTTG CTTCAAGTAG 1140

TTTTTCGCCA ATTGGATTCG GTAGGCTAAG ACAATTTCCG TAAACGTTTT GTTTGTTTTT 1200

TCTTTTAAAA AATTCGATAA GTAATTCGGA TGAAAATGAA ATTTAGCGGC GACTTCTGCT 1260

AAAGTGACAT GCGCAATCTG TTGCTCAATA TACGCTAAAA TCACCTCGAC ACGTTGATGA 1320

TTCGACAAAT AATTATCTTG CATCTTTAAA GCTTCTCTAG GCAGTTGACC TAGTTCCACC 1380

ACTAGCAAAA CAAAGGCCGC TTTGGTCACT TTATTATTAA AATAGGCCAT TTTCACAATT 1440

TGTTTTAGTA ATAATAGCGA ATAGACGTGA ACATCCGAAT TTGGCTGGCT GGCAAAAACG 1500

AAATATCGAG GAATGTTTTC AAATTCACTG CTAGCAATTT CTGTAAAAAA ACGATACATG 1560

ACTGGTTCTT CCGCCAGCTG ATTTAAGAGC GTATCAAGAA AATAGTGCTT TTTAAAATAA 1620

AATATAATCA TAGACATTCC TTGCCCCTGA TAGCTAACCG AGGTGGCCTC ATTGACAATC 1680

ATGACTTGGC CAGCCGAAAA CGAACACCTT TGTTGATCCA AATAAGCATA GCCGTCTTGC 1740

TCTAAACAAT AGAGCATCCG AATAAATCCT TTCGGAACGT CAATGGTTTC CGAAGATGCC 1800

AGCATAAAGC CCGCAATTTC TCGATGTGGA TTTTCCTTAA ATTGCGCTAC TTCATTCTCA 1860

AGAGCATTGG TAGTGGTTAA ATAACAATCT AAGGTCTCTA AAAACTGATA AAATGCTGCA 1920

TATTGTTCTT CTTTGCTTGC CAATTAATCA CCTCATAATC CAACACTTTT TACTTTACTC 1980

CCTCTATTTT TTTCTTTGGC GTTTCCTTCT ATACTAGATA CATGGTAACA CGAAAAAAGA 2040

GATTCAACAG TTTTTAGGAG GAATTTTTTA TGAAAATTAG TTTTATTGGT GCTGGAAATA 2100

TGGCATCCGC TATTGCCAAA GGTGCGCTAA AAAAGCAATT TATTGCCGCA GAAAACCTTT 2160

ATTTTTATGA TATTCAAGTC GAAAAAACCG CGGCTTTTGC ACAAGAAATT GGTGCACACG 2220

CGGTTGCTTC GCCTCAAGAA GCTATTACAG TAGCTGACTT AGTTATTTTA GCAGTGAAAC 2280

CGCAATTCGT TCAAGCGGCT TTACTTGAAG CAAAAGAAGC AATTTTAGAC AAGCAACCGT 2340

TAATTGTTTC CATTGCGGCA GGTACGACTA TTGCAGAATT GTATCAACTG TTTGAGACTA 2400

CCCAACCGCT TCGTCTCGTT CGTGTGATGC CCAATATGAA TGCGTTGATT GGCGCGGGTG 2460

CAGCAGCTGT CTGTGGTAAC GCTTTTGCAT CCCCTGAAGA CATCCAGACT GTTTTATCGT 2520

TGTTTCGAGC AGTTGGCCAA GCCTGGGAAT TAGAGGAACA GTATTTTTCG ATTTTTACTG 2580

CTATTGCAGG TAGCACTCCT GCGTATGCTT TCTTATTTAT TGATTCGATT GCCCGAGCAG 2640

CCGTTAAAAA TGGTATGAAC AAAGAGTTGG CCTTAGAAAT TGCCACACAA GCTGTACTAG 2700

GCAGCGCTCA AACTTTGGCA AATAGCACAG AGAATCCTTG GACTTTAATC GACCAAGTCA 2760

GTTCTCCTGG TGGAACCACG GTTGCTGGGA TTGTCGAATT AGAAAACAAT GCGTTTATTT 2820

CAACAGTCAT CAAAGGGATT GAGGCCACCA TCCTTCGGGA TCAAGAATTA GCCAAACAAG 2880

ACTGATAAGA ATAATTACAT GAGCGAATAA ATAAGAAAAA GCGCTGAAAA TTCAGCGCTT 2940

TTTCTTATTT TAGTTGAATG AGTAAGCCAA AATGATCACT GACTATCGGT GTTTTCCTAC 3000

CATCAAAAAT TACTTCATAT TTTCGTACGT GCCACTGTTT TGGAACAAAT GCGTAGTCAA 3060

TCCGCAAGGC TGCTTCATTT TCTTCCCAGC CATCTATTTT TTTCTCTACT GTCGCTTCAC 3120

CGCTTGTCTC TTCCGCTACA ACAAATGCAT CTTGAATCGG CAAGTAACTA TTTTCCACTA 3180

ATTGATAGCC AGTTGTACCA GCTGGGTTGT TTAAATCGCC TAAAATGACT AACGGTTGTT 3240

GCCCCGTCGC TAAGTATTTC TCTAATTGTA GCCATTCATA GGCAAAACCT GTACAGGGTG 3300

TTTCCCACCA AGAAAAGTGA CCAGAGACAA CAGTAAGCGT ACCTTTTGAA CTCTCTGTCT 3360

CCGCTACTAA GATTTTTCTT GTTCGATAAT TCGTTGGTTC TTGGCTTTCT GAAATAAGGA 3420

GAGCTTCACT AGTCAACGGA CATTTCGAAA GTAGTGCGTT CCCTTCTTCA TAAATAGCAT 3480

AACCAATGTG GCTCATTTCC CAACTCCAAT AATAGTGTTG GCCTTTTTCA GCTAGATATT 3540

GAACGATTAG ATATGCAAAA TTATCTTCAT GGATCGGCGT TTGGGTCGCT ATGGGACAAA 3600

AAGTAGTTAA CTGTTCTAAC GGCACTTTCT TGGAAGCGAC TTTCTGATTC ACTTCTTGTA 3660

AGGCAATTAT TTCACTTTCA GAAGATAAAA TCACCTTGGC AATCTCCTCT AATTTTTTTA 3720

ATGGTTCTTC TTCTAACCAG CTATGAGTAT TGATTGTTAA AAGATTCATC TTTTCCCCTT 3780

CTCTTACATG TTATTAGGTC TGTGAGTGGG ACAAAAATCA CTTTGGATTT TTGCTTCACG 3840

CGCAAAACCT GATAAACGGC GGGAACAGAA CCAACTcCTT CGGAAATAAG CCGAAATTAT 3900

CCAAAAATTA AAAAGCAATT TCCGGAAATT CCTTCTTATT TCTCGGAGTT AAACGGTTCT 3960

GTCCCGACCT CATACCTAAT CATTTAAATT TCAATCTGTC CGATCACAGT TCCCGCAGTG 4020

GTGGTTCCTA GTTGATTAAT AACTACTTGT TCCACTTTGT CGCTGTTTGT AAAGGCGACA 4080

ATAATCGTTG TTTCTTTGCC AGCTTGTTCA ATCACATCCA AATTCATTTT AGCTAGTTTC 4140

GTCCCAGCTT TCAATGATTG TCCTTCTTTA ACAAAAGATT CAAAAGCAGG TGTTGCCATT 4200

TCAACTGTAT CAATTCCCAT ATGGACAAGT ACTTCAATAC CTTCTTCTGT TTGTAGCCCA 4260

ATCGCATGTT TGCTTGGGAA AACACTTAGA ACTTTCCCCG AAATTrGTGC CACCACCTCT 4320

CCTTCTAGAG GCTTAACTGC AAATCCATCC CCCATCATTT TTTGTGAAAA GACAGGATCA 4380

TTGACTTGCG CCATTGGAAT AACTTCCCCT GTCGCTACAG CCACGAAATC TTTTTTCTTA 4440

CCTAAGAAAT TCGTTGTTGG CACTCCTGCT GTACTTTCTG CTATAACTGG TTCTGGAATG 4500

TCAACGCCGG AAGCTAGTAA ATCTTCAATA TCGGATTTTA AAACATCGGC TTTTGGTCCA 4560

TAAACGGCTT GAACGCCATT ATCTTTCACA ATCAAGCCCA TTGCGCCTGC CCGTTTCCAC 4620

GCCTCTTCCG AACCGACTTT TTCTCGATCC TTTACACTGA CACGTAAGCG TGTCATACAC 4680

GCATCAACTT CTTTGATATT TTGTTTACCA CCAAGTAAGT AGACAATTTG CGCGATTTGC 4740

TGATCGACGA CGCCTGAACC AGCCGCGCCA GATGCGATTT CTTCGCTGTT ATCATTGTCA 4800

TAGTTTCCAT TTCTTCCAGG TGTTGCGTAA TTAAATTTTT TAATTAAGAA ATTCGCTAAG 4860

AAATAAGTGA CAACACCAAA AATGATGACC ATTAAAACAA AATTGATTAA ATCGCCACCT 4920

AAACCAGCTT TTATTGCTAG CGGTGTTCTT GTTAACAATT CAATATTTCC AAACGAATGC 4980

ACACGCAATG GTAAAATATC AGCCATTGCA AAAGCAGCAC CTTGGATCAC CGCATAAATT 5040

ACATAAAGCG GCACTGCAGC AAACATAAAC ATGAATTCTA GCGGCTCTGT CACACCAGTT 5100

AAGAAAACAG tAAAGCAGCA GAAAAATACA TTGATTTATA TTTAGCTTTT TTATCTGCAT 5160

CGACATTACG ATACATCGCC AAAGCCATCC CCATTAAAAT CCCTGAAGAa CCAATCATTT 5220

GGCCTACTTT GAATCGAGCT GGTGTCCAAT TTTCTAAGAC AAACTGATAC TTGCTCATAT 5280

CACCAGCGCC TTTAAGATTC ACTAAGTCTG TTGCCCAAGC CAACCATAAA GGATCTTGAC 5340

CAAAGACTTG GGTTCCAGCT TGTGCGCCAG ATAAAATTTC ATACGTTCCA CCTAATTGTG 5400

TATAGTTGAT TGGAATCGTC AACATATGAT GTAACCCAAA AGGTAATAAC AAACGTTCCA 5460

ACGTTCCATA TAAGAATGGC GCTAAAATAG GTGCACTATC TTGAGATTGC GCAATCCATA 5520

ACCCAAAATT ATTAATTCCC GCTTGAATAT TTGGCCAAAT AAGTGCTAAT GCAATTGAGA 5580

CAATTGTTGA CCACAAAATA ACGACAAATG GGACAAACCG TTTACCATTA AAAAaTGATA 5640

GCGCATCTGG TAATTTCCGA TAATTGTAAT ACTTGTTGTA AGCCATCGCA CCGACAAAAC 5700

CAGCAATAAT CCCTACAAAA ACACCCATAT TTAATGCCGG AGCTTCTAAG ACACTTGTAA 5760

AGAATCCCTT CACCATAATC TTGGTGCCAA ATAAGGTATG CGTGAAAGCT TGTTCATCAG 5820

CCAACATTTC ATTTGTTACA CCAAAAATGG CTCCAGTAAT ACGGTTGATT AAAACAAAAG 5880

AAATCCCCGC TGCAAATGCG CCACCTGCAC GATCTTTGGC CCAACTGCCA CCTATgTAAC 5940

GCAAATAGTA AATGTAAGTT GCCAATAATT GCCCAACCGA TACTCTCCAG AACTCCGCCT 6000

GTTGTTACTA ACAAGCCTAA ATTAGGATCG ATTAAAGGAA GCGATTTCCC AATACTAATC 6060

ATTAAACCCG CTGCGGGCAT TACTGCCACA AC 6092

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ATAAACTATC AGCATATTTA TTTAAAGTAC GAAGGCTTAG AAGGAGCCTA GGCGAAAGCT 60

GAAAATAATG CACCCTCTTA TGAGATATTT CAACAAACGT GCTTTTTGCA CGTTTGTTTT 120

TTTTTATCAA AATGAAAACG TAGAGGAGGG ATGGAATGGG TGAAGCTAAA GTAACTAAAA 180

CTTTCCGATT AACAGAATTA GTGGCAAGTG ATTTAAGTTG TAAAGATTTA TTTGATGAAC 240

TTATTGCCGT TTTAGAAATT TTAGATGTAG AAGTTGTTAA TAAAAAAATA GTTTATTTCT 300

ATAAAAGAAA CGTGAAAAGT AAACAAGAAA AATTAGAAGT TTGTTTTACT AGAGAGAGTA 360

TTCTGCACTT AATTGGGATA AGTTATTATG ATATTAATGA AAGAGAAACC TCTAAGTCAA 420

GAATGAAAAG TAAGTATGCT ATTGAATTTT ATAGAGACTT TAAAAGrAAT AAATTGAACT 480

TTTCAAAATG TTGGGTAGAA AGTACAAGAA AAGTAAAAGA TAAGCtcAGG TATTGAAATA 540

CATTAAAAGC ATAAAGACAG ATGTGGTCAG AATAGGCGCT GACGGACAAT TAAGAACAAT 600

TCCTATGACG AACACAATCA GTACGCCTAA GATTGGTTTA GGGATTGGCT TATATCATGA 660

TCATCCAGAA TTCTCAATTC CTCGTTCTTG TTTAAATCTT GCTCAGGATA AAGAAGCGAA 720

ACAACATACC TCGTTTCGTA ACGCCTGTCG GTGTACAAAA ATTTGGATAT ATGAAAGAAC 780

AGAACAGGGT ACTTGGAAAT TAGAAGATAG GCAAGAATTT TTTAAAAAAA TACAGGCAGA 840

AAAAAGTAAG AAAAAAAGAA GAAAAAAGTA AGATTACGTC ATTAACTTAG TTTGTAATTT 900

GCTATATATC GTCAGCTAAT GATGTCGTAG AATGAAAAAA GGGGTTCTCT TATACTAATT 960

TTTGTAAAGA ATTAAATTTA TTTTCTATTA CAAGTCCAGT ATAGAACTTA TTACTTACmT 1020

AACAGTACTT TTAGAAAAAt CAGAAcCAAA TTAAAGAGAG TAGCCCCTTT GnATTTAAAA 1080

TTTAATAAC 1089

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AGGGTCTTTT ATAaTCAAGG AACAATGAGT GAGAACGATT CTCAATAAaT GTAAAATAAC 60

GACAGAAAAA TTAAAGAGGA ATGGTTATGA ATTATTaGAG GCAGAGGACT TAACTACAGG 120

ATATGGTCGT CAAGTGATTA GTGAAGCGCT GAACTGTTCA TTTGAAGCGG GAACTATTAC 180

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AAGTATTATT GGACCAAATG GTTGTGGCAA ATCGACCTTG TTAAAAACAC TTGCACGTAT     240
TTTGCCAGCT GAGAAAGGCA AGGTGTTCAT TAAGAACCAA GAACTTCAAC ATTTTTCTTC     300
AAAAGAAGTA GCGCAAGAAC TAGCGATCTT ATCACAAACG CCAGAAAATA CAATCGATTT     360
ATCTGTTTTT GACCTCGTCT CTTTCGGGCG ATATCCTTAT CAATCGGGCT GGAAAAGTGT     420
CACCACAGAA GATCAAGAGT ACATACAATG GGCATTAGAA TTAACAGGCT TAACTGAGTT     480
AGCTAGAGAG TCTGTGGCAA TTTTATCAGG TGGACAACGG CAACGGGTTT GGATTGCTAT     540
GGCGCTAGTG CAGGATACAG ATATTTTAAT TTTAGATGAA CCGACCACCT ATTTGGATCC     600
AGCGCATCAG CTAGAAATTT TAAATGTGTT AAAACGAATT AATCAAGAAC ATCAGAAAAC     660
CATCGTGATG ACGATTCATG ATATTAATTT AGCTTCTCGT TTTTCTGATC GCGTGATTGC     720
GATGAAAGAG GGAAAGATTA TCAATGAGGG AACACCGCAA GAAGTGATTA CTGTTACTGG     780
CTTAGCAGAT GTTTTCGCTA TTCAAGCAGA AATTAGTTAT CATAGTCAGA CACAGCGGCC     840
ACTAGTGCTT TCTTATGAGT TGATGGAAAT GGAGCTGGAT GGATGAAAGG CATAAGCGGA     900
TTTTATAGAC ACCAATGGCA AGTGTTGCTT GTCTGTCTTT TTTTGCTACT GGGGACAATG     960
CTTCTGTCAT TGATGTTTGG TGCGACGTCG GTTTCGATTC AAACGATTAT TGATTCATTT    1020
ACGCACTTCG ATGCGACCAA TCAAGCGCAT CAAGTCATCC AAACGGTTCG GTTGCCGCGG    1080
ATTTTAGGGG CCGCTTTTGT GGGGGCAAGT TTAGCGGTGA GTGGGGCGTT ACGCAaGGGA    1140
TTACACAAAA TCCATTGGCA GATTCTGGCT TGCTGGGTAT CAATGCTGGG GCTGGCTTGG    1200
GCTTGGCGCT TGTTTTTGCT TTCCTCCCTC AGGCAAGTTA TTGGTGGCTT TTAGTTGTTT    1260
CTTTTCTTGG TGCCGGCGTG AGTGTGGCAC TGATTTAwTA TCTTTCTAAT CATTCAATTC    1320
GAGGAGCAAG CCCCATGCGT CTGACCTTAG TGGGAGCTGG TATTAGTGCC CTTTTTTTAT    1380
CATTTAGTCA ATTCTTAGCC ATTCAGTTCA ATTTGAGTCA AGAGTTAACG TTTTGGTTTC    1440
TTGGCGGTGT CAGCGTTATT TCTTGGGCAC AATTAAAAAT AGTCGTCCCT ATCTTTCTGG    1500
GCGCATTTGC ATTAGCAATT CTGATTAGTC CGTCGGTGAC TATTTTACGG TTTGGCGATG    1560
ATGCAACAAT TGGTTTGGGG CGAAATCCGC AGCGTATTCG GTTGTTTGCC AGTATAACGA    1620
TTTTGCTTTT ATCAGGATTG TCTGTGGCGC TAGTTGGCTC GGTCAGTTTT GTTGGTTTGG    1680
TGGTGCCTCA TGTGATGCGA ACAGTTTCTG GAGAAAATTA CCGGCGCTTG ATTCCGTTCT    1740
CGGCGTTAGG TGGTGCGCTC CTCGTTTTGG TGGCAGATTT AATCGCTCGA ATGGTGAATC    1800
CGCCTTTTGA AACACCATTT GGGATTATCA CGGCCTTAAT TGGCATCCCA TTCTTTCTTT    1860
ATTTATTTCG TAAAGGAGGG AAACTAGGAT GACACAGAAA AAAGTGTCTC GTTGGGTGGC    1920
TATCTTAATA GTTGGGATTA TCCTAACTGC TTGTATCAGT TTAACGCAAG GGGAATTATC    1980
TGTTTCCGTC ATGGATTTAA AAGCCCTTAT TTTGGGACAG GGAAGTCAGG CCAAACAACT    2040
GTTAGTTTGG GATTTTCGGT TACCACGGAT TGTGCTTGCG GTCCTAGCGG GCGCAGCTTT    2100
AGGCTTAAGC GGCGCTATTC TTCAAGGGAT TACTCGGAAT CCGTTAGCAG ATACTGGGAT    2160
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TTTAGGTATT AATGCGGGTG CGGGTTTGGC AGTGATTTTG TTTATTAGTT TTGTTGAGAC 2220

GACAAGTATC ACAACGTTTG CACTTCCACT CGTGGCCTTA GTTGGCGGCT TGCTAGCGGC 2280

TGTTGGGATT TTGGTAATCG CGTATCATCA TCGTTTAGGA TTGACGCCAG TTCGAATGGT 2340

CTTAGCGGGT GTCATTTTGA GTACGGGTAT TTCAGCACTC ACCTTATTAA TTACATCAAA 2400

AATTGACACT GAAAAGTACC GTTTTGTTAC AATGTGGCAA GCAGGCAGTA TCTGGGGCAG 2460

TAATTGGTTC TTTGTGGGCG CTTTGTTGCC TTGGCTAGTC ATCGGGTTCT TTTTTGCGAT 2520

GAAGCGTCAT CGTCTGTTGG ATATTTTACA ATTGGGGGAC GAAACAGCTA TTTCTGTAGG 2580

TATTGCTGTG AAAAAAGAAC GAATCGTTTC GTTGCTGTTA GCGGTGATGT TGGCGGCATC 2640

AGCGATTTCC GTTACAGGGG GAATTAATTT TTTAGGTTTA CTTGCGCCAC ATATTGCTCG 2700

CAAATGTGGT TTTACGCAAC AAAAACAGGT ATTGCCATTG GCGGCGTTGT TTGGGAGTTT 2760

ACTTTTATTG GTTAGTGATA CGATTGGTCG GCTATTGCCT GGCAATGGAG AAATGCCTGC 2820

AGGGATTATT ATTGCGATCA TCGGTGCGCC TTATTTTCTT TATTTGTTAA TCAAAAACAAG 2880

CGATTCGTTA TAAAAAAGAA TCAAAAGCTG GGTCAATCGG TCGTTGTGAA AGCAACTGTC 2940

ATTTGCTCGG CTTTTTTATT GGCGGATTTT TGAAAAAATA GTATGATAAA TGCGTAAGAG 3000

GATTGAATGG AGGATGAAAG AATGGAAAAC TTTAATTTTT ATGTACCAAC AGACATCCGT 3060

TTTGGGAAAG ATCGTTTAGA CGAATTACCT GCTGTGTTAG ATCAATTTGG CAAAAATGTC 3120

TTACTTGTTT ATGGTGGCGG TAGTATCAAA CGTAATGGCT TGTACCAACA AATTACTGAT 3180

TTGGCCCAAA AAAACGGGCA TACACTGATT GAGTTGAGCG GTGTCGAACC AAACCCGCGC 3240

ATTGAAACCG TTAGAAAAGG AATTGAGTTG TGTAAAGAAA ACCAAGTCGA TGTTATTTTA 3300

GCAGTTGGCG GTGGTTCAAC CATTGATTGT TCCAAAGCAA TAGCTGCGGG CTTTTATTCG 3360

GAAGAAGATA TCTGGACAGT TATTGCAGCC AGAAAAGGGT ATACTGGTCC TGCTTTACCA 3420

ATCGTGACCA TCTTGACTTT AGCAGCGACA GGTAGTGAAA TGAACGCAGG TGCTGTCATT 3480

TCTAACTTAG AArCCAATCA ArAATTAGGC TTTGGTGGTC CGAATATGAT TCCAAAAGTT 3540

TCGTyCTGGG ATCCAACGAA TACTTTT 3567

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7893 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TTTAGTGGTT TGTTGATGTT TTTAAGTAAA ATTGGCACAT TGTTTGGCTG GCTTTCACTT 60

CTGGCAGCTG TTATTGGCTT TGTTATTTTT TATAAACGAG CAACGACCGC TGAACAGCCA 120

CTAGTTCGTT TGACAATTTT AAAAAATCCC GCCTTCGTTT TATTTTTATG TGGCTTTTTA 180

GTTTGTCAAT TCTTATTGTT AGGTATTTCC TTTGTCTTAC CAAATTTTGT TCAAATCGTC 240

CTTGGAAAAA ATGCGTTTGT AGCTGGGCTA GTCATGCTGC CAGGTGCTAC AGTTGGGGCC 300

ATTTTGGCAC CACTTTCTGG ACGAGTGTTG GaTCAATACG GCGCTAAAAA ACCTATATTA 360

TTTGGCTTAA GTTTGGCGAC AATCGGTTGG CTAGCTTTAA CAATTTTACT AGAGATGCCT 420

GTTTTATTAG GATTCGTCGC TGGACATGTT ACCTATATGA TTGGTCTAGG TTTTGCATAC 480

AGTAATATGA TGACGACTGG TAtGAGCTTG TTAGAGGAGA AAGATTTTGG CGACGGCAAT 540

ACGTTATTTA ATACACTTCA ACAATTTTCT GGCGCTATTG CGACGGCCAT TGTAGCGACG 600

ATTATTAATA TCGCTCAAGA CCACGCAGAT AATTTTGCTC AGGGGACAAC GATGGGCTCC 660

CTCATTTCTC TGATTTTCTT GTTAACCTTA TTAGTAATTG TTTTAATTGC TTGCTGGAAT 720

TATTTCCGCA AAAAAGCTTA AAAAAAAGCA GCTGGTCAGT TCCATAGTGA CCAGCTGCTT 780

TTTTTAGTTT TCTAAAGATA GTTGTTTTTT TGTTCTTCTT GCTTCCGAAT ATAAAGTACG 840

AACAAGACAG CAATTAGCAC GATAAAACCA CCAAAAATCG GTGTATATGT TACTGATAAA 900

TGATCTGTGA CCACCCCACC TGTCATTGAG CCGACGGTAA TCCCAATATT AAAGGCTGCA 960

ATATTAAAAG CTGAGGCCAA AGTGATATCT TCTGGAACAT ACTTTTCCGC TAATTCTACA 1020

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ACTAGCAATC AGTCCCACCA AGCCAATACT GGCTATAAAA AGAAAGGACA TATGCCAAGC 1500

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CCCTCCCTTA TTTTTCATTC TTATCTATTA TACGTGATTT TnAGTCATTC GGCATCTTTT 7860

TTCTTTTAAT GAGTCACTGG CGCAACCATT GCT 7893

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 17082 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GCGCAAATTG GCTACCAATC TAAATnACTT TCAGAAGCGT ATTATACGAG CATGATTGTG 60

GTAATTATCT TAACGACCTT AGTTGCACCG TTCTTATTGA AATACTTTGT TAAAAAACAA 120

GAATCTGCGT TGCAATAAAA AAGATGAGCA GAAGTTGTTG ACAAAAAAAT AAAATAGCTA 180

TATGATGAGT TCAAGATAAA CGACGGCATC AGGACCCGTG GCCCCATGCG TTTTAATGAC 240

TGGCGCTTTT AAGCCAAATA AAACCGCTCC CCCATGTTTT GAGTAGTCCA TTTCGTCTTT 300

CATGCCATGC AACGCATTCT TTAATAATAA GGCGCCCATT TTTCCTTTGA CACCTTCAGA 360

AAGAATCGCT GTTTTCAGCA AGCTCATCAT GTTCATAGCT GTGCCTTCGr tGGATTTTAA 420

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CAAATGTTCT GGTTTATTGT CTGCATTGGC TCCTAAATCT AACATGTCAA ACCCTTTGTC 720

TGGTTCTCCC ATGACAGGTA AAGTTGACAT CAAACCGGGA CGTTCCACAT TTTTGATGCG 780

GCCGACAATG AACAGACCCG CTGCTAATAG CGCTCCGGTG TTGCCTGCAG AAAAAATCGC 840

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TTTTAGATGG AACAACCGCT ACTGGTACAT CGGCAACTTC TGCTGCTTGA TCAGCTGCCA 3840

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GGTTGAACGC CTTCATCTAA TTCATGCGCA CGTTTGCTTG CT 17082

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CTTTTAACAG AGAACCTGAC TATTAGTGAA AAAAGAAAGC AACAGCTAGC CTTTGAAGTG 60

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ATTGTGACGG TTGACCAAAC GGGTAATTTA ACAGCAGTTA AGAGTGGGTG AAGCGAAGGT 180

AACrGTCAAA ATTAAaGGAA CAGAAaTTAG TGATACAATT CCTGTGACTG TTGTAGCAGA 240

AAATAAACAA TATGCGGAAA TGCGAGCAAA ATGGAAAATG CGATTGTTAG GTACAACGCA 300

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CTACTATGAA CCATCAAGTG AGCTTTTTGA AAAACCAGAA GTTTATGATG CGATTGTTAA     540
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GCCAAAAATT GTTTTATAAG AAATTCGTCC TAATTTTTGC GTATCGGTAA TATGACAAAT 4320

GGCTAAAGTA ATTGAAGTAA AGACCATCGG CACAATCACT AATTGTAGGC CGTTGATAAA 4380

TAGTTGACCA ATAATATAGA AAAGCCCAAT CGCAGATTGT CCTTTTTCAG GATCTGAAAT 4440

ATCTTGGAAA AGAATCTGAT TGATTGTCTG CCACACAGCG CCTTGATTGC TGCGAATAAG 4500

GTGCTCTCTT AAAAATAAAA AGCCGAGCCC AACGATTAAT CCTCCCACCA ATGAAATCAC 4560

CATTTTTTTG GTAAATGAGA TACCTTTCAC TTCA 4594

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

TTTCGGTCAC TATCACCATC TCTTGAAAGA AGTTCAATGG CTACATCTCC GTTTAGCTCT 60

GCTTTTGCTT TATCTAAATA CTCTTTGGCT TTTTTGGCGT CTGTTTTGAC AAGAGCGCCT 120

GCTTCTTGAC GAAAATCTTC ATTCGTTTCT GGGTTATATA CAAATTTTTC TGGAATGTAC 180

CCATAAATTT CTTTTGAGCC ATCTGCTAAA ATATTATCGA CTAAACTTTT TTTATCCAAA 240

GCATAAGCTA AAGCTTTGCG GACATTCTCA TTTGCAAAAA TGGATGGTTT TTCGTTTCTT 300

TTTTGGTTTA AACGTAAGGA ATAGACTTTT GACCGTTCGA TTGCTTCATA GTCTGGGTTG 360

TCTCGATTTT GTTTAGCAAA ATCTCCTGTT AAGACAGCCA CATCTAATTC ACCTGATTCG 420

TACAAATTAT AAACGGTATT GGTTTCTTTA AGAACTTCAA AATGAATCGT TTCTGATTTT 480

ACTTTTTCTT TATCGTAATA GTAGGGATTA CGCACAAAAT CCCACGACAT CGCTGACTGA 540

TCCCAATTTT TCATTAAAAA CGGACCATTA GATACAATCA TTTCACTAGA AGTGCCATAG 600

GCTTGTCCTT TTTCTTTCAC GAATGCTTCG TTTTGTGGGA AAAATGGAGA AAATGCCAAT 660

AACGACGTAA AATATGGTAC AGGCTTTTCT AAAGTAACCT CCAAAGTATA ATCATCAAGC 720

GCTTTGACAC CCAATTCCTC TGGTGCTTTT TCCTCTTTTG TAATAGCTGT TCCGTTCAGA 780

ATCGTTCCTT CTAACAAGAA AAAGTAATTG GCTTGGTTTT TGGGATTCGC TAATTTACGC 840

CAAGCAAAAA CGAAATCATT GGCTGTTACA GCATCACCAT TGGaCCACTT GcCATCTTCT 900

CTTAGTTTAA TGGTATATCG TTTGCCATCC TCAGAAATTT CTGGCATCTC TTTAGCAGCA 960

GCAGGTATTA GTTGATCTTT TTCATCCAAT TGATATAACC CTTCAAAGAC ATTGGACTGT 1020

GCGTTAATAC TGGCTTCATC TTGTGTAAAA ATAGAATCCA TTGAACCGAT TTCCGAGTTC 1080

TCCATTAAAT TTAAAACTTT TTTCGAGACA CTGGTTTTCT CAGTTGCTTT CTCGTCTATT 1140

TTTGTwTCTG CTGTTGTGCC ACAACCTACC AAGACCGTAC TAACAAATAA CATAATCCCC 1200

ATCATTTtTA ACTTTTTCAT ACTATTCCCC CTATGTGTCA ATCAAACGGC AACTCTTCCA 1260

TGGAAAGCCG TTCTTGCGAA ACTATCAAGC ATGCGTAGGG CAAGCCCTCA TTTTCGTACT 1320

CAAATTCTCC CCGCTGGTTG TCAATTGGGT CTGCACGCAA TTGCATTTTT GCCGGCTGAA 1380

AGTCTGCCTG GATCTCACTA TTTGCGACCA TTCTAAAAAC ATCTAAATTG CCGAAATAAT 1440

GATTCCACCG CTGTCTATCC CCGTCTCGGT AAGCACCTCC GCCAAAAGAC AAATCCGCAA 1500

AGAGCCAGCC GTACGGTTTT ATATAAAATT GTGCCCAATC ATGACAGCCT GTATAATGTG 1560

TAGAAACATA TAATCCCGAT TGCCATTTGG CTGGTATCCC TGCAATCCGA CAAAGCGTGA 1620

TAAACAAAAT CGCTTGCACG CCGCAGTCAC CTTTTAAATT AGTTGCAGCA TACTCTGAAA 1680

TATTGGAAAT TGTAAAATAT TCACGCATGA AAGAATAATG AATCTTTGTC GTCACAAAGT 1740

CATAAATCAA GCGTGCCTTT TTTAAGGGaT TACTTTCATC GCCCACAATC TCATCTGCTA 1800

AATTTCTTAA ATAAGGCGTG AATCGAATAT GCGGTAACTG TTCCTCTAAA TCAAAGCTTG 1860

GTTGCATTTT GTCTACGTTA TTTTCTTCTA ACTGTTGGTA AACCATCCGA TTAACATAAC 1920

AATATTCAAC TGTAAACGTT TGATTTTCTT TTAAGATTGT TTCAAAACAC AGTGTTCGTT 1980

GAGGCGCATC TTCTGCCGCA ATATAGGTTG CTTCAGGTGA CGTAGCTAGG ATTTCAATTT 2040

CTGATTGTTG TTGACACGCT TTGGGCAGCG GCAAATGGAC ACGAACACGC TCACCTGGAC 2100

GCTCAAATTC TTTTTTCACC TGAATGGTGG CTTTAATTGT TGTTCTCACT TTTCTACCAC 2160

CGTTTTTTTG CATTTGTTCG ATGTTCTCTT TTAGTTCTTT TTTGCGGAGA ATTTCTAATT 2220

GATTGCTTTC TGCTTCCCGC AAACGTGCAA CATATGCCGC ATTTGTTTTA ATTAAATTGG 2280

CCAAAAATCG AAGTTGGAAA TACGGTTCAC CATCAATATA AACCCAGTCC ACTAATCCCG 2340

TTTCTTTTAA ACGAATTAAT TCCTCTGTTT GATAATCCTG AAAAGTATCT CTCATCATTT 2400

GATCAGCTTT TGcAAAGcTA TGAGGATACT CATtCATACG CATCATTTtA ATGgACAtCT 2460

TTTTCaATTA TCAAACGTTC TTTTaATGCC TGCGGAAGTT CTTTTGTCAA CCAAAAmTCA 2520

ATGGCAATAT CCGCACTTGC AAAATCGCCA AATTCTTTCA CCCTTTGAAT TTCCTCAGGC 2580

AAAGGAACAC TAAGATACTT TAAATCATAC TTCATTTACT TTACTCCTTT TTTAATGAGA 2640

AATGCCTAAT CCAGCTGCTT CTCCTAATTC CAATAATGGT TTTGCTTCTA AGGATACGCC 2700

CCCAGTTACG GGCGCAGTTT CTAAACCGAA TGTCGCATCT AAATCTGCTC GTGTGATATT 2760

CTTTTGAGCA GCAGCTAAAT GGGCAGCAnC CGTGATGCCA ATGGTTGTTT CTTCCGCCAT 2820

ACAACCAATC ATGCATTCGA TGCCTGCTGT TTCACAAATC TGATTAATTT TCAGCnCTTC 2880

ATGAATGCCn CCACACTTCA TTAATTTTAT ATTGATAACA TCGACTGTGC CTTTTTTAcT 2940

AATTCCAACG CATCTTGAGC ATCAAAACAG CTTTCATCAn CCATAATTGT C 2991

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

TTGGACCCCC CAAATTCTTC CTTCGTCGAA ATTAACCACT CCCCCTTGGn TGATTGGATC 60

AAGGTCTGGn TTCCTTTACG CCCCAGGCCA TTGGGGTGTT TCCACCAAAn CAAACCTTGG 120

ATCCCGCTGG TTAAATTTCA CATATCACCc ATTGATTGGA AATCaAAAGC TATCTTcTTT 180

AAATAAGATT ACTTATAAcG AGAATTTATT GACAAATTAA GACAAGAAAA CAAATATACA 240

GAATCAACTA TTCAAACGTG GCATAAAATT GTAATGAGGA TGATTAACGC TGCGGTACAC 300

AATCAAATCA TCCCTAGCAA CACGCTAACA GGCTTTAAAT TTGATTTAAG TAATAATGTT 360

CGTTCGTTCT CTAAAAAGGA ATTACAGCGA TTTGTGGCGG TTTTAGAAAA CGAAGATATT 420

CAAACGCAAG TTATATTTTT AACTCTGCTA AAATCTGGAA TGAGGAAAGG CGAACTGATG 480

GGGCTGCGTT GGAGTGATAT TGATTTAACC GAAAAATATT TCGATATCAA TTCTACACGT 540

GGTGATTACG GTGAAAATAA ACCTAAAACA AAAACCAGCA TACGTAAAGT TTATTTTGAC 600

AACTCGTTAC TCACTTTAAT AAAAAAATAC AAAAATCATG AGAAAGAACG GCTTTTCAGA 660

GAAGGGATAA TTTTAAGCGA TAAGGACTAT TTTATTTTAA GTTCTCGAAA TTTACCTATC 720

AAACAATCAA GAATTACGTA TATGTTTCGC CTGTTATGTG AAAAAGCAGA AGTTCAAAAC 780

ATAACCGTAC ACGGCCTAAG ACATACCCAT GCAACGTTTT TAATTGAAGC AGGAGCAAAC 840

ATTAAGTACG TTTCAACTCG GTTAGGACAC AAGAATATTA ATATAACTTT GGATGTTTAT 900

AGCGATGTGC TAAAAGAAGA AGAAAAAGAA ACAGCTGATA TGATGGATAA ACTTATTGAG 960

AACTTGTGAT TTGTGGTAAA CCTGTGGtAA AAACATTAAA AACCATTGAT ATATAAGCAC 1020

TTTACCACTC CCCATCTGAA ATTGTAAAAT AAGTTGtTGT TTCTTTTCAG TCCAAGTAAA 1080

AATATATTTC ACTAAACGGC CATTGTTCCC TGACGAATGA AGAAAACTGA GTTTACTTGG 1140

GCCACTCACT GTCATTTTTT CAGGTACAGC TAGTAAAGTC CTCCGAGCTG ATTGGTTCAA 1200

TTTATCAGGA AATGAAAAGC TTTGTTGTTC TTCAAAAAAC CAAACTTCTT GTGTTTCCTC 1260

TAAAACAATT GCTTGCTGTT GCGCAAAACG AAGTTGTTTT TCTACCGTAG CAAGAAACTG 1320

TTCAATTTTT AACGTTTCTT GCCAGCGGTG AATAGCGAGT GTCGGGAGCA TAGTCATAAA 1380

GCAAACAATC GTTAAACTAA CAAGTGTTTC CATTAATGTG AATCCTGCTG ACTTGTTCAT 1440

TGCTTTTCTG CTGTATATTT ATCTAACTGC TCTTTAGTAA TGTAGCCTTC GTTGACTAAT 1500

TCATTTAAGG AAGGCGTCTT ATTTTTTTCT AGTGTGTAGA GCTCGATTTG TGATTCTACA 1560

ATTTTTACGA TTGCTTCATT GCCTTTTTTA TCAACTGTTT CTTTATGTTT CGCTAAGTTA 1620

GGGACAAAAA GTAAAATCAA TACGGAAATA ATCAATAAGA CAATCAACAT TTCTAATAAT 1680

GTAAACCCTG CGTATTTTTG tTTCTTTTTC ATTATAAAAC TCCTTCCATA TTGcCATAAw 1740

TAGGCAGCAA CaTTGCCCCA TAAACACCGA TAATTAAACA AGCAATTATG ATAAAAATAA 1800

GTGGTTGAAC GAGAGTAATG ACTCGTTCAA TTTTTTTGAA AAAaCCTTGG AAACAGACAT 1860

TACTATAAAC CATCAaCTCC TTGCCTAATT TTCCTTTTAC TTCCCCTTGT TGAATCATTA 1920

AACCCAATGC TTTCGTAAAA AAAGGATAAG CAGCTAATTG TCTATGTAAG GTTTCACCAA 1980

CTAGCAGTCC TTCACTAATT GCTCCAGCTA ATTCTTTCAT TAAGGGGTAA TTGGTTGTAT 2040

GGCGCATCAA ATCGATGACC TCTTTCATTT CTAATCCTTG TGCAAGCAAC TTCCCCCATT 2100

CTAGTGCAAA AAAAGCACTG ACGTATTCCC GATAAAGGCC ACGGATAATT GGCAGTTTCA 2160

GATATACGAA GGCCCGCTGA ATAGCAGACT GATGCTTCAA ATAACGGTTT AAAATGAAGA 2220

AACTAAATGA GAGGACAAAA ACTAAGGTAA CCAGAATGTA TGGACTGTAA ACAATCAGAA 2280

GAATCCCAAT ATTTTTAGAA TAACTATTGG CATCATTTTC CATTAATTGG GGCAATAAAA 2340

ATTGCCGAAT ACCAACAATG ACGAGAATCA AAAAAACAAT CAGGAGCAGC GGATAACTAA 2400

TTATTTTATA GAACTGTTGC CGATATTTTT CCGTTTGAAA AAAATGTTCG GAAATCGCTT 2460

GTAGTGTCCC CACCAAATCC CCGTGTGCAG TAGCAAACGA CAATTGTGCC GAGACCATTG 2520

TTGAAAATCC TAATTCTTCG ACTAAAGCTT GTAAGGCAAT GCCTGAGGAA AAGCCTTCAA 2580

CTAAAAAAGT TATACTGTGC TGAGGTAAGG CGTTTGATTT TTTCATGAAG GAAAAACTTT 2640

CTTGTATATT AAAACCATTT GCAAGCAAAT CCGCTAATAG TTTCAGAAAA AGCTGCTGTT 2700

GTTTTTTCGT TAATTTATTC GATGGCTTGA AAATACGTTT TTTCTGTAAT AAACCCATAC 2760

GCCCACGCCT TTCTTAGATT CTTTTGCCAA CTACTCTTTA TAACGGCTTC CTTAAAGAAG 2820

AAATAATCAT AAAGAATTCC CGCTACTTGT TCCTTATTAA TCGTGGTTGT CAAAATCTGT 2880

TGATAAATGA TACCTTGCAA GCATTCAGCC AATTCATGCT CTGGGCCACC TAATTCTATC 2940

AAACGCCGTT GCACCCCCAA TAAGTTACGG GCGTGAATTG TCGCAAAAAT AGTATGACCC 3000

GTTAAGGCGG CTCGAATAAC TGCTTGAGCC GTCTCGCCAT CACGAATTTC ACCAATAATC 3060

AAAATATCAG GATGATGGCG TAAGCAAACT TTTATCAAGG CTTCGTACGT TAACTGAATT 3120

TTTTCATTTG TTTGCAACTG TAAAAACTGC TTTTCCTCAA TTTCAACAGG ATCCTCAATC 3180

GCTATCACTT GTTGTTCGCC ACTTCTTTGT TTAGCCACAC GATACATGGT TGTTGTTTTC 3240

CCAGAACCAA CTGGCCCACT GAATAAATAA AGTCCTCGTT TCTGACAAGA TGCTTCAATT 3300

TCATTCAGCT GGTGGGGAAA GAAAAAATGT TCAGCTTGTt CACCaAATCG GTGCAAAAAA 3360

CGAATTACCA AGCTCTCTCG ATTCTGAAAA TCTCCCACAG ATGATAAACG CAAGCGTTGC 3420

TtCGTCTCGC CaATTAGATA AGTTGTCGCG CCTAATTGTG CTTTTCGTCT TTCTCCGACA 3480

TCCcATGCCG CcTATAAATT TAAAGTGGAA AATTAACTTT TCGCCTATTT CTGCGGAAAC 3540

TTGtGTGTAA AGTGTCCGTT GCATCCCTGT CCGAAAAGAG ATGGCTATTT CGGTATCATT 3600

GGGTAAAAAA TAAACGTCTT GCGCCCCATG AAGGACGCCC CATTCAATTA ATTGATGAGC 3660

CAATTTTTTT ACATTkTCAG TCATTCATTT CCTCCTCTCA CTAATAAACT ACGCATTTAT 3720

TTTATGATTT CAGCAAAAAA AAGAACCTTC ACCATTaAGA TGAAGGTTCT TTTTTTGAAG 3780

TTTGCGCTGT CCATCTATCT TCCCCAAAAT AGTGGAACTC CTAGACACTT AGTATTATAC 3840

TAAAAAAATC TTGCGTTTAG TTTTCAAAAA TTTCTCTGAA TCACAAAATT TTTGAGAAAA 3900

ACTATGATAA TCCGATTGGA TCGTTTACGT TTTTGGCTTC GTTTTTTGTT TATTAACTAA 3960

ATAAACTGGA ATTCCTAGAA GCGTAATCCC TATACCAATC AATGCTAGAA TAGGCTGTGT 4020

AATACTCGTT GTAACCAAGA TGAAGATACC ACCTAGACTT GCGATAATTG GAATAATTGG 4080

ATAGCCAGGA ACTTTATACG GTCGTTTTAA TTCAGGTTCT CGTTTTCTTA AAATAAAAAC 4140

AGCTAAGAAA ATTAATAGAT TAAACAGCCA CATAACAAAA ACTAACATAT CCGTCAATAA 4200

ATCGAAGGTT CCGAAAAACA TCATGATAAT GGCTACAGCT AACTGGAAAA TTCCAGCAAC 4260

GTAAGGGcAC AACAAAGCGT TTAGgACAAC TTTTGAAACT GAACGACTAA AAGGCATCAG 4320

ATTATCTAAG GCTAAGGGCA TAAGGG 4346

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

CTTCATTCGA TTAATAAATT CATCCCAATT TACTTCATTG CCtTTAAACT CAGGTCCATC 60

AACACAGGCA AATTTCATGG TGCCATCAAC AGTGACCCGA CAACCGCCAC ACATGCCTGT 120

TCCGTCAATC ATAATAGGAT TcAAGGAAAC ATAAATTGGT AATTGATGTT TTTCAGCTGT 180

CAAGGTACAA AATTTCATCA TGATGCTGGG CCCAATCGCC CAACTGCACG CTACAGATTC 240

ACGTGCAATA ACTTCTTCCA TCGCTTCTGT TACTAAGCCC TTTTTACCTA ATGAACCATC 300

ATCCGTTGTA ATGATTAGCT CATCTGaATA mCGACGGCAT TCTTCTTGTA ACAGAACTAA 360

CTCAGCTGTT CGTGCTCCCA AAATCGTAAT CACTCGGTTG CCTGCTTCTT TTAAAGCCtT 420

GATAATTGGA TAAATAGCCG CGATACCAAC CCCGCCACCG ACAACCATCA CCGTTCCATA 480

TTGCTTCACT TCTGTGGGCA TACCTAAAGG TCCAGTGATA TCCAACAAAG AGTCTGAAGT 540

TTTAAGTTGG GAAAGTGCAG CTGTTGTCTT ACCGATTACT TGGAAAATAA TTCGAATACT 600

GCCTGCTTGT GGATTTGTCT CCGCAATCGT TAAGGGGATC CGTTCTCCCT TTTCGTCAAT 660

TCTTAAAATA ACAAACTGTC CAGCCTGAGC ATGTGTCGCT ATTCTTGGCG CTTCCAGCCA 720

AAAATCAAAT GTATTACTAG ATAATTGAGT CGATTgAAGA ATATTAAACA TTGAAATACC 780

TACCTTCATC GTTCCTTTTC ATTCTGACTC CTACTTTCTT AAACCCTTAG GCAACGCTAT 840

CAGATAAAGT TGTGGCGACA CTTTTAACAA ATGTTTTTAG CATTTCGATG TCTTCTTCTT 900

CTGCATTGTT TTCAATTTCA ACTGTTTCAG CTACTTTTTT AGCACCAGCT TTTTCAAAAG 960

CTCCTACAAA ATCATGCGCT GATTTACAGA AAAATTCACC ATATTCACGA TCACCGGAGC 1020

CAACAACACC AAATGGCTTA CCTGCTAAAT CCTTCTCAGT TAATTCATCA AAGAAATCTT 1080

CAAATTCAAA AGGCAGTTCC CCATCACCAT AAGTATACGT TGCGATAATA CAAGCATCTG 1140

CATCATCAAA GAAGTCTACA TCAACTTCTG AACATTCTTC ACGTTCTACT TCAACTCCAG 1200

CTTCTTGAwA CTGTTCTTCC AAAATCTCGG AAATTTCTTC TGTGTTTCCA GTCATACTTG 1260

CATAAACAAT TTTTACTAGT GCCATCTTCA TTCATTTCCT TTCTTTTTCC TAAATATTTC 1320

AATGCATTCA AATGCAATTG TAACCCCTTA CATTAATCCT TAAAAAAATA ACTTTTACAA 1380

ATGATTTTAT TCACAAcTAA TCTAACTAAG TATGTACTCT TCCCCTTTCG AGATAGAGTA 1440

TTTTTTACTA CGTCTTTACT ATACCACATT CCAAACCTTT TTAACAATAT TTTTAAGGTA 1500

AAAAAAATAT TATTTAGGTT CTTTTTTATA AAACGTTTTT CCTTCTTCCA ATCATAAAAA 1560

TTGCTTCTAA AACCGCTCCC CCTAATGCAC GAGCTTTGTC GGAGATCGTC AAGCAATCGA 1620

CTTTCTCAAC TGGTCGAGGA TCTACATCTG CACACTTCAA CCCTTGATAA CATGTTACCT 1680

TTTCTGAAAT CAATCCTCTC AAAGTCCCTG TCAGAGGCGA ATAAACTGGA ACCTGATCGA 1740

TTAAAAATAA TGCTTCCCCT TTCAACACGA GATCCCCTAT GTTTTTAAGG TGGGTAACTT 1800

GTCCTGAAGC AGGGGCATGG ACAACTCGTT CCGCACTTTT TCCGCCAATT TCACCTGGAA 1860

TACCTGTATT AGGTAAAGCT GTTCCTTCAA AGTATAAACG TCCCAACCTA TGGCCACGCA 1920

TTGTCTCAAT CACAACATCG ACATCTTGCG GTGCTGAAAA GCCTGGTCCT AAAGCAATCG 1980

TAATCGGTGC CATTCCTCGA TGCGTACCTA AATTTTTCTT AGCCAAAATC GCATCGATAA 2040

CAATCAGTGG TTTCAATTGT TGAATAGCAC TTGCTGTTTG ATCGACAAAA ACAGGCAGCT 2100

TATTTTGCTG CCAACATTTC GCGCAATCCT TTAATGAAGT AATTCGAACA GCAACCAAAT 2160

CTTCCACTCT TTGTTCTTTC TGAAAAATAG CATCACAAAC TGAAACAGTC CGCCGAATGG 2220

CCAGAGGACA TTCTGTTTCT AATACTAGTA TTTTAAAGCC AACGTGCCAT AATTTTTGGA 2280

TAACACCTGT CGCTAGATCG CCCCCTCCGC GAACAATCAC TAATTTTTCT TGGATGTTTT 2340

GACTGATTTC TCCCATAAAA TAAGTCCTTT CTCTAATTCC ATATTGCAAG CAATAATCTT 2400

GTCTAATTTT TCAAAACAGC TTTTGGGTAA TTGAAGACAG ACATTCATCG CTTGAACGAA 2460

CTCTCTTCGC GTATGGGTTT GATTTAAACA TAAAATTCGT TGGCCTTGGC TCTCTTTAAA 2520

CAATCCTTTT GGATGATCAA TCAGTTGAGC TAACAATGTT TCTGTGATTG GTTCTTGTAG 2580

TTGCGCATCG GTTAATTCCA AAAAAAGCGG CAACCGATGA ATGGTCGTTT CATCTATCTT 2640

TTGACCAATC ACAGAAATCG GAAGCACACC AATTGTGGTG GTTGTTTCTT TTAATATCAC 2700

GGGTTCATAA GAGGACCAGC CTTTCAAAGG TCGTTGTTTG GACCCATCCG CTTCTAAAAA 2760

AACTTTCGTG AAGTGCTGAA ACAATGTTTG AAACGAGGTC ATTGCAGGCA TCGTtAGTTT 2820

TGTTTGGTTG TTGATAGCGG TTCCTGCTAA AGTGATTCCG CAGATATTCG GCGTTATTTT 2880

TTCAAAATGG TTTGTATAAA AATAATCATA CAATTGACGT TGGGGAAACC CAATTTTTGT 2940

AGTTGTACTA ACCAGAACAG CTTCCTTTCG ATATGTTTTT GCTAGCGCCC ACATTAAGCT 3000

TGTTTTCCCA CCGCTACCAA CAATCGACAC AATCTCCTTT CCTTGTAAAT CAAAACACTT 3060

TTTTAAGGAC TCCACAGTTG GTACCTCCTT TCCCCAAGGT CATTTTTCAC AGAAAAAATA 3120

GAgGCTACGC GTACTTTTGC TTCTTCTAAA AAACATACAC TGTGAGTTAT TTCCGCTTCA 3180

TTAATGAGTA AACCGATCCC ACAGCCATCC GTCAATGATG GGGGCAAAGT AAAGACGCGA 3240

ACAGCCACCT TTCTTGCCAA CAGTACTTGT TCCGCCTGAA CAGCATAATG TGTATTCGGA 3300

AAGGTTAGCA AATACTCCAT CTTTTCACCT TCTTTTTTTG TTAAAGCGTA ATTACTTTAG 3360

CCGCTTGATT CATTGTTTCA ACAATTTCGT ACATATTAGT AATAGAGCCG ATAGCTAAGG 3420

TGTCTGTTAA ATGATAAAAA TCTAAACAGG CCCCACACGT TTGAATCGTG GTTCCCTTCT 3480

CCGCTAATTG TTGCAAATCA GCTAAGGTAT TCGCTGCTTG ATTCGTTAAA AACGCCCCTC 3540

GATTAAAGAA TAATAGCTGT GTAGGAACAG TTTCTGCTTC TGATAATGAT TGAAGATAAC 3600

TTTTCATTAA TAGTCGTCCT AGCTGCTCGT CTCCAGTACC TAATTGATCG GAGCCAATCG 3660

TAATTACTAA ATCTGTTGCT GACTGACTTG TTTGTTGAGT CGCTTCTTCA GGTACCGTAA 3720

TTTTGACAGA GAAAACCGTG GCTTCTAtnT GctTCGCAGT CAAAGTGGCC TGTTTTTTAG 3780

TAGCTAATTT TTTTAAATTT TCAATGGCTA CTTCGTTATC GACTAATACC TCGATAGTGC 3840

CTCCAGCTAA ACCTAACTCC GCCAAAGCTT TTTTTGTTTC AATCACAGGT ATTGGGCAAG 3900

GTTTCCCCAA TGCATCTACT AATTTCATAT TTGGCCCTTC TCTCTATAAA AGTACTACTG 3960

CTTGTTGTTC TTTTGGCAGA ACCTCGCCAA TAATTTTGGC AACAGGGTCC TCTTTTTGAA 4020

TAGCTGCTAA ACAGGCTGCC GCTTCGTCAG CAGCGACACT AATTAACAGT CCGCCAGAAG 4080

TTTGTGGATC AAACAAAAGT TCTTGCATTT CCATAGAAAT TTTTGAATAA TCGATTGTCG 4140

TTCCGATTGT TTGGCGGTTT CTTTGCCCAG CTGCAGTGAC TAAACATTCT GCGGCGTAGG 4200

CCAACGCTCC TGTAATGGTT GGTAATGCTT CTGTATCAAT CAGTAATGTT ACCTGATTAT 4260

CAGCCATTTC TTTTGCATGA ATTAATAGAC CAAACCCAGT CACGTCAGTA CAAGCATGTA 4320

CTGCGTAGGA TCGAGCATTC GCAGCGGCAT ATTTATTTAA ACGTTCCATC GAATCTTGTG 4380

CGATTTTTTG TTCCGTCTGc TTCGCCAATT GCCCCCGAAC AGCCGCTTGA ATAATTCCTA 4440

CACCTAATGC TTTAGTTAAA ATCAAGACAT CCCCCACCTG TGGCGTATTA TTATGCCACA 4500

AATTTTCTGG ATGAACTTCT CCGGTTACCG CTAGACCATA CTTGGGTTCA TGGTCATAAA 4560

TCGAATGGCC TCCCGCCAGT AAAGCACCCG CTTCCTTTAA TTTTAAGCTG CCACCCAAGA 4620

GCATTTGTTC CAACCATTCT TTTGACATCT TTTGTGGAAA ACAAACAAGA TTTAGCGCAT 4680

AAAGGACTGT TCCGCCCATG GCATAGACAT CACTTAAAGC ATTAGCGACC GCAATTTTTC 4740

CAAATGATAA CGGATCATTG ACCATTGGTG AAAAAAAATC TACCGTTGAA ATCAAAGCTT 4800

TTTCAGACGT TATTTGGTAA ACAGCGGCGT CGTCGGCATG TTCAAATCCG ACGAGTAGCC 4860

GCTCATTTGC CGGTGTTTCG GGTAAGTGTT GCAACAATTG GTTCAGTACA CGGGATTCAA 4920

TTTTTGCCCC ACAGCCACCT GATGTACATT GTGATAAAAA ATCCATGCTG TCCGCTCCTT 4980

CTCAAATTAG TAGTTCTTGT AAAGCGTGAA TTGTCCAAGT AATTTCTTCA GGCGTTGTCT 5040

GCCAACCAAA GCTAAAACGT AAGGTGCCAG TTGCTAAAGT CCCAGCTGTT TGATGGGCTA 5100

ATGGTGCACA ATGCAAACCT GCGCGCGTCA TAATGCCATA TTGTTCTGCT AGTTGCTGTG 5160

CCACTATTGT TTCTTCCTGA TTCCACAGTG TGATAGAAAC AACAGGGACA GTTTGTGCCA 5220

CGTCCTTGGT TCCTAAAATT GTGACAGGTA ACCCTGATAA ACCATTTAAA AAATTCTGCA 5280

TTAAGGTTCG TTCATGCTTT TGAATCGCTG CTAAACCAAT TTTATTCAAC TCTTTAATAG 5340

AACTATTTAA GCTTAGAATA CCTAAACTGT TTAACGTACC AGCTTCAAAT TTATCTGGTA 5400

AAAAAGAGGG TTGATCAAAG GAATTAGAAT GGCTACCAGT GCCGCCCGCC ATCAGTGGTT 5460

TGACCGCTTC AGCCCCTCGC TCACTAAAAG CTAACCCACC AATACCTGCT AATCCATATA 5520

AGCTTTTATG TCCAGTAAAG GCTAACACAT CAATGGCCAT CTGGGTCATT TTTATTGGTA 5580

AAAATCCCGC CGTTTGAGCC GCATCCAAAA TAGTTAGTAA TCCTTTCTGT TGAGCCCATT 5640

GAAAACATTC TTCAATGGGT AAAATGGTGC CTAAGACATT GGATGCGTGT GTCATCACCA 5700

AGGCTTTTGT ATTCGTTCGC CAAGCTCGCT GAATATCTTC TACTTCTAAC AGGCCAGTTT 5760

TTTGACAAGC AACATATGTC ACTGAAATGC CTCGTTCTTT CTCAAGTAAG TGAAGAGGTC 5820

TAGCTACTGC ATGATGTTCT AACATAGTCG TAATCACATG GTCGCCAGGT TGTAAAATCC 5880

CCGCTAATGC AAGATTTAAG GAAGTTGTTG CGTTATTCGT AAACGTAATC TGAGCCGCAC 5940

TGGGTGCCTG AAAAAAGTCT GCTAACAATT GACGTGTCTC TAAAAGAGGA AGCCCCTCTC 6000

TAAGCAAAGG GGCATTTCTT CCGTAATTCA TGAACTGATT TTCTGCTAAA TAGGCAGTCA 6060

AAGCCTCAAT GGTTGCTGGA AATTTTTTAT AGGAAGTCGC TGCATAATTT AAATAAACCA 6120

AGTCCTTCAT ACGTTTTTCC TCTCTAACTA TTGGTTTCTT GAATTAATTT TTGGTACTCT 6180

TCTGGCGTGT CGATATCTTT CAAACGGCCA GGAGTCGCTA TTCTCAGCAT CTGAACTGCT 6240

TCTGGAAAGC GTTCATAAAT CATGCGTCCG CCTTTTTCAC CAGTCAATGT TAATAGTTCT 6300

TGTCGAAATT GATTACCGAA TAATACTGGA CTACTAGGAC AGCCATCTTT TTGTAATGGC 6360

ACTACAATTT TATTTCTCTG ACATTTATCT AACACGAGTT GTAGCATTTT AGGTGTTAAC 6420

AATGGTTGAT CGCTAGGTAA GTATAAATAG CCAGCTCCCC GAGCTTGTTC GGTTCCTAAA 6480

CGAATACTGC TACTTTGTCC TTCTTGCCAT TGATGATTGA GAATCAACTG AATGTTCTTA 6540

GGTAAAGGAA ACGCTGGCTG ATTCTCAGGC GAAACAACTA AAATCCGTTC TAATACGTCT 6600

AATTGATTCA CTAAGGTTAA CGTGTGCTCT AAAAATGTTT TTCCTTGATA TTTTAAGAAC 6660

AATTTATTTT GGCCCATCCG TTGTGAATTG CCCGATGCTA GAATAATGAC ACTAACGAGT 6720

GACATGAGTT GTCTCCTTTT ATCTTTTTTT CTTTTGATAA GGGGTATTTT CTAAAGGCAG 6780

ACTTGGTCGG AGCTGACCAT CCAAGGCAAA ATATGCGCCT GCTAAAGCTG GTGCGGTAGG 6840

GATCGTTGCT AACTCACCTA CGCCTTTAAT TCCATAAGCT AAACCTTCGT GAAGATTGTC 6900

AGCATGAACC AAAATTGTTT CGATTGGTGG TACTTGAGTG GCGTTCACTA ATCCTAGCGT 6960

TGCATATTTT GCTTTAACAT AGCCTTCTTC TAAGGCAAAT TTTTCAGTTA AAGCATACCC 7020

CATGCCCATT GCAATCCCAC CTTCAATTTG ACCTTCAGCA GCTCGTGGAT TCACCACTTG 7080

CCCCATATCA TACGCAGCCA CAAATTTAGC TACTTTTCCT TTGTCATCTA GAATAGCTAC 7140

TTCAGCAGCA TAACCATAAC CAGCATGACT AACTGGACTT TTTTTATCAT TAATTAATGG 7200

ATCCGTTTTC GCTGAATATT CCCCATAAAA TTCTTCGCCT TCCAAATCGC TTAAAGCACG 7260

TCCCATATCA AGCTCATACC GTAATTGCAT TGCCGCTCTT CTAGTTGCTT CTCCTGTGAA 7320

GAGTGACTGC CTCGAAGCCG TTGTCGTTCC TGAATTCGGT GTTCTTCTTG TATCAGGGGc 7380

TTCCGCAACA ATCATTTCTG GTGGTAAATT TAATGTTTCA CAGGCAATTT GCGTCGTAAC 7440

GGTTGCCATC CCTTGACCGA TACAAGCAGC ACTTGTGCGG ACATGTATTT TTCCTTCTTC 7500

AACAGAAATA ATACAACGCC CTGTATCAGG TAGCCCCACA CCCACGCCAC TATTTTTAAA 7560

GAAACTAGAA ATTCCAGCAA CTTCCGCTTG TTCATAGACG TCTTTAACCG CTAACAAGGC 7620

TTCTTTTAAC GCTGCATTTT TCGAGACCAA TTGTCCATTC GGTAAAGTAT CTCCTGGGGC 7680

GACGGCATTT TTAAAGCGTA TTTCCCATGG TGATAGTCCG ACTTTTTCTG CTAACAAGTT 7740

TAAATTACTT TCAATTGCAA AAGCCGTTTG GCAAACACCA AATCCGCGAA ATGCACCTGC 7800

TGGCGGATTA TTAGTATATA CAGCAAACCC TTCCACATCA ATCGTTtGAT ACTTGTAGGG 7860

ACCTGCCGCA TGTGTACAAG CCCGTTGCAA TACCGGTCCT CCTAAAGAAG CATAGGCCCC 7920

AGTATCCGCA TAAATCACTG CTTTCATTGC AGTTAAATTG CCTTCTTCAT CACAGCCGGT 7980

CGTAAAGTCC ATTTCCATGC CATGGCGTTT GGGATGAACC ATCAAACTTT CTTCACGGCT 8040

TAGCAGTACT TTTACTGGTT TCTTCAATAA CCAAGCGGCT AAGGATGCAT GATGCTGAAC 8100

ACTCATGTCT TCTTTTCCAC CAAAACCACC ACCAACAAGT TTTGATTGAA CATGAATTTT 8160

TTCCTTGTCT AGCCCTAGCA TCCGAGCCAC TTCCCGTTGT TCATCATAGA TACTTTGACC 8220

CGCACTAAAG AGTAAAATGC CCTCACCTTC AGGTTGTGCA ATCGCACATT CGGGCTCCAT 8280

AAAGGCATGT TCATTAAygG TACGGAATAA TGTyCTGTCA CTACAAACGC AGAwTTTTCT 8340

AACACTTCCT CTGCATgCCA CGTACCAAGT GTTCaTGaGA CAAGATATTG CCCTTTTCAT 8400

GaATAGCTGG TGCACCTTCT GCTAAAGCAG CTTCACAAGA AGTAAGCGGT ATCATTTCTT 8460

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CGAGTGCTAC TGCATCCCCA ACATACCGTG TTATTTCTCC TTCTGGAATC ATTACATCCC 8580

AATCGGAAAT AAATTCTAAA TGACCAATTT TATTATTTCC TGGAACGTCT TTAGCTGTGA 8640

ACACAGCCAC ACAGTCAGGA TGCGCCAATG CTTGGGTACT ATCGATTGAT AGAACTTTTG 8700

CGCGAGGATA GGCACTCCGC AAAGCAGATG CATGaAGCAT TCCTTCTATG TCAATGTCAT 8760

CTACATAAAT CCCTGTTCCT AAGGTTTTCT CCACTGCATC GACCCGTTGG AAGTCTTCCC 8820

CTAATTTACC ATTTGAATGk TCTTCTGGAA TGCTCGCTTC TTCACAAAAC ATTTTAGCAG 8880

CTAACTGAAT GGCTTCTATT ATTTTCACAT ATCCTGTACA ACGACAAATG TTTCCTCGTA 8940

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AAATAACCAT CCCAGGGATG CAATACCCGC ACTGAACTGC ACCCGTTTTT GCAAACGCAT 9060

AGGCATAGAC ATCTTTTTGC CGTTGGCTTA AACCTTCGAT TGTCGTGACT TCTTTACCAG 9120

CTAATTTTTC TAGAGTAAAC AAACATGCTT TGGAAGCCTT TCCATTTACT AACACCGTAC 9180

ATGCACCGCA AGAGCCTTGG TTACAGCCAT CTTTTGTTCC AGTTAGGCCC AGATCCTCCC 9240

GCAAAAAGTC CATTAATTTT TTGTTTGTTT CACAGGTTTC ACTTTGACCA TTTACAATAA 9300

TTGAATACAT TTCTTGCACC TCGATTTCTG ATATrGTTTA GTGTTCAATC ACCkrGATTA 9360

TACCACAAAT CTCCGTTCTA AAAATTATTT TTTAGCAAAA AAAGTTTTTT ATTTAATTTA 9420

AAGGTTCGCA TTATTGATAG CGCTGTTGAA TTAATTCTCC CGCGATGCTA ATCGCTAACT 9480

CTTCTGGTGT TTCGGCTGCA ATGTCTAAGC CAATTGGCAT GAAAATTCTT TCAATTTCAG 9540

TCATTGTATA ACCGACCTCT TTTAACCGTC GAACTTGTGA AGCAATTTTG TGTTTGCTCC 9600

CCATCACACC AATATATTTG GCTGGTGTTT CCAATAACTG TTTGGCAACG ATGAAATCAA 9660

AATTGTGTCC TCTGGTAATT ACTATACCAT AATCGTCCGC CGTTATTTCA ATAAACGCAG 9720

CTAAATTTTC TAAAGGAATC ACCCGTAGTT CTTCAGCTTG TGGAAAAGCT TGTGCCGTCA 9780

AAAATTCTGG ACGATCGTCC ACTACAACGC AATAAAACGA TAAATAGTTT AAAATAGGTA 9840

CCAATGCGCG TGCAACATGA CCACTTCCAA AAATATACAC TTTCCCTACT TGGAGGATCG 9900

CTTCTGTTAA AAAAATTATG TCCTCTTTTT GCTCACAATG GATACCTTTA GGTAGCAAAC 9960

TTAATTCCCC CTCCCAAGAA GTGGAACCAA TCAATTCGCC TGTTTCACTA TAAAAGGATA 10020

CTTTTCCTAA ATTGTTTTGA TCTAGTTCAG TCACTAACCA ACCTTGTTGG TTATTTTGAA 10080

AATGCGTTTC TATGGATTCA CACAACTCCT TTAAAAATGG CGTTTCCCAT GAAAGATAAT 10140

GGAAAAAAAT CGTGACATTC CCGCCACAGA CCATACCTAA ATCAGCAATA TTATTCGGGG 10200

CTAAAATAAA TTGACGTTGT GCATTTTCTT TCTCAAGAAC TAGCTTTTTT GCCACTTGTT 10260

CAGCCTGAAA TTCAACCGCC CCACCACCAA CAGTTCCGGC TATTCTACCT TCGGCGGAAA 10320

CCAGCATTCT AGCCCCTTGA CTTcGTGGTG TGGAtCCtGa ACTTGTACCa ATCGTTAATA 10380

ACaTCGTGTC TTGCTTTTCC AAtATTGCCT GtTTCAAACG CTGAAATACT TCTCTCATTT 10440

CAGTTCCTCC GATACTACAT CCTGTTCTTT AAATATTTCT TCAAAGCATG CCTCTACCTG 10500

TTGATACACT TTTTTCTCAA ATAAAAGATA TTGATCAATC AACTCTTTTC CTTGA 10555

(2) INFORMATION FOR SEQ ID NO: 234:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCCACTCAAC GTACATTTAA AACATACCCT ATTACTATAC AGGATTCCCT TTACTTTTTC 60

AAGATGTTTT TATGATTTCA AGACAATTTT TTTATCCGTT ATTTTCTTCA TGAAATGCGC 120

ATCATGCTCA ATCACTAGCA TTGCAGGCTT CACAGATAAG ATTAGCGCTT CTAATTGTTG 180

ATGATTAAAC ACATCCAAGT AATTAAGGGG TTCATCCCAA ATATAAAGCT CTGCTGATTG 240

AGACAATGAT TTGGCTACTT CGACTTTTTT CCGTTGCCCC ATACTCATTT GTTCAATTCG 300

ATTAGTGAAA ACGGnCACGC TCCATCCCAA GTTTTCGTAA GTTATTTAAA AATTGGGTGT 360

AATCTAACTG ATTTTTCTCT GCAAATTCGG aTAAAGTTCC TTGATTGTCT TCATAATCTT 420

GGCGCACATA AGAAATGGTT AATTGGTGaG CCAAAGTGGc TTCGCCTTCT GaATCCCCAG 480

AAAAATTaTC CAATAAAtAC TGaATCaAGC TCGrTTTTCC TGaGCCATTT TTTCCTGTTA 540

TTCCGaCAAT TTCTCCCGCG tTTATTGaAA AAGaAATTGG cGCmAACAGC CAATTTTTCT 600

CGTAGCCTAG ACGAAGCTCT TCCACCGTCA ATAATGTTTT GTGATGCGTT GGCTGATAAT 660

CCATTGACAA AGAATCAATA TACTCAAGAT CTTTTAATAG TnTTTCTTTT TCTGCTAAnn 720

GTGTTTCGGC GCGTTGTTGG AATATGTTTC GA 752

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

TTGATATCCA GTTTGTAATA ACCATGGCTA AAACAATCGA AACAATCCCT GGATCAAAGA 60

CTGTTAGCAT CAAGATCATA ACAACTAAGT TAGGAATACC AGAAAGAACT TCTAAAATAC 120

GTTGCATTAC TGTATCGACA CGACCGCCGA CTAACCCGGA AATCAGTCCA TACGTTACCC 180

CAATCGTAAT ATCTAGAATT GCCGCGATAA ACGCAATTAA TAATGAAATA CGTGTTCCCA 240

TAAATAAACG ACTTAGGACA TCACGACCTA AACCATCTGT TCCTAGATAA AAGTTTACGT 300

TATCTGGAAC GTTTGCTTGT GCATATTTAT CAACTAATTG ACCAGCAACT GTTGTTTTAC 360

CATTTAAACC ATTCACGCTT TCCAAGCCAG GAATTCGTGG TGGTAAGTTA ATGTAAGAAA 420

CATTTTGTTT CGTTGGGTTA TGTGGTGAAA CCCAAATGGT AATAATAGAG ATAAAGATAA 480

TAACTGCTAA GAAACTCATT GAGATAACTG CAGCTTTATT CTTTTTCAAA CGACGCCATG 540

AGTCTTGTAA GAAACTTAAA GACGGTGTGG CAATACGCTC TCTTTCTTTT AGAGTTGAAG 600

TGTTTAGAGG CTGAAACTCA TCTGCCGGAA TATCTTTAAT CGCTTGTGGT AGATTATTTT 660

TATTGACTGT TTCCATTAGC CTTTTGCACC TCCTGATACG CGAATTCTTG GATCAATTAA 720

ACCATAAAGT AAGTCAACAA TCAGAATTAC AACAACTAAC ATTGTTGAAT ACAAAATAGT 780

TACTGCCATA ATTGTTGGAT AGTCGTTTGT CATAATTGAT TTTACAAACT GTTCCCCAAT 840

CCCAGGGATG GCAAAAATAT TTTCTACTAC TAAAGAACCT GTgcATTAAA CCAACGGCTA 900

AAGGTCCTAA TAAGGTAATC AATGGAATTA AACTGTTTCT TAATCCGTGG CGGAATGCAA 960

CTTGCCAGCG ACTCAAGCCT TTTGCTTTGG CTAATTCGAC ATAATCACTA TGCAAGACCT 1020

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CTACCATCTC GGTTCGAATA AACCTAGCCG AATCGGCCAT GGGACTCATT GCCAAGGCAA   1080

TAGTTGGGAA GATTGTGTAG GCAAAACCAT TCCACATAGC AATTGGTAAG ATTCTTAATT   1140

TCATTGCAAA AATGTATTGT AATAATACCG CGAAAACAAA GTTTGGAATA GAACGACCTA   1200

AAATGGCTAA CAATGTTGCC AACGTATCTA CCCAAGTATT TTGACGCATC GCTGCGATAA   1260

TCCCCAATAA AATACCGACT AACGTACCAA AGATAATCGC TTGTCCTCCC AGTTGAAGGG   1320

ATGGCCCAAT TCGACCAGCT AATAACTTAG CAACAGGTTG GTTTTTAAAT TGGAATGAAA   1380

TACCAAAGTC TCCTGTTACC AGGTTCTTTA AGTAAATTCC GTATTGAACA ATCACTGGTT   1440

TATCTAAGCC AGATTGTTTA TTCAACATAG CGATTGTTTC TGGACTAAGT TTTTCTTGGT   1500

TGGTATAAGG CGTACCTGGT AATAATTGCA TTAAGAAAAA CGTAATCGTT GCGATTAACC   1560

ACAAAGTGAT AATCATGAAA AAGATCCGTT TAAGAAAATA TTTTCCAAAA CTATTCAATA   1620

ATGACACCTC CGAGATTTTT TTGACTTCCT CAGTTATTTT CGTTAAAGTA ATGACTAGAT   1680

AGACCACAAT AATAGATAGG GTGAACACAT GAraACTTTT AAATGGCCAA tTaTTACAGC   1740

CGTTATTTCC AGTATCGGCA TTTTTCTTTA CTTATTAATA AGTAAAGAAC CTATCACTAC   1800

CTCCTCATTA TCAGATACCT yCTTTATCGT TTCGCTTTtC TTTTTAATTA TCGGCATTGC   1860

TTTATGGATT ATATCCTCTG GCTTTTTCGA TAACTTTCAG CGCTCAATGA AAAACGCGTT   1920

TCGTTTTAAA AAGAAAAATG AACCGAAAGA GTTTATCCCG CTTTCAGTCA TTGGCGATGC   1980

ACATCGCTCT TTCTGGCTAA AAACTGGGGG CATCTTACTG ATTCTGTCTT TAGGCTTTCT   2040

ACTAnTTTAC TTGGTCTAAG ACAAGATAGC AAGAGGACCG TTGCCTTTTA TTCCATGGCA   2100

AAGGTCCTTT TTTGTTTGCT ATCGATCTTT TGTCAGGTTA TTCTGAAATG TATGCCCATT   2160

TGTAGTCATA CGTTGCGCCA GCAGGATGAA CTGCGACATC TTTGACTTTT TCAGCACGTA   2220

AATGCGCTTC TGATTTTTGG AATAATGGTA CCACACCCAT GTCTCCCATA ATCGTTTTCT   2280

CTGCATTTAA CATATCATCC CAACGTTTTT CAGGATCTGT CGCATCTGCA CTACTTGCTG   2340

CTTTCACGAA CTTGTCAAAC TCTGCATTGT TATAACGTCC ACGGTTATAT GAGTTATCTG   2400

AAGCAAATAA GTCTAAGAAA CTACTTGGAT CAGCATAGTC AGCACTCCAA CCACCGATTA   2460

CTGCATCAAA GTCGCCTTTG TTTGAACGAT CTAAACGAAC AGAGAATGGA ACCGGACTAA   2520

CCGTTACCTT CACACCATCT AAAGCATCTT GAATTGACCC TTGAACAAAT TCAACTGTTT   2580

TCTTAGAAGA ATCTGCATCT GAAGAAAGAA TATCCATTGT TAAGGTTGAA ATCCCCAATT   2640

CTTTTTTCGC TTTTTCCCAG TATTCTTTAG CTTTTTTCGt ATCATATTCA ATTTGaCTAC   2700

CTGCTTCTTT AGCAAAGTCT TTGCCGCCAC TTGGGtCTTT TGCCATATCT GCTGGTACTA   2760

AACCGTTTGG cTCGATAGA                                                2779
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(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 10955 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

GTGGCAGCCC AGCAAGTCAA AGTGCGCCCG CACCTGATGA AGTGTTGGCG ACAAGTATTG 60

GGACGTATGA AAATCGAACA TTGTTGGTTC CAGATGGGCG TTTAGCCTTA ACTGCCTTGC 120

ATAAAGGAAA AGATTATCAA GGCAAACCAA TGTTTTATGT CCTGTTTGAA TTAACCAATA 180

CAACCGAAAA AACACAAAAT ATTCAGCTAA TGATTCAAAG TTTTATGGAA GTTAGTCAAA 240

CTGTCCACGG AAAAGCCCAA AATTTACAAT ATGCAGTCTT AACAGATTCA CCTTTCCAAG 300

ACAAATTAGA TCGTTTAGCA GATGAAATCA ATCCTGGTGA AACAATCCAA GGCGCTTACC 360

CGTATGAATT TATTAATGAG AACAAGCCGG TCCATTTTAA ATTTAGAGAT CGCCTTCTCA 420

GTCTGGATGA ACCCATTGCA TCAGAAGAAA TTACCATTAC AGAAAAAAGT TTGGTCCGCT 480

AGCTTAGCTA GCATTGGACC AAACTTTTTA TTTATTATTC AGACGGAAAA GATTCTCCTT 540

CTATAAAACG TGTGTAAATG TGTTCGCTCT CAGCAGCTTC TCCCCGCATT AAATGAATAA 600

TTTTCTCTGC AGCCACCATG CCCCATCGAT GTTTAGAATA GGCAATTGTT GCTAATCGCG 660

GTTGCACAAA CGCACCTAGT TCAGAATTAT CAAAACCAAT AATCCGAATG TCTTTCCCCA 720

TTTGGTAATT TGTTTCTGCA ACATATTTAT AGACACCAAT CGCCATTTCA TCATTAAAAG 780

CAAAAACATC GACTGGTTCT GTCTGTGGTT GACTCAAAAT TTTTTTAGCA GCCGCATAGC 840

CAGAAGGTTC GGTAAAATCG CCTTGGATAA TTTCATAAGG TATCCCAAAA CGAGTTAATT 900

CTCGTGTACT AACAGCCAAT CGTTCTTGGC TATCATAACC TTTTTCTGGT CCAGAAAGCA 960

GAAGAACTTT TTTTGAACCC ACATTGACAA ATTGCTCAAT TGCCTGCGTG GCACCGCCAc 1020

GGTTATCCAA GAGAACTTGC CGAATATTCC TATGCTCAGT GGTTCGATCA AGGACAACGA 1080

TCGAATGGCC TCGTTCAGCA AACTTTTCAA TTTCTTTTGT TGGAAATGTC CAATCTAAAA 1140

TAATTGCCCC ATCCACCATT TTTTCAGGAA TGAAAAGATG TGACTTTTTA CCGCTGCAGA 1200

CAATCATCTC ATAATCAAAC AGTGCTAAGC CTTTCTTAAT TCCCTCCAAC AATTCACCAT 1260

AAAAACTACC GCCATAATCA GCCAAATAGA CACCAATAAT ATTGGTTTGA CGACGTTTTA 1320

ATGTGCGAGC GGCCATGTTA GGAACATAGT TTAGCTCTTC AGCAATTGCT TGGATGCGCG 1380

TTCGTGTTTC TTCAGTTACC TTTGAACTAC CATTCAATGC GTAAGAAACG GTCGAGATTG 1440

ATACGCCTGC TTTTTTTGCA ATATCTTTAA TTCCTaCCAT GGACTACTCT CCTTTCTAAT 1500

GGTAAATTTC AATAACACTT GCTTCATTTA ATAATGAAAG CACCTCGTCT TTTTGAACTT 1560

CCATTCCCCC TTCTCGATAA GGGTTTTCTT CAAACTTAAA CGGAACCTCT TGACCATCGA 1620

TAACTATTTT CGCTGACTGA TTTGGATAAA ATTTATATGT GACAGGTTTA TCAAACAATT 1680

GGTAAGTTAG TGTTAAACCA GACAATTTTT CTGGTAACAT GGGATCAAAA ACTACACTTT 1740

GGGCCTTTTG CCGAATCCCT AAAACAGCTG TAATTAATTG ATTTAAATAA ATTCCCGGCC 1800

CGCTTGAATA AATTCGCCAA CCACCTTTTA CCCCAATACT TCCATCTTTT AGTTTACCAA 1860

AATTTTCTTG TGATTCATAC CTTGTTTTAA AATCGCCATC GGAACTACTA AAATAGGCAT 1920

TGGCTTGACG TAACTCTGCA TTGTGAACCA CTTCTTTTAA TTGAACTGGA TTGATTTGCA 1980

TTAATGCTTG CCAGGTTTTG TCTCGCTGAC CAATTTTCGC CATCGCTTCT GTATAGCGAA 2040

TGTGCGCATG AACATACTGT AAGCCAATTT CGCGACCAAA ATTAGCCGCC TGTTCTGCTC 2100

GTTTAAAATT AGTGCTCACA CCGCCTCGAT AGTTCGCTGG TTTGTTCATT AAGCGCACGC 2160

CATCAGGAAA CGTTAATTCT TTTTCAATAA TTTCTAAATG ATGACTTACT TGTTCCGGTG 2220

TTAATAATTC AGCTAACATA CTACGAGTCA TTGGCAATAA TCGATATTGA ATCCCTGTTT 2280

TTTGGTCATT TGGGTGAATC ATTTGTTCAA AAGTTTCTGG CGTTTCCATA TAAATAAACC 2340

CTGGAATCGT TTCATCTGCC AACATATATT TTTGAAAATC GTTCTTTATT CCTGCGACTA 2400

AAATTGCTAA GTGCTGACTA TAAGTAGCAT CGATTTCCGT AATTAAAGCC GCAAATTTTT 2460

TCAACACTTG ATACGTTAAG GCAACGGTCC AACTACTAGC CATTTGCTCT TTAAGACGAT 2520

TATCATAAGG TTGTAACGTG TCATCCCAAT CGCCGTCGCC ATAACAAGAT AGAAAAGTTT 2580

CTGGTAAAAA ATGTTGTTCA ATATAATTTA TTTCTTTTTT CAAATGTTCA AATAAAGATG 2640

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TTGAATAATC TGCGGTTTGT TCCAAATAAT CAGTCACTAC TTTCAATGGC CAGACGATAA 2760

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GCCAGTTGCC ATCGTCCTCA AATTGATTTT CAAATAGATG CTGAATAATG GAGGCCACGA 2880

TCTTAGGCTG TTGCGTCGCA AAGAAAAATT CTGTCGGTCC TTGCGACACA TCTCGTGTGC 2940

CCCAAGCTGC TCCACCATAC TGTTCTAAGC CATGTGGCGA CAAATAATGA ACGAGCATAT 3000

TATGAGTATA CCAACGAGTT AATTGATTCA TTTGCTGCAC ACTTGAGTCT GTGTGTGTTA 3060

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ATTTTTGGGT CTTTTCGATT GCCAAGACTA ATAATTCTGC TTCAGCTCCA CCAAATAATG 3240

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AATTTTCTGT GGCAGAATGA TTTCCCGTCA CTCGAAGCGT TTTGCCAGTT TGTTCTAATT 3360

GATAGGTTGG TACTTCTTCC GGTCCTAATA ACAAATGGTT AGAAACAGCC CACATATATG 3420

CATCCTTTTG ACTGGTCACT TCCAATTGAA TCACTCTTGA ATCAGGCGAA GTGAAGGTGC 3480

GTACACGAAT TGTATCCTTT GGCAACTTAT AATACCACGT AGCAGAGTTC AACCCCATTT 3540

CAAAAGCAGA AGGCATTGTT AGTAAGCGCC ATAAGCCATT CTCTAAAATG TAGATTCGTT 3600

GACCAGAGCG TTTCATAACG TTTAAAGCGT TTCGGCTATT ACTCATTAAT TTGTTCATGG 3660

TCGTATTTCC TAAAACTACT TGTGAATTGA AAATGCCATA CATATACACT GTCGTACTAA 3720

GCAAAGGTTC GTCAACCGTT AAGCCTTTAC CACTTAATAA AATGTGGCCA TGCGCTCTTT 3780

CCATGGCAAT TTCTTTTTCT TGAAGAACAA CATGATGGTA ATTTTCCGTG AAAAAGGAAT 3840

ACGTCTGACC TGCTACTTTT TCAATTTGTG TCTGAAGGGG ATAAAGTGCG GCCAATTCTT 3900

CTTCTGTTAA TGGATTTCCT GTGATAGGTT CTCCTAAAAG TTTCGGAGGA TAGTCCTGTG 3960

TTCCTTCTAA TGAATCGAAT GTCACAGTTT CATAAATAGC TTGTAAGGCT TCTTTCGATA 4020

AAAAAGGTTC AGCTAATGCT TGCGGATGTG TTTCTGTTAC CGCACCATAA AAAACAAATT 4080

CCTTACTTTC ATTCGTTAAT TGGACGGCTT CCGTTTGTAA AGCGGTGTAA GCAAATTCAT 4140

ATTGATAGAC TTCATTTGCT AAATATCTTT TCCCCAATGC TTCTGGTGTG TTTATTTGTT 4200

TAAATGAACG TCCGAAAAAT TGATAGCCGT CCGTTGAGTA GCCTACTAAT TTTTGAAAAC 4260

TCCCTTGAAT AAGGGCTGGA AACTTCTCAT TTTGCGGTTG ATTTTGTCTT GATAAAACAA 4320

CAAGCTCTTC GCCCTCTTGC CAAATGTGAT GATCAAGATA CTGCGACACA TACGCTTCAT 4380

TTGACTGAAC GGCTCCTTTT GTCGCTAAGC CAATATCTTG ACCATAAACA ATATCTACTA 4440

AGCCAGTTCC AGTGACATTA ACCCGCCAGA ACCATTGATT GCTTGGCCCC AAACGAAAGT 4500

CAACTTGGTA ACGAACCGCT TCAAATTCAC CCCGCCATGT CAATTGATTA TCTGAAAGAT 4560

AAAAATCACT TTGACTGTTG GAACCAATCA TTGGTCGATA ATTAATTGTG TCCCCTGTAA 4620

TTATCCGCAA ATAGAGTTGG TTCATACTGC CGTCTAAAGG ATTACCTTCT AATTGATTAA 4680

TCATCATGCC ACAGCTATTC AATTCTTTTA AATCACCTGT CTCTAGAAAT GTAGCAACTG 4740

TGTCTGCTTG CTTAAGCTTC TTTATCTGCA TAACTTATCC TTCCCATCTT ATTCATTTAA 4800

CGTGACTGTT GCGGTTTGTA CATCGCGACT ATTTCCACCA ATCATTACGA TAAATTCACC 4860

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AAACTGAACT TCTTTTTCTT CCTTTGGTTC CAGCCAAACT TTTTGGAAAT CTTTTAACTC 4980

TTTAATTGGG CGAACCACTT GTCCCACCAA ATCACGTACA TAAAATTGCA CGGTTTCCTC 5040

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AAATGTTAAT GCACTTAGTT GAATTGGTTG ATAAGAGAAA TGACTATAAC TTAAGCCAAA 5160

TCCAAAGGGA TATTTAGCGT AATTAGAGAC ATCTAAATAT TTAGAAACAT ATTTTTCTTC 5220

TGGTGCTGAC TCATAAGGAC GCCCAGTATT GTCGACATTG TAAAAAATTG GCACTTGACC 5280

AACCGTTTCT GGAAACGACA TACTTAAACG ACCACTTGGA TTGTACTGTC CCCACAAAAT 5340

TTCTGCTAGC GCATTGCCCC CTTCTGTTCC AGGTTGCCAA GCTTGCACAA TTCCTTTTGC 5400

AACATCTATC CCTTGCAAAT CTAAGGGCCG GCCACTGTAG ACCGTGACAA CAACATTGGG 5460

ATTTTTCTCA ATAATTTGTG CAACTACCGC TAATTGTTTT TCGGGTAGAC GAATATCACT 5520

GCGACTGGCA GCTTCCCCAC TCATCCAATC TGTTTCGCCT AGTGCCACTA CTACTTTATC 5580

TGCTTGACTA GCTAACGTTA AAGCCTCTTC AATGGCCGCC GCGGTCGGTT CAAAGTAATC 5640

AAAGGGTTCT TGGGCAACTA GAAGATTTGT GGTTAATTTT TGGGCCCCAG CCACGAGGGA 5700

AATGGCTTCT TCTTTCTTTC CTTGCCATGA CCAAGCCCCT AAAATATCTT GTGATTGGGC 5760

CCCTGGGCCG ACAAGCGCGA TTTTTTCTTG CGGTGTAAAA GGCAAAATAT TTTCATtTTT 5820

TAAAAGAACC ATTGATTTTT GAGCAATCTT TTTAGCTATT TCTCGATGTT CTTTGCTTAA 5880

AATCACTTCT GCTTCCGCTT GTTCATCCGC ACCACGATAG GGATTTTCAA ATAAGCCTAG 5940

CTCATTTTTT AGTTTTAAAA TTCGCATAAC TGCTTCATCA ATAAGTGTTT CAGCAATCCG 6000

GCCTTCTTCA AGTAATTCTT TTAAATAATC TGGATAACAC GTGGTCATCA TTTCAATATC 6060

TACACCAGCT TTGATAGCCA ATTCTGCCGC TTGTTTTTCA TCTTTGGCAA CGCCATGAGG 6120

AATTAATTCT TTAATCGCTC CCCAGTCTGA AATCACAACC CCTTCAAATC CAAATTCATT 6180

TCGTAATACG TCTCTAAACA GCCATTGGTT GCCTGTAGCA GGAATCCCAT CCaCTGTATT 6240

GAAGGACGTC ATGACAAGTT TTGCACCCGC ATCTAATCCA GCTTTATAGC CAGGTAAATA 6300

CATTTCTCTT AGCTGCCGTT CAGACATATC TACCGTATTA TAATCCCGAC CAGCTAAGGC 6360

ACCACCATAT GCCGCAAAGT GCTTCACGCA CGCGGCTACT CGCCAATTGT CTTCTTTTAA 6420

ATTTTCTCCT TGGTAACCTC TAACCATTGC AGCAGCTAAG CGGCTGTTGA GTAATGGATC 6480

TTCACCTGTT GACTCCATGA CACGTCCCCA ACGTGGATCG CGCACTAAAT CAACCATTGG 6540

TGAAAAGGTT ACATGTAATC CTGAAACAGC AGCTTCTTTT GCTGAAATCT CCGCCATTTT 6600

TTCAACCGCT GCTTCATCCC AAGTGCTTCC TAAAGCCAAA GGAATCGGAA AGATGGTTCT 6660

GAAACCATGA ATAATATCCG CCATTAAAAG TGTTGGAATA TTTAATCGAT GATTTTGCAT 6720

ATATTCTTTT TGAACACGTT TTGCTTCGTT TGCACCGGAA ACACCCAGTG TTGTCCCCGC 6780

CGTATCAATC GTTTCTTGAC TTAGTCCTAG CTCTGACATA GGGCCGGTCT TTTCTTCTGC 6840

TTTATCTGAA TAAAACGCTG CTGCTAATTG TAATAATTGA TTAATTTTCT CATCAATTGT 6900

CATTTCTTCG ACTAATTGAA TCAGTTGATT TTCTTTCATA CTCTCACCTT TCTTCAATAC 6960

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AACTTGCGGT TTGCTGTACT TGCCAACCTT TTACATAAAT ATAATCAATT TCTTCTAATT 7080

CCGCCCAAGG TTTTGTGTAA GTAAAATTTT GAAATGTTCC TCTTGGGCCA TAATGAGTAG 7140

CTAAATTTTT GCTATCTTGA AATTTTTTTT GAACAAGTTG ATGAACCTCT TCCCCCGACT 7200

CTGCATTAAA ATCGCCCATT AATAAAGTTG GATACTGTGC AATTTTGTCA TGTAACTCCT 7260

CTAAGATAAC GGTCATTCCT GCTAAACGAG CATGAGCTGA AATATGATcC AAATGAACAT 7320

TGATGACTAA AAAAGGCGTA TTTTGAGTCG TTTCCTTAAA TAGTCCCCAC AAAGCAATTC 7380

TTGGACAGCC AGCTTCAGGA TGGATACTTG GCTGCTGAGG TGTTTCAGAT AACCAAAAAT 7440

ACCCTGTATC AATAGCCTGA ACTTTTTGTT CGTTATAGAG AATCGCTAGT CCTTCTCCTT 7500

GACCATCCCC TTCTCTTTCC GCAGAAAGAC AGGTGAATGT TGTATACGCC TTTAAATCCC 7560

TGACTTGATT CGGTCGTACT TCTTGAATAC AACAAAGGCT CCAATCATGA AAATTGATTA 7620

ACTGACAAAC AGCCTCTTTA CGAAAAGACC ATTGCCAATC TTGGTCATAC TCTGTATCTA 7680

CCCGGACATT ATACGTAGCT ATTTTCATTT TTAACCTCCT GCAATAGTTG TTGAATTTGA 7740

CGCATCTCAC GACGGATCTG GGTTGTTTCA CCGCCACCAT GGCCTTTTTT CCAATACACT 7800

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CTGACTGCTT TTCTTGCCTT TATCTGATGA TAAGAAGGGA AAAAATCTTT CATCGGACAT    7860

ATCGGATCGT GACTCCCAAC AGAAGCAAAG ACTGGATTTT TAATTTGCGA AACAAAGTGA    7920

CGACTATCAA AATAAGGAAG GACCGCGGCA ATTTTTTCAT GCGCTTGAGG ATGCTCTTGT    7980

AAGTACTGAT GAATAATTTG ATACGAACCC GTTCCTTCTG CTACTCTATT TTCTAAACAA    8040

GAATGACTTG GAACATCTGC AAAAGTAGCT AAAATCGGGA AGTCGACTAA ACTGTTCACC    8100

ATTAACACTA CGCCACCCCC TTGGGAACCA CCACGAAGAA TGATTTGGTC CTGATTAATT    8160

TCAGTAAAGG TCCGCACCAC CTCTACGCTA CGTAAATGGT CGGCAAACAA GCGGCGTTGG    8220

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TATGGCACGC GATCTTTGGT TAATCCCCCT TGACCTCGAT TATCAATGAC AAAACAAGCA    8340

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AAACAGTCAA TCACTATTGG CTGTTTCCCC GCCGTTTTAG GaAGTAACAA ATAGCCAAAG    8460

ATGCGCTCAC CTAGGAAACT TAAAAAGTCG ACCTGTTCCA CTTGAACATT TTCCAATGGA    8520

TAGTCAATGA CCCGCCGATG GATATCTAGC GGTATTTTTT GAAGTTCTTC CTTGGTCTTT    8580

TGCCAAAACT CAAAATACTC ATTCATGTTC CACACCTAAC ACTTTCTGAA AAAACGCAAC    8640

TTGAAGAAAA GCCGTTGTCC CAAATCCTAA CGCAATATAT AAAAACAAAT TAAGCTTATA    8700

GAAAAAAACA AACGTTAAAA GAGGTAAAAT AAACAAAATA ATCGCATTTG CACTATTACT    8760

TAAGACCACA TAAACCGTCT CACCTAGTGT CTTTTTAACG GACCAATTAA AAACGGAAAA    8820

GAGAAAAAGA AAACTCGTCA AAAATAATGC AACAAAACTT AATAGAAAAA TAGCTAAGAA    8880

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AATAATGATC AAGTTGGCAA TAAAAGAAAA AATCCGATAA TACCAACCTT CATATGCAAA    9180

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CTCCTCTCTT ACTTAAGTTT GTCTCTGTTT TCCGCCATTT TCTCAGATTT TATTTTTTCA    9300

ATTGCATCCC ATTTATTTGA TTTTAAGAAT GCTTTGTAGT CTTCTAAAGA TTTGTCAAAG    9360

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GCTTCATTCG CACGAGCTTC CGGCGTTCCT GCATCTGGAT TAATATTTTC AATTACGAAA    9480

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ACTTTTAGTT TATTGACACG GTCGTTGTTA AAGTATAGGA AACGACTAAT GCCATATTTT    9600

TTGTTGTAGG CATCATTGTC TGTTTGTTCT AATTTTTTCA CTTCTGGTAA ATAATCAATT    9660

TTTCCTTGAT CATTGTACGC ATAAGTAACT CCTTCAACGC CATATTTTGT TAAAATTTGT    9720

CCCGGTTCAT CAATTAAATA TGTGAACAGT TGAGTGACTT TTGCTGGATC TTTCGCATCT    9780
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TTCGTAATGT AATTACTTAA CCAACCTGAA ATGCCGGTTT GATTTAATGT TGGTTTTCGG 9840

CCAGAAGTGC TACTTGGTCC ATCAATGGCT ATATAACGTG TGCCAGATTT TTTCATAAAT 9900

TCTGTGAAGT TCCCACCTTG ACCACTGGTT CCAGCAACGA GCATGGTTGC ATAATTTCCT 9960

TGTTTCACTT TTTCATCAAA CGTTGCCCCA TCATCTGTGA AGCTATCATC ACTAATATTG 10020

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CGATCATAGT ATTTACCATT TTTATCCTCT AAAGGAACAC CTAAGAAGTC TTGTAATTTG 10140

TCTAAAAATG GTCCTGCACC ATCGCCCACT GTGGTGAAGC CCATTGGGGT CATCTCAGGA 10200

TATTTTTCTT TAATCTGTTG CATGACTTTT TCAAAATTTT CTGGTGTTGA AACGTCTGGC 10260

TTGCCTAATG CATTATAGAC ATCTTCACGA ATAACAAAAT TATCATTTAC TGGGATATTT 10320

CCACTTTCAT AATCCGCTTT TGTATTAGAG TAATTAGGGT AACCATATGT TTTTCCATCC 10380

TCTAAGGCAT ACCATTTAAA CGTATCTTGG TTAACAACTT TCATTAAATA GGGGTCATAT 10440

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TTTGAATCAT CGCCGGAAAT AAATTCAATA TCCACATTTA AGTCTTTTTT AATCTGCGCA 10620

GTGGTCACGT CTTTTCCAAA AGGCAGCGCC GTCCAATCTG AGTTAATATA CCATTTAATC 10680

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CGATCCTTAA TTGAGACATC TGAGCTAGCT TTCTTTTCCC CACCGCTACA GGCCGCTAAA 10800

CTAACGACCG CCGTTGCCAC CAATAAACCG CCTAAAACTT TTTTCATATT GTTCCCTACT 10860

TTCTTTATTC TTTTACTGCA CCGGCCATCA TACCGCCGAT AAAGTGTTTT TGTAGTAATG 10920

GATAAATGAT TAAAATTGGT ATCGTTGTAA TGACA 10955

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GCTAGtCAAG GATTAAATGA ACGTGCTGAG TATTTAGACA TCAAACAATT ATCGTCTATG 60

TATTCAATGT CTGTTCCTGA AGTTGAACAA AATTTTGTAA AAGACAAACG TATGCAAATG 120

ATCGAAAAAA GAAAGCCTGG TACTAGCAAG GGAAAAAGAT aCTGGCCtGc TAAAGAAGCt 180

ATAAAAAtTT GtAATGACAT CmTGAATcAT TGGGATTaAA GGAAAGGrCg ATACAGAAAC 240

AwTGGACAAC TTaGTAATTA TGAAAAACCA ACAAGCAGTA ACAACTAGTT TGCAAGTCGC 300

AGAAACGTTT AATAAAAATC ATCGTGATGT TTTAGCAGCG ATTGATGATT TAmAAGAGGG 360

GGTTGCGGAA AATTACGCAG GGCTATTTTA CGAAGATAGC TATATTCATC CACAAAACAA 420

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ACArAAATAT AGACAAaTCA TTATGAACCg TGACGGATTC mCGCTACtAG CaATGGGATT    480
CACTGGTCAA AAAGCTCTTA AGTTTAAACT GAAATACATT GAAGCTTTTA ACCAAATGGA    540
GGAACTGCTT AAAACTCAAT CAAACTTACC GATTAATAAC ACAGAATTGT TATTAGAAGC    600
TGCGTTAAAA CATGAACGTG GATTGACTCT TGTAAATCAA CGTTTAGATA AGCTAGAAAC    660
AGAAACTACA ATTAATAGAA GCCAACAACG AAAGATACAA GGGCTAGTTT CATCAACTGT    720
TATCAAAGTA TTAGGTGGCA AAAAAACATT GGCTTATCAG GATTCAAGTA TTAAGCAATC    780
AGCCTTTAGT AATTGTTATA AACAATTGAA AGCATTATTC GATGTAGCAT CTTATGTAGA    840
CATTCCAAAA GTTCGATATG AAGAGGCTGT AGCTCTAATT CCTAGATGGA AGCCTAACTT    900
AGAATTACAA GCAAGAATTG ATATGGcTAA TGaTAATGGa GATATGnTTT AAAGAAATAG    960
GATAGTAATG ATAAArGGAT AAGCCTTAmC TTATCCCsGG TTwAAAGTAG TGtCAmCAAT   1020
AATAGCtTTT TGATCCATAT CACTTTTGAT GGATTCAATA ATTTCTAAAA CAGAAGATTT   1080
ATAGTAATAA GTCTTGCTTG ATGCGATTAC TTCATTTTCT TCGGTTTTAA TTACAAAATA   1140
GTATTTTTTA TTAGAAGCTT TCTTTATTAC AAAAAACATT TTGACACCCC GCTTTCAACT   1200
GAATTATATC AAAAAAATTA TaGGAGGGTA AATATGAnAG CAaTwCGTGA aGCaCGATTG   1260
ATAGcGCtTA TTATTGATGA TTGCGCTAGG TGTGTTATTG AAAAGCCACT TTTCAGTTCC   1320
AGTGTTGGCA ACAATAAGTG TACCTCTTTT TATCCGTTGG TTTTTCAACT GGGATGAAGC   1380
GGAGTATCAG CATTTTCAAA AAAGACAAAA TAAAAAGCCC CAATCGTCTG CCAACGATTA   1440
GGACACATAC AAAATGAACT AAGGAGAGTA TACCAAAATG AACGATAAAA TTCAAAAATT   1500
GATTAAAAAA CTAGCAAAAG AATGCCAGAA AGAAGATGTA GCTTTATCTT TGGCAGCTAT   1560
CGATTTAGAA GGAGAGATGG CAATATCTCA AGTTGGAAAA GGCACGATAG TAGCCATTGC   1620
TGCACATAGC CAATATACAC TAACAAAAGA AAAACTGGAA CAATCAGATT GTGATTGTCC   1680
AAAACATCGT TTATTAAAAG AGATGTACGG TACTGAAACA GAAACTACGA CTAAAAATAC   1740
ACATACTTTT GTCACAGATG ATCCAAACGA TTTGATGGAT ATATTATCGA AGATTTTTCG   1800
AGGTGAGTTT AAATGACTAG AAAAGAAAAG TTAAACCAAG CAAAAAGATT AGCTGATTTA   1860
TGGTACAAAC AACAAAAAAG TCAACTATAC ATTGCGCAAC AAAAAGAGCA CAGAGGGATT   1920
GCATGATGAA AAAAGCGACT ACGCCGCCAA GCAAATAGTC GCATACAAAA TTATACTAGA   1980
AAAATTGTAA CACAGAAAAG AGGTTTTGTG AATGAATCGT AGAGAAGCAA ATGCACTAGA   2040
CAGATATTTA ACAGAGCCGA CTGAAAAACC ACATAAGGAA ACCTATGAAG ATGATCCaGT   2100
GGATACTACT GATTATTTTG GAAATGaAAT TGCTGATGAA GACGGTGTGT TTGAGATAAC   2160
TTTTGCAATG AAATGTCTTT ATACAGGACA ACCAGTACTC ACTTGTAAAA AAATTGCTAC   2220
ACAAGATACA ATCGTTGATT TGATAGAAGA ATTAGGCGAA GAAAACGTGT ATTTAATTGA   2280
ATATGTGAGT TCAGGAAAAA GATATAAGGA GGGCTTATTG AATGACTGAA GCAACCAAAA   2340
CAGATTTTTC TAAGTTGAAT GTTTATCAAA AATTAGCGTA TGTGAGACAA AAAGCACCAT   2400
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ATATTCAAAA AAGTAAACGT GGCCAGCAGT ACAGCTATGT GGGGTCAAGC GATGTACTAT 2460

CCGCATTAAA TACAGTCATA AATCAAGTTG GATTAATTTT GAAGCCAGAA ATTGTTGCTC 2520

ATCAAGTTCG GGAATCACAA GATGAGGTAT GGAAAGCGGA TAAAGTAAAG AAAGAGCCTG 2580

TAGCCAAAAA ACGTACAACG TATTTTACAG AGCTAGAGTT AATGATGACA TGGATTAATA 2640

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CTAAAAAAGC ATTTGAAGAA TATAGTGCTT ATGATTATGG TGTTATTTCT AAATTGCTTG 3000

CGAAGTGGAT AAATTTTTAT GAATCTAGGC AGAAGGTTCA AGAAGATAAG AAGTGATTGA 3060

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GATATAGCTC GTTGGAGTTA TGACGAACCA AATGGATAGA GGAAGTTTTA AAGTATTAcT 3300

ACGAAGCTAA aAGTGGCGTG TATTTTGAAC ATAGTAAGGC TACACGACAT GAAGCAACAG 3360

AATGGATTAG TTTTTTAATC GAATTCATTT TGAAAAATGA TGTACCACTA GAAAAGAGAT 3420

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TAAACGTTGA AGAACGTAAG AAGTTGAATA TCGGAGGTTA ACAGTTTGGT AGAGGAATTA 3720

CTTGAAAAAT ACAGGCAATT AACATCGAGT CAAAAACTAT TTTTTGAACT ATTAGCATTT 3780

GTCTATATCG GTTCAAGAAA TGGTAAAGGA ATAGCTATTG AAGCACAAAC AATAAAAAAA 3840

GTCGTTAACG GAGAAATTAA GCATAAATAT GTTTATACGG TCGTTGTTGA TGAGGAGGAT 3900

AACTAGTGAA TGAACATAGA GGATATTACG CCATTATCCC AGCGATTGTT CGCTATGATA 3960

ACCACTTAAA TGGGAATGCA AAATTATTGT ATGGAGAGCT AACGGCATTA GCAAATGAAA 4020

AAGGCTATTG TTGGGCAACG AATCAATATT TTGCAAATCT GTATAACGTT AGCAAGCGAA 4080

CAATTATTTC ATGGCTGAAA CAGTTAGAAG AAAGAAACTA TATAAAAATA CAAATTTTTT 4140

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AGGGGGATGA AGAAAATTTC ACTACCCCTA GTGAAGAAAA CTTCACAGAG AATAATACAT 4320

TAATTAATAA TACmAAGAaT AATACAAAGA ATATATATAG TGTTGAACAA AGTTCAACCA 4380

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CCAAaGaGCa ATTCTTAAAG AAAATTAAGT CAGATGAAGA CTTCGAACGG TTTAAAACAG    4500
GATACAAAGC TTATCTTAAG TATATCAAAT TAAACGACTG GTATCATCCA CAAGAATTGT    4560
TCCGCTGGAT ACGTGATGAA CGTTTTAACG ATGAATACGA CTTGTCTGAA ACGGCAACGC    4620
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TCACTGATGC TGCCGAAGtA TTTTATATAA AACcGATGgT CAAaTtGCTG TAaTGGTTtG    5100
yCAAAAGTTG TACAGTATGC GACCACGAAC AGAACTAGAA ATTACAAGTT TGGAGGAACA    5160
AGTGTAGTGG GTAAAACGGG TAAACAGATC AAAGAGAATT ATTCGGTTAG AAAGCGAGTA    5220
AAGAAGATGC TTAAATTTAA aGaATTTAAT ATTCAATTAT yCGACGTTCA CATTTATATA    5280
AAAmGGCTAA GTAGTTTTAA AACCAACAAA AAATAGTATA AAAAAACTAA CTAGTTTCCG    5340
CTAGCTAGTT ATAGATACAT TTTCATCTCA GATAGAGACA ATTAATAATA CATTACTATG    5400
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TGTTTTCCGC CAGTTGTTCT TTAGGTGTGA GTTAGCACTT TCCCCAAATA AAGTGCTATT    5520
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TTTACCAGAA GTTAATGTAG AAAAGGAGGA AATTTATTTC ATAAATAAAA TCCCCAAGAA    5640
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TTATTAGATG GAAAATATCA AATGAATAAA GATGATGTGA AAGATGACGA ATGGAAGATT    5760
GTAAAATATT GTAGAATTAT TATTGTTTTC TTTATAGTCA ACCAATAATT TGTTGACTAC    5820
AAACATGTAT GAGTGATGAA TATTTTGATA AATAAATAGC CAGTCGGTTT CCGCCGACTG    5880
GCTGAGAAGT GAaTAGCTAT TGGAATAGTA TyCTaGTATA ATTTATaTCa TATGGAGTCG    5940
CTGATGAGCA AAGAATAAGC ATTTCTTATA TATGTTTGGA TAAATaAAAA AAGCTACTTA    6000
GTTTCCGCTA AGCAACTCTT AAATGATGAT ATGTTTATTA TAnACTATTA TACCATAAAA    6060
GGAGCGATTT CACTTGATTC TATTGTTAAA AGAAGTAGAT TTTCGACAAA CAAAAGCGAA    6120
TGCTAGAAAT GTGTTGAAGA GTTTTAGACG TTTAGAGCGA ATAGCTGGTC GCTCTTTGAT    6180
AGATTTAAAA TCACCAATTA TTACAGATAT GCCTAAAAGC CAAAGTCACG GGAATAAAGC    6240
AGAAGATGCG CTAGTACAAT TAGTAGATGC AGAAGCAGAA AGAGACGCAA TTGTATCTGC    6300
GCTTATGGCA TTGAGCCTAA CTAGCAGACA AATTTTGCAT TATAGTTTCT GTGTGCAGGA    6360
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TCATTACTCT AATaCAAGtA GCTAGGGAAG TTGGATATTC CGAAAGAAGT ATTCAACGAA 6420

TGAAATCAGA GGCTTTAATT GAATTTGCCG AAGCGTATCG AAATGGAAAA ATAATTGCAT 6480

ATAAATAAAA TTTTTGGCGG TTTTTGGCGG GAAGTTGGCG GTTTTAACCA TATTAGGATG 6540

TTAATATGGn AGTGGCGAAG TAAGGAGACG AGGTAAGCCT GCATTACCTA CCTAGCTCCG 6600

TTCC 6604

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTAACTTGT GACAAAGTCG TGCATGGATG CACTAAAAAG ACACCCTATT GTGGTAGGGT 60

GTCTTTTTTT GCTGTTTAGA CAGCAGCGGT TGGAAGCAAC TTGTTTATTC CTCGTTCTGT 120

TTTTCCAACC AAATGGTTAC AAGTTTCAGG ACAATCCCGA CAAAAATCGG CACAAGAATT 180

TTTGTGACAA TCTCGTACAT GTGATGCACC TCCTTTCGAG GCAAGTCGCC AATTTGAGTA 240

TAGCATAAAA AGTTGTTCAT TTATTATTGA AATTATTATA AATGGAATAA GTACGTGTTT 300

TCTGGTTTTC GTAACTAGAG AACACGTGCT TTTTTCTTTC AACTTTTGGC ACAATGGTTT 360

GTGCCAAAGT ACGACTTTTT CCAGATTTGG AAAGCGGATA CAATTTAGTC AACAAGAAAA 420

GTTACTTGAG AGAAGGGGAA TAAAAATGGA ACAAGTACCA GAAAAAAATA AAGTATCAAT 480

TAAAGCAAAA GTCCAAAGAA TTGGCAGTAC CTTATCTAGC ATGGTGATGC CCAATATCGG 540

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CTACACTGGT GGGAAAGTAA TAGCAGGTGA TCGCGGTGCC GTAGTTGGCG CAATTGCGAC 720

AATGGGCGTG ATTGTGGGAA CCGATATTCC GATGATGCTA GGTGCCATGA TTATGGGTCC 780

ACTTGGTGGC TTTACAATTA AGAAATTTGA TCAGTATTTC CAACATCGGA TTAAAGCTGG 840

TTTTGAAATG TTAGTAAACA ATTTTTCAGC TGGATTGATT GGTTTTGCGT TACTTTACTT 900

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GTGCTCTTTT TAAACAATGC GATTAATCAT GGCATTTTAA CACCCTTAGG GACAGAACAA 1080

GTCTTATCGG CTGGTAAATC AATTCTTTTC CTATTAGAAG CAAACCCTGG TCCTGGGTTA 1140

GGTGTCTTAT TAGCATTTAT GTTTTTTGGA AAAGGTGCGG CAAAATCTTC TGCGCCGGGA 1200

GCAATAATTA TTCATTTCCT TGGTGGTATC CACGAAATTT ACTTCCCATA TGTAATGATG 1260

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GCCCAAAAAG TGAAAGAAAC CCAArCTGCT AAAGCAGCAT CAAAAGGATT AACTGTCACA 1560

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GGCTCTAGTG CAATGGGTGC GTCTATCTTA CGGAAAAAGG TCCAAGAGGC TGGTTTAGTA 1680

CAAACTGTGA CAAATCGGGC CATTAATAAT TTGACCGATG AGGGAAATAC ATTGATTGTC 1740

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CAAAGAAAAA AACGACGCAC AACCAACAGT CTCCAAAGCA ACACCTGCTT CTGAAATTGA 1920

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ACAAAAGAAG AAGCTATTCG CTTTTGCGGC GAAAAACTAG TCGAGGCAGG CTGTGTTGAA 2340

CCCGCTTATA TCGAAGCAAT GATTGAAAGA GACCAATTGC TATCTGTTTA TATGGGGAAT 2400

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TATGATAAAA ATGAATATTT ATTCTGCTT 29729

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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GGGCGCCAAT TTATTACGGG AAATCGCTGT GAACGTGGTG CACGAATTAA AATTAAACGA    1920
GAAGAACGCA AAgTAAATTT GGTTGATTAT AAGTACCGCA AGTTATTTAA GTACCGACCT    1980
TTGCGGGAAA ATAAAGCGTT TCGTGGGCGC TTGGGTATCC CTAGAGTCCT AAACATGTAT    2040
GAAAATTATC CTTTGTGGCA TACATTTTTT ACTGACTTAG GCTTTCGGGT CGAATTATCG    2100
CCACGTTCTA ATAAGCAAAT CTATGAACAA GGCCTTGAAA CGATTCCCAG TGATACGGTT    2160
TGTTACCCAG CGAAAATGGC GCATGGACAT ATTCAAGCAT TAATTGATGC GCAAGTGCCA    2220
ATTATCTTTT ATCCTGGTGT TGTTTTTGAA CAGCAAGAAA CAGTGGAAGC AGATAATCAT    2280
TTTAATTGTC CAATTGTGCA AAGCTACCCA GATGTTATTC GAAATAATGT GGATGCCATC    2340
AGAGAGGGCC AAGTGGATTA TCGAAATCCC TATCTTAATT TAGCGAATGA AGCTGCAGTT    2400
GCCAAAGTTT TAGCTGAAAA TTTTGCTGAT TTAGGGATTT CCTTAGAAGA AATTCAAACA    2460
GCGCTGCATC ATGGTTATCA AGAATTAGCA GCTTTTAAAA AAGAAATTCA AGAAAAAGGC    2520
GAAGAAACGT TAGCCATGTT AACTGAAAAA GGCCAGAGAG GGATTGTCTT ATCGGGGCGA    2580
CCGTATCACT TGGATCCAGA GATTAATCAC GGCATTGCCG AAGTCATTAC ACAGGAAGGA    2640
TTCCATGTCT TGACAGAAGA CAGTATCTCG CATCTTGGAG ACGTGCAGAA TTTACGTGTG    2700
GTGAATCAAT GGGTCTATCA TTCTCGCTTA TATGCGGCGG CTAAAGTAGT GGCTAAGACG    2760
AAAAATTTAG AACTTGTCCA ACTGAATTCC TTTGGTTGCG GCTTAGATGC TGTGACAACC    2820
GATCAAGTAG AAGAAATCAT GGATCGGTCT GGCAAAATTT ATACAGTCCT CAAAATCGAT    2880
GAAGGTGCGA ATTTGGGCGC AATTCGTATT CGGTTGCGCT CCTTGAAAGC GGCTGTCAAT    2940
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GAGCGGGAGA AGCAACAGTT TGTTCCGCAT ATGCAAATGG AAGAGCCAGA GAAAATTGTG 3000

TTTACAAAAC AAATGAAAAA AACACATACC TTACTGTTAC CAATGCTTAG CCcGATtCAT 3060

CAATCTGGAT TAGTCGATGT AGCATTACAA GCTTCTGGCT ATCATGTTGT CTGTTTGCCT 3120

GCGCAGGATA AAGAAGCCGT GAATGTCGGG TTAAAATATG TCAATAATGA TGCGTGTTAC 3180

CCAGCAATTA TTTCTATCGG ACAACTAGTC GAAGCTTTGG AAAGTGGTCA ATATGaTTTG 3240

GATAATGTCA GTGTCTTAAT GACGCAAACA GGGGGCGGTT GTCGCGCAAC GAATTACATT 3300

CCCTTATTAC GAAAAGCCTT AAATGATGCT GGTTTTTCTC AAGTTCCTGT AGTTTCAGTT 3360

TCGATGGGCA ATAAAGGGGT CGAATCCAaT CCAGGATTTA AATTTACGTT GCCAATGATC 3420

AAACGCTTAG TGGTTGCCTT TTtATATGGT GaCTTATTCG AACGAGTAGT TTATCGAACA 3480

AGACCTTATG aAACAGAAAA AGGAATGGTG GATCAACTGC ACCAAGATTG GCTAAAAAGA 3540

GTGGAAGCCA ATGTCCGGAA TGGTTCGCTG ACACAATTTA ATCACTTCAT GAAAAAAATT 3600

ATTCGGACGT TTGATGAAAT TCCTTTACAA GAGATAAAAA AACCAAAAGT CGGTGTGGTC 3660

GGGGAAATTT TAGTGAAATA TTCGCCGACA GCGAATAATG ATATTGTGCG TTTGCTAGAA 3720

GAAGAAGGTG CTGAAGCAGT TGTGCCAGAT ATTGTTGGCT TTATGAACTA TTCTTTGTAC 3780

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TTTGCGATAA AAATCATTGA ATTGGTAGAA AAACCAATGG ATAAGGCATT GAGAAAATCG 3900

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TCAATTGGCA ATCATACGGG TGAAGGTTGG TTTTTAACAG CTGAAATGAT TGAGCTCTTA 4020

AAACACGAGG TGAATAACAT CGTTTGTATG CAGCCgTTTG GATGTTTACC AAACCATATT 4080

GTTGGAAAAG GGGTCGTGAA AGAGCTACGA CGTCAATATC CGCAAGCAAA TATTGCGGCG 4140

GTGGATTATG ATCCAGGGGT ATCTTTGGTT AATCAGTTGA ACCGAATCCG TTTGATGATG 4200

GCCACAGCGA ACAAGTTGTT GAAAGAAGAA AATGTAAAAA GATAATAACT AATAGAAATT 4260

CGTTTAAAAA CATTTGACTT GGTCACTTTT TACTGACTAA GCCAAATGTT TTTGTTATAA 4320

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AGGAAGCGTA AATGGTTCAA AATATACCAA TTTATATTCA AATTCACGAT AAAATCAAAG 4500

AAGATATTGA AAAAGGTGTC TGGAGTATCG GGGATCGTTT GCCCTCTGAG CGAGAATTAG 4560

CCTTGAAATT TGATGTTAGT CGAATGACCT TACGCCAAGC CATCCAGACT TTAGCAGACG 4620

AAGGGATTTT AGAACGAAAA ATTGGTTCAG GAACGTATGT AGCACGTAAG AAAGTTCAAG 4680

AAACAATGAC AGGTACCACT AGTTTTACAG AAATTACCTT GTCTCAAAAT CGCGTTCCTT 4740

CTAGTCGGAC GGTGTCTTAT TTTGTAGCGA AACCTAGTTC TAGTGAGATG GAAAAATTAC 4800

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CGATTTGTTT TGAGGTGGCG AGCATTCCTT ATTCATTGGT CTCGCAATAT GGCAAATCTG 4920

AAATCACGAA CTCTTTTTAT AAAACACTTG AAGCCAAATC TGGCCACAAA ATTGGCCATT 4980

CTAACCAAAC AATCTCTGCT GTTCaAGCAT CGGAACAGAT CGCAGAATAT TTAGAGATTA 5040

AACGAGGCGA TGCGATTCtG CGTGTGCGCC AAGTATCCTA TTTTGAAAAC GGACTACCTT 5100

TTGAATATGT TCGTACGCAG TATGCAGGAA GTCGATTTGA GTTTTATTTA GAGAAGTAGA 5160

GAAATGATAA GTATAGAAAA ATGCCAAGAA ATAGGCTGAG GTArGATATT TtAaCCTCCA 5220

AArGTkGTAT CTGAAAAaTA CAATTTTTGG AGGTTATTTT TTATGrACTT ATCAGGTAGA 5280

ATTCAAATTA AAATTAGTGA AAGCATCTCA ATTCAmATAA ATATTGAATA GAGTAGCAAG 5340

TCTGAATACC AAAAAAGTGA GATGGTTTGT CCCGCTATAA ATATTGTTAA AAATAAACTT 5400

ATAATAGCTG CTAGTTTATT TGCTTTTATT CTTTTTTTGG CTGTAGTTCA TTTTTGTCCA 5460

TTTTTTACAT TTCTTTTTTA AACTGTAACC TAATATAAGA TATACCCGTT CAACGCTTTA 5520

ATCAAATAGT TGCAAAATCA GCAGTTGTTT TGCAAATTGT TACATTGAAA TTGTTAGTTA 5580

TTACCAATCA ATAATACTTA TGATTGTCAA AGTTATTATA TAGATATACT GAAAGAGAAA 5640

TTTATTTTCT TTTTCAATAA AAAGTTTAGC GGAAGGAGTG ATGCGGAATG AAAAAAATTA 5700

ACGTACGTAA AGCCGATACA GTTGATGCAA CAGCATGGTG GATTATTATC TAATTTGATA 5760

ACCAAATAAC GGTTAGACGA GATAGAAATA TCTCGTCATT TTTTAATAAG GAGTGAAAAA 5820

AATGAAGTAT AAATATCCCA GAATAAAACC AATCTATCCA TTATATCAAT TAAATAAAGA 5880

GAGATTTAGA GTTGGGGCCC AATTAGGAAT CACTATTGAA TTTGATGATG ATGAAGGTCA 5940

ATTTTGGACA TTATCTAATT TACTCGATGG AGTTAGATCG TTTGATGAAG TTGTCACAGA 6000

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GGAAAAGATA AATAACTTGA AAATACTATT ATTAGGTCTT GGTGGAGGAG GATCAAATAT 6240

TCTAACGGTA CTAGCGGGTC TTGGCCCCAA GATGATtAGA ATGGTGGACT ATGACCGAGT 6300

tGAAGCAAGT AATTtAGGTC GTCAATTACT ATATAGAGAA GCAGATATTG GTGAGAAGAA 6360

AACTGTAGTT GCTAAAAGAG CCATTAATGA AATGAnACTC AAATATTAAC GTTGAAACTG 6420

TAGATAAAAA AATAATAGAT GTGAATGATG TTGTTGAATT GACAGAAGGA ATAGATATCA 6480

TTGTTTGCGC TATTGATGAA CCCCCTTTCC TTATACATAG AATTGtGAaT GAAGCTATTG 6540

TAAAAGTTGG TTTGCCGTGC GTGTTTGGTG CCTCACAGGT TAGCCGAGGA AGAGTATACA 6600

CTGTAATACC CCAGAAAAcA GGATGCTTTG aTtGCATGAA TTTGAACTtC AGTAAAAATG 6660

ACCCTAAATT TGTTGAACAA TTTGTAGGTT TTAGAAATAT TCAATTTGCT CCCCCATCCA 6720

TAGCTTATGG TCCTGGTATC TTTCAATTAA CAGCATCAAT TGTAGATGAG TTAATAAGAG 6780

TGGTAACAAG ATATGCTGAG CCAAAAAGTT TGGGAACGCA ATATGAAATT AACTATGAGG 6840

ACGGAAACTC GTTCACGCAT AAAACTTGGC CAAGGTTTGA GAGTGAATGT CCAACTTGTG 6900

GTAAAGGAGA TGTCTCCCAA TGGGAAATAT TTCAATATTA TCAAGAGAAG AAATAGGCCG 6960

AGACTATACC GAAGCTCGTA CGTTAAAACG TAAGCTAAAC AATGGCGATT GGGTTTATGT 7020

ATCAGAGGTA CTTAATGAAT TAGTTgAAAA TAAAATTATG ATAAAAAAAG CCGATCAGAG 7080

AGATGATTAT AAGCCGCTAT TTGTCGAGCC TAAGAATATC TTATTTAAAA GCTCCTCTTT 7140

CCTGATTGAT GTTAACGGTA TTGTTGCGTT TACGATTAGC ATATTTTTAT TCGTAATCAA 7200

GGGGTCTCCT TTTGGAAGTG CAGTAAATGT TTTGTTT 7237

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

GAGGATTTGA TTTGATCnTC TGAGTTCACG TgkCGCTAtC agcTCTGATA cTTAcaCTTT 60

AcGTCGGAcC CAgAAcAGGC TTATTAGAAA TGATTCaAAA gATGTtGgCT GTTCCCgArT 120

GTGTTTGTGT TTtATTTGTA TAATTAAGTT GaCTATTTCC tTGGAAAATw cAGGAGTCAG 180

ATGCTAAATA ATTTTTGCAT CTGACTCCTG TTTTCTTATT TTAAACGATG GATTGGTTCT 240

CCAATTCTTT AACGTATAAA TAAAAAGAGC CAAAGTCTAA GCGATTCATT TGTAAAGATT 300

CATGAATTTT TGTGAACCCT TTACTTTCGA AAAATCGAAT CATTCTATGG TTTGTATGAT 360

TAGTTTGAGC ATACATTTTA CGTCTTCCTT CCCAGACTGC CCGTTTCTCC AATTCATGGA 420

ACAATAAACT GCCATAACCC TTGGCAATAT AATTAGGCGA AGTTGCAAAG CGCTTTAACC 480

AAACAAAGTC TTGTTCCTGC TCCATACAGA ACGTTGCCAT TGAAAAAATC ATTTCTTCGT 540

GCACTAGCAA ATATAATCGT TTTTTTGTAA TGTCTTCTTG GATATCTCCT TGAGAAGGAT 600

AGTCCTTTGT CCACTGTGTA ATGCCCACAA CATCCATATA TGCCTTTACT TCTGTTAAAA 660

ATTGAAGAAT CATCGGTAAC TCTTTCTCAT CAGCCACTCT AATTTTCATT GTTTATTCTC 720

TTaATAAGGT AACAATAGAA TCGACAAGAC AATCACACTA ATAATGCCAA TGATGGTCGG 780

TACACTCGTC CGTTTTAAAA TTCTGATGGG ACTAACTCCT ACTGTTGATG CGACAATCAT 840

GACAACTGCT GCTACAGGAG AAATCGTTCT AGTTAAATTC GCAATCATCT GCATTGGCAA 900

GGAAATTAAG ATGCCATCAA TCCCAGCTTT TTCAGCAATC CCAGGGATTA GTTCGATAAC 960

CGCATAAAAC ATTGCCAGAC CACCACCGCT TAAAATTCCA AAAAGGGTCG TTGCACCGCT 1020

GAAAATTAAG GTCGTGACAA TTCCTGCTGA ACTTGATGCT TCGACAGATG CCATAATACT 1080

ATCAATAATT CCTAACGTTT GAAtCGCAGA CGTGAATAAT GAACCGCCTA CGACAAGCAT 1140

CACAACTTGA CTAAACCCTT GCCCCATTCC TTTAAACATC TCGACAGCTG TATCTTGAAC 1200

CTTTTTAAAA GATTTCAAGC GAACGyCTCA ACCAATACAG CGATGAAGAA AGAAATAAAT 1260

GTAAGAACAA AAATATCCAT CGTTATTCCT TTAATAAACA TTCCTGCGAT TCCCACTCCA 1320

ACAATTAATA ATAGCGGTAA TATTGGCAAT ATTGCATAAA ATTTAGGAAC ATCAAATTCT 1380

TTTTGTTTGC TTAAGCCCTC TTCATTTAAT GAGACATAGG CAGCCTCACC TTCTTTTTTA 1440

TCGCAGTATT TTTGCCAGAA GTACTGTGCA ACCGCAATGA TTAATAACGA TGGCAGCGAA 1500

ATTTTGGCAT TCCATACAAC ATAATTTAAC ACATCATAAC CAAGGGTATT TGCGGCGATT 1560

ACGTTATCCG CGCCTAAAGG TGTTGGCATG ATAGTTGCCG TCATTGCAAT CACACCTGCA 1620

GCAGTTAATG ATGAAATCCC CATGCTGGCT AGCATCGGAT ATAATATAGA CATTAAAATA 1680

ATCGCTAAAC TTGATGCACT AGGAACTACT AGTGACATTA AATTTCCAAT TAAAAAGACC 1740

ACAGGGACAA ATAACGATTT ACGTTTAATC TTCATTAATG GTTTCACCAA AAAGTTGACA 1800

GCCATCTGAT TGGCCCCGAT TGCATTCATA TAGCCTGAAT AACCAAAAAG AATCATAATT 1860

ACAATTCCTG CTGAACTCAC TTGTGCAATA ATTGTATCTT TAAACTTCAA GAAAATATCA 1920

AATAATCCAA AACCGGTTCC TTCTCCTGCA GGATAAATGG GATGCCCTAA CATCCATGCA 1980

CATGCAAGT 1989

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GCTTCATTAC TAAGAAATAA GGTATGTAAA CAAAAACAAC TAAGATTCGG TATTTTTCCA 60

GAAAGAGTTA TTATTTAAAT GTTTTTAAAT AAAAAATATG GAGATAAATG GCAGATCGTT 120

TGTTGCTTTT TTTAATyTCG AATTATCAAT TAAGTACAAC ACTTTATCCT GTAAAAACTT 180

CATACGATGT TTTyCATTTT AAGCACTTTT GTGGTCTAGT CTATGCATAA AGGATTGAAT 240

ATAATTATCT GGAATTAAGA TTATATCTTT CTCTTTTGGT AGGTACTCTC TTAATAATCT 300

ATTTGTATTT TCATTTAGTC AAAAACTGGG TAAAGGAGTC TACAAAGATA AACCTAAAAA 360

ATAATTTTGC ACATATGCTT GATGaCCTTC CTGGAGTAGC TGATAATGCT AAAAAAATAT 420

TGTTTGATAT GAAATGkACT ACTGkAATAG ACGATTGTAA TGTtCATTTA CGAGATGTAC 480

TTAATTTATT AGAAGATGAA ATGCACAGCT TTAGaTTATC TTCTATTGaA GCtAATGATT 540

TAGaTAAACT AtATGATACT TTTTATTACT ATGGnAAAAA AGamCAATTA ATAGAATTTC 600

TGCTTGACCA GATGACTAAT GCGATAAATT TTAAACAAGC TGATAAGGAT TTTCTTATTT 660

ATTCATGGCT TGTAGAAAAA CTTACTGAAG AACAAATATG CGAAATGCTC GCGAGAATTA 720

ATGAAAATAC CCAATACCAT TGGAATAACA ACCTTAATTC ATTTGTTGAT GAGTTCGTTG 780

CTTATTATAA AGAAACAAAT GGAATTGATC TAAGAATAAA TTATTTGGGA GCAATTTATA 840

CTAATTTAAA AATTCTCAGC GATGAATATA CTCTCTCTAT CTCAGATTAC GAGCTTATTT 900

TCAAATTTTT TGAGGATATA ATAGAGAGTC ATAGCGAAAC AATATTTGAT TTTCAGCGTA 960

AATATAAAAA GGATATTGAA ACAAATTTTG GTAATAGTTT GGAAAACTTT CCTAAACTGA 1020

ATAAGTTaTT GTTCGAATAG ATTTTGAAAA GCTTACAATA AATAAAAGTA TTAATTTTTG 1080

TTACATCAAT TAATCTCTAA TTCATGAATT TCTTTTTTGA TTCTATATAT AGTTTGTCTC 1140

GTAATATTGT AATCTTTCGC AATCTTTGAG ATAGCAACCC CATTCTTAAG ATCCTGAACG 1200

ATGCTTTTAT AAACAAGGCG ACGTTGGGGA TCTTTTGTGT CTGCACTGTA TAACTTAGGA 1260

CGACCTTTAT AGACGCCGTT TGCTTTCGCA ATCTTTATCC CTTGTGCTTG GCGTCTTTTA 1320

GATTCCGTAC GTTCTTGCTC GGCAATCATG GCCAAAATCT GAATGATTAG GTCTTTGATA 1380

AATTTATCTA GGAGTGGATT TCCGATTGCT TCAGCCATGA TTGGTAAACT GGTAATAATT 1440

AGCCGCACAT TTTTCTTCTT TAGATAATTT ACTGAATCGA TAATCTCGTC ATAATTACGT 1500

CCAAGTCGAT CGATGGCCTC TACAATAAAA ATATCTTGGG CTCTAACAAA ATCTAGAGCT 1560

TCCTGAAAAA TCGGTCGATG AGTAATAGTC GCTCCGGATT GTTTCTCGAT AAAAATTTTT 1620

TCAGCACCAA ACTTGTTCAT TtCCTCAATT tGACGTtGTT CATTTTGATC GATTGATGAA 1680

ACTCGAATAT ATGCAATTTT CCAAATtTTT ACCTACTTTC TATAATTTTT AAAAtACACC 1740

CTAATCATAC ATTCAAAAAC CATATTTTTC AAkGTtCTGT TGGTGTCTAT TTAGGGGTCC 1800

TTAATTAGAC AATC 1814

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TATGGTTCAA GGTCCAGTGT TTaATGAAAG ATATGTTTGG TCAGACTAAT CGAATTGTTG 60

TTCATGTTAT TTTTGAAGAA TGGTTGGAAC TGTTCAAAAC CGTTGATGAT ACAGAAGCTT 120

CTAAAATGGA GAACCGCTTT GTTGCATAGG AAGGAAGTGA GAATATGCAG TATCTAATTG 180

ACAGTTATAG TGCGTATACG GTTGATGGTG GTTTGTTGGA TAAAGGATGG CAAGTAGTGA 240

ATTGGTTCTT TGTAGATATA CCATTCTTTA TCTTACGAAT GTTTGTTTCT TTTTTTCTTT 300

TTTGTGAGAA CGTCTTAAAC CAATCTAGTT TCTTTGAAGG AAAACAAGAA ACAGTATTGA 360

ATATGTCAAA AAATGTTCTA AGTGGCATTG GTGGCAAGGG ATTTAGAGGT GGTTCTTTAC 420

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GAAGCTTTTC AAAAGTATTC CTTCATTATT TAGCAGTTGT TATTTTGTTT GGTTTTTGGT 540

TTGGCTCTGT ATCAACGTCA ACAGGCACAA CAAGTGGCTC AATGTTCTTG ATTCAATCAA 600

CTAACGCAAT TGCTAAAGGA GTACAAAGTA CGTTTACTAC AAGTGCCAAT TTAGGAACAG 660

AAGGTTCTAA AGATGGAGAA GTATACCAAA GTCCTATTTT TGATGCCACA GTAAAACAAA 720

CATTTAATTT TGTAAATAGT GGTTCACTTG ATGGGAAAAT GGAAAATGGT AAAAAGTTAG 780

ATGAAGGTAA ACTACTAGAA AAGCCTAAAT TGTCTAAAAA AGAAAAAGCA AAGTTTGAGG 840

ATGAAAGAAG TACCTATATA AAAAATAATG AGAAAGATAA TCCATACTTC TCACAGGACG 900

GAGCAAAAAC AATGGAAAAA GCTTTTGGCG TTGGTGTGGG TTTAGTCAAT TTAGCAGTCT 960

TAGCAGTGCC TGTCACGTAT ATTAATATTA TGCTAAATGT AATTCAAATC ATTGTTGATT 1020

TACTCATTCT TGTTTTTCCG ATTATTGCGT TGGTGTCTTT CTTCCCTCGG TGTCAAATGA 1080

TGATGTTTAA ATTTTTTAAA TCATTAATTG GCATTTTATT TTTACCTGTA GTTTTCGGTA 1140

TATTTTTGTC TGTGTTATTT TGGATCAATA AGTTAATTGA CCAAGCGTTT TTAGGATTGA 1200

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TGGATAATTT TGAAGATTTA ACAGATGATG AAATGGATAA TTCTTTAGAA GAAATTGATG 1800

TTCCTGTATT AGATGAAACT GTATCTGATT CTGATACTTC TTTAGCTGAT GAAAGTAATA 1860

TTGAGTTAGA GCCAATTATT GAAAATGAAC TTGATAGTTT AGATTCAAGT GTAGAATCAA 1920

GTGAAAATGA TAGAGAAGAG CCAATTCATG AAGTTGATGA GCAAGAAATA GCGGACAATT 1980

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AGGACGAAGA GTTAATTTAT TAAATTTTGC AAAAAGTCAA AAAAAGGAAT GGAAATCAGT 2640

AGCTTTACAA ATGGATTTTG CGTGGAATAA GGATGGTTCT GATAGTGACT TACTTAAAAG 2700

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AATGTCTAAA TCAAAAGATG TGAATACACT TGCGGTAGAT AtTTTGAAGC TGTGGGAACG    2760

AGCTGGAACA AAAGATGATC CCGCAGaACA AGTAAAAAGA AAGGCTAGTG CTAATAATTG    2820

GTATAAACGA CTTTCTACAG GTTCCATGGG CGGAGGTTCA GCCAATGTTG GTGGAGGAAA    2880

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TCCAAATTAT TcAGATATTA AAGCAGGAGA TGTCATTAAT TTTGGTCAAG GTGGTGTGGC    3120

TACTAGTATT TATGGGCATA CTGGTGTAGT GGCAAGTGTT GAAGGTAAAA ACAAGTTTAC    3180

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TAAAGAGTAT CGTGTTAAAT TTTCTGAGGG GATTTTTTCA AAGATTATGT ATATTAAAGA    3480

AGTGCAACGC ATTTCAAAGA AAGTAGGTAG AAAATGAAAA AGTTAAGTTT AGTAGTTTTA    3540

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GCGGCTTCGT CAACAACTGA ATTGGTGACT ATGAAACCAG TTGATAATAT AAATACTACG    3660

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GCAGAAGAAA AAGTATCTGA TACTTACCAG TTGGTGGAGG ACTTTGGaAA TACTTATGCm    3780

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AATGGTATAA TGTATGTATA AGTGAGGAGA TGAGAAAATG AAAAAGGTAG TTTCAATTTT    4140

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TAAGCGATTA GATAGTACTA AAAGTAAAGT AACCTTTGAT GATATGAAAG CTAGTGGAAA    4440

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ATTTTTAAGT GGCTAAAATT TGGCTAAAAC ACTTTGAAAT GTATGGAAAT GCTGGATTAT    4560

TTGTAAAAAT AATGTTGATA TTAAAGCATT TGTGTGGAAA ATACATTTTA TAATTTACTC    4620

GTAACGCGTA GGTCACAGGT TCGATCCCTG CAGCTGGCaT CTAAAAAAAC AGACAGGcAC    4680
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TACCATCTGG TAGTGCCTGT CTGTTTTTTT AgmTAAAATT TTGGaTTAGT GCAAATGaAG 4740

CAATGCCTAC CAGTACAATA AGCAATAAGT TTTTAGTAAG TATTGCGGCT AAAATGGTAG 4800

GAAATGAAGC GAATAAATaA GGAAGATTGA GGCTTGGTAA ATGCCCAATT CTTTGTTCAA 4860

ATAAGCTACT AAACCATAAG GCGGACATAA TCACAATTGG AACAAAACTT AGATATTCTA 4920

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GATGTCCCAT TCGAAAAAAT CACTG 12445

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

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TCGTCTTCAG CACAATAAAC ATAGTGTCCA TTGAGAATTT CACGGAGCTC ACGATCTTTC    240

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ACCGTTTTTA AAAGTTCATT GACTTTTTCT TCCCGCTCTT TTGGTGTTTT AGCTAATCCA    720

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GATAGTTTTT CAAACGTTTT TCAGCATTAG GAATGCCGAC TAATTTTAGT AATTCTAATG   1740
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TTTCTGCTGC CATGACAAAC TCTTGGTCTT TTAGTTTCAt GGTCkGGGcT CGCACAATCc 2520

TGGCCATkGA tATCCAGTTT GTAATA 2546

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

AACTTACCAA GAATCGCTTT AGAAGCGCAA GGAAGTCAAG AAAAGTTCTG GCAAATTTTA 60

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AACGAATACG GCTATCATTT TAGTGTCTAC TCTACACCGA GCGAAAGCTT GACTGACCGT 420

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TACTTTTCCC GCTACCTGAA GGACCAACAA TTGTTGTATT GCTGCCTGTT TCAAATGACA 4140

AATCAATATC AGAAAGAATG CTACGACCAT TTACTTGATA AGACACGCCT TCTGCTCGCA 4200

ATAAATTACT CATGTTTCTC TCCTTTTTTA AATGGAATGA TATTCTTTAT ATACTTCTTG 4260

TTTTTTTACA TTTCTCAATT TAGCCACTTC TTTGATTGCC TCTTTTGAAC TCCGTCCCTC 4320

TTCCTCCATT AAAACTTGCA CATGTTCCTT GAGGGAAATA GCTGGCATTG CTGCTATTGT 4380

CTCTTTCTCA CCAGTAAACC CGCTAACTAA TAAACAACAC TCGCCTTTTA GCGTATTTTC 4440

TGCTAAATAT TCTGTTAGTT CTCCTAAGGT ACCACGCAAA TACTCTTCAT GAAGTTTCGT 4500

TAATTCCCGA CAAATCACAG CGGGGCGTTC TTGACCATAG ACTTCAGCAA ACGTTGCTAC 4560

CGTTTTAGCA ATCCGATAGG GGGACTCATA AAAAATCTGT GTCGGCCGTT CTTCTTTTAA 4620

TGCTGATAAC ACGTCTTTCT GTTCTTTTTT CTTTCTTGGT AAAAAACCAT AAAACGTAAA 4680

TGGCTGTGGT AAAAGACCCG AGGCAATCAA AGCGGTCATT CCTGCCGTAG gTCCTGGCAA 4740

GGCAATCACT GCCAGTTCTT CTTCAAGACA TGCTGTAACC AATTCATGGC CAGGATCACT 4800

AATTGAAGGC ATACCTGCAT CGCTAACTTG GGCAATCGTT TCACCATTCA GCAATCGTGT 4860

AATCAGTTGA GGAATTCGCT CTTTGTAATT ATGTTCGTGT AAACTAATTT GTGGTGTTGT 4920

AATCTCAAAA TGATTTAGCA ATTTTTGTGT GTTTCTTGTG TCCTCACTAG CAATCACCGT 4980

TGCTTCTTTC AATATGTTTA AACAACGAAT ACTCATATCT TCTAAATTGC CGATCGGTGT 5040

TGGGACAAGA TACAATTTTC CTTTTGTTGT TTGCTTATCA AAACTTTTCT GTTTTTGCAT 5100

AGCGCATCCC TCATTTTCCT TTTTCGTTCT ATAAATAGAT AAAGGTTTGA TTTGACAATC 5160

GATTGACTGT CAAACCAAAC CTTTCCTTTT TATTTGCAGT GTCCACTAGA CTTAACGCGT 5220

ACGTTCCCCA TAAATAACAT CAAGACAAAA GGCACATTCT TCATCATTTT CACGTCTTGA 5280

ACCATATAAA ATATTGCAGA CATGGAAGCC CTCTTCATAA AGTTTTTCCA AATTCATACG 5340

TGATTTTGAT AGCTCTTGTT TTTCAGTTTC AGTTGTATTT CCTGCTAACT TATTCAGTTC 5400

TTGGAGATGC TCTCGTAAGC GTTGGTTTTC GATTTCCAAC GTGGTATTTT TTTCTACCAA 5460

CTCATGGAGT GCTGCTTTAA TTTCTCTTAA TTGTGTCACT GAACTGTCTA AATCAGTTTC 5520

CAACGAATTT AATCCATCAT AGAGCGAACG CTTATCCATT TTGATCACCT TTTTCAGCAG 5580

CAACTTTCGC AGTAGCTTCT TTGATTTCTT CGTAATCATA ATCCGCTGCG ATTTCACGAC 5640

CATGCAGACG AACTTTGACA ATCCGACTTA ATAGATTCAA CCCGACGACT TTGCCTTTGC 5700

CATCTGGTGT TATTACTTCT TTTCCATAAT CTGGTAATTC TTTTTTAGCG GCTTCATATT 5760

CGTCGTTTTC GTATTTCAAA CAACACATTA AGCGGCCACA TAATCCCGAA ATTTTGACAG 5820

GATTTAAAGA TAACCCTTGA TCTTTAGCCA TTTTGATTGA AACTGGCATA AAATCTCCTA 5880

GAAATGTTGA GCAACATAGT TGTCTGCCAC AAGGGCCAAT GCCACCTAAT ATTTTCGCTT 5940

CATCTCGGAC ACCAATTTGa CGTAACTCAA TTCGCGTCCG GAAAATAGCC GCTAAGTCTT 6000

TGACTAATTc ACGAAAATCA ATTCGCCCAT CTGCCGTAAA GTAAAAAATC ATTTTGCTAC 6060

GATCGAAGGT ATATTCTACT CGCACTAATT TCATTTTTAA GTCATGAGCT CGAATTTTTT 6120

CATTGGCAAT GCTTTTGGCA GCTTCTGCAT CAGCCAAATT TTTTTGTTCT TTTTCTAAAT 6180

CATTGGCTGT TGCTTTATTT AAAATGGGTT TTAGGTCCTC TGGTAAATCG TCTGAATCGA 6240

CTGTTTTTTT AGGAATAGCA ACAGTAGCTA ATTGTTTTGA CTGTTGAGAT TCAACGAGTA 6300

CTTTCTCATT ATAAATATAC TCAGATTTTC CAGGAGCAAA ATAATAGATA TGACCGGCTT 6360

CACGGAAGCG AACTCCTACT ACTTCTACCA TTTTATTCCT CCTAATCTAG TTCAAGTGAA 6420

CGTCGCTTCA ATCGGTTAAG GAACTTGCTG AAACAACTAA GTTCCTACTA TATTATGAAA 6480

CTGAATGCCA CTTGGCACTT TTTTCCTTTA TGATTTAGGG TGAATCATTT GGATAACTAA 6540

TTGTTCACAA ACATTTTGCC AACTAACATT GGCAGTCCAT TTTTGGCGTG CTTTCAAAAT 6600

TAGCGCCAAC CGTTCCGCCT GCTCTTCCGT TACTTTTTTG GCTTGCTGTG TCGCAACACT 6660

TTCTTCCAAT AATTGACGGT AATAAACCAT GAGCAAGTCA AAGCTAAGCG CTTGTTGTTC 6720

TTTTTCCTTA AATACTTTGA CCATTTTCTT CTGAACGTAG ATAAATGCCT GTAAATCATT 6780

ACTTTTTAGA TAATTAAACC ATTGCAAAAT GATTTCCCTA GCTTCATTAA ACCATTCATC 6840

TTGAGAGATT TCaACTGCTT TCTCAAAACT ATTTGTCAGT TCAGCTAAAA GGGTTGCAGT 6900

CTTTTCACCA ATCCCCTGTT TGATTAAGCG ATCAATTAAT GTTTTTTTGA CTAATGGTTG 6960

AAAATGTAAG GTTTGGCATC GTGATTGAAT CGTTGGTAAA ATTCGAGAAA GCGAAGTGGT 7020

TTCTAAAATA GCTAAAATTT GTCCTTCTGG TTCTTCTAAA AATTTTAAGA GACTATTaGc 7080

tGCGCCGGTA CTCATTTTAT CTGCTTCTTG AATTAAGAAA ACTTTTTTAG CAGTCTCGAC 7140

CCCACTTTTA GAAAACTCCG CTTTTAATTC ACGGATTTGG TTCACTTTGA TGGTTTGCCC 7200

ATCTGGCGCA ATTCTTAAAA CATCTGGATG TTCATTTTCA TTAATCCGCA CACAATTATG 7260

GCATTCGTTA CAAGGCTGTT GATTTACTAA ATTCGTACAA AAGACATGTT TCGCCATCCA 7320

TAAGCCAAAT TCTTGTTTTC CAGTTCCTGT ATCTCCTTCA AAAAGATAAG CATGGGCAAG 7380

ACGACCATGC TCAAAACTTT TTTGGAGTTG CTTGTACAGC AAAGGTTGCA TTTGCTGTAG 7440

CTGTTGTGCT TCATTCATCT TAATATTGAT GGAATCCTTC AACTGGTAAG ACGAAGCAAG 7500

TAGCGCCGCC TACTTCAACT TCCACAGGAT AAGGAATTTG GCCATCCATT GTGATATCTA 7560

AAGTCACAGG TGTTGAAACA TATTGTTTTC TTGATTGACA TGTTTCTTTA ATTAAAGCTA 7620

ATGTTTCGTC GACACGTTCA TCATCAATCC CAATAATAAA TGTGCTGTTT CCCGCTTTTA 7680

AGAACCCACC TGTTGAGGAT AATTTTGTAG CACGAATATT GGCATCAATA AATTCGTTGG 7740

CTAATCGGTT ACTATCTTtG TCtTGTACAA TGGCTAAAAT AATCTtCATG GTCTACACCT 7800

TCCTATAATT AAAAGTTTTC TGGATAACGT TCAATAATCG CCTGATACGT TGCTTCTACG 7860

ACAAGTTCTA AACTCATCCG TGCATCAATC TTTTTGATAC GTTGTGGATT TTCTTCTGcT 7920

AATTTCAAAT ATTCATGACG AACmCGTTGA TGAAATTCTA ATCCTTCTGA ATCTAAGCGA 7980

TCAATTTsCT GTGTTCGATT TTCTTGAATC CGCCGTAAGC CAGTATCTGA GTCAACGTCT 8040

AAATAAATTG TAAAATCTGG TGAGACACCT TCTGTCGCAA ACGCATTAAT TGAAGCAATG 8100

Gn 8102

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1670 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

AATATTTATT TTATAGGAGG AGAAAGTTAT GGGGCATCAA TTGAGCACTC ATTTTTTTAA 60

CAAGAAAACA GGGATTATTT CAACTTTTTT AAGTTTGATA CTTTTAGTCG GTGGGTTACT 120

GTTTGCACTA CCTGCATTTG AAGTACAAGC AGCATCAACT GTTACACCTA AAACAGTCAT 180

GTATGTAGAA GTAAATAACC ACGATTTTAA CAATGTGGGa AAATATACTT TAGCTGGAAC 240

CAATCAACCT GCTTTTGATA TGGGGATTAT TTTTGCAGCC AATATTAATT ATGATACGGT 300

CAATAAAAAA CCTTACtTAT ATCtAAATGA ACGGGTCCAA CAAAcTTTAA ACGAAGCTGA 360

AACACAAATT CGTCCaGTTC AAGCACGCGG CACTAAaGTC CTATTGTCTA TTTTAGGCAA 420

CCATGAAGGC GCTGGCTTTG CTAACTTCCC AACTTACGAA AGTGCGGATG CCTTTGCAGC 480

TCAATTAGAA CAAGTCGTTA ATACGTATCA TTTAGATGGT ATTGATTTTG ATGATGAGTA 540

TGCTGAATAC GGAAAAAATG GGACGCCTCA ACCAAATAAT TCTTCGTTCA TTTGGTTACT 600

TCAAGCCTTA AGAAATCGCT TAGGTAATGA TAAATTAATT ACTTTTTATA ATATTGGACC 660

AGCGGCTGCG AACTCTTCAG CTAATCCTCA AATGArTTCT TTAATTGATT ATGCTTGGAA 720

CCCTTATTAT AGTACCTGGA ATCCGCCACA AATTGCGGGG ATGCCTGCTT CTCGTTTAAG 780

TGCTTCTGCC GTTGAAATTG GTGTCAATCA AAATCTAgCT GCGCAATATG CTAAACGTwC 840

AAAAGCGGAC AATATGGTAT TTATCTAATG TATAACCTCC CAGGAAAAGA TTCATCTGCG 900

TATATCTCGG CGGCGACACA AGAACTTTAT GGTCGAAAAA CGAACTATTC ACCAACTGTT 960

CCAACACCTT AATATTATCT CGTGTCTACA AGCGCCAACA TGTAAAGAGT TAAAAGCCAG 1020

CTTACTACAA GCTGGCTTTT TGGTATCTTG AGCGAATAGT TTTACACAAA AAAAGACCCG 1080

CCCTTTGGGT AAGGACGGGA AAGGAGTTAA AAATGAAAAA GTGTTTTGTG TTGTTAAGGT 1140

TGTTTGTTGA TATGCTTATA TCTTACAAAC TAAATGTGAA GATTTTGTGA TCATTTCATT 1200

CTTATTTTGC TACTTTTATA GGAATTAAAT AGATTGCCAC GAGACTATCT TTAGTTGCCT 1260

CGTGCATCCG TTATTCTGAC TGCTCCTTGT GGTGATACTC TGAAAAAACC AACAGTCCCA 1320

GTCCCTCCAT TTGCAGCCAT CTGTTTCGAT TGGGCTCTAA AAAAGAAGTC ATTTCCATTC 1380

ATACCCAAAA ATCCAAGGTT CGTATCATTA TTTTCTGCAT CAGTCAGTGT CTTTCTAATA 1440

TATGTCTCTG CTTTTTCTTG TGTATCGATG ATTTTTGCCT CTTCATTTTG GTCTTGATTT 1500

TCCTCTTCAG AAGAACGATA GTAATACTCT TCCGCaGGAT AATTTCCACT ATCTTGAGTA 1560

ATTAACAATC GCGGTTTCGT CTTATCCGAT TGGTCGCCGT TAGGATTTTC AACACCAATT 1620

TTATATAATA ATAGCGCAGC ACCAGTAGGC CCCCACCTAA TACTTAAGCT 1670

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TACCGAgGTG TATCAgCGAT TCtaGTAAtC CACAaGTTCC ACTACAGAAT CAGAAtCTTA 60

AAAGGTCTGG CGGAAGAAAA AACGCTAAAA GAAAAAATCC CGTCCTTAAA TCAAACAACG 120

ATTAAGAAAG TCACTGATAA TGAGTATAAA CGCATTCTTG TGaTGGAAGA AAAGGCTACA 180

GGAACGACCT ATAAAAGTAT TTTGATAAAA AAACAAAATC GCTTAAAAAT TGTCAACGAA 240

ACAACCGATG AATTGTTATA CAATGGAACC CTATAAGAAC GAAACCATTC AATAAACTCA 300

AAAGTATAGC CATTGTTTTC AAAGAAAAAT TTCTTTGGAA ACAATGGTTT TTTTATTGAC 360

AAAAGAATTT CTAGGATATA TAGTTAGTTA CATAAGTAGT TAACCGTTTA AGCGAGGTGT 420

AAAAATGGAA TTTAATTTTT CGGGGGAAAA GCCTTTATTT CAGCAAGTAG CCGATCAGAT 480

TGCCGAAGaA TTTTTAATGG CGCTTACTTA GAAGGCGAAC AAATTCCCTC AACCACAGAA 540

ATATCAAAAA GTTATCAAAT CAATCCAGCC ACCGTTTTAA AAGGAATGAA TTTATTAGTA 600

GAACGACAGT TGATTGAAAA GAAACGGGGG ATTGGCATGT TTGTTTTACC AGGCGCTCAA 660

GAGAGAGTAA GAAGTGCACG GAAAGAAGAA TTTTTAAATA AAGAAGTCTT AGAAGTTGTC 720

GCAGAAGCTA AAAAATTAGG GATTACAGCT GAACAATTAA AACAACTAAT TGAAAGAGGG 780

TATGACGCAT GAGTTTGCGG GTGGAATCAG TAAGTAAAAA ATATCATCAA AAACAAGCAC 840

TAGATAATAT TTCaATTACT TTTGAAAAAG AAACGATTTA TGGGCTCTTA GGCAGAAACG 900

GGGCTGGTAA AAGTACGTTA TTAAATATCA TAAATAATCG AAGTTTTGCC ACTTCAGGTT 960

CCGTTAAATT GGCGGGAGAA ACAGTGACCG ATAATGAGGC TGCTTTGACT CATATTTACT 1020

TAATGAGTGA AGATAATTTG TTTCCTCCTC AGTTAAAAAT TAAAGATATT TTTAAAACGA 1080

CTGAAGGTTT TTATGGATCC TTTGACTGGT CTTTAGCCGA ACAAATGTTA AGCGATTTTG 1140

ATTTAGATGG TAAAAAGACA TTCAAAAAAT TATCAACTGG TTATCGGAGT ATTGCTAAAC 1200

TAATAGTGGC GCTATCCGTC CCCTGTGAGT ATATTTTTTT AGATGAGCCA GTCTTAGGTT 1260

TAGACGCCAA TCATCGGGAA TTATTTTATA CTTATTTAAT TGAGACATAC CAAGAACGTC 1320

CCCGTACGTT TGTGgATTTC TACCCATTTG gATtGGAAGA AATtGCGAAT TtATTAGAAG 1380

ATATTATCay CATTGAkCmA gGGAAAATTG ATCCGCGCAG AATCTATTGA AACCAATTTG 1440

AAAAACCGGT CGC 1453

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TAGGAGTGAC AACAAATGAC AATTGATTGG ACAAAAGAAG TCGAAGCACG TAAAGACGAC 60

TTATTAGAAG ATTTACAAAA CTTATTACGG ATCAACAGTG AACGTGATGA TGCACAAGCA 120

ACACCTGAAG CGCCCTTTGG ACCTGGGCCA GTTGCTGGCT TAAAACACAT GTTAGCGTAT 180

GGTGAACGTG ATGGCTTTAC GGTGAAAAAT GTCGACAATT ACGCTGGACA CATTGAATAT 240

GGTGAAGGCG ACGAAACGTT AGGAATTTTT GGTCATATGG ACGTTGTTCC TGCTGGTGAT 300

GGTTGGGAAA CAGATCCTTA TGAACCAGTC ATTAAAGATG GCAAAATTTA TGCACGTGGT 360

GCAAGCGATG ATAAAGGCCC AAGTATGGCT GCTTATTACG CAATGAAAAT TATCAAAGAA 420

TTAGGCTTAC CCGTGTCTAA AAAAATTCGT TTCGTAGTAG GAAGTGACGA AGAAAGCGGC 480

TGGGGCGATA TGGATTACTA TTTCCAACAT GAAGAAGCGC CAGACTTTGG TTTCTCACCA 540

GATGCTGAGT TCCCAATTAT CAATGGGGAA AAAGGAAATG TGACTATTCG TTTAACTTTC 600

CGAGGCGGTA ACGGCGCTGA TTATAAATTA GAAAGCTTCA AATCTGGCTT ACGTGAAAAC 660

ATGGTTCCGG GAACAGCAGA TGCTGTTGTA ACGGCTGCTT CAGCAGACGA AGCGGCTTCA 720

CTAGCTGCTA GCTTTGAAAC ATTCATCAAA CAAGAAGCAA AAATTTCAGG TAACGCAGAA 780

CTTTCAGATA AAACAGTGAC TTTCCATGTA GTTGGTAAAG GTGCTCACGG TGCTAGCCCA 840

CAATCTGGAA TTAACGCAGC GACTTTCTTG GCAACTTTCT TAAATGATTA CAGCTTTGCA 900

GAAGGCGCAT ATAGCTTTAT TAATACCATT GCTGAATTTA TCCATGAAGA TTTTTATGGT 960

GAAAAATTAG GCGTGGCTTT TGAAGACGAA AAAATGGGTA AATTGACAAT GAACGCTGGG 1020

ATTGTTAACT TTGATCCAGA AAACCCTGAA AATAGCTTAG TAACATTAAA CTTCCGCTAT 1080

CCAAAAGGAA CTTCAGCAGA AGAATTACAA GCAAAAGTTC AAACAACAGT CGGTGAAACG 1140

GTCACTGCAA CACAAGGAGA TCGCAACCAA GAACCGCATT ATGTACCAGT TGATGATCCA 1200

TtGGTGGCAA CGTTACTACA AGTTTACGAA GACCATACAG GCGAAAAAGG CCAAGAACAA 1260

ATCATTGGTG GCGGTACTTA TGGCCGCTTA TTGAAACGTG GTGTTGCCTA TGGCGCAATG 1320

TTCCCTGGCT ACACAGACAC AATGCACCAA GCCAACGAAT TTATGGAATT AGATGACTTA 1380

TTCCGAGCAG CTGCTATTTA TGCAGATGCG ATTTATCGTT TAGCGAAGTA AAGTAAAAAA 1440

GCyGTTTTCG ATTTTCGAAA ACAGCTTTTT TTTGCAATTT TTGCCTTTTA AAAAcCCaAA 1500

ATCAGAACCG TCAATTTACT GAAAATTTCT TGCAAATCAA CGGATCCCAC GATACGATAA 1560

ATAGGAGAAA ACGCAATGAG TGAAACACTT ATTGTTAACT ATTTAATCAA AGGACGTGTG 1620

AAGATGAACG TAGAAGAATT AGTTCnAAAA GCmAAAGATT TAATTGGAGA AGGCmACGTG 1680

GAACATGCGC AACAATTCAT TGAAGAACAT AAAGATGAaT TaGGCGrACA CTATCmTAAA 1740

ATTACmGCGA TGTTAGCTGA TmCAaCGACC GATGGTTtGT TTGaTAAAAT TAAAGgATtG 1800

TTcAATAGTT GAAAAAAATC 1820

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

GACATTTAAT TGAACAATTA GAACAACACT ATCACGGAAT GATAATAGTA CTTTATACAA 60

AAAATTGTCA ATCATACGCA GCATCCTTAA ATCAAAAAGG CATAAAGACG ATACTTTTTG 120

ATAAGAAAAC TTTGTTGATT ACAACGGCGA TTTCATACTT GAAGTCAGCG CCGTTAATTT 180

TTGTAGATAA TTATTTTCCA GAATTGGCAA TTTTAAAAAA AAAGCAAGTA GTTATCCAAT 240

TATGGCATGC TAATGGGGGC TTTAAAACcA GTTTGGCTGG GGTGCTTATC ACACGAAACA 300

TAGAAGTAGC AAGGATCAAA TCAGGTTTCA AAAaGTTtAC GmTAAAATGA ATTATTTTAT 360

CGTTAATTCA CTAAAAATGG AAGCAATTTT TAGAAACAAT TATCGTCTCG AGAATGCTCA 420

ATTTTGTCAT TTTGGTTCGC CGCGTCTTGC TTATCTTGAA AAATTAGAGG TAGGAGAAAC 480

AAATCAGAAT AATAAAGTTT TATATGCACC AACTTACCGA GAgGGAATGA ATGAAATGAT 540

GCTTGTGATA AATCAAGCAA TAAAGGCTTT TTCTGCTATG CCAAATTTTC ATTTTTATAT 600

GAAATTACAT CCATCAATCC AGTTAGATGC CATTGAACTA CCGAGAAATG TTTCTATTTG 660

GGAAAAGCAT ATTTTTGAAA GCTTTAGTGA AATAGGgCTA CTTGATTACT GATTATTCGA 720

GTGTGGTCTT TGAATACATG CATGTTAAAG AGCAACCGAA CATTTaTTTT TgTCCAGATT 780

aGAAAAtACG CATTAAATCC TGGAATkGAG CCTGATTTTT TTGAATATTT ACCAGGACCG 840

TTAGTTGaAA ATGaAAAACA GTgGATgTGG GCATGtCAAA TTTTcCAtAA ATAGTTAtAA 900

rGAkAATaTT ACtrGAtTaA CGAGGAATnG G 931

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CCTATGTAAA TAATGAAAAT CCCATATTTT CCAGAAGGGA TAAATGTGAG TTTTGTTGAA 60

ATTCTTGGCA AAAATCAACT ATTTGTTCGA ACGTATGAAC GTGGTGTAGG TTTTACAAGT 120

GCTTGTGGGA CAGCTATGTG CGCAAGTAGT TTACTTTATA CGTTATTGAA AGATGGTGTT 180

TTTTATGAAG AAATAACCGT CAAAAATACT GGGGGTATGG TGAAAACAGT CGTCCACGAA 240

ACGTCAGATG GCAGTTATTG GATGGAATTA ATTGGGAATG CCACGATTAC GCATTTGATT 300

GAAGGATCAC TGACTGATTT ACTAAATGGT GCATTTGAGA AAATAACTAT CACTGAAACG 360

AATGAACAGA AACATTATCA AGAATTTCTG CAAACACTTT CTCAAAAATA ACAATTGTTC 420

CTTGATAAAG CGCTCTTTTA TTTTACAATT GTGTTAAGTT CTTGTTCCAA AAAATAAAAA 480

ATATTGCTTG AATAAGCAAA CTATGAGAAA ATAAAGGGCA TGAATTAAGA ATTATTCTTA 540

GATAAACGAG GAAGTGTCTT ATGAAACTAT GGAAAAAAGT AGTACTGGGC TTCTTGAGCG 600

TCTTGCTAGT GGCAGTAGCT GGGGTATGTG CTTACGGGAT TAAGATGTAT TCAGATGCCA 660

ATTCAACAAT TAATGGGATC TATCAATCAG TTAACCGTAA GTCCAATAAA GGAGCCACGG 720

CCAATATTGA TGCGCAAGAA CCATTCTCTG TTCTTTTAAT GGGGATTGAC ACAGGCGATT 780

TAGGTCGAAC AGAACAAGGT CGTTCAGATA CTACAATGGT TGTAACCATC AACCCGAAAG 840

AAAACAAGTC CACAATGATC AGTTTGGATA GAGATATTCT AACAGATATT GTTGGAAATG 900

ACACACAAGA CAAATTGAAC CATGCCTATG CATTTGGTGG CGCCGAAATG GCGATTAATA 960

CAGTCCAAGA ATTACTGGAT ATTCCCATCC ATCACTATGT ATCCATCAAT ATGAAAGGGT 1020

TAAAAGACCT GATTGATGCG GTAGGCGGTA TTGAAGTAGA TAATACGATT GGTGAATTTA 1080

CGTTGGACGG TATTACTGTT CCAGCAGGTA AAATCmAGTT AGATGGCACG ACAGGTTTGG 1140

CTTATGCGCG GATGCtCaCG AAGATCCTGA AGGAGATGTG GGTCGTCAAC GCCGCCAACG 1200

AGAAGTTGTT GAGAAAATTG TGCGCAAAGT CATGAGTTTT GACGGTGTTT CAAAATATCG 1260

AAAAATTCTT GATGCTGTTG AAGCCAATGT AAAAACAGAC TTAACTTGGG ATGACATGAT 1320

GGACATCCAA TCAAAATATT TATCTGCCTT TAAAACAATT GACTCTGAAC AATTACAAGG 1380

ATACAGTGCA ACCATTGATG ATATTTATTA TCAAGTCCTA GATCCAAATA GCTTATACAA 1440

AACACAAACA ACACTCAGAA AACAACTTGG TTTAAAAGAA CATGCTTCTG AACGTGAAAA 1500

AGATTTAGCC TTTTATAATC AGTTTAGCTA TGCTGTTACA GATACTGCAC TGATTGGTGA 1560

ATCTGGTGAT TCAAGTGCCA ATAGCTCTAC TAGTTCGAGT AGCACAGCGG ACACCACAGC 1620

CGGACAAACA GAATACAACG GcAATACGCA ACAAGCAGCA GAAGGAACCT ACGATCCGAA 1680

TACGTACGTT GACCCAAATG CGTACACAGA TCCAAACGCT TATGCTGATC CAAATACGTA 1740

TGTGGATCCC AACGCACCAC AATATTAATC TGTTAAACAA GCTCGAAAAC TTCTATTTCT 1800

GATGGGAAAT AGAAGTTTTT TTCTTTTATT CTAGAAATTT TTTTCAGAAG GTGTTATAAT 1860

TGGACTATAC CAnAATAAAC CGTAAGGAGC GTGTCAAAAT GCAAATTATC CGTGTAGCAA 1920

ATGCAGAAGA AGGCGGCAAA AAAGCGTT 1948

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TCAAGCCAGC AAGTAAGGAA rGArGTGTrG ATTTCCyGtC CyGaCTTtCC TACTATCGCA 60

TAAAACTTCC CAAGTTCAAA TTTTTGATTT ACTCCTGACA AAACTTTTTC TTTAGAATTT 120

GCATAACTAT ATGCTACATT CTTTATTTCT AATATATCCA TTATTTTCTC CTAACTTATT 180

TTTGATAAGA TTTCTTTAGG CTTCTTGATT AACATTAATG AAGAAGCAAA TACAACTGAT 240

AAAACAATAA TACTTATTAA TATTAAATAA CTTTGTCCAA GCGTTGTTAT ATTTGACATA 300

AAACTACTAC TATTTATTnA ACTTCCaCCG GAAATCATTG rATCCTCTGA GTTAATGAAT 360

CCATCTACAA TTACTTTTAG TAATACATTT CCTAAAAATA AGGAAGATAT TATACTTGGT 420

ATCGAyATGA ATATTAACTC GAATATAAAT TGCATTATAA TTTGTATCTT AGATGTTCCA 480

ATAGATAAAA ATATACCTAT TTCATAAATT CTTTCCCTTA ACCATAGAAT CAAGATTAAT 540

GAAAGAACAA CCATCCCAAC TAACATAATA GAATAAGTCA TTACTTTTAT TATATATTTT 600

ATTCCACTCA CTGACTCTAA AGACTCTTCA AACGCATTAG AATCTTTTTC AACAAAATAC 660

TTTGACTCAT CAATTTTAAG CTCTTTCAAT TTGTTTAAGG CTAAGTCTGT AGATTCTGCA 720

CTACCAGAAT ACATTAAAAT TTTATTTGCA ATTTCATTAT TTTCTGAATT GTTTAATACC 780

TCTTGGCTTG TTGAATAATC TACAAACACC ATATTTTCAC TAAAATCAGA AGATAATCCT 840

GTATATGTTT CCTGTTTTTT ACCAGAAAAG ATCCCTATAA TTTTAAATTT ATGACTTTTT 900

ATTTTTCCAC TTTTTTCAAT ATCTAGTAAT TCAAGATCAA CTTCATCACC TAATTTTAGA 960

TTGTTTTGTT TAGCAAATTC TTCATGAACA ATAATTGAAT TCTTATCATT TTCTTCTATA 1020

TTTTCACCTT CTTTAATTGT AAATACTCCA CTACTAAATA AAATATTTCT TTTAGTATTA 1080

TTTGTAGCTT CGAGTGAAAC AACATTCTTA AATTCGTCAG ATAAATCTTC TCTATTTATT 1140

CTTTGTTCTC CGCTAACTAC TTTAGCATCT TTTAGTTTTG CTAATCCATC ATATTGAATT 1200

ATTTTTTCTT CAATTTCTTT TAATTTTTCA ATATCTTTAA ATTGATTAAC ATTAAAATAT 1260

TTACCATCTT TTTTTGTTAT TGATATTGAA GAATTAGAAC TTTCATATAA AGCCTTTTCT 1320

ATTTCATTGC TTGATTTCAT TATTGTTAAA CAAGAATACA AGCAAGAAAG AACTATAGTT 1380

AATATGATAA AAATTATTAA AGTTCTATTT TTCTTTCTTG TAATATATGC TATAGCATTT 1440

TTTATCACTT TCCTAACTAC TCCTCTCTAT TTTCTTACTC CATAACTAAT TGCATCCACT 1500

GGACAAGCAT TTTTACATCG TCCACATCTG ATACACTCCA GATGATTGCA ATTCTCAACT 1560

GAATCTTTAT TCATTTGGCA AACTTTTTTA CATTTTCCAC AATTAATACA CTTATCCTTA 1620

TCCAATCTAT ATCTAAATAT TGAAATAGGG TTAAAAATTG AGTAAATAGC TCCAAGTGGA 1680

CATATATATT TaCAAAAAGG TCTATATATA ATTATAGAAA GTAACAAAGT AACTATTAGA 1740

ATGATTCCTT TCCAATAATA CAAGAAACCT ATCGTACTTC TCATACTTTT ATTTAATAAA 1800

ACAAGTGGTA ATCCTCCTTC CAGCATACCA ATCGGACAAA TAAGTTTACA AAAATACGGA 1860

GAACCCTGAC CTAAAATATC AACCAAAAAT AAAGGTAATA TTAATGAAAA ATACAAGTAA 1920

TATTATATAT TTCAATTTTC TCAAATGTTT ATCAAACTTA AATGTTTCAA CTTTTTTAAA 1980

AAAGGGAATC TTGTGTAGCA AATCTTGAAT CAATCCAAAT GGACACAGCC ATCCACAAAC 2040

AAATCTTCCC ACCAATGCTC CTATAAAAAA CAAAATCCCA ACTATATAAT AAAATAACTA 2100

ATCTTATATT TTGAATTTCC AATTACTGCC TGTAGTGATC CTATTGGACA AGAACCTTTT 2160

GCTCCCGGGc ATGAATAACA ATTTATACCC GGAACACAAA TTTTCTTTAA ATTCCCCCCG 2220

TAGATTTTAC CAGTCTTAAA CCCTTCaAAG TAAGAATTAG TAATTAAAAA CCAAACGGrT 2280

TGAAATAAAT GCTTAAAACG ATCTCTTATT TTATATTTAT CTTTTTTTGt ACTACCATTT 2340

ATAATATTtT TAATTCTATC CaATTCCAAT ACACTCCATA CAAATTCTTA TCGCCTTATC 2400

CmAGaCmACy TTAGTTTCtC CcATTACTAT CAACAAAGAA AGTCTCTGGC ATAGCCTGTA 2460

TACCATTCAA TCTACCATTA AAGTTTGTCT TATCTGGCAT TAAGAAAGGA TATGAAGCCT 2520

TTGTCTTTTC ATGTATTAAC TTTGACTTTT CAATTGCTTC CTTGTTTTCA CCGTTATCAT 2580

CAACAGGATC TGTAACAACT CCAACGATAT TTACACCCTT GCTTTTCATT TCATTCTGAA 2640

CCTCAACCAA ATCAGGAATT TCCTTTACAC AAGCTGTACA CCAAGTTGCA AATACATTTA 2700

CCATAGTAAG ATCATACTTC TCAAAATCTT TACTTGTAAA ATCCTTGCCA TTTATGTCCT 2760

TTGTTGATAG TTTACGTAAA TCTTTAACCG ATTCTTTGTT AAATGCTTCT GTATTTTCTA 2820

AATCAGTTTT TTCTGATAGC ACAAAACCAT TTTTAGGACG TTCTTTTTTA TCTATAATTT 2880

GAATCTCAGT TCTTTTTAAT TCATCCAGAA GATTACTTTC AGCTCCGCTA TTTGTGCTTA 2940

AATAGCAATC GTATTTTCCA TCACTTGAAA CTCCTATTTT AGTATGAGTA TCACATTTTA 3000

TAATTTTAGA TTTTTTTCTT CTGATGTATT TTTTTCAAAT ATACCAATAG TCCCaATTCT 3060

TTCAAGCTCA TTTTGCCAAT TTTTATATCC ATCGCCCATC TTTTCTATAA CgCATyCTTT 3120

TGgTtCTtCT GTCATTTTTt CAAATGTCAA AATAGCATAC TTTAGTTCTt TAwCyATAGG 3180

ACTTnGAnCA TCTAACAnCG CTAnCTTTTa TCAGCTATAT AATTTCTAAA TTTGTCTGAG 3240

AGTTTAAATT TAAGCCCTAA ATATTCATAA ACATATTCTT TCTTtGCCTC CaATGTATAA 3300

TCTGaTGGCT TAAAAGTTTC ATTTTTGcCA TTTGCATTAA TTGACATGCC TTCCTCTTCA 3360

GAACTTATGG ATTGTCCTTC TTTTATTTTT ACTTTTTTGA CACCCAACTG CGCTTAAGCT 3420

CAAACATAAT GCAAGTAATA GGCATGCTCC TCTTGGTACT ATTTTTTCAT AAATTATTCC 3480

TCCTTTATTT TTTACACAAT AGCATTTTAT AGCTACTTTC AATAACATTC TACACACCTT 3540

TTATGAAACG TTGATGAAAT ATAATTTTTT ATTTTTCCAA ACTATGGTAT AACAATATAA 3600

GTATTATGCT TAAAGTTGTT CTTACACGAT TAGTATATGA TCGATTAATA TATGAGCAAG 3660

CACAGTAAGT GTACGGACAC TTACGAAAAA AATGATGAGG CAGCCCTTTG GGATCTGCTT 3720

CTTTTTTTAT CAATTTTTAA CTTGTTAGGG TGTACCCTAA GACCCCGAAA TACATTCAAA 3780

GGAGGATTAC CTATAGCAAA TAGAATACGA AATGAAAGGC TTGAAATTAA ATTAACAGAA 3840

GAAGAAAAGG CTCTTTTTGA GGAGAAAAGA AAACTTGCGA AATGTAAAAA TATGAGCCAT 3900

TTCATCCGCA AGTGTGTTTT AGAAAAAGAA ATATATTAAG TGGATTTAGA GCCGTTTAGA 3960

GATTTACAGG GTTTCCTTTC CAATGCTACC AGCAACATAA ATCAGATTGC AAAGCGTGTG 4020

AATTCCACCG GCATAATCTA TAAGGACGAT ATAAATGATA TGAAAAAGCA GATTGAGTAT 4080

TTCTCAAAAG AGTTGTGGCA AATACATTCT CTGCTTCTTA ACAGAACTTC CGGAGTGTTA 4140

AATGAGAGTG TAAAATATTT TGTGTAAATA GAAAAAAGAA AGTCCCTTCT GTAGAATAGA 4200

GTTACCACAA CACATTCACA GAAGAGAGGA CTTCCCTATG AACGATTTTA CTACAGAAAT 4260

TCTAAAGACT CTAGCGAACA AAGGCGATTT GAATGAATTA TTCCGTGTCC ATTTGGAGAA 4320

AGCAGTCAAT ACGCTTCTCA AAACGGAGTT AACGGCTTTC CTCGATTACG AAAAGTATGA 4380

TCGCATTGGT TTTAACACGG GTAATTCTCG TAACGGCTCC TATGACCGTA CGGTCAAGAC 4440

CGAGTATGGG GAACTTCATC TCCAGATTCC GCGCGACCGC AATGGCGAGT TCAAGCAACA 4500

GACTGTTCCT GCTTATAGAC GGACGAATGA CACGTTAGAG GAGACCGTCA TTCACCTCTT 4560

CCGAAAAGGT ATTACCATGT CGGAAATCGC AGACTTGATT GAGAAAATGT ATGGGcATCA 4620

CTACACGCCC CAAACCATGT CCAATATAAC AAAATCATTT aCAGAAGAGG TAACGGCGTT 4680

TaAaGGGcGG GAcTTTCATG GACCGTTATG GCGCTATTTA TTTGGGCCnC ACGTTTTTCn 4740

CGTAAAAGGG AAAAnCGCCA CGAAG 4765

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4054 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GTGTGTCTAA CGGTTCTAAT GGTTTATAAA CGACCGCATA TTTAATCCCA TATTCTTTTA 60

ATTTTTCTGG AGATAAACGA GCAmTAATCG CATCTTTTTG CATCAACTCT AAAACAGGGG 120

TCTGATTTCC TACTTCAACA TTGATGTGCG CATAGCGATT ATAAATAAAT GTGTCTTTTC 180

CTTTTGGATC TAATGGTTTC CAAGCCTCTA AGTCAGGTGT AAAAGCAACA CCGTTAAATG 240

TATGCACACC TAACATTGGC AAATAGCCAT ACATCAAGCG TTCGCCCACC CACAATTGGT 300

TGGGGTCTTT TTTGTTAATT TCTTCCACTT CTACCGCTAA TTTTTkACCA TAGACAGCAG 360

AAACGCCACG AGAAATTGGA TTTACAAAGG CTCCAGAAAC CATAATGATT CCTAATAAGA 420

CAAGGACAAA TAACGTGCGC CAACGTTTAA ATAAAGCAAC AATTAAAACG GTAGCGACAA 480

CTAAGACACC AATGATGTCC ATTCGTGTAA CGTATAACCG TAAATTGCCC GTATATAAAA 540

CAAAGAAATA CAGAACAACA TTTAATCCTA GTGCCCCTAA CCAGGCCATC ATTGGAATTT 600

TTGCTTGGCG ATTCCATAAw TAATCGATGA mCCwTAAaCT TAACAACACA GCGGCAAaCC 660

CGAAGaTAAC ATCGCCCGTT GTTCTGGCAC ATAAGACCAC AATGTCAACT TAGCAAAAAT 720

TGTTGGAAAT TGCACGCTCA TCCaAACTAA GTTAAATAAA CAATACACGA ATAAGACAAA 780

ACCGTAAATG tTTTCTTTGA TTTTTTTATA AAAAATAAAT GGTGAGAGCG GCAAAATAAC 840

AAAAAATAAT TGATAAAAAC TACTGATTTC CGAATTATTG GAATATGGAA CATCTTGAAA 900

CGGCATTTTC CAATTTGTTA AAAATAACAA AATATCGCGT TTAGGCATAT CGCCACCTAA 960

ACTTACCCGT TTTCCTGGAT AAGCGGTATC CATTACTGCT TTTAAGGAAT CCAATGAGCC 1020

ATATAGCGAT CCGCCAACAA TAATCGCCGT CATCAAGAGT GCCCCrCCTA TCAGGACCCC 1080

ATCCCACTTA TCCAACTTAA TTTTTTTACG AAATTCTAAA AAGAATAAAA TTAAAAATAA 1140

TAAAATCAAA TAACCAAGTG GTACTTGTAA CGCAGGATAA ATAACTAAAA CAAATCCTGA 1200

GGCCATAATA ACAGCCGTTA TCGCACAAAT GACACGACGT CGAACACTAC TATGATAATA 1260

GAAATAATTA TAAATTCCCA CTAAAAAACc TAAGCCAAAA AATACTAAAT CTCCAACTGG 1320

CGAGACAAAC CACCATTGAA GGGCCGAAGA AAACGGAATC CAAACACTTG CTAACAAAGC 1380

TAAATATTTA TTCCGCCGTG TGACGATCAA GCCAATTTCA AAAGAAAATA AAATTAAGCC 1440

AATTAATTTA AGATTCCAAT ACCATGATAA GCCATATTCT TTGCCTAATA GTACATAGCC 1500

CCACGTAAAA GGTTTCGCTA ACGTGGCCAA ATTCCACGCT GGTGAATTAT AGCCTACCAC 1560

CATGTCTTGC CCATTTAACG TAATCACATC ATTATGTGTT TTCAAACCTG TTTGTGTTTG 1620

TGAGAGGCTA AATGGGGTTT GAACGAGCCA TTCATCCGAG CGAACACCTC TTGGTTCACC 1680

AGCAATTAAT GAACTTTTTT GACCATCCGC ATATTCAGAA ACATACGCAT CCCACATGTT 1740

TAATGAACTA CCATGGACTT TAAAGGCGAC CAGTAAAATA AAAATGACTG CCGCTAGCAG 1800

ATAGCGCCAs GTrAACAAAT GATCAACCAA GCGAGCACTC TGCTCAGCTT GGTTGCGTAA 1860

TGGTTGTTTT TCTTTTCTTG TAGTTAGTTG TTGTTCCATC TTTTCGCTCC ATTTCGTCAT 1920

CCGCAATTGC ATCTAGTCAA TTCGTAATGA AAAGTTGGGA ATATCCCTTG TCAGATTAGG 1980

ATTATAAAAT GGATCATTTT CAATTAAAGG TCCCCATTTT TCTTCCATCA TCACTTTTTC 2040

TTGTTCAAAA CGTTTTTTCT TTTTGCCTTT ATCATCATAT CCACGAGTTT GAGATTCAAA 2100

ATGATAAAGC TCTGCTTCAT GAAGCCAGAC ATTGTCACGT CCTAAAGCTT GGACTTTCAA 2160

GCATAAATCA ACATCATTGA AAGCTACGGT AAACGCTTCT TCAAAACCAC CAACTGCATC 2220

AAAATCTGCT TTTTTCATAA GTAAGCATGC GGCAGTTACT GCTGAATAAT TAACATTAAT 2280

AGCTAACCGA CCAAAATAGC CTAAGTCACC ATGGGGATAA CCATAATGAC CATGTCCAGC 2340

GACACCACCT AATCCTAAAA TAACGCCTGC GTGTTGGACC GTATTATTTG GaTACAATAA 2400

TTTCGCACCT ACACAGCCAA TCCGTTCTTG CTGAGCmAAT GAAACCATCA AGGTTAACCA 2460

ATTCTCTGTA ATCACTTCGG TATCATTATT TAAAAATAAT AAATACTCTC CGTGCGCTTT 2520

TTTCGCTGCA CGATTGTTAA TAGTTGAGAA ATTGAATGGA ATATCGATTG ATTCAACGAA 2580

AAAGCGACCA GGTAATTGTT GTTCAAATTC TGCATATAAT TCGTGCATTT TTGGATCTGT 2640

ACTTCCATTG TCAGCCATAA TAATCTCGTA ATTTTGGTAG GTTGTTTTTT CAATAATCGA 2700

TGAAACACAA CGTTGTACGT CTTTATAGCC ATTTTTAGTT GGAATAATAA TTGAGACTAA 2760

CTTTTCAGAT TCAATGTCAT AATAAACATC GTATAAGCCA TTCGCCGCCC CATGCGTTGC 2820

ATGACCATTA ATTCCTCGAC GAACGAGCGC ATCTTGCACG GCTCTTAGCC CCGCTTCAAA 2880

AGCATAACCT TTGGAGCCTT GATCCACTGC TGTTGAGGTT GGCAGCATCC GCCAATAGTA 2940

AAGAACTTTT GGAATATGTT TGATGCGTTC TTTTGTCGTT TTTTCAGTAA ATCTTAAGAC 3000

TAAATCGTAG TCTTGAGAAC CTTCGTAACC TTTTCGAAAG CCGCCAATTT CTTCTAGAAT 3060

ACTCCGACGA TACACGCCTA AATGCGAAAT GTAATTCGTT CCTAAAAGTA AATCAGGTGA 3120

CCAATCTGGT TTAAAGGCTG GATCAGAACG ATTTCCATCC ATGTCAATCT TATCTTCATC 3180

ACTATAAATT AAATCCAGTT CTGGGTTTTC ATTCAGCACT TTAACCACTT CATAAAAAGC 3240

ATTGATCGCT AATTCATCAT CGTTGTCTAG TAAGGCGACA AATTCTCCGG TAGCAATCGC 3300

TAAAGCAGAG TTGGTTGCTT CGGAAATATG ACCATTTTGT TCACGAAAGA CGACCCGAAT 3360

TCGCTCATCC AATTGCTGGT ACTCTGTTAA AATCTTTTTG ACATTAGGAT CTGTTGAGGC 3420

GTCATCGGCC ATACATAATT CCCAGTTAGT ATAGACTTGA TTCAAAATAG AATCAATGCA 3480

CAACCGAAGC CATTTTTCTT CAACATTATA CACTGGCATC GCAATGGAAA TTTTAGGCTG 3540

ATAATGAAAT GTTGCGATTT CTTGCGTCAT CGCTTCTATG TCTAGTACTT CATTTCTAGC 3600

TAACCAGTTA GGATACGAAG CTTGATTTCT TAGTTTCTCA ATTTTCGCTC GTTGAATGGT 3660

ATGAGAAATA CCATTTTTAG CCATATACTT AAATCCTTTT TTGGCTTTTA TCCAAAGACG 3720

AGTTACTTTA TCTTCTGTCC CTGGAATCAC TGGATATTTT TTATTCAAGG GAAAATCCAC 3780

CGTTATAACA TGTGCTGATG ATTGAAAATG AAAAGGGAGT ACTTTTTTTT GTTTAATTCC 3840

TTCAAGTGTA ACAACAAAGC CAGCTTCAAT CGCAGGCTCT GTTTGATAAA TTTGATTAAC 3900

ATCTTCACGT AAAACGCGCT GAATGTTATA AGCGGACACT TGGTTTtCAT TATTAATTGT 3960

GAAAGTTGGG CTTTCTTTAG TGATtGTAtC TAACGCCCAA CCTGTAAtGG TTAAaTtATT 4020

tGTTGTTTTG TCGCGATAGA TACTATCAAA GATC 4054

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3074 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGCTCATAGT TTTTCATAAA AGAGTTCATC CGCTTAGCAG TAGCTTTAGA TACACCATTA 60

CCAGATTTAG TAGTATTATC AAACGGCTTT TCGAATAAAT CCTTTGCTGA AGCTTTGATT 120

TCTTTTATTC CTGATTTGCT TTTTTTAACT GCTTTATCAA TACCTTGAAC TAGAGGACCC 180

AATAAAAAAT TATCCTTTGA TGATTCCCAT AATTCACTAA TTTTTTTAGA GATATCGGGC 240

CATTTTTCTT GCAGTTTCTT TCCAAATTTA CTTCCAAAAA TTGATCCTGC AGCTGTTCCT 300

AAAACGCCAC CAATTAGAGT ACCTAACGGA CCAAATGTTG TCCCTGCTGC TGCACCCAAT 360

TTTGCGCCAG CTAATGTTGC TGCTTTAGCG CCTAATGCTC CACCAACGAT AGAACCTAAC 420

GAATCACCAA TTTTTTCAAA CTTATTATTT TTATTAATTT GAGTTAAAGT TAAACCTGCC 480

GAAATATAAG ACAATAAAGG AACCGATTTG GCAAACCTTC TCACTCCGCT AAAAAGTTTA 540

GTACCTTTTC CTATTTTGCC AACAGATCCA ACCGGTAAGG ATTCCTGTAT ATTTGGACTA 600

GCAGTAGTAT GCGTTGGTGC GCTAGCTTTT TGAGCTGCAG AATCAACATC TTCTAAAGCC 660

TTTCTTGTTT TAAAAGCTTC TCTCTGAGCA GTGTTCCCAA GCTTTTCTAG TTTACCAATA 720

ATACCTAAAA TTCCCTTTGA GACTCCCAAG AGCGGTTTTC CTACTAGCTT AAACCCTAGC 780

AAACCGCCAA TACCATACGT GGCCCATTTG CCAACTTGTT TCATAGCAAC AGGGTTTTCA 840

TCAGTAAATT CTTTGAGTAT ACGAATGCTT GGCTTAATAA TATATTTAAA CCCTTTATCC 900

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ATTACGTTAA ACATATTTTT AGCACCTTCT GAAATGCCAG GTCCTATAGC TTTGCCTACC     960
TTTTTAGCTG TAGGAATTAT TTCATCAACA AAATAATCTT TTGCTTGTCC AAAGTGTTTC    1020
ATTACCTGTT TTGCTGTTGG CTCAACTTTT GCGCCAACAT TTtCTAACAT ATCTGGTAtT    1080
TCTTCACCTT TTTTTACAAA ATCTGTCGCT TTGATAATTA GTGGCGTGAA TATTGGTAAC    1140
AAACCTTGCC CTAACTTCGC CGATGTTTCT TTTATTGATT CTGTAAAAAC ACGGGTGGCA    1200
TTTGCAGCTT GATCACTTGT TCTTGCAAAA TCGCCTTGGG AGTTCTTAGT TTTAGACATT    1260
ACGTAGTTAT AACGTAAGCG TACTAATTCT TCCTGACTTA GAGAATCTAA TTTTGCTTGT    1320
TGAACCTCTT CACCTTTAGA TTCTGCTTCT GTTAATTTTA ACTGCGCATC TCTAGCTTCA    1380
ATTGAATTTT CACCATGTTT TTTAATGGCT TTATTTAAAC GATCTTGAGC TTTTTCTCTT    1440
GCCATGGCAT TCTTTGCAGC CTTAGAATTA TCTACTGACG ACTGCAACGC TCCACTGGCC    1500
ATCGCAAACT GTTCCAAGTT GGTTTGAGTC ATAACAATAC CCAAACCTTT TAACGCCTCA    1560
GTTTCACCAG TGAATACACC ATTTAATGCA GTATTTACAC GGTCAATTCC TATATTTTTA    1620
AATGAAGCAA GATCTCCTGC CAAGTCAACT AATGAAGTAG ACATTTTTGC AGCTTCTTCT    1680
GTGCCAATAC CCATTGAAGT TGACATATCT CCATATGTAG CTGCTAAGTC TAACGCTGTA    1740
CCTTGTGCCA AACCAATATT AGTCAGTGTG GACTTCGACC AATCTTCTAC AACTTTATTG    1800
TwATCACCAA AAGCTACTTC TACTTTGTTT AAAGCTTCAT TAGTATCAGA TGCATAGTCA    1860
AAGGCCTTTT gCCTGcTCCT GCGATTGCTG CACCAGCTAT CAtTGCACCA TTTCTTATCT    1920
TTGTAAAAGC ATTCCAAGCA ACATCTGAAG CCTTTGTTGC AACAGTACCT ATATGGCCAA    1980
TACTTGTTTG TACACCCTTC GCAGCTTTTC CAACTACTTT TAGAGATGTT GCACTAGATT    2040
GAGCGAAAAC ACTCGCAGAA TTTTTACTTT TAwCaAACTG aTTTCCaAcA TCTTTTAcTT    2100
GtTTTTCaGT TTGTTTAgCa GAGTTkGTTG TCtTTTGCaT AGAATCTTTT GcTCGaTTTC    2160
CgAACTGGAC AACTTTATCT GTATTTTGkT TTAAAcCTyC ACTATTTCTT TTTAAAgAGG    2220
TTGTGGCGCC ATCTATGGAT TTTGCTGAAT TTTGATAAGT ACCTTCCATT CGTGCAGCTT    2280
TAGCAAGAAT TTTATCAGTT TCTTCATTGG CACGCTCTAA CGATCTATTA TTTATTTTCC    2340
AATCGAGTTC GATTACTGAA CTACGTAACG CATCTGCCAT TATTAGATGA CACCTCCTCT    2400
TGATTTAGTT AGATTTATTT TTTGATATGC tAcTTCGTTC CAAACTGCTA GCTCCTCTGC    2460
CGTGGCAATA TCGACTTCAT CTTTAGTGGC AATGCCTGCT ATTACAGGCA GCCACCTAAA    2520
CATATCTTTT TGAACTTCTC TTTCCGTAAT TCTCGGATTA GGGCTAGTTA AGCATTCGAC    2580
CAAGAAAGTT GTCGGCTAAT GCCATAACCT CACGATATCC TTCGTGTTCA TCCCAATAGT    2640
CCCAGTTCAA TTTTGGTGTA ACAATAACTG AGTCCATAAG TTGAGAGTGG TAAGCAACGT    2700
CAGAAAAAGT ATTTGACGGT CCTTTTGAGT TATCTAAAAT CGCTTGAGCT GCACGTGTTC    2760
CAGGGAATTG AAATGTATAT TCCACATCTT CAACAGTATG TTTTTCTTGT TTTCCGAACT    2820
TATTAAATGG TTTTTTTTCT GCTTCTGGAA TGTTATTTTT CACTTCTAAT TCTTTTACTT    2880
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CATCyTTTTT CGTCATGATA AATTCCTCCT AAAGTTAAAT AAAAAGCACt TAACGAGATG     2940

TTaAGCGCyT AGtTATATTC GTGTTTGTAA TCTAATGCTT TAATCGTATA AGAACGAGTC     3000

GGAACGCCTT TACCAAACGA TCCATCAGGT GTTTTTTCAA TATAGGCTTT TGATGCCCAT     3060

GCTTTTTCAG TTGA                                                       3074
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(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

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CTTGTGATTG TAGATGAACC GCAGATTCCT ACGAATCCAG TGCCCTTTTA TCCTTATGTA       60

ACGAATCCTA ATCTCGTGCT CTTCCGGTTT CACGGACGTA ATGCGGCTGG CTGGTTAGCC      120

AATGATGCAG AGTGGCGAAA AAAAAGAACC CTTTATCATT ATAATACGCA GGAAATCGCT      180

GATTTAAGCG AAGCTGTTTT AAAAATGTCG CAAGAAGCTA AAGAAGTGGG CGTAATTTTT      240

AATAATAATT CTGGCGGCGA TGCCGCAGAA AACGCTCTAC AGATGCAAAA AGTCTTGAAT      300

TTGAGTTACG ATGATTTGAA TCCAAAACAA TTAGATTTAT TTTGAGAAAG AAGGTAGCTG      360

AATGTCTGAA AAGCAATCCC CTTATGAAAT GGCTTGTGCA TTCCACGAGG TTTTTAATCC      420

ACAACAACCA GAGCAACCAA CTGCTTTTTC GCCAGAGCTA GCCAGTCGAC GAGCAGAGTT      480

TAAAGTCGAA GAACTTGTAG AATTTTTATA TAGTGCTGCT GATAATGACC AAGTGCTTTT      540

TCAACAATTG GTCAACGGAT TAAAAAAATC TGTCGATAAA GCAGAGCAGA AAGTCTTGGC      600

GAAAGGCAAA CCAGTATCTG ATCCTTTAGT GGAGGAAGTG GATGCACTAG TTGATTTATT      660

GTATTTTACT TATGGTTCGT TTTGCTTAAT GGGCGTCAAT CCAACAAAAA TTATTGAAAT      720

CGTTCATCAA GCCAATATGG GGAAATTATT TCCAGATGGG CAGCCACATT ATGATCCAGA      780

AACAAATAAA GTATTGAAAC CTGAAAATTG GGAACAAGAT TTTGCGCCAG AAGCTAAAAT      840

TAAAGCGGAA ATTCAACGCC AATTGAAAAT TACTGaAACC AATGAAAAAG ACGAATGAGA      900

AAACTCATTC GTCTTTTTCA TTAATCATGG AAGAACGTCC GATATAAGGC TTTGATGGCT      960

TTTTCCTCTT GTTCTTTTTT GATACCAAAC ATAATACTTA CTTCCGAAGA TCCTTGGTTA     1020

ATCATTTCTA AGTTGATTTT TTCTTTGcTA ACGCCATTGT ACTTTCAGCA GTAACCCCAA     1080

TTCGTTGGCG CATGCCTTCC CCGACAATCA TAATCATAGA AAGATGATGC GTGATGCGTA     1140

ACTCATCAGG CGCTAAAACT TCTTGGAGTT GAGCCATCAG TCGATTTTCA ATTTCAGTTG     1200

TTAACTGGTC TTCTCTTAAA ACAATCGTGA TGTCATCAAT TCCTGAGGGC ATATGCTCAT     1260

AGCTCAAGGC TAATTTTTCT AGTACTTcTA AGAGCCGTCG CCCmAAACCt AATTCTCTAT     1320

TCATTAAATA CTTACTAATG TAAATACTTG CGAmCCCTTG ATCACTAGCA ATTCCTACAA     1380
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CAGGAGCATG CTTCACTTTG CGAGAGGTGG TAATTAGGGT GCCAGGATGA TGTGGGTTGT 1440

TGGTATTTTT GATAACGACT GGAATATTTG CGCGATAGGC AGGCATTAAG GCTTCGTCGT 1500

GGAGGACGGC AAAGCCTGCA TAAGCTAACT CCCGCATTTC TCTGTAGGTC AATTCTTGAA 1560

TCGTTTGAGG CTGTTCAATA ATTCCAGGAT GGGCGACATA AATTCCGTCC ACATCGGTAA 1620

AGTTTTCATA CAAATCTGCT TGAACACTGC GGCAACAATG GACCCTGTGA TATCGGAACC 1680

GCCACGAGAA AAAGTACAAA TTTCGCCGGC TTCTGTATAA CCAAAGAAAC CTGGAATAAC 1740

CAAGATTTGT TGAGTCTCAC GATAGACACT AATTTTCTCT AAAGCTTTTG GTAAAATGCG 1800

GGCATTGCCT GGCTCAGGTG TCACTAGG 1828

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

GGCCGCCACG GTTTTGGTTG TTCCCGCCAT TGTTATTTTG GCTGGTCCGA TTTTGATTCG 60

TTGTAGAACC GTTATTGTTT TGGGTATTGC GGTTTTGATT GTTTGTATTT GTTnGATTGC 120

TACGGTTTTG TGTGTTGCTT TGGCCGTGAC GATTTTGGTT GTtGttGTTt CTTkGTtGyC 180

CATtCGTkGA TkGATtGTTt GGACGATTTk GGTwATTtCT TkGTtCACCA GGTTTATtGT 240

yCATkGGTTy CTTATTGGCT GGTTTATTTk GTGTkGTTkG TkGCTTtTGG TTGTTTGTTG 300

CTTTTGATTG AGTATTTACG GTACTTCCTC CtCCGAATGC TTGACGAAGC TTTGTTTCTT 360

GCTCGGAACT AATTGCGCCC aTATGGTTTT TAACATCCAT ACCTAATTGA TGCGCTTTAT 420

CGACAACGTC TTTGCTTGCT TTATTCATTT CTTTTGCTAG TTCATAAATT CTTTTTTTTC 480

CCATGCAATC ACCTTCCTAA CCTTTTAGTA ATTCCTTGAT TTTGGTGGCA AATCCTGCAT 540

CAGTTACTCC GATAACCATT CGTGGTCGCC CAATCGCTTG GCTGAGCTCG AATTGACTGA 600

ACAGTTCGCT AACAGGAACA TTATAATAAG AACTTTTGTC CTTGATTTTC TTTCTAGTAT 660

TCTCACTGGC ATCTTGCGCA ACAAACACAA ATTTCGCTTT GTTTGCACGA ATATCTTTAA 720

GGGTTAATTC CTCGCCTGTG ACTAATTTAC CGGCGCGCAT TGCTAAACCT AAAAGGTTCA 780

AAATTTTGGT TTTATTTTCC ATCGCCAAAC AACTCTTTGC GGGCTTTTTG ATGTGTTACA 840

TAATCCAATA GTTCTTGATA AAATTCATCA CTTAATTTTG TTTCTAAGAC ACGATCAAGA 900

ATTTTTTTAT CCCAAGCTTT TTGGACTTCC GCAGGATCCA AATCAACGTA AGCGCCACGT 960

CCAGGTAATT TACCAGTTGG ATCTAAGGCC ACCTCGCCTT CTTTGGAGCG AGTAATTCTG 1020

ACTAATTCTT TTTTCGGTTT CATTTCGCCT GAAACAACCG ATTTACGCAT TGGAATTTTT 1080

CTCTTTTTCA TTTTTTCACC CTCCAAAAAC GTTATTCTTG TTCAGGTAAT TCTTCTGTAA 1140

TTTCTGCTTC AACAACTGCT TCTTCAGCAG CCAAGTTTTC GTAATCATCT GCCGTCATAT 1200

CTGAAtGGAT AATTGCTTCA TCCATTTCTT CTGCCACTTC GGCAACTTCT TGATTGGCTT 1260

GTTGTTCATA AAATTCAGCC ATATCAGATT CTGATTTGAT ATCAATTTTA TGGCCCGTTA 1320

ATTTAGCAGC TAAGCGCGCA TTTTGACCAC GtTTACCAAT TGCTAATGAC AATTGATAAT 1380

CAGGTACAAC AACTGTACAT GCTTTGCTAw TTtCTGGATC AAAAaTAACA TCTAATACTt 1440

GAGCTGGAtT CaAGGCATTA CTAATATAAA TAGCTGGATC TTCGTTCCAT TCCACAATAT 1500

CCATATTTTC GCCTTTTAAT TCATTCACAA TCGCTTGGAC ACGTTGGCCT TTTGGACCAA 1560

CACAGGTACC CACTGGGTCA ATATTAGGAT CTGTTGAACG AACGGCTACT TTTGAACGAT 1620

CGC 1623

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

ATGCCTGCCG GTCGACTCTA GAGGACCCCC GCATGAACCA GACGTGACGG CTTTGATTCG 60

TCTAAGTGAT GTCTATGAAA TTCCTTTAGC GACCAATATT GGCAGTGCTG AAATTCTTTT 120

GAGAGGTGTC GAGGCGGGGT TTGCGGACTT CCGTGAGGTT ATCCaTGAAG GGGATCGTCG 180

ACCGTTAGCT TTTTAGAGAA CCTTAATGGT TATTTTGACT ATTTTGTGGT ATATTTTATG 240

AGGACTTTTG TCCAAATAAA ATAACAGAGT AGGAGACAAA GCGTTAAGTG CTAAAAGGAT 300

GGGATGTTGC CTTTTGGACG AAGAACATAA ACAGTGTGTT GCTAGAAAGC AAAGGTTCTT 360

ACTTTGCTTA TCATCAGAAC AACACGTTCA GCTTTTTAAT GTTCGCGGTT TTGTTTTCGC 420

ATTCGCTGCA TGGTTCGTCA TGTAGCAGCT CTTAGAGGAG ATGCTAAAAA TGACAAAGAA 480

AAAATTTGGC ACAAAATCCA TTGCGTTAAT GGGCGTACTC ATTGCGGTGG TCGTTGTCTT 540

TTCACGCTTT TTTGCGTATG AAACAACGTT TTTAAAAATC AGTTTCACGT TTATCCCAGA 600

ATCATTGATT GGGATGATTT TCGGACCTTT TTGGGCTGGA ATCGGCACGG CGGTGGCTGA 660

TGTGGTAGGA ATGTTGCTTT TTCCAAAGGC AGGCTATTTT CCTGGGTTTA CTTTAAATGC 720

CTTTTTGGCT GGTGCTATTT ATGGTTATTT CTATTATAAG AAAGAAATGA CATGGCAACG 780

AGTGATTTTG GCGACATTGT TGGTCACCGT TTTAATTAAT ATCATTTTAA CTCCTTTGTG 840

GTTAAGTTTA ATGTATGGCG TCAATCTAGC AAATTTTGCT TGGTGGGTAC CACGCTTAAT 900

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TCGGCGGATT ACTAATCATC GTGCGTGCAA TAGTCATTAA TTGTCGTTGT CCTTCAGAAA 1380

TTTTAACGCC TTGGGAACCA ATCTCGGTAT CTAGTCCTTG AGGTAAACGC ATGACGAAAT 1440

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TCTGTCCTTT TTCATACAAC GTTTGATTCA ATGCTTCAAA TGTTTCTTGC GTAGCTTGTT 2160

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AGTTTACAAT AAAAATAATC GGCGTACTGA TAAGAACCAC TAATGTGAGC AGGGGACTTA 2340

GCCGAATCAT AAAGAGCAAA GCAACAACGA CGGTGGCCAT GCCAGAAAAT AATTGGTTGA 2400

AGACAGCCGA GCAAGCCATT GAAATATTGT CAATATCGTT GGTAAAGCGA CTGACGATAT 2460

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GCGCAnCATT tGACTTGTCC TTTACCCACC ATTGTATCAA CGGATTTACC TATATAATAA 2700

GTCATGAGGA CAGTCGAAAA ACCACTGAGA ATTCCTAGGA TTAAGGCGCC AATAATTTCT 2760

TTTGGATAGC GTAGTAAATA CGGCTTAAAA CGTGAGAAGG CACCAAAATG AATTTTTTTA 2820

GTTTGCATGG GTATCCTCCT CCTGTGACGC AACGATTTCT TGATACTCTT TAGAAGAAGT 2880

AAGTAATTCT TCGTGGGTGC CAAGGCCAGC GACTTTTCCA CTATCTAGGA CTAAAATTTG 2940

ATTCGCCGTT GCAATCGAAC TCACGCGTTG TGAAATTAAA ATAACGGTTG TCTCTGCTCG 3000

TTCTTTTTGT AAAGCACGAC GCAGATTCAA ATCTGTTTGA TAGTCGAGGG CACTCAAGGA 3060

ATCATCTAAA ATAAGTAAAT GCGGTTTCCT AATCAAGGCA CGGGCAATGG TCAACCGTTG 3120

TCTTTGTCCA CCAGAAAAGT TTTTTCCGCC TTCGTTAACA GGCGTGTCTA ACCCTTGGTC 3180

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TACACCATTA ATAAAAAGGT TTCCTGCACT CACATCATAA AATCTGGGAA TGAGTTGGGT 3420

TAAGGTACTT TTCCCGCTGC CGGTAGGTCC TGTGATGCCG AGAATTGAGC CTTTAGGAAT 3480

CGTAAAATTG ATATTTTCCA AAGCCAAACC GGCCTCTGGT TCATAGCGAA AATCTACATG 3540

GTCAAAGGTA ATATCACCAA ATTGTGGAGA TGTTTTTGCT GATTCTGGTG TATCTGTTAA 3600

C 3601

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

GGATGATTTT CAAGAGGAGA ATCCTCAATT AGTCTTGATG GATATTAATT TACCTGTTTA 60

CGATGGGTAC TATTGGTGTC AAAAAATTCG TGAAGTTTCT AAAGTACCAA TTATTTTTAT 120

TTCGAGTCGT AGTACCAATA TGGATATGAT TATGGCGATG AACATGGGCG CGGATGATTT 180

TGTCACAAAA CCGTTCCAGA TAGATGTTTT AATTGCTAAA ATCAATGCTT TGTTGCGCCG 240

CTCTTATAAC TATTCCGATA CGGATAGTGA AGTGCTTTCA CATAATGGCA TTACTTTAAA 300

TGTGGACAAT GGACGAATGG AAATCaGAGG TGAAATGATC GATTTAAGTA AAAATGAATA 360

CCGATTACTG TATCTTTTAA TGAAAAAGCA CGGAAAAATT TTAACACGTG AAAAACTATT 420

GCGCGCTTTA TGGGACGATG AACGTTTTGT GGATGACAAT ACGCTGACGG TAAATATCAA 480

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CGTCGGTTAT ATGGTGCCCT AGATAGGAGT AGACAATGAC CATTCTAAAG TATTTAAAAG 600

ATCGCTGGTT ATTACTAATT GGTTGGTTAT TTTTTCTGTT CTTAACTTGT TTTATTTTAT 660

GGTTGGCTCC TAATGTCCGC TTAGATTGGA CAGTGGTTGG CTATATCTTT TTACTGCAAA 720

GTGTTTTTTT ATCGCTATTT TTAACAATTG ATTATTATTT AAAACGTAAG TGGTGGCTTT 780

CGTTGGCAAC GGAAAAAGAG CCGCCTTCTT TACAAGAATA TTTGAATACA GCAGAAAAAG 840

AAGAAGAACT ACTTGTCCAA ACGTATATTA ACGGTTTATT GCAAGAGCAC CAACAAACCA 900

TGCAGCAAGC AATTAACAAC CAACAGGACC AAAAAGATTA CATTGACTCT TGGGTTCATG 960

AAATCAAAGT CCCCCTAGCG GCTATCACGT TACTGGTACA ATCTGTCGAA GATGATATTC 1020

CAGAGAAAAA ATATTATCTA TTGGAAAATG AGTTAGGTAA AATTGATGAA TATGTCGAGC 1080

AAGTCCTATA TTATGCTAGA CTGGACAGCT TTTCTCGAGA TTATTTACTC CAAGAATATT 1140

CTTTAAAAGA AATTGTGCAA TCTGTTGTTC GTACGCAAGC AAATTATTTT ATCCAAAAAA 1200

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GGGGCTTAGG AAATATTTGT ATGTTATTAA CAATGCGTGA AATTGGCTTA GCTATTAGCT 2460

TCTCTTTATC ACAAATGGGG aTTATTATTT CGACTCTTGG GGGCATCTTC CTTTTAGGCG 2520

AAAGAAAATC AAAAAAAGAA ATGTTTTATG TTaTTTnTGG TTGCATTTTT GTTATTCTAG 2580

GTGGTATTCT TTTAGGGTAT ATGAAAGCGT AAATAGTTTA TTTACGCTTA TTTTTTTTAC 2640

GGGGGTAAaC ACATgTCTAT TTTCAGAAAA AAAGAAATCA CTGTGCCTGT CAATGACAGT 2700

GGTGGGATGA AAAAAAATCT TAAGACGATG GACTTAATTT TTCTAGGAAT TGGGGCTGTA 2760

GTAGGAACAG GGATTTTTGT TGTGACAGGT GTCGCAGCGG AACGCTATGC AGGTCCAGGG 2820

CTCGTCTTAT CATTTCTGGT AGCAGCAGCC GCGATTATTT TATCTGGTTT ATGCTATGCA 2880

GAATTTGCAT CACGTATTCC GGTCATTGGT GGGCCGTATG CCTACATGTA TGTGGTCTTT 2940

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TCATCCGTTG CTTCAGGTTG GTCAGGCTAT GTCCATGGCT TTTTGGATAG CTTAGGTTTT 3060

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TTACGTTTAA ATAACTTAAT GGTTTTCGTG AAGTTTGGGA TTATTTTATT ATTTGTTCTC 3240

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CATgATAAAC CGTTGTTAAA TGCTGTTGTT CATAAATTTT TTCATCGGT 9589

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GGTCCTTATC ACCTTTACCT TCCAAATAAA TCAAAATAGC GTACGcAwAw CTTgGTCGAC 60

GTTGTTCAGT AACTTCAAAC AGTTCkTCTk TCAAATTTTT TAAtACGTCG ATCTGCTCaT 120

TAACCCcGAT TGAAATCATT AGTATCTATT AAACCgTTAT CCATTTCAGA TTGCCTTTTT 180

TCAACCAATG TTTTTAAATG TAGTTCTATA GAAGCTGTTT GAACCATGCT TCTAATTAAA 240

TCTTCTGCTA ACCCTTCACT AGCTTGTTTA TTTTCTGCCA TTGTAGCTAC CCCCTAATTT 300

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CGTTGCATCG TATCTTGTCG ATTTTGTTTA CGATTGTTTT GAGTTCTTTC TGCTACTTTA 960

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CTTtTCyAAw AATATCTGnn ATAACTGTAA CTTTACTTGG TAAATATCAG GATATTGGAA 7980

AATTTAATnT TC 7992

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AAGAAAACCT TGAATTTGTT CAAGGGCAAT TGCAACAAAA TTTACCAGGT TTAACAATCA 60

AATTAAAATC ATTGCCTTnG CAAAATCGTT TGGATTTACA AACAGCAGGT AATTACGATT 120

TAGCCTTTGG AACATGGACG CCTGATTATG CTGACCCCAT TAATTTTTTA GAATTTTATG 180

ACTCGAAAAG TGGCTTAAAT ACTTCTGGTT ATAACGATTC GGCGTATGAT GCGGGTCTCC 240

AAAAAGTTAG AAAAGATTAC GCCAATGAAC CTGAAAAAACG CTGGAATGAA TTACTAAGTT 300

TAGAAAAAAC ATTAATTGAA AAAGATGCTG GTGTTTTACC CTTATTCCAA GGAGCCATTG 360

GTTACTTGAA ATCAGATCGC TTACAAGGCT TGCAAGTATT TTCTTTTGGT CGCACAGTAT 420

CCTATCGTTT AGCTTATGTA GAAGAATAAA TTGACTTCTG AAAAGTCCTA TCTTTTGAAA 480

AAGTCTGCTT TCTGTTTTAT CCTTAAAGAA GGAAAATTAA CTAAAAAAAT CAACTATGAA 540

AGGTAGGTTT TTCAAATGTT TAGCTTTCTA TGGGCATTAA TTGTCGGAGG AATTATTGGC 600

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GTCTACTGAA AAATCTTTAC GGACTCGTTC ATACACACTT GCATAAGCTG TGAGGTCCTT 7380

TGAGAGCGGC TCTTTAACAA GCTTTTTGGG AAGATGTGTG ATATGTACGA GAAAGGGTGT 7440

ATCTTCAGAA TAGCGTACAC GCTTGATTCT ATAATAAGAA GCGTTAGCTG GTAAGCCTAA 7500

TTCCTTTAAA ATTTCGGCTT GATTATCTTC TTCAATTGAA AGGACTTTAA CTTTTTCAGA 7560

GTCTAAAGAA TGCAACTCGA TATCAGAAAA TTTTACATTT TGAGAAACTT TTGATTTCGA 7620

AACAAAGGTC CCTTTTCCTT GGATACGATA CAAGTAACCT GCACTGGTCA GCTCATTCAG 7680

TGCTTTGACA GCTGTGATAG AACTAACAGC ATATTTTCGT TTAATATCGG CTTCAGAATA 7740

AAATTTATCA CCAGGAATAA AGGTATGATT TTTTATTTCA CGTAAAAGGT CTTGTTTAAT 7800

TTGTTCATAT TTAGGTAACA TGCGATTGCC TCCATTCTAG TAATCGAATG AATTAAGCAT 7860

AACATGTTAA CTAGCCTTTA GCAAaCACTT TGAAAAAGAG GAAAGACAAT TTTTATTTAA 7920

gtTCAAAAAA aAATaATATA TTAAGAaTaG GTTTACGGAT AACTTAGTAT GTGTTATAGT 7980

AAGTTCGTAG AGAACATAAC ATGTTAAGTA GGGTCACCTA CATCTAGGGA GGGAAATTCG 8040

TGGAAAACAT TGTACTAATT AGTCATGGTA GCATGGCTGA AGGCGTCAAA GTTAGCTTAG 8100

AAATGATCGT TGGTCGGCAA GAACACGTGC ATACAGTCTC ATTACGACCA GATAGCGACA 8160

ATCTTCAATT TGAGAAAGAG CTAAATGAAA AAATGAAAGC CCTTAACGGT ACGACACTGA 8220

TTATTGCTGA TTTACTAGGA GGAACGCCAT GTAACGTGGC AACTAAGAAT TATTTGAACG 8280

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AGGCTGGAAT GAATCAAGCG GAACaAGAGA TTTCAGAAGC CAGCAAAGAA AAAGAGTTAA 8460

GTAACTATAG TCAATATGCT GGAAAAGAAA ATATTGTAAA CACACGGATT GATGAACGGT 8520

TAATTCATGG ACAAGTAGCG GGAATTTGGT CGACAAGTCT TAGTACACAG CGAATAATTG 8580

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CTTCTTCGAT GCGTTTATCT GTTCTTGGAG TAGAGGCTGC CGCTAAAAAT ATTCaATCaG 8700

GAAAATATGG TAAACaGCGT TTATTTTTAT TATTTAAAAA TCCGAAAGAT GTGCTCCGCT 8760

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GAGCACGCGA AGTAACAAAA AGTATTCAAG TTTTACCAGA AGAAGAACAA ATTTTTGAAA 8880

CAATCGCTTC AAAAGGCGTC ACTGTGAcAG CCCAATTAGT TCCAAACGAT CCAGTCGTTG 8940

ATTTnATGAA AAAATTACGC GGCTAAAACT GTCAGACTAA GAAAGAATAT n 8991

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

ATAnAAGTAn ATAmAATGGC GATTATTGCT GTCTGAAAAG ATAAAAGAAT TGGTCGAACA 60

TCCATTTTCC CACCTACTTT GTTAACTTAA AGCCAATATT yTCAAAATAT TTTCTGCATT 120

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CTTTACCAAC TGGATAGATA ATTGGCTTTT TCAAAACAGC TTCAGGCATG GCCGCAACAA 240

TCGCTACTTT TGAATTGGTT GCTGCATCTG TCGCATAAAC TAAGCCAGCT TCTGCACTTG 300

CATTAGCTAC CCATTCAAGG ACTTCTGTTA CATTCGTGCC AAAGCTTGCG TGTTTTTCTA 360

CATAAGACCA AGCGCCTAAA GCTTTTAAGC CTTCTTCGGC ATATTGACCA GCTGGAACAC 420

TTGCAGGATC ACCAATTGCT AtCATTTGGG CTTTTTTTAA ATCAGAAAAA TCATGCCACT 480

TTGCTTGATC TTGGTTAGGC ACAATAAGAA CGAGCTGGTT TTCCAATAAA GGAACGACAC 540

TTTTTTTATT AATTAGTTTT TCTGCAACCA ATGCATTCAT TTGTTTTGTC GAAGCTGAGA 600

AAAATACATC GGCTTTTAGG CCTTTTTCAA TTTGCATCTG TAATTTTCCA GAACTATCAT 660

AGGTTCCAGT TACCTGAATA TCTGGATGCT CTTTTTCAAA GGCTGGAATA ATTTTCTTCT 720

CCATGACTGA TTCTAAGCTA GCTGCTGCCG CAAGGGTTAT TTCTTCTTTT TTTGTTGAAA 780

CTGTTTCTTT TTGCGGCTGA TTTGTACATG CAGCAATTAG GGCAACTAAA CTGAATAAAC 840

TAAGCAGGAA CACAGCCTTT TTTTGTTTAG ACATTTGAAC GCCTCTTTTC TTTTATAAAT 900

ACCCGCCATA ACTCAAGTCA ATAATTTCAG ATTTTTTAAT CACTTCTTTG GCCATTAATC 960

TTGGTAACAA CAAATCAAAA ACCGTTTTTT CTGAAAATAA AACACCACCT GGTAAGCCAA 1020

TGATCGTCTG CTCTCCTTTA TAAGCCAGCA AAAACATTGA GCCTGGTAAG ACTGGTGTCC 1080

CATGGGTTAC GATTTCAGCA CCTGTCTGCT TAATTGCTAA CGGTGTCAAA TCATCAGGAT 1140

CTACACTCAT ACCACCTGTA CAAACAATCA GATCAACCCC TTGTGCTAAC ATCTTTTTGA 1200

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TCGCAACAGT AATTTTTTGC GGCTGATCAT CGACAATTTC TTGCTTGACA ATCGTAACTA    1260
AAGGATACGC GGAGAACTTG GCTTTTAACA CAGGGTAAAA AGCATCCTCA ACCAATCCTG    1320
TGTAAACTTC ACTGCCAGTA GTTACAATCC CGACCCGTAT TTTTTTGAAA GGTTTCACAG    1380
AGATTAGTGG CTCAGACGTG CTGAGCTGGC GTGCCTTTTC TAATTGGCTT TTAGAAATTG    1440
TTAGTGGAAT CACTCGAAAG GCTGCAACTT TTTCATCTTT CTGAACTTCT ATATTGGTAA    1500
CTTTAGTTGA CAAGGCGAGA CCTTCAATTT CATTTAAAGC AATTAATTTT TCTCGATTGA    1560
CTTTTAAAAG ACCTCTCGTA CTAGCTTTAG CAACAATTTT TCCTTCATGG ACTTCACTCG    1620
GCTGACATGA GTCATCTGTT AACAGGTTAT ACAAAAATGT CGCkGCCTCT TCTTCATGTA    1680
TTtCTGCTGG ATCCAAGGAA ACAAACAGAT GTTTTTTCCC TAATGATAAA AGAATTGGAA    1740
TATCTTCTTG AACAACTATA TGTCCTTTTT TAAAACACAC TTCCkgGTCT TCCCATAGTC    1800
AATTCGCGTA AtATCATGAC TCAATGGAAG GCCAACTGCC tCTTCTGTTC GAATTGTTTT    1860
CATGGTTTAT TCCTCATCAT GTATGATTTT TTTATTTGTG ATTAAATCCA AAGCGTGGGG    1920
CAAAACAGGC AACAAAAAAT GCAAATGTTC TGTTACACTT TTCGGGCTAC CAGGCAAATT    1980
AACAATGAGC GTGCGTCCTC TTTGAACAGA AACGCCTCGA CTTAACATAG CAAATGGTGT    2040
TTTTTCCAAG CTAAGTTGAC GCAAGCCCTC ACTGATCCCA GGAATGATTC GCTCTGCTAC    2100
ACGTAAGGTA GCTTCTGGGG TCCGATCCCG TTCACTCAAC CCTGTGCCGC CTGTCGTTAA    2160
AATCAAATCA CAGGTCTTAG ACCACTCTTG CAATAGCTCT ACTAATTGAT TTTCTTCATC    2220
TGGTAAAATG GTTTGTTTGG TTACCTGGTA GAGCGCAGGT AACTGTTCAC GAATCAAGGG    2280
CCCCGATTGG TCGACAGCAA GTCCTTGAAA GCAACGATCA CTTAATGTTA CAATGCCAAC    2340
TTTAAACAAC GTCTAACTGG TCTCCTTTTT TAATATGACC TTCTGTCACA ACAACTGCAA    2400
AGATTCCTTC TCTAGGCATG ATGCAATCGC CCACTCGCGC GTAAATCTGA CAGTGTTTAT    2460
GGCACTCTTT CCCAATTTGA GTAACCACCA ATTCGGAATC GCCTATTTTC ATTTTCGTTC    2520
CAACAGGTAA TTGACGTAAA TCAATCCCTG AGACGATTAT GTTTTCCCCA AAAGCACCAT    2580
TGCCAACCCG AGCTCCTTTT TCATTGAAAG CCGTTATTTC TTCAAAAGAT AACAAACTGA    2640
CTTGTCGATG CCAATTACCG CCGTGCGCAT CATTTTCTAA TCCGAAACCT TTAATTAAGT    2700
TGACTTCAGG AATTTCCTTT TTCTGTGTGC CTCTTCGCGG GCTAATATTT ATTGCAATAA    2760
TTTCTCCTGT TTTCATACTT ACCCTCCTAT TTGTGACATA AATCGTTGTT CTCCTTGTTG    2820
TTCCAAGAAA AGATGTTTTT CAGGCTTACA GGCAATGCCA CTCTTGATAA TCCCTAACAA    2880
TTCTGCTGTT TGTTCCATAG CTAAAGCTTC CTTTAACGAG TAGCCGTCTG CAGAATGCAG    2940
GCACGTTTTT AAATGGCCGT CTGCAGTAAT TcGGATTCGA TTGCACGTCT CGCAAAAACA    3000
ATGCCCTAAT GCACTAATAA AACCTATTTT CCCTTTAAAA TCTtTTAAGG CGTAATAACT    3060
AGCAGGGCCA TTGCCCAATG GTTTTTGGTA TGGTTGTAAC GTTCCATAAT ATTTGGTTAA    3120
AATGGCTTCT ACTTCTTCTT GTTGCTTACC TGGATGCTCC TTCCCTAATC CAATTGGCAT    3180
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CATTTCAATG AAACGAAGAT GCACAGTCTC TTTCTTmGCG ATTTCAGCCA GTyCTACAAT 3240

yGTTGCTTCA CTTAGCTCTT TCCTAGCTAC AGTATTAATT TTGATATTAG GTAATCCCAC 3300

ATCAATCGCT TGTTCTAAGC CCGCCAGAAC ATTCCTTAAC TGACCAACTC TTGTTATTTC 3360

ACGAAATTCT TCTGGATCCA AAGTGTCTAA GCTAATATTA ATGCCGTCCA AGCCCGCCTC 3420

TTTTAATCCT TGAGCCTCAC GAGCTAACTT CATGCCATTA GTCGTTAAGG TTACTTTTTC 3480

GATGCCTGAG ATTTGCTTTA TCCTTTTAAT TAAAGAGAGT AAATTCGGTC TAACAAGCGG 3540

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AATAATCTCA TCATCTGTTA GAAGCTGCTC TTTTTTTAAA AAGCAAAGAC CTGTTGCTGG 3660

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TCACGGTTAA ATGCATCTTT CATGCTGTTC ACTCATCACT TTCCTTTGAT TTAATTGAAG 3780

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CTAAACAAGT TTGATTGCGC CAATCAAACT GAATTTCACA CTTTGTCAAA GCAACCAAAT 4020

GACACAAAGG AATCCATTCA AACGTTCGTT TTGCGGCGGT AATCCCAGCT ACTCTTGCTA 4080

CCTGTAATAC TTCACCTTTT TTAATCATTT GGGTCTGGAT CGCTTCTGCT GTCGCTTCCA 4140

ACATGTGAAT TTCTCCATAA GCGAGGGCTG TTCTTTCAGT GTCATTTTTT TCCGAAATAT 4200

CAACCATGTG CACTTCTCCt TGTGTATTCA AGTGCGTAAA TTCCT 4245

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4013 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

TGAAATCAGC ATGGTACGTT TAAACCAAGA TTGTATCCGC TTTAAAAAAC AAGAATGATT 60

GACAAAAATT AACTTTACAC TATAATATTT TTAATAGATA ATGTTGAAAA TTGAAAAAGG 120

CAATGGTAAA AGGGGCTGTT AAAATGTCAA AAAAAACAAT TATGTTAGTT TGCTCCGCAG 180

aATGAGTACT AGTTTACTTG TTACAAAAAT GCAAAAAGCA GCATTTAATC AAGGCTTAGA 240

TGCCCATATA TTTGCGGCTT CTGCATCGGA AGCAGAAACA AATTTAGAAA ATAATCCAGT 300

CGATGTGTTA TTGTTAGGTC CACAAGTTCG TTATATGAAG AGTGATTTTG AAAAGCGTCT 360

ATCACCAAAA GGTATCCCAA CAGATGTCAT TAGCATGTCT GATTACGGCT TAATGAACGG 420

GGAAAAAGTG CTGGAACAAG CCTTGGGTTT GTTAGCACAA GCAGATAAAA AAGAGTAAAA 480

ACAAGTTGTT TTTTCGAGAA TCTTCGAAAA AGCAACTTGT CTTTTTTTAT GACTTTAGTT 540

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AATTAGTCCT GTGAGCTAGA GAAAGACAAC TGTCTTTAAT TTTTTACTTT AATCTAGATA 660

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AAAGTAGTAA TTCAAAGAAT GATTAACAAT ATTTTATATA CGAGTCATTA TAGTATGGCA 780

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GTTTAAAAAT AATGAGGTTA TTTCATAAGG CATACTTTCT TCATACGTGA TTTCTAAAGG 900

ACTATCTTTA TCAAAAGAAA TAATTTGTGA GTCAGGCATT GCAAGTAATA TAGGTGAATG 960

AGAGACAATA ATAAACTGAG ACCCCTCATC AATTAGTTTT TTTATAGATA TCATTAAGGC 1020

TAGTTGGCGT TGAGGTGAGA GAGCCGCTTC AGGTTCATCT AACAGGTACA GACCATTTCC 1080

TCTAAACCGA TGGTTCACCA GATTCAAAAA ACTTTCGCCG TGTGATTGAT GATGTAGGGA 1140

TTTATCGCCG TATTCAGAAA AATCTAAGTC TATATTTTCT GCATATGTAG CAACATTGTA 1200

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TTcCATTTtc ACCTGaAAAA AAAGTAATAG GttTTTAAAA TTTAGkGaAT nAAATTTATT 1440

CmGcCCTTCA ATTTTTGAAA AAACAGAATC TTCTTCAAAA GCTTTGAATT CTAGTCTTTT 1500

TAAAAAAATA TTTTCCATGA TAAAGCTTGC TCCTTTCTAG TCTTTTCAAA TTAAAGCTTG 1560

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GCATGGACGT AAAATAATTA TTGAAGAAAC AGAACGTTCA ATACAGACAA AACTGGTTTA 1860

TTTACCAACA ATGTTAGAGC GTTCCCCCCT AACAATTCAA TGTCAGCGGT GCGGGGAAGT 1920

CGTATCCAAA AAAGAAAACA GACTGGCGAC AAATGTATAC TACTGTCATG CGTGCATTCA 1980

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AGGCAAAACA GAAATGtTAT TTGCTGTTTT ACACCAAACC TTACAAGAAG GGGGGCGGAT 2220

TGCGCTGsTT CGCCGCGTGT CGATGTTTGC TTAGAACTGT TTCCCAGAAT CCAAGCGGTT 2280

TTTCCTCATG AAGCAATTGC TTTACTCCAC GGAAACAATC AAGAATCGTA TCGTTATACG 2340

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CGTAGGCCAT TACCTGTGCC ACGCCGATTT TGGGTTCAGT CGTGGCAACG TCTTTCTAGC 2640

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CTATTTTGCC CAAGCATTTC ATTAATTCAC CAATTGCATG CATTAATAGC TGAGCGATTT 2760

TCCGACAAAG AAGTTGTCGC CGTTTATGGT AGTGATGAGc TTCGCCTGGA AAAAGTTCAA 2820

GCAATGCGTC AgcAGAAAAC GGATATTTTG ATCACTACAA CCATTTTAGA ACGTGGTGTG 2880

ACTTTTGATG CAGTCTCAGT TATTGTTTAT GGTGCCAATC ATCGAGTCTT CACTTCTTCA 2940

ACACTTGTCC AAATTGCGGG CCGAGTCGAT CGAAGACAAG AATTCAATTA CGGCGAAGTT 3000

TTATTTTTAC ATGATGGGGA AACAAGAGAC ATGAAAGAGG CAATTCGGCA AATAAAGCAA 3060

ATGAATCGCT TGGCTAGTAA ACGaGGGATG TTAGATGGAT tGTAAAAATT GCGCAAgCCC 3120

mTTCGTTTGG AGATAACATT AAAAATGCTC TTACGTTTTA ACAAATGGAT GAGCCCTTCa 3180

CTTTGCCcAG CACTGCCAAG CAAAGTTCCa GAAACTGCCA ATGACAGGCA CTTGTTTTGG 3240

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TCCAGAGTAT TCTTTTCATA ATGCAGCGTT GTTTCATTAT GATGAAGGAA TGCAAGAGTG 3360

GATGGAACGC TATAAATTTC AAGGAGACTA TCGCTTAAGA ATGTGTTTTA ACGAGGAAAT 3420

CAACTTTTAC TTTCAGCAAC AGTCTGCGGA CTATATTATT CCGGTGCCCT TATCCGAAAA 3480

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AAAAGAAAAG AATTCATAAA TTTGATGACT ATTTTGTTGG CAAAACCCAG ATTATTCGAT 3840

ATAATGAAAT TAAGAAGAAG GGAATTAAAG AGTGGTCCTT TAATCTTTTC TTTACTGGTA 3900

GATGAAAGGG GTAATTGTTA TGTTTAGATA TAATGTACGT GGAGAAAATa TCGAGGTAAC 3960

CGAAGCGATT CGAGACTATG TTgAGAAAAA AGTCGGTAAT TAGAAGATAT TTC 4013

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4951 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

TCAGTGAAGA TTGTTTTATT TTCGTTATAG ACGATGGTAA AGATGCTTTT tTATCCACCC 60

ATGATACAGG TTACTTTACG TCAGAAATGT TTGAATATCT TGAAAAGAGC CACTTACTTC 120

TTAGTATTGT TTCTTTAGAT TGTACTAGTC AAACAAACGA AACTGGCAAT AGTCATATGA 180

ATTGGGAAGA AAATTTAAAA TTAATTGCAG AATTAAAAGA AAGAAAACTC GTCACAGATA 240

AAACGATTTA CGTTGCCAAC CATTTTTCTC ACAATGGCGG CTTGTCTTAT GCGGAGATGG 300

CGGCTTTATC TCAAAAGCAT GAAATCATTA CGAGTTATGA TGGTTTAGAA ATACTAACTT 360

AATCGGATTA TTTGCCTTCT TTTCAGCACT ATTATATGCT TTTAACCGAT AATTACAAGG 420

TACTTTTATC GTAACTTACA CTATCTTAAA AAACAAAAAT ACTCGAGATT TCCCGTGATT 480

CTGGAAATTC CGAGTATTTT TATGGTTCTT TACGCTGCTG GcACAGCGGa TAAACGTTTA 540

TTTTCTTCTT CATTCACTCG ATTAACAATA AAGTTATAAT TCACTTCATT TAGTCTTTGA 600

CCATGATTTC CTGTTTGCTT AATGCCGCCA TTGGAATGAA CACCAACTAC TTCAACCTGA 660

TCATTATAGA TTGGTGAACC aGATTGaCCG CCGGTTGTAT CGATATCATA AAATAGTAAT 720

GGATTTTCTA AGTCTGTAAA GTTAGATGTA AACAAATCAT TTTCATGAGA CCATTGTGTG 780

TGGTTTTTCT CACCTGGATA GCCTGATATT GTGACATGGG TATCTGAAGA TTCAAACTTT 840

TTCAAAACAA ATGGCGTTAA AATTTCTCCC AACTCTGGGC CATCTGGACG ATCGTTTTGT 900

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GCATTCGGAT TTAATACTTT GGCATTCTTA AAACTTTCAG CCACATGATT ATTGGTGACA 1080

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TGTGCTTTTT CAATGCCTAA GTTCTGGATA ATGGTGTAAC CAATCCGATT AATAATTCCA 1680

CTATTATAAT GAACACCGCC TTGATCATAA TAAGGCGTTC CTTTATACCG TGCTCGATCG 1740

TCGTATTGAG CCATGGTTTC TGGTTGTCCG TGTTTACTTG GCGTTTGTAA ATTTCGAATA 1800

CCTGTTTTTC GGTCAACACT CTGAGTATCC GCACCAATTT CTGGATTAGA TGCACCCGAA 1860

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ATCCCTCGAT CATCAATACT GTGTCGTTGG AAATGATCTT CATAATATGT TTTcACAAAT 2160

TTTCCATGCG TATAGGCGTC AACAGCATTC TGATTTAATG CTACTAGTGA TGGTGCTTGA 2220

ATAATAGAAT AATTATTTTT GCCATCAACT ACTGCATGGT AAACCCCTGT GTTATCCGTT 2280

CCGTGTAAAG CAATTCCCGT ATTGCTTTTT TCAACTGGCA CATTAAACGC TACTTGAAAA 2340

GAGTTTTTTA ACGTTACTTC ACTACCGACA TGTTCCGTTA AATCTTGTTT TTCCATAATT 2400

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cGATTGCATC arCCGATTGA ATTTTCACTA CTTGATCAAC TGGATTTCCt GTAACACTTG 2640

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CATATAACAA TCCCCAACCG TGCTCTTCTG GATTACTTTT AGAACTAAAT TTGGTTTTCT 3360

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TCGCGTTATC TAATAGAATA GCCAACAAAC GAATCACAAC CACTAAGTCG ATTGATGTAT 3540

CAAGAATAAA TACTTCTGGC ACATCAACAA TCACTTTTAG TTTTGCTTGC TTTGCGGTAT 3600

TAATTTTCAT ACTTATGAGT GCCTTAAGTT CCATATTTTT CAAACGATTT AACTTCATAA 3660

GTTCAAATTC TTCATTATCA ATAATTTTTT TGGTTGGTGC AATCGTTTCT TCATAAATTC 3720

TTTTGATTTC CAGAATATCT TsGkATGAAA TAGCAATTTG TAAACTATAC AATAAATTTT 3780

TATAATCATG ACGAAACATC GCTAGCTCTT CGTTAATGGA TTCTATTTTT TCAGTATAAA 3840

TCGTTAAATT ATTCAATAAT TGAGTGTTGA TACGTTGTTC TTCCAAATAA GCTTCAATGA 3900

CTAAGCCAAT CAGAATTAAA AATAAACCTA CACTTATTAA TAACTCCAAT TTAGAACTAT 3960

TTACCGTGAC AAATCCTCGC ATAAAGTCAG GTGAAATCTC TGGCGAAATC AAAAACACAA 4020

AAAGTAACAA CAGAATCAAC AATAAAAGTA AACAACCAAA AAAAATTCGG CTATTTTCTA 4080

ACACACGATT TAATCTTAAA AAAACACTAT TGGGAATTTT TAAAGCAATC CAGATATTTA 4140

TAAGCAACAG AAGAACATTT GAGGcAaTCC ATAATAATTT ATTTTGATAA ATCTGTTGAA 4200

AAAAAACACT TAAAATCGTT TGCTCCGTGT AATTGATAAn CGAAaCCATA AGCAaTGTAA 4260

AAnCAGACAA AAATATCGCT TTAAAAATTG AGAACCTCTT TTTGTGAATG AGTAAAAATC 4320

CTGTAAAAAT AACGACTGTC AGCGCATAAA TCAACCAAGA GTAGCCCAAC ATTAATGCCG 4380

CAAACGAACA AAGATTAATG ACAATAAGCA ATGAAAGTAA CGGTATTTTA CATTCAATCT 4440

TGATCAATGT TACTCGTAAA AAGACAAAAA CGATAAAGCT AGATACAAGC AAAACGTTAG 4500

TAGCTAATAA CGACAAAATC ATTTTTCAAT ATTCTTTTTA GGTTTTTCAG TTTGTCCCAT 4560

CCATTGTCCA AATATATTGG GCGAATTTTG ATTTAATCTA GGCTTAGTTC CCACACCATC 4620

ACTAACTTTT GCAACTCTTT TTTCAATAAC ATTTTTAATT ATTTTTTTAC CAAATTTCAT 4680

AAAAACACTT CCTTCAATTA AATTTTTTGT TACAGGGAGT ATCATCAGAC CTTGGATGAC 4740

GAGACCGTAG AGTATTACTG AAGCAATCTT TTCTTTGACA AACAGACTAC ATAAAATAAG 4800

TAAACACACC CTTATAAGGC TTTGCTTTTT GAGCACGTTT AAATCAGATG GCTGAACAGG 4860

TTCAATCGCT GTTCCTTGTG GCGCATACCA ATAAAATAAT ACGACTAAGA GGCACATCAA 4920

TAGAATTTTA TAAATAAACG GTAAGCTCAC A 4951

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

TTAATTGATA ATCAAAGTAT AACATTTTTT AATGAATTTA CATAATAATA CAAGTGGAGG 60

TCTGTTCGTG AAGGTAGCAG GAGACAAAAT AAAACAAGCG AGAAAACTTA AAAAAATCAC 120

ACAATCAGAG CTGGCTAACG GCATCTGTAC GCAAGCAACA ATTAGTAATA TTGAAAACCG 180

TAATCTATGT GACAGTTTAG ATATTTTCTC ATCTATTTGC CTCCGATTAG ATTTAGAAGT 240

AGAAGAATGC ATGATGATTT CTGAAGAAAA GAAAATTGAA AATCTACTAA ACAAAGTCGA 300

GGATTTATCT TTACGGTTAT TTCACTTAGA GGCCTACAAT TTATTACAAG AAGTGCCTGA 360

AGGTCTTATC TTATCTAATA ATGAACTAAC GACTAAATTG TTATATTATA AGGGrATTAC 420

TTGTTTATTA GGAAAAAAAG ATAAAGCAGA GGCCTTGTTT TACCTATACC GGGGCGCGGA 480

AATTGACCGT AAAGTCAATA TTTACAACAT TTTAAGCCTG AATGCGCTAG GTACGCTATA 540

CGAACTGGAA AAAGATATGA GAAAAGCGCA AGTGTATTAC GAAAAATCAT TACAAGAATT 600

GGAACAATTT AAATTAGAAT GTTCCTTGGA GCGTTGTAGA ATTTATTATA ATTCTGCTAA 660

ATTCTACTCG GAAATGAAAG ACTACCAAAA AAGTGTCATT TTAAGCGAAA AAGGGATTCA 720

GATTTGTCGT GACAAACACT CCATTTATTT GCTAGATTAT CTTTTATATG AAAAAGCCTT 780

TAACAAACAA ATGCTCGGGG AAGACACAGC CGATGACTAT CGCCAAGCCT ATTATTTTAC 840

ACAATTTTTT GGCAATACGG AAGTCCTGCA ATATATTGAG AAAGATATGA AAGCTTTTAA 900

TATTTCCTAT TAATTTAATC AAAAAGCCGA TAAAAGCTGA AAACTCAGTT TTTACCGGCT 960

TTTTGAAAAA TATAGGCAAG TTGCTTTTAA AAATCAGCAG TCACGGTTAC GATAAGCAAG 1020

ACGAAgTATT TAGGAGGATT TAAAAATGAA AAGAGTAATA TGGTTTAGAC GTGATTTACG 1080

ATTACAGGAT AATAAAGCAT TAGCACACGC GTTACAAAAT TCTGCAGCTG ATGAATTGAT 1140

TTTATTATTC CAAATGAATC CTCAACAATT TATTCAAGAA AGTGCTAATC ATAACGCTTT 1200

TTTTGCAAGC TTAGCCTCGT TCAAAGAACG AATCGATCAA GAGGCACATT TACAAATCAT 1260

GGTCGGCGAA CCATTAGATT TATTTTCACG TTTGAAACGC AAATTACCCG ATTGGCAGGC 1320

CATTTATTTT AATGAAGATA CTTGTGGCTT TGGGGCAAAG CGGGACCAGC AAGCTATGCG 1380

CTTTTTTGAA GAAAATAATA TTCAGTCTTT CTCTTTTCAA GATGCCTATT TGCATGGCTC 1440

TGAAGAAATT AAGAAGAACG ATGGCAGCAA GTACCAAGTG TTTACGCCCT ATTACAATAA 1500

ATGGAAAGAG GCGCCTAAAG AAACACCGAT TCCTGTTTCC TATACAGCTG mAAAAATTTT 1560

TAGTGCGTGT CTTTTTCCAG AAGAGGAAGC AGCTTATCGT GAACAGATTG CGAGGATtCC 1620

TTTAACACAC TATAGTGTCG GCGAAGAAAC AGCCAGAAGG CGCTTAAATA CTTTTATTGA 1680

TCAAAAACTT CAATCCTATG AAAATAAGCG TGATTTTCCT TATCAGGATC AAACGAGTCA 1740

TCTGTCTACT TTTTTAAGAA CGGGAGAACT TTCGATTCGC ACCATTTGGC AAGAGCTTGC 1800

ATCTGTGCCT TCTAGCTTAA GTAAAGAAAC CTTCAAAAAA GAATTAGCTT GGCGCGACTT 1860

TTACAATATG ATCTATAGTG CGTTTCCACA ACAAAAAGAG GAAGCTATTC AAGAAAAATT 1920

TCGTTATATT CAATGGACAA ATGACCCAGA AATGTTTGTC AAGTGGCAAA AAGGGGAGAC 1980

GGGGTACCCT ATAATTGATG CCGCAATGCG ACAACTGAAT CAAACTGGTT GGATGCACAA 2040

TCGCTTAAGA ATGATTACTG CCTCTTTTTT AGTTAAAAAT TTACACATCG ATTGGCGTTG 2100

GGGTGAAAAA TACTTTCAAA AAATGTTGAT TGACTATGAT GCTGCCAATA ATATCGGTGG 2160

CTGGCAATGG GCTGCTTCAA CAGGAACGGA CGCTGTCCCT TATTTTCGGA TTTTTAATCC 2220

AATTATCCAG TCAAAAAAAT TTGATAATGA CGGCCAGTTC ATCAAAAAAT ATGTTCCAGA 2280

ACTTAAGCAA GTGCCACAAA AGTATATTCA TCAACCAAAT CTAATGAACG AaGCCTTACA 2340

AACGCAATAT CATGTACATT TAGGAGAAAA TTATCCAAAA CCCATTGTCG ATTATGCATC 2400

AAGTAAAAAA CAAACATTGT TTCTATAksA AGCGAGCAAA GAAATtCATC AAGAAATGAA 2460

CAATCCAAGG TTTCAATAAA CAGTAAACCC AACTAGCTTA GCAAACAACT TGTAAGGTTA 2520

GTTGGGCAAA TTAATTAGTC GAAAGAGAAG TGCnATTTAT CGGCTAAAGT TTTTTATTCT 2580

ATTCTAGTTA ACATAATATA CATTATACAA AGTAGAGTAA AAAGCATTGA AAAGCAAACA 2640

AAACCAGTCT TTAGTTTATC TAGACTGGTT TyGTCACGTA CGTTATATAA ATTATGCTTG 2700

TTGCTTGATG GCTTGTGCGA CACGTGCTCC ATATTCTGGA TTtACTCTAG TGAACAAATC 2760

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AATTTGACGC GCGATGaTTt CTTGaTTTTt CACTTgACCT AAAgATGCCG CTATATTGTT     2820
AATTAAGTTT TCTTTTTCTT CGCTTGGCAG CAAATTATAC AAAGCGTTTG CTTGTGTAAA     2880
GTGATCTTGA TTATAGCTAT AATTACCAAC ATTTCCTTCA ACTTCAAAGG AACTAATTTT     2940
CGCTGTAGGA TCTTCTTTTG GTGTTTCAGT ATAACTATTT GGTTCATAAT TAATTTCGCT     3000
ATTGCCATTG TTAAAACGCA TATTGCCGTC TTTTTGGTAG TTATTTACAG GCGCTTTTGC     3060
TTGGTTGATT GGCAATTGGT GACTATTAGC GCCCACGCGA TGACGATGTG CGTCCCCATA     3120
AGCGAACAAA CGTCCTTGCA ATAATTtATC CGGAGAAGCT TCAATACCAG GAACGAAATT     3180
CCCTGGTGAA AAGGTTACTT GTkCAACCTC TGCAAAATAA kTCkCTGGAT TTCTATTTAA     3240
AGTCATCGTG CCAACkTCAA TCAGCGGATA CTCTTTTTGA GAAACCGTTT TTGTTACATC     3300
AAAAAGTGTT TCTTTCATTG TTAACGCATC TGCATACGGG aTAATTTGCc ACAGATAATG     3360
TCCAAGAAGG AAATTCtTGA TTTtCAATtG CATTATGCAA ATCTyCAATA TGGrAATCTG     3420
GGtTTtCCCa GCAATTTCyT CTGCTAATTG ACTCTCTAGA TTTTTGATTC CTTGATTCGT     3480
CTTGAAGTGA TATTTAACAA AAAATACTTC TCCAGCAGCA TTGACCCATT TGAATGTATG     3540
GCTACCAAAA CCATGCATAT GACGGAACGA CAACGGAATG CCACGATCAC TCATTAAAAT     3600
TGTTACTTGA TGAAGACTTT CCGGTGAATG AGACCAAAAA TCCCAAACAG CTTCTGGACT     3660
TTTCAAATGC GTCCGCGGAT TTCTTTTTTG GCTATGAATA AAATCTGGAA ACTTAATTGC     3720
ATCACGAATG AAAAAAATGG GCGTATTATT GCCAACTAAG TCGTAATTTC CTTCGTCTGT     3780
ATAGAATTTA AGCGCAAAAC CGCGAGGATC ACGCAATGTA TCTGATGAAC CTAACTCTCC     3840
AGCTACAGTT GAAAAACGAG CGAATAAAGG TGTTTCTTTG CCAACTTCAG ATAAAAAATC     3900
GGCTTTAGTA TATTGTGCCA TTGATTGGCT CACCTTGAAA ATCCCATGAG CACCAGCACC     3960
TTTGGCATGA ACAACCCGTT CTGGTACGCG CTCACGATTA AAATGAGCTA ATTTTTCTAA     4020
TAAATGAACG TCTTGGATTA GGACAGGACC AAATTCTCCT GCAGTTAGCG AATTTTGATT     4080
ATCGCCAACT GGACTTCCTT GTGACGTAGT TAAATGTTGA TTTTTCACCT AAAACACTCC     4140
TTCATCTAAA ATTATACTCA TTGTATAAAA AAACCACTCT GCATAACAAA AATAATGCTT     4200
AAAAACACTC GAAAACATTT GTTATTTAAT AGAATGATTA AAAATAGCAG TAGAATTTAA     4260
ATCAAAAACA AATGTATTAA CTTTAAACTG TTTACACCAC CAAAAATAAC AACCAATAAT     4320
TCAAAGAAAA CTAAAATGCT GTTTTTTTAT TCAAAAAAGA CCTAGCATCC CAATCATGCT     4380
AGGTCTTTCG TTACTTTTTT TGAGCGGCCG TTTTTATTGG TCATTCAGCG TTATTGATTG     4440
ATCGCAACAG TCGTGTCTTC AGTCGATAGA CCTGTCATAG AGGTGCTATC GGAAAATATT     4500
TTTTCAACTT CTTGTTCTGA TAAAATATTy TCTTTCTTAG GCATkGAAAT CGTCGCTTTT     4560
TTGGCTTTTT GTGTAATGCT AATTTTACTA GATAATGATT CAAGTCCCAT ATCAACGTTC     4620
TTGTCTTGCT GCGGTTTCAC ATTAATCAAC ATATTTGTTT TATTTTCTTT TGTATTAACA     4680
GAAACTTTGG CAGAAACATC TTTGACTTTT TCGAAAGGAT CTTGTTCTTT ACCTTTTTCA     4740
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GATGTTTCTG TCGTAATTTT GATTAACTTT TGTAATTCTT TTTTTGTAAA CGTATGGGTA 4800

ATGGTGTCCC CTTTTTTCTC GAACGTATCC TTGTCTAATC CTTCTAAAAA CTCTTTGTAT 4860

TCCTTAGCAG ACTGTTTTCG TTCTTTTTCC GATTCTTGAT ACTCTTTGAT TGTATCTTGC 4920

CATTCTTTCG TACTTTCCTC GTTCATGGCT AAAAGATCAA TGTATTTTCC TTTTAGTTTT 4980

TCTGTATCTA ACTGAGAACT ATCGATAGCA CCGTCAGTCA TTGAGTCTGC GACAGCGACA 5040

ATATATTCCA TCATATCTGT TGCTAAATAG AGTTTTGGCT CTTTGCCCTC GTTATCTAAC 5100

GATCCAACCA ATGAAATCGG TACATCCATT CCCATCGCTT TTAATTTCAT CTCTAAGTTG 5160

AATGCTTTTT CTTTTTTGGC ATCTACTTGA ATCTTCCCAG AAAGCGATGC GTCTTTGATT 5220

TGCGTGATGA GCATCCCAAT CATAGGATTC GTTTGTGmAC CATCTTCTTG TGAAAAT 5277

(2) INFORMATION FOR SEQ ID NO: 263:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

TCACAATAAA TAAAGAAAAG TAAGAGGATA AATAACAAAA ATCTCATCAA ATTGAAAAGA 60

AGAAGTGGTT GTTTTCACAA GTGTGAAGAG GGTTAATTAA ATACAAACAA GATTTCAATT 120

ACATTACAGA AATTTTAAAA CTCAAAATTT AATACGTTTA TTTCTTGTTT CAATAGGAAA 180

TTAACGGTAA AATAGAAAAG TGAGACAGTG AGGAGGAAAA ATGAATGAGC GAACAGTTAA 240

CAAGAAGTAG TAAACATATT CAAAAAGCTC TTAAAAAGCA AAAAGCTTAT AAACGTGCTA 300

CCGCCGTTGC GGGGACTTCA ATGATTTTAG CACCTGTGGT TGGTGCTGCG GTACCTGCCC 360

AAGCAGAATC AAGCCAGCAA GCATTTATTA ATGAAATCGG AAATTCAGCA GCAGCCGTTG 420

CCAATAGCAA TGATATGTAT GCTTCCGTCA TGATTGCTCA AGCGTTGCTA GAAAGTAGTT 480

ATGGTAGTTC TGGGTTAGCA TCTGCACCGA ACTATAACTT GTTTGGTGTA AAAGGAAGTT 540

ATAATGGACA ATCTGTTTAT ATGCCAACAA AAGAATATTT AGACGGACAA TGGGTGACCG 600

TCACAGCwGC ATTTAGAAGT TATAATTCTT ATGCGGAATC GTTCCAAGAT CATGCCAATG 660

TTATTCGTTC CACTGCTTTT GGGGATACAT ACCATTATTC AGGCGTTTGG AAGAGTAATA 720

CTAGCAGTTa TCGCGATGCA ACAGCCGCTT TAGCTGGAAG TTATGCAACT GATCCAGGCT 780

ATGCCGAAAA ATTGAATTGG TTAATTGAAG CATATAATTT AACTCAATAT GATTGGGGAG 840

CACCAGTCGC TCAAACCACT AGTTATTCAG GACTCACCGG GAACCGTTGA T 891

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AATTCTCTAA TTCGGATAGT TTGGCTGGCT TAAAGTCCAC ATAATCCACC TCTGATTATT 60

TTTTCTTCGT ATTTATCGTT CCATTGGCCA TTGCTTTCTC TTGTAAACGA CGCTTTTTCT 120

TTTTAATTTT TGATTTTTTC TTACCCATAA ATTTTCCTCT TTTCATTAAT TAATATCTTA 180

TTATTTCTTT TTTTCAGTCG CAAATCCCAT GATGaTTTGa TTCTTTAGAT ATCGTAATTG 240

CTGTCTGGCA TATGCTTCCT CTCTACAGCA AGATAATCTA TAGTTAATAT CCTTTAAAAC 300

CGCTAAATCA AAATTGTATT TGCCCAGTAA TTCATTAATT TCTTCTTCAG CTGTTTTCAT 360

TTAATTCTCC TTTAGCGTGA TCGGTCTGCC ATACTTTAAA ATTTCCCAAG CGCCATCTTT 420

CATATTGGTT TTATTCATAT GATTTCTTTC ATCACGAGCA ATTGTATAAT CGAAAAATAA 480

ATCAGCTTGC TCTGATCCAT GCAGGTACTC AACATACACG CCGTCTACTT GACGGCCCAG 540

TATATATAAT TCTGGATAAC TTAGCATTGT TGTTCTCCTT CAAGAGATAT AGTGGCCCCA 600

GTGaTTTTTA AGCCAATTAG TTTACTTAAA ACCATAATTG CTTCATCCAC TAGCAATCCA 660

TCTCGTTGAA TAGAACTGGC ACATGTAAAG CGGTCCATGC TTACAATCTC ATCCACCGTA 720

ACAGGATATG GAATAGTaAC GCCTGCTTTT TTGGCAATTT GTTCAATAGC TCGGACATGC 780

GATTTATTCG ATGCTAAAAT ATACTGACCT GTTCTAGCTG ATTCTTTAAC TAGCTCTGTT 840

GTTTTTCCAG TCCCTCGATC TCTTGCTATA ATTTTCATCT ATTTGGCCTC CTCACTTAAT 900

CCCCAAAAAG GCTTTACCTT GTAAAACTTC TCAACTTCTC GATTTAAAGA TCGCACCATA 960

CTTTCTAAGA CAGTTGCTCG TGTTCCTAAC GTGACATTTT GCTTTTTCGC TTTTTTAACA 1020

CTTGTAATAC CTAAGTTGTG CCTTAGTTCA GAAAAAATTA GTATTCCCTG ATTGCTATAT 1080

TTCCATTTTA AATCTGGATT GGCTTGAATC TTTTCCCATA ATTCGTTAGT GACCACTAAA 1140

TAGTTATAAT CACCTAAAAA CGTCTGTTTC GCAGAACTTT TCAAGTCTGC CATTGTAACT 1200

TTAATTTCAT AGCATCTAAT GGTGTTGTCA GTAGAATAAG TCATAAAGTC GACTCTTTCT 1260

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TGCCACAAGC ATTTCTCAGC TTGTCTGGTT AAATCAGTTT TCATTCACCA CCATCCGCTT 1380

TCACAGCAAA CGGCCAATAG CGCTCATCAA TTGCTTTGAT TTCTTGTTCT GTGAATATTT 1440

CTTGAACCAA CCCAATCAAA TTATCTGACC AGTCAACAAT ATTATATTTA CCATTTTCAT 1500

GATCAAAAAC CAGTCGCTTA TGCACATCAT CGTTTTTTAT GAAATCAACA TAATACAATT 1560

GCTTTTTCTC TACTTCGTAG CCGTTATCAA TCGCATTCAA TAGTTTTACT TTATTTTCTG 1620

GATGTAAAAG CCAACCCTCA ACATCGTCAG TTATCAATGT ATATTCGTTA TAATATAAGC 1680

ATTCTAACTG TTGACCAACG AATACCATAA ATGCAGCACC AGAACTTAGT TTTTTATCAC 1740

TAATTTTCCC TTTTAACCCA TCAAGCCAAT CAGCCACAAA TTTCTCTTCA TGCGAAAATA 1800

TAACTTTTCC CTGTACTTTG AGCTCTTTTA TGACGTCAAT TGCTGCATTT ACTCCGTCGT 1860

CATAACsTCT TGCCCATTCA TCTTCTGCCT CGCAGCCTCC GATATCATAG AGCGCTTGAA 1920

TTAAATCTTC TTTTTCTTGT TTATTCACCG CTGATCCTCC ACTCTAAAAA GTTCGTCTTC 1980

TAGTCCAGTT TTTTGATACT TCAAAAATTC AGTAATTATG ATCGGTTGTT TATTACGCCA 2040

TGAAATTTCA GTAATATCTG TATTTTTAAG AATTACAGTT GATGGCAATG CACCTTGTGC 2100

ATTTTCATTA ACATAACCCC ACGAACCTAG GTCCATATAT TTTTTAGGCT TCAAGGAAAA 2160

AAAGGAAAGA TATTCGCTGT TGCAGTCTCT GACCACATAT TTAAACCCTC TTTTAAAAGC 2220

TTCTTCCATA ACCTCTAGCG CTTCAGCTCT TGGTCTAATC TCCATTATCT TTTTTATTCG 2280

ATCTAAATAA TCACTCATTC CGCTTCCTCC TGTTCAATGG CCCATCGGCT AAACGCTTGT 2340

AAGACTTGTA ATTGCCCAGT TTTTGACATA TATCTGTAAC TTCTATAGAC AGGTCTATCA 2400

CGATAGTCTG GTTTTATAGA ATTAACTCTC AGTCTCCAAA ATAATTCTAT AGGTTCAATA 2460

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TATGGTCTTT TAAAACCTTT TACGATGAAT AAAACATCTT CtGCTGACAT ATTTCCTTCT 2580

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CCCTCCAACA GTTCTGGGTT TTCATGGATG TTACCGATGA CTAAATAGCC ATCGCGATAC 2700

AAAATATTAG ATTGACAAAA TACAAGAtCT AAAAATTCCC AGAAAAAGCG CCCATCTGCA 2760

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ACATAAGGAA ATTCATCCCA ATTAAAAGTT GTATCATAGC TTCCTATCTC TATTTCAGAC 2940

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TTGCGCATAG TCTACATCGT AAACAATTTC GCAAGCTTCA AACGTTTCCC ACGTGCCATT 3240

TATATTGTCA TCATGTTCGA CTAAATCCCC CTCAAAAATT TCAACGCCGT TCTTGTCTTT 3300

TAAGCCTGTT GATTGCATGA GAACATATTT ATCAATCATT CCCCACATGC CATTTTCTAG 3360

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TTCATCAGGA TAATACATTA TGTTTTCTTC TACTGAATAA GCTCTAAACT TCGGAATCAT 3480

CTTCTTCACT CGCTTTCTAA TATTTCCACT TCTTCCGCTG AAAGAAAACT AGCAAGACAA 3540

TTTGCATCAC AAAACATATT GTCTGTTCCA TCTTCAAACT GGAAAAAATT AACTATCATA 3600

AAATTGTCTC TAATTGTTAA ATATGaTTGA TTAGTAAATt CTCCATCATT AAACAATGCG 3660

TTACCACAAT TGGcACAGGT AGAGCTATCT TTCTCAAAAT TCGGATAAGT cACAATTTTT 3720

CACTACCcTTC TGATTATTTA ATTAATACAT AAAATCCATT TTTCTTTGCA ACGTCTCCTC 3780

GAATTCCCAA ATGGCCTTcC AACTCTTCAA AGGTCCTTTT TGTAATTTTG GAAAGTTGCG 3840

TATCATAGCC CAAATTTCTA AGTGTCACGT ATTCATCTGG TGTTAACTGG TCTAAATCTA 3900

TcgCaCAAGT GGCGGAAAGC GTTCAACCGA CGACTCAAAT ATCACACTAG TTAATTTCAT 3960

TTTTtCACCC TCAACAATTT AGAATTAATT TTTTACGGCT TTCGTTAAAT CAAAACCAAG 4020

AGCAGTTGGA 4030

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TAATGCAATG CTTGCAGCAG ATTACTGTAT TATTGTTCTT CAAACACAAG AGTTATCTTT 60

AGACGGTGCT CAAACATATA TCGCTTATAT GCAATACTTA GCTGACACAT ACGATAATGA 120

TTTACAGGTC TTAGGTATAA TTCCTTGTAT GTTGCGTCCT GGGGGTAGGG TAGACAATAA 180

AGTATTAGAA CAAGCAAAAG AATTATATGG AGGAAATGTA TTAAACACTG TTGTAAAATA 240

TCAAGAACGT TTAAAAGTCT ACGATGTTGA GGGAATTAAA ATTAGTCATA ATTACACAGG 300

TAAAGCAGAC GGTTGGGACG TTAAAGCGCA TAAGGTATTT ATTGACGTAT TAAATGAATT 360

AGATCAACAT CAACTAGTAC TAGAAGAATT GGAGGGATAA AATATGAGTA ATAGTTtCGA 420

ACCTATTATC AAAaCTAAGA AGAAAAAATC TTCTTTAGAA GAAAAGCATG TTAGTGTTAA 480

AGGAAATGAT AATTTTTCAA GAGATACTAC AAATAATTTT GCTACAAAAC CTACATCAGT 540

ATCTAAAAAA ACAAGCACAG ATAATAGTGA TGTTAAGCCT TCTACAGTAG ATCGACGATA 600

TAAAGCTACT ATGACTCAAA AAATATCTCC TTCAGTCAAT CTTAAAATAA ACACTTTAAA 660

ACCCTTTCTT GGTGATTTAG AAAACATGCC CAAAGCCACA GTAAATGATA TTTTGAACAT 720

CTTGCTAGAT AATTATGTAA ACACAAAATT TTCTACTCGC CAACAAGAAG CATTCAATTC 780

TATGTATAAC ACACAAATTG AACTTTTAAA GAAGTAGTAA GTTTAACTTA GGTATACCAG 840

TATACTGGTA TACCTAAAAA AGAGAGTATT TAATATACTC TCTTTTTTTA TATTATAATT 900

TATGATTCCG CATTATAGAA TTCTTCTTAA TCGTGTATAT TCGTTTACAT AACGAGCATT 960

TATACTTGTC TAAATCACTC GACACTCTAC TTGCAAGACA GCCACACGAG CACTGCACAT 1020

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TCATAAAAAT CTCCATCACT GTAATAGTCG TTAATGAAAG CATCAATTGT TTTACTTTCT 1140

TCTTCGGTTA ATTCTGAAAA TTCTACATCT ATAAAAGGCT CTTCTACAGT TCCTACTGCA 1200

GACCATTTCA AAAAGTTATG AATTTTAATG TGCCTTATGT CGTAGAAATC GATTTGAAAA 1260

TCACTAATTA AAACAACATC AAACTCAGCC ATTCCACGGA AAACACCAAA CACATGCGGT 1320

TTTACACGAT CATATTCATC CAATGAGTTC AACTGGATTT CAAGCACTTT ATTTTGTTTA 1380

ATTGAGCGTT CTAATAAGTA TTCTATTTGT ACTTGAGATT GCTGTGGCAG TCTTTCAATC 1440

TCTCGTGCAT TAAATTCATC CGTTTCTTTG ATTGCTGCTT GCAACTCTCC TAAAGGGAAA 1500

GCAGTTGGCC ACTTCAAATC AAAAGGGCGG TCTACATAAT CGTTATAAGG TGTAAATTCC 1560

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ACTAAGCCCG AACGATTCAC AGcTGTCGCC CCtTCAAGAA GTGAGGACGC ATGGATCAAT 1680

GCTTTAAAAC CAAATTTCTG ACGAATTTTA TCAATTAGAA AGTCTAACTG ATTGTTTAtT 1740

ATTTGTTCTT CAGGAGGGGA GAAGAGATCT ATTTGAAGTG TAGTATCCCA AACCAGCTTT 1800

CCAAAGGAGA CTCCTAAATT TCGAATATCC ATGCCAGGAA CATAGTTTTC TCGAAAAAGT 1860

TTCAAAACAT GCTCGGTTAA CACTTTTGTG TTGTTGCTAC GAGCGATTTT AAGCTGTTTT 1920

CGCCAATGAG ACCTGCCCAG TCCATCAACT TGTCCTTTAG AATAACCAAC AAAAATTGAA 1980

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CCGAATGATT TTTCTTTGGC CACCTGGCTT TTTTCTCCTA AAAAACTACG ATCAATGCCC 2160

CAAGCATGTG CGAACAGTTG TAATCCCATG ACACCAAAGC GGTGTTTTAA TAGATAAGGA 2220

TCTGCTTGTG CTAAATCATA AATCGACTCA ATTCCTGACA TCTTTAAACG AGCAGCCATA 2280

CGCTTGCCAA TCCCGCAAAA TTCAGTGATA GGGGAGATAG ACCAAACTTT TTCTTGTACA 2340

TCTTCATATC TCCATTCTGC AACAAAACCT GGTGTATTTT TTGCTTCGTT ATCTAGGGCC 2400

AGCTTTGCTA ACAATGGGTT ATCTCCAATG CCAATCGTGA CGTATAGCCC CATATGGTTA 2460

TAAATGACAC GTTGAATAAT TTTGGCCAAT CGATAAGCAG TATCACAATT AAAATACTTC 2520

AGAGAAGCAG TTATATCAAT GAAGCTTTCA TCTACACTAA AAACAGAATG GTCTTCATCT 2580

GCCACAAACC GTTTGAGCAG ATTATTAATT TCACTATTTC GCTTCATATA TAAATTCATT 2640

CTTGGTGGAA CAATAAGCAA TTCTGGGTGA TCAGGCACTT CATCTTTACG AGTCACATTA 2700

GAAATTCCCA GGACTTTTTT TGCCATTGGC GAAgcAGcAA GyACwArTCC GCCTGCATTA 2760

TCCGCACCAC TCATyACTAT AAGCATTGTT TTrAGGGGAT CTAAGCCACG TTCTACACAT 2820

tCTaCGCTCG CGTAAAaGGA TTTtACaTCG aTrCAAggAC ATCTCTCCGg GTTCTTgGAA 2880

TAATCAAtTT CATGCAAAAA CCCGTCCTTT CGAGTTACAT TATACGAACT AACGTTCTTT 2940

TTTGCAACAA CAAAATTTCA GTTTTCCGAA TTATTTTAAA TTTAAAGTAG CTCAGAAATC 3000

TACAGTCATT ATTTTTTTAG TTTGTTTTTA ACGCGCAAGT AGATATCAGC CAGCCAGTAA 3060

ATAATTGTAA TTAATACTAT TACTTTTAGA AAGTTCACCA TGAATACTAG ATTGAATGCG 3120

TATTTTAACC ACAACAGCCA TAATATAATC GCGATAACTA CTTTTCCAAA GGTATTcaAT 3180

TTCCtAACCA ATAACCAATG TAAAAAATCT TCTCCTTTAT TTTTAGTAGC TCTATATTCT 3240

TCTAGAATAT TTTTTTTCAT GTTTAAACCt CCTTTTTTCT CrTCTTmTAT TmACATATAT 3300

ATAATTACAT GTTAATATAm ATAwATGAAA AAGAAAGGAG GTAGTTTTCT TATGAAAAAA 3360

TTAGCACTAG GTTCATTGCT TTTAGTTGCT CTAGGTGTTA TCGGGACATC TTTTGCTTTA 3420

ACTACTGAAG TAAAACAAGA GGCTGGATAT GGACATCCTC TTATTGATCA CAAAATTTAG 3480

TCTTAAAAAG GACATAGCCT TGAATATTTG TAAAGGTTAT GTCCTTTTTC ATTTTTATCT 3540

CTTATTACTA TTTTCGGGCC GTCGTATAGA TTCCCCCAAC CTAAGAACTT TTCATTTGGT 3600

TGAGCTGACT AAACGAAgGG AAACCAAACT AAAACGTTGA AGGCCAGTTG AGCAAAGCGA 3660

AACTAATTAT tCGTCTTTTC GGGTTtGACC AtGTtCCTGG TAtaAAAAAT TATTCGTAtT 3720

TAAATAGAAA TATTTTTATT ATTTCCGCCT GCAGATCACC ATTTAATCAT GTAAAAGCGA 3780

ACGTTAAAAC ACCTTCATTG CATAACTACC GATCAATATT TGTGAAAATG GCTTAGAATT 3840

GCTCTCTCAA ATCTAAATTC TAGTTTCTTA TTTTACTTTT GGTACTAATT CATTTATTTT 3900

TGAAATATTT AAGGCAATCA TTAACTCACT GATTGTTTGT ACACCTACTT TTGTATCATC 3960

AAATAGTCCT TCATTGTACA TTCCATCTAG TAATACTGGG TCTATTTGTA CATTTCTTTT 4020

CAGTTCGTCA ATTGTCATTC CTTGTTTATC CATGATTTCC TTtAACTTGA TkTCCATTTG 4080

ATTATTCTTC ATAACTTTTT CCTTCTTTCT TTTTTATCCC TTATTACTAT TTTCAAnGTG 4140

GCACATA 4147

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GTTCTTCTTC GAATTCATCT CCAATTACCT CGACTTCCTC ACCTTnAATA TCTGGTnGGT 60

CAAAACCAAA CTCTGTCATC TCAAAATCTA AmTCTAAATC TGCTAATTCA TCTAACTCCG 120

CATTTAATAA TTCTTCATCC CATGTAGCAA TTTCTCCGAC CTTATTATCA GCTAAACGAA 180

AAGCTTTGAT TTGCTCTGGA GTCAAGTCAT CAGCAATAAT TGTAGGTACT TCTTTTAGTC 240

CCAAATACTT AGCAGCTTTT AATCTTGTAT GCCCATTTAC AATGACATTA GAAGCATCTA 300

CCACAATAGG AACTTTAAAT CCAAACTTTT CGATACTTTT AGCAACTGCA GTGATAGCAC 360

CTTCATTATG TCTGGGATTT TTTTCATAAG GTATCAAATC TTCTGTTTTT TGTACTTTTA 420

TATCCATATA TGTAGAACCT CCTTGTATTT AAGTATCTAG TGGGATTCGA ACCCACGAAT 480

GCTAGTTTTG CAAACTAGAG CGTTGCCACT TCGCCATAGA TACATGAAGC AAACTTATAG 540

AGCAGTATAA GCTTGCTTGA CTAAACGAAA CATTTATTGA CATACATTTT TTATTTTGTG 600

AATCACTAAA ATTCACAATG GACCAGATAG GATTTGAACC TATATTCAGC ATCTGCCTAC 660

TTCCTTTATA TGCACTTAGA TATCATTACG CATAACTGAT CCATAAAATA TGCAACAAAA 720

AAACCGACTG CATAATTTGC AATCGGTTTT GTGTTTTACA TATTTTTCTA TACTAGTATA 780

ATAACATCAT TTTTATGACT TTATCCGCCA TAAAACCGCA AAAAAACCAC AATTTCAGTC 840

AGTCGCACTT TTATAGCATT GAAGCAGACC AGATTCATAT GCTTCAGCAA ATTCAAGAAG 900

TGCGACaCaC TTTAACGTTT CCACGTTGCT AACAGAATAA CCTAGTTCAG AAGCAATCCA 960

AACATTAGTT TTCTTTTCAA CACTGCAGTA AGTATAATAC AATAGTTGTC TATTTATCAA 1020

TGACAATCGG GCCAATGCAT TATCTATTTn TAATTTTTCT TTTTCCGCAT CAATTTTTCT 1080

AATAAAATGC TGTTGAGATC GATGTGTATT TGTGTGCTGA ATAGGCACTT CTTTAATTAT 1140

CGGCGAAGTT ATATTAAATT GAGGTGTTCC TGCAATTCTT TGCAGCCGTC TGTATTTTTT 1200

TAAAAGATTT CGTGCATTCT GTTTTGTTTT TTTGTCATCA ATATCAGGAA ATAGCTGCAT 1260

TTTTTATCCC TCCGTGATAC AATATCTATG CAGCGTTTAT TTCGGGAACG CTAAATCACA 1320

CATCCGAATT ATATTTGAAG TCGGTTTTTG TTTAATATTT TTTCAAGATG CCAACCACTC 1380

GCCGTCTAAC GAGTGGTTGT TTTTTTTATT GTCTATCATC TTTTAATTTT TCCAGTTCTT 1440

CTTCCAATTG TATTTTTTGT TTATATAGCG AACTTACGCA CAACGCTAAC AAAATAATTA 1500

CAAGCCATAA GAATTCATTT AGTGTTATCA TATCTATTCT CCAGTTAATT AAATATTTTt 1560

ATTCCTCCAA TGCCCAGCCC ATTAATTTAA CTATTTCAAA TACTGCATTC CGCCTTACAC 1620

CAGTTGAGAC ACCtAGGTwA TTAAACTTCA AAACATCCCT GTCTAgATTA TTTGTAACTG 1680

TTTCAAAATT CCTAACATCT TCarasTTCA TTGTTCCGCC AGTCGGTAGC CATATAATCa 1740

AACTTTTTGA TTTTTCCATT TAtTGATCCT CCTCACTTAA TCCCTAACAC TACATATCCA 1800

TCTTGTTGGG CATAATCTGT AATGTAAGTT ATTTCTGCAA CATGGACATC ACCTGTATAT 1860

TGTCCGTCTT GATATTCGTT TAAGCGTAAT ATATCGCCGT TTTGATAGTT TCGGTCATTC 1920

TTACGTATTT CAAAACGCTT ATCACCTGAA ACAACCGCTT CAAAGTATTC TGGTAAGATT 1980

TTTAGTTCGT GAATGGTTGG TTCTTTCTCA ATTCGTATCC GTTAGCTAAT GCATCAATCA 2040

ATAAATCTCC ATTTGTCTTA AACCACTTAG AAAATTCAGC AGTTGGCATT GCACTTGAGA 2100

AAGAAACTGc CGAACCGATa ATGTCTACTT TATcAGAACC CATTGaTAAA CCTTCTTTTA 2160

TAAATTCATC GGCACTTCTA GGCAATGCAG CTTTTTTCGA TTCTtTAATT GTTTTGCTAA 2220

GCTAATTGCT CTTTCGTTGG CATAGTCAGC ACCTTTCAAA TAATCAAGGC TATCTGTAGA 2280

AACTTCTAAG CATTCTAACT CTTCAATCAA TTCTTGTTTT TCCATTAGAG TCCACCTTCC 2340

AAAACTTTAA ATGTACTTTT ACGCTCATCG AATAACGCTT TATTTATTTC CTGTTCAGAC 2400

CATGGAACAA TCATTTGTGC TGTGTATTCA ACAACCAGAT CAACAAACTC ATAGTTAATA 2460

CTATTAATTG AAATCACTTC ATACGCCATT TTTTTATCAC TAGAAAATAT GATATTTCCT 2520

ATTTTAGCTA ATTTTGGCTA ATCTTAGCGT GTCATCTTCT TTACTTTGAT GTAACGTTCA 2580

GTGAATGTAA AATTCATTTA TATTATGATA ATCGTTATTC GCCTACTTTT TGGACCAATA 2640

TTTTACTCTA ATCTTACAGG TTACTAAAAT ACAATTTTTT CAATCAGTAT GCGGGATAAC 2700

AATAT 2705

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

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GGTAAGTAGA TCCCATGGTT GATTCACCTT CCAAAAACnA GCACnCATAG AAGAGCTTCT     60

TAAATCTTTC CCACTGTGCA ACATAATTAT AAATAAATTT CTTTGGTGTC ACCTCGCCAA    120

AGGCAAAATC CATATCATAG TATGCGGGAA TTATTATCTC TTTTTTCGAA TTTTCAGGAT    180

ATAAAATATT TTTCTCCAAA CGCGCCTTGG CAGCTTTAAA TTCAACTGAT TGTTCTCCTA    240

AAACAATTGC CTTAGAGGAA ATACCGCCAT TATAAAACAT AGCTACATCT TCCTTATAGC    300

GATTTGCCAT GtCAACTwGa GCCAAGCGGG CACTAAGTTC TtTCCCCGCA TTACGTAATT    360

CCCaTAAAAA ATACAACaTA ACAATAATAA AAACTATAAT TAGCCAAGGC TTTAACGACC    420

TTCCTATTCC TAATAAATAT AACCAAATTT TCTGCAAAAA ACTAACCTTA GGTAGCGAGG    480

TCGTTTTGGA CATAGTATCA GTAGTAAGTA GTTCCTTAAT CCGAGTGGTG ACAATATGTA    540

TTCCTGCATT AAAATCCTTT AATTTATAAA AATCTTTCAC GGTACTATCT GTTATTTCAT    600

CGGTTAAACT ATCTGGGATT ATCTCTTCAA GCCCATAGCC TACTTCAAGT CTTGCTTGCC    660

TGTCTTTGAC AGCTACTAAG TAAATCACTC CATTATTATA AAGTTTATTT CCGATACCTA    720

ATTTATTACC TATTTGATTG GTAAAGCTTT CAATCGTTTC GTTTTCAGGA ACTkGCTCAA    780

CTGTGATAAC CATTAGTTGT GGTTTCGTnT CCgTCTTACT AArTTCTTGa TTAATTTTTk    840

GTACATTATT AAkGACTTCy TCGTTCAAAA TTTGTGCATT AyCTGAAACA AAAAGATGAT    900

TTyGaTTAAT TTTTACTACG ACATCGTCTG TTGGAGCTGA ATAAGTCCTT TCAAATCGTT    960

TTAAGAAACT CATTCCCAAA TAGATCCCTA TTAAAAGAAC AGCTAGATAA ACTAAATTCT   1020

TCATTACAAT ACTTTTTACT TTTATTTTTC GATACTCCCC CACGCTCATT TGTAATTCTA   1080

TCCCTACTTT ATTTTTCCCA TACACTGATT TTTTCTCCCT TCCACTCCTA CCGAATGTTC   1140

TAGCTCTGaT TTTCCACAGA GCTAAATAAA TTTTTTTGTA TTAAAAATTT ATTtTCTTAA   1200

TAGTTAGTAT ACCGAATATA GACGTTCAAA TCTCTATCTT TTTAACTAAT TTCTGTTAAC   1260

ACGCATAAAA AGAACGTAAC GCCTAGTGGA TAAGCGGTAC Gn                      1302
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(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

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AAACTTGCAA AAGAGAACGC AAGCAAGATA ATAGAAGACG GTTTTATATA GATAGCTACC     60
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GnAAAGGGTA CCAGAAACCA AATTAAAAGC CTAGAAACGT TGGAAAATCA ACGTCTAGGC 120

TTTGTTTTTA GACTATTCCC ACTCTGTAGT AGAAAGAATA GTTTGACTTA CTTTTGTTTG 180

TATATCAAGG TTTAAGTTTG GTTGAATTGC TAAAATATGG CTTAAAATGA TATATACTGT 240

GATAAAACTG TGATAAACTT TTTTGATGAA AAAATAGATT TTAGTAATTA AAAATTTGTC 300

TGAATTTATT TATATGCTTA ATTTGAATAA TGTTCTTTTT TAGTTTTATT GATAATTTAA 360

AATTTACTAT GTGTTTTATt GTAGTAATAA TTtAAATATA CAGAAATTAT GGkTTTGTAT 420

AGkAGTTTTT ATTATAAAAG TATTGAAAAT ACAGGTTTTT AATGTCTTTG TTTGCATAGT 480

AAATAAGTTA AAAAATAACT TTTGTGTTAA CACTTATTGC kTTTTGAATT TATTATTTTA 540

AATTAATCTG GAATGATATt GTTATGTATA AAAAAACTAT GTTGTTTAAA CTTATCGACG 600

TGGTATAATT AATATAGGTA TTTTGAAAAT AAAAAGAAGG GGTATTTTAT GTTTACTAAC 660

AATAAAAATA AAAGCTTATA TTTTGAAAGA ATGCAAATGA TTGATATGAT AAGAAATTTG 720

GACAATATTA GTTACAAAGA GTTTCCTAAG TTTATnGGGG AGCTGTACAA TCTTATGGGG 780

TATAAGGTAG AaCTTAATGA GAGAtGAATA ATATTGATTT ATACGCAAGT AAGTTTTCAG 840

AAAAGTTAGC AATACAGGCA AAAGCTTACA GCTTAAmCTA TAATAAGTCG AAaGCAATTA 900

ACmAAAGAAG aGTAGAGTCA TTTGCTTTGC AAGCAAGAGA AAAAAGAAAA AAACCTATAT 960

ATATAACTAC AGGAGTTTAT ACAAATCCAG CATATATAGA AGCTAAAAAA ATTGGTGTTA 1020

CTTTATTTGA CAGAAAAAAT ATTTTTGATT TAATTTCAAA GGCTGATCCT AGCTTACTGG 1080

TCGAGGTTAG TTATTTGGAA TCAGTTGAAA AACACGATTT AAAAAAATGT AAGCATTGTA 1140

AAATTGGGCA TGCTACGAAA GTTTACTCAG AAGATACGAG TAAGTTTTAT TTTATTTGTA 1200

TGGATTGTAA GAAACATACA TAGGGAGAAG TAAAAGTCTA GTAACGTTTA GTTTCTAGAC 1260

TTTTTTATTT GAGTAAAATC TCTTTAAGTT GTGTTTGTTG TTGAAAATAG TAACTATTAT 1320

AAATAAGATT GGCTTGTTTA TAAGATAAGT TGTGGGAATA GATTAATTCG TCAAGAATTC 1380

TTATCTTGAG AACTATATCG TTTACGTTGA AAAAACTAGC CATTTTTTCA AGATCATCAT 1440

AAGTACTAAA TGCATACTTT AAGGCTTTTT TATTAATAAG TAACATTCCG GCACCCTTAT 1500

TTGCTCTGAA TTCTTTAGGA TAATCTTCAG GAAGATAGCC CTTTTTTATA AGTAGTGTAT 1560

CAAATGATTT TTCATTGTTA GGCATATCTG TCGTATAGTC AAAATAATGA TGAATTATTT 1620

CGTGCATTTT CGTAAAATTT TTAATTTCTA TTTTCAAGTG TTGGGCAGTC GCTACCATAG 1680

TTACATCACC AATTTTTGTT ACTGATCCCC AGATTAATTT TTTAGaTTGT TTTTTGAATG 1740

GATAATCAAA AAAATCAATG TTTTCGGTTT CTTTTACGTA GGCTTCAATA TCATAACAAT 1800

TGATGAGTTC TTTTCTTTTA GACATATTGA TTGAAATTTC ATTTATAAGT TTGTCAGTAA 1860

ATGCCTGTGT TTCGAAATAT AATTTTTTCT TATTTAGTAT CATAAAAAAT TACTCACTCT 1920

TTTTTTTTCT TTCTTTTGCT CGTTTTATAA GAAATTCTTG AAAATCAATC AATTCTTTTT 1980

CTAATTCTTC TATGTCATCA GAACTTAAAT CATTAGTGTT TAATCTGAAA TGTGAAATAA 2040

TATTTTGTCC AGCTTCTTTT TGATTATTTG AAGGTGTTGT AGGGTTATCA GTGCGTCCTG 2100

TTAAATAATC AATTGAAACA TTAAAAAAAT CAGCAATAGC AGTAAGTTCT TCTTCTCTTA 2160

ATGGACGTAT TCCAAGTTCT ATTTTATTAT ATACACTAAC ATTAATGTCT AGTGCGTTTG 2220

AAATTTCTTT TTGAGTGATT TCTCTATTTn CTCTtAATTG TgTaTCTTTT CGTAAGTnTT 2280

CATACTATAT CTGTCCTTAT CTAATGTTTA T 2311

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CAACACCAAT TTTATATAAT AATAGCGCAG CACCAGTAGG CCCCCACCTA ATACTTAAGC 60

TTGTAATTGG TCGCGACTCA TCAGTAGGTG AATCCTTCGT AATCATTCCT CCGGTATTTG 120

TACTACCATC AGGATGAATG ATCAAACTCT CTCCTTTACC ATTTTTCCAT ATTCCAACTA 180

AAGTAGTAAA ATCGCCAGCA TTAATCGCTG TAGTATCTAA ATCAGCTACA GTTAGCTGAC 240

TATTGTTTCC ATCAGCTGTC GGCTCTTCAT TTTTCACTGA TTCGTTAGAC TCGACACTGC 300

TGCTCGCTTG TTCGTTTGTC TTATCAATTG TTTCACTCGT TTTTtCATTC GTCTCTTCAA 360

CTTTAGAGGA TGCCTCCGTT GAAGCGGTTA CTTTCTTTnC TTTTGGTTCC CGACAaGCAG 420

TTAaTGATAA AACCGCTAGC ACGACAAAAA aCGCTAACAT TCCCTTTTTC ACGCCTATTC 480

ACCCCGTTCA ATGATCTATC TTACTAGACT ATTGTACTAT TAATTCAACT GTTTAGACAA 540

ATATTTATGG AACAGACAAA AGTTGAACCT GTCATTGAAT GCTTTGTGTC ACATGGACCT 600

ATCAATCAAC TTTCTTTTTT CTATGTATTA TATGAAAAAA AGTGAGCCAT CAGTCAAAAT 660

GACCGATGGC TCACTTTCTA AATCTTCAAA TAAACGAACA AATGGATTAT TCAGGTAAAT 720

CTACATTATG ATGGACTTTC TGAACATCTT CTAAATCTTC TAAAACGTCT AACATTTTTT 780

CAAAGTTCCC TAAATCGTCG CCTTCTAATG TTACTTCGTT TTGTGGAACC ATTTCTAACT 840

CAGTAACCGT GAATTCTTCA ATGCCTTTTT CTTTTAACGC TTCTTGTGCA TGGTGGAAAT 900

CTTCTGGTTC TGTGTAAACG ATAATTTGAC CGTCTTCTTC AACAACATCG CGAACATCAA 960

TGTCTTTTTC CATTAAGTAT TCTAAAATTT CATCCGCATC GTCACCAGCA AAGCCAATGA 1020

TACCTGTATT ATCAAACATG TAGGAAACAG CACCGCTGAC ACCCATGTTT CCGCCGTTTT 1080

TACCAAATGC GGCCCGCACA TCTGCTGCTG TTCGGTTCAC GTTGTTTGTT AAAGCATCAA 1140

CAATGACCAT TGAACCATTT GGCCCAAATC CTTCATAGCG TAATTCAGAA TATTGTTCAT 1200

CTGCTGAACC TTTTGCTTTT TCAATAgsGC GATCAATAAT ATGTTTTGGT ACATTGTATG 1260

TTTTGGCGCG TTCGATTACA AACCGTAATT TTTGGTTTGC ATGAGGATCA GGGTCTCCTG 1320

ACTTCGCTGC TACGTAAATT TCAATCCCGA ATTTTGCATA AACACGGCTA TTGTTTGCGT 1380

CTTTGGCAGC TTTTTTCTCT TTAATATTTG CCCATTTACG GCCCATATTC TCACTTCGCT 1440

TTCTCTGATT TGTTGTTAGT ATCTTATCCC TTGTTTATTA TACTGGGGAA aCTGATTTTT 1500

GTTAAGTATT TtTTAGGTAT CTGGCGAAAA TCGTAAGGGA AACCGACCAA AATTTTGTTC 1560

TTTTAAAGAA GAATCTCCCA TTTGGTATAG TTGATgGCGC GAATATCTAA CGAAAGCATT 1620

GCGCGGTTTT CyTTAGATAC TTTGGaAATT ACCGGCAATT GAATCTGTGC yTTGGkTTCy 1680

TTTAGATAAG CTTGTCCCTT TGGCGTAAAT CCTAGCACAT GGAGATAACT GkTTTGcCmA 1740

ACAGTTTCAA CTTCTTCTTT GGTCATATTT AACAATATAT AGGTTGCTAA TCGTTGCAAT 1800

CTTGTCCAAG TATAACGCTT CGTTTTCATA CGTTCCATTA ATTCGTGAAA AGAACCTGCT 1860

GCTTGGATTT GATCTTTTAG TCGATATTCA AGTCCTTCCG TCATTTGGTA AATGGCTTGT 1920

AACTCTTCTA ACGAGGATTG AACAATTTTA TACTTTAGGA AGGGCCAATA ATTTTCCCAT 1980

GAAATCATTG TCTGTGTTTG TAAATGTTGT GCGGTTATAG AAGGCACCGT TGGCAGCACT 2040

TGCGTTATTT CTTGTTGAAA AACACTTTGC CTAATCGCCG TGGCGCTAGC AACTTTCCCA 2100

GAAATCGTTG CATCATGAAA GCCCGCTTGT TTTCTAGCAA TTGGGTAGAG CGTCATCGGG 2160

GTTGGATACG TGGCATTTTC CTTTGCATAA CTCATCCCCA AAATATGATT AGGCGAAGAA 2220

AAATCAAACC TGCTTTCAGG ATATACTTGA CGAAAAACAG CAGTCATTTT TTGTGGATAA 2280

CTCAATTGTT TGTCTGTCAA TGCGTGGAAC GTTTGATCAA TTAAGGATTG ATTTTCTTGG 2340

ACAAACTGGC CGAAAGCCGC ATAATCAATT GCGCTTGTAC TATCTGTTCC AAAACATAAG 2400

CTCTCACATT GCAACGCCTG CAATAACTTT ATACCGCCTT TGGCAAAGTA ATCCGCAGAC 2460

TGTACCGACC AAGCTGTCGG CAATTCAATG ACTAAATCCA CACCATTTTG CAAAGCTTCT 2520

TCTGCTCTGG CCCACTTATC TAGTAAGGCT GGTTCTCCTC TTTGTAAAAA ATTTCCACTC 2580

ATTATAGCAA TCACTACTTC AGCTCCGCTT TGTTGGCGAG CTTGTTGGGC ATGATAGCGA 2640

TGTCCATTAT GAAAGGGATT ATATTCCACG ATAATGCCAC AGGCTTTCAC TCTAGCCACC 2700

TCCGTTATAA AAAAATGGAC TTATCAGCAA AGAGACAAAC GTTTTTAAGC GCTGTCCCAA 2760

GCTCATAAGC CAAATCTTAT TAATCTCTTT GACAAACAAA GAACCAGCGT TCACTTGTTT 2820

CAGTTGGTGC TTCATCTGTA AAATCTGCAT AAACTTTGAC GTTCATGAAA CCAGCACTTT 2880

CTAACATTCG TAAATAGTTA TCTAACGAAT AGGTTCGTTC TTGATGCAAT TCATCATACC 2940

GAACAAAGTG CTCATCTGTT TCCTGTTCTT TCACAAAAAA TGTTAAGAAA TGTTCGATGC 3000

TGTGTTCTTT TTCACCAGCG TAACTATCCC ATAGAAAAGC AAATTCTTCT GTTTGATAAT 3060

GATAGCTATA TTCTGGAAAA ACTGAATCAA TTTTGTAAGT AGAATGAACA TCAAAAATGA 3120

ACGTTCCTTC CTCTTCTAAC GCTTGATAAA CTTCATCGAA CACTTGTTGT ACTTCTTGGC 3180

GaTTAGCCAT ATAGCACAGT GAATCAGAAA AACAAGTGAT GGCTTGGTAT TGTCCCACTT 3240

CAGATAAATC TAGCATATTT CCCTGAACAA ATTGAACTGG CACTTCTTCT TCAAAGGCCC 3300

GTTCACTAGC AATCATCAAC ATTTCTTCTG ATAAGTCTAA GGCCGTCACA TCGTAACCAC 3360

TTTTCGCAAA ATCAACTGCT AAAGCGCCTG TACCACAAGC CATTTCAAGA ATTTGTTGGG 3420

TTCCTTGTGG GAGATGACGA TTGGAAAAAT CCAACCATTT TTGGTATAGG CTTTCGTCCA 3480

TCACTTCGTC ATAGACGAAA GCAAACGTTT CATAGGCCAT TTTAGTCGAC CCAAGCGCTT 3540

AGATCAACCA TTGGGGCATC TGACCATAAT TTTTCTAAAT TGTAAAAGGC ACGTTCTGAA 3600

GATTGGAATA CATGGACAAT AACATCGCCT AAATCGATTA AAATCCATTT TCCGCCTTCT 3660

TTACCTTCCA CACGTTTGAC TTCAACTTGA TTTTTGGCTT CTTGTTCGTT AATTTCATCA 3720

ACAATCGCAT TGATTTGACG TTCACTATTG GCTTGGCAAA TTAAAAAATA ATCTGCTAAT 3780

AATGAAATCT CTCTTACGTC TAATGCGACA ATTTCTTCTG CTCGTTTTGA ATCTGCTGCT 3840

TTGACAGCAA TTTCTAAAAT TTTCTGGCTA TCTATGATAG TTCCCTCCTA GTAATTCTTT 3900

CTTCTTTTAT TTTTGATTAA CGACCCATTG ATTGTAGGTC TCTAACGTTT TTGGATAAAT 3960

TTTATGTTCT TGTTCAATCA AATGTAACAA GGTATGTTTC GTTTCATAAG CAACCGCTGC 4020

ATCTAAGTCA ACAAGGGCAA TTTCACGGGC TTCTTTCACA CCTGGGAAAA TCACGTCCTG 4080

GTTCAATGGT AATCTGCGAC ATAAATAATT TTATCTAGCA AGCTCATCTT AGCAGCCCCA 4140

GTTGtATGCA CACGaATTGc CTGCAAGATT TCTTCGTCAT CAATGGCTAA TTCCCGTTGA 4200

ACAATATCCG CCCCAACTAA GCCATGCCAA ATTTCATTGC CATAGTTTAA TAAAGCCAAA 4260

TCAAAACCAT CTCGGCGAAT AATCAACTCG AATTCATCGT TTGGACGTTC TTTGGCGTAA 4320

TCATGCGTCA AAGCAGCAAT ACTGGCTTTC GCTTCATCGG CACCATATTT CGCTGCCAAG 4380

GCCACAGCTG TTTCCTCGAC TCCTAACACA TGGCGAAAAC GGCGTTCACT CATTTGCATT 4440

TGAACTTTTT GCATTAATAA TTCACGTTGT GCAGCATCAT AATTTGTTAT CCAGCTCATC 4500

TTGATACAGT CCCTTCTCTT GAATATAGTT TATCACATTC TCTGGAAGAA GATAGCGTGT 4560

TGAGCAACCA CTTTTGACTT TTTGTCTAAT CAAAGTGGAA CTAATCGCCA TCTGCGGAAC 4620

ATCGACCCAA ATAATTGGAT AGGTAGATTC CGTTGGATAA TTAGGACGCC GAATGCCGAC 4680

AAATTGAACT AAATGGAGTA AGTCATCAAT CCGATGCCAT TTGGGCAAGT ATTCCACCAT 4740

ATCTCCACCA ATTATAAAAT AATAATCAGT ATCTGGATTG GCTTCTTTTA AAGCTTTCAT 4800

CGTATCATAC GTGTAACTTT TGCCTTTGCG AATTAACTCA ATTGGCTCAA TATCTAAGCA 4860

GGGATTATCA GCCACTGCTA GTTCTAACAT CGCTAACCGA TGTTCACTGC TAATTGTTTT 4920

CTTTTCGTCT ACATGTGGTG GTAAGTACGT AGGCATTAAG TAAACTTTGT CCAAACCTAG 4980

TTGATTTTGA ACTTGATCGG CCATGACAAG ATGTGCTAAA TGAACGGGAT TAAAATTACC 5040

ACCTAACAAG CCGACTTGCT TTCTTGTTTG AAAACGTAAC GGTTCCTCTT GCAAGAGAAC 5100

GTCCGCTCCT TGACGCGCTT GTCTTTTTTC TCCCATTGTT CATCCCTCCA ATATTAAATC 5160

TCTTTGACTG CTGCTGAAAT TTTTTGATAT TTTTCTTTAC TTGATGGCTT GAATAAGACC 5220

AACACGCGAC CAATAATTTG TACCACATCG CAATGAATGG CTGCTGTTAG TTCTTCTGCA 5280

ACCTCTTCTG CTACTTCATC TGTATTTTGT AATAACGTAA TTTTAATCAG TTCACGTTTT 5340

TCCAACGCTT CATCAATTTG TGTAATCATT GCGTCATTCA AACCACCTTT GCCTACTTGA 5400

AAAATAGGTT GTAAATGGTG TGCCTGACTA CGTAAATAAC GTTTTTGTTT TCCTCTAAGT 5460

TTCAAATTGT TTGCCTTCTC TCTAAAATTT AAATTAATGC TTTTCTACGT AAAACATCGA 5520

CACCTTTAGG CGCCCAACCA GCGACTACAC CAGGTTCTGT GACAGTAATC CAACCTAGAC 5580

CAGCAAACAC AATATCCGTT TTTTCTTTCA CGGAAAATTC AAAGCGCACT AATTCAGGAA 5640

ACTCAGCGAC TTCATCGGCA CGTGGAGGCT GCAATAAGCC ACCAACATGT TTTTCATAAA 5700

AAGCATCGGC GGTTGCTGTT TTTGTTCGGT GTAATTTTAA GTCATTGGAA ACGTAGGCAA 5760

TGAAGGAACT TTTAGCACCT TGGACATAAT CAAAGCGAGC CAAGCCACCT AAAAACAAGG 5820

TTTGTTCAGC ATTTAATTGG TAAACTTTCG GTTTGATTTC TTTTTGCGGT GCAATAATTT 5880

TCAAGTCTTT TTTaCCTAGG TAATGTGCCA TTTGATGACG GTGAATAATT CCGGGCGTAT 5940

CGATTAAGAA GTGGCCATCG TCTAATGGAA TTTCAATTTT ATCTAGCGTT GTTCCAGGAA 6000

ATTGTGATGT CGTAATCACA TCTTGAACAC CCACTGTTTG TTGAATGATT TGATTGATTA 6060

ATGTTGATTT TCCAACATTG GTCACACCTA CGACATAAAC GTCTCGGCCT TCACGATATT 6120

TTTCGATCGT ATCTAATAAC TCTTGCATTT CTTGTGGTTT CTTGCCACTT GTTAGTAAAA 6180

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CTCCGATAAA ACGATGTAGT CCTGGAATAA GAGAGCCATT AAAGTCAAAA ATATyCmcTA 6360

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AAACTTCCCC TGTTTCCATT CCTTTTTCGA AAGCTGTTTT TGGTGTATAG CCTAATTCAT 6540

GAGGATTTTC CGTTTGGATA ATCGCACCAC AGCCAATACA ATGAATTGCC TCTGTCATTC 6600

TAATCCGCCT CTCCATGTCA TTTCTGGATG TTTTTTTGAT AAGTATTTCA TAATTTTCCG 6660

TTCAAAGAAC CGATTGATTC TAGTATTCCA GCCATCTGTA TCGACAATCG GTTGAACTAA 6720

AACATTGCGT ATACCCGCTG CGTTAgCTCC CCGAATATCT GTCATAATCT GATCGCCGAC 6780

CATTAACATT TCAGATGGCT TCAAGCCTAA TTTTTTTTCT GCTAATTTGA AGCCACGTGC 6840

GGTTGGTTTC AAGGCACGTG CTACATAATC TAAGTCAAAC TTTTCAACAA CGCGTTTAAT 6900

CCGGCTGTCT TTGTTGTTTG AAACAACGAG GACAGTAATT CCTGCATTTT TCATTTCTAA 6960

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CACTATGTAG TTTCTTCGAT TTTAAGAGAC TGAAACATAA CTAAACAATT ATGCTTCAGT 7200

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ACGTAACGCT TTGCGATACC CTTCAGGATT AGGTGAACCA AAATTACGTT CAATATTTTC 7920

TGGTAGATTT CGACCTTtTT GGaTACCTAC CACTGTAACT GGGTTTCCCT TGACAAAGTA 7980

GCAACACCA 7989

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

AAACACAAGG GAAATTTGAT TATTCCTCAA AATATAGCGG TGTGCTTTGT GAAAAACATT 60

GGCATTTAGA TGAACAGCGC TACCATGCAG ATCCTAGAGC AATTCATTTT ATTCGCTTAT 120

TTTCGCAAGT CTCCTATGAA AAAGTCCAAA ACATTCAAGT AAAAGAAGAA ACTAAGAAAA 180

GTATTCGAGA AACGATTGAT ATGTTATACG ATGAATATGT TGGTTTGCAC TTAAAAAGTA 240

AAAAATTTAT TGATCAAATG AAAACGTGGG AAAATACGTT AAAAATTCCG CCACGAAAGA 300

AGGAAGAAAA ATAAACATwA ACAAGCAGAC GTTTTtCTAA AAAAAATTTG ACAACTTCCC 360

TCAGACACCG TATTATGATA GAGAAGTTAA ATACGTACGA AGAAAAAGAG AAGTAAAAAG 420

AACCCTCTGT TAAGCGAATC TGGGAGAGTG GGAGCCAGAA ACACGGAACT TTTGAAAGGC 480

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GTCTCCTCTA TGTTAAAACA AACTGCTTAG CCAAAAACAT GGAGTAGATG ATGAACAGCA 720

CAAGGTGACC AAAGGGAACG TTGTAACCGA ATAAAAAAAG CAAACAGTTA ACACCAAAAG 780

AAAAAATAGT AACGTTTATT CAAAAAAGCT CAATTGGCGC AAAGGCGACA GAGTAGATGA 840

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TACATTcCAG AAgCAAAGCC AATCCCTATG TCTATAAAAr ATATTCCAAG GaGGaAAACA 960

ATGaAAAACa AGTTAACCGT ACaAGAAATG aTTTTAACCt TGCaAAAATT TTGGTCaTCT 1020

AATGGCTGTA TGTTAATGCA AGCCTATGAT ACAGAAAAGG GAGCCGGTAC CATGAGTCCT 1080

TACACGTTTT TACGTGCCAT TGGACCTGAA CCATGGAATG CTGCCTACGT AGAGCCTTCT 1140

CGTCGTCCAG CTGATGGACG CTATGGTGAA AATCCGAACC GTCTATACCA ACATCATCAA 1200

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TGTTGTCACA CCAAGCCGTA TCCAACTTGA AGAAAAAGTA ATCAAATTTT TAGATGAACA 1980

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AATTGCTTTA GATGCTGAAG GAAATTGGTC AAAAGCTGCA CAAGGTTTTG TACGCGGCCA 2160

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TATCGCTGTT CGCAATGGGG ATAATGTTCA CCTTGAAAAC GTGATTAAAG GAAATGAAAA 2820

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CGTTTGCTTT TGGTTGGTTC GTTTTTTGCG TTACTTTGTT TGTTTCTTTT GGTGTCACAT 4320

CCTTGATAGG AGTAACCACT TGTTTTGGTG GGTTATTTTT CAATTCTTCT TGTACTTGTT 4380

TTTTAATTCT TGGACGTAAG AGGATATTTG TGATGGCAGA TTGAATACAT GTGAAAATAC 4440

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TAATGGTGAA ACAATCAGCA TTGATTTCAT TGTTTTCTTT TGTTCTTCAG GAATACCAAT 4560

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TGGTTGCCCT AAATTCATTC CTAAGAAGCT TGCCGTGGCA ATACCTTTTG TATAACGAGC 4680

AGCAAAGAAC AGAGAAGAGA AAATAGGCAT TTGAATTAAT AAAGGCAAAC AACCAATTCC 4740

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TAAAATAATG ATCCGTACAA TAATGGTGAT AAAAATAATC GCCCAACCAT AGTTCGAATT 4980

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AAAACCTTCA CCAGTTGGTT GTCCATCTGC TCCTGTTTTC ACACAGCCTG ATAAAAACAT 5100

TACTAAAAAT AGTAAGCCAG AGCCGTAAAG CCATAC 5136

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GGCGAAATTG TTGAAAAAAA ACTAGTTACA GCACCTCTGT CAACTGAACA AATTGATCAA 60

GCAATGGCCG AAATGACAGG TGAAaTCACA CAAATCCCAC CGATGTTTTC TGCGGTGAAA 120

GTCAATGGTA AACGTTTATA TGAATATGCG CGGAACGGGG AAGAAGTTGA ACGGCCCCAA 180

CGAAAAGCTA TGATTTATTC ATTTGAACGC ACTAGTGAAC CAATTTTTAA CGAATCCGCT 240

CATACACAAA GTTGGCGGTT TAAAGTGGTC TGTGGCAAAG GAACCTATGT GCGGACACTA 300

TCAGTGGATA CTGGCAAAAA ATTAGGCTAT CCTGCCCATA TGTCGGATTT AACGAGAACG 360

GCAAGTGGCG GTTTGCAAGc tGCGCAATGC TTAACGTTAG AAGAAGTAGC CAAACAAATG 420

GCTGCTGAAA CAATCGATCA ATGCCTGTTG CCCATTGAGA CAGCAGTAGA ACAATTCCCA 480

CGAATTGATT TATCAGATGA ATTGTATCmA AAAGTAAAAA ATGGCATGCG TTTGCACmAA 540

AAAGAATTAG GrATAAAGGC AaTGCCAGAA TCCTTAGTCG CCTTATTTTA CCAAAATCAA 600

GTGGTTAGTT TATACATGCC ACACCCAACG CATGATAAAT TATTGAAACC AAGTAAAGTT 660

CTACGGAACA ATTAAATAAA AAAGAAGGAA GTTTTTGCAC ATGCAAGTTA TTCAACTACA 720

TCATCCCTAT GAACCCAATC AAATTCCTAA TGAAGAAGTC GTGATGGTCC TAGGCTTTTT 780

TGACGGTGTT CACAAAGGCC ACCAAAAAGT AATTGAAACA GGTAAAAAGA TTGCGGAGGA 840

AAAAGGCTTG AAGTTAGCTG TGATGACCTT CAACCAAcAC CCAtCAATCG TTTTTCAAAA 900

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GCCGCAAGAT TTTGTCGATC AGTATATCGT TAATTTAAAT AGTGCAGTGG CAGTCTCTGG 1080

GTTTGATTAT ACGTATGGTC CTAAAGAAAT TGCTGGAGTC AAACAGTTAC CAACTTATGC 1140

GCAAGGCCGT TTTGAAGTGG TGACAGTACC AAAAGAAGAA ATGACTGGTG CCAAAATTAG 1200

CTCAACAAGA ATTCGCGAAA AAATGGAAGC CGGCGAAATG GAGGAGGTCA CGGAGTTGTT 1260

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TGGCATTTTT CAACATGCTT TGCTTATCCA GAAACACACC CTGCAGAATT AGAAGCCTTT 2220

GAAGCAGAAC TCGGAATAAA TGAATAAAGA ATAATAAGAc GCGACAACTA CTAGTTAAGT 2280

ACTGGTGGTT GTCGCGTCTT TACTACTTTT TATTACAAAG TAGTTGACAG AACCGGTACT 2340

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ATTGACACAA AGGAGATAGC TTTCTGTATA AATTAATTCT TTCTCTAATG GAATCGAGGT 7200
ATCCAAAAAT ATCCCAATCC CAATGTCAAT TAAATCTGTT TCCAAGGCTG TTTCAAGATC 7260
GTAATAATAC TTAAAATCAA TACTTACATA CGGATAGGAT TGATTAAATA ACAACAAGAC 7320
```

TTCTCCAAAT GCTTTATCTA TATCAATTAA GTTTGTTCCA ATCCGAATGG TCGTTGTCGA 7380

TCCTTGGGTC ACTAATTCAT TAATCTCTTC TTGCGCTTCC TTAATGAGTG CAAAAATCAT 7440

TTCTGTTCGC TTGGCGACGA CTTCGCCTGC TGGAGAAAGC CGACAATGTT TCTTGTCTCT 7500

TAAAATTAAT GAAGCACCTA ATTCACGTTC CAACTCCTTG AGCTGGGTAC TTAAATAAGG 7560

TTGACTCGTA TGGAGCTTTT GAGAAGCTAA AGTAAAACTC GCATACTTTG AAACTGCCAT 7620

AAAATATTCT AGTTGTTGTA ATTTCATTTT CCTCACCGCC GTTTCTTTAA CTATACAAAA 7680

AATAGCAGAA GAAAAGCTTC TCGACAAGGC TATCTGATGG TCTTTAGATT AATTTAACCA 7740

GTTATGATTC TATGAATAAA TACGAATCAT ACCAGAAAAC CATAGTAAAT AAGCGGATTA 7800

TTTTTCTTTT TGTTACTGAA TGGACAAAAA GTTATCTACT AAAAACTTTT TCTATATCGT 7860

TATTTTTTCA TGGAAGAATT ATACTTGCTG TTGTAATTAA ATAAGATTTG TTAGGTGAGG 7920

CTCCTATACA AACATAGGCT ACTGCCCAAA AATGTCGAGA GACGCCAATG GGTAGAACAG 7980

GAACTGTCGA ATGAAGGCTT TTCTTAAGGT AGCTAAAAGC AATCGCTTTT TACGTTGTAT 8040

AGTGCTAAAG CTCAACGATA AGAACGATTA TTCTTTGACA CGTtGAGTTT TCAGCGTGTC 8100

TTTTTTTGTG GAAAGGGTGA GGAAAATGGA AGATGAACCG ATCGTCAATT CAAGTCAACC 8160

ACAGATAAAT GAGGTGAAAG AAAATGGAAA AGAAAATGCG TCACTTGGGC CATGACTATA 8220

GTTACAAAAA GTTTGCCCAT TCAGAAGTAG AAAAAGTTTT ACAACGTTTT GGCTCAACTT 8280

GGGATGGCAT TAAACACCAA GATATTGAAG AATTACAAGA ACGTTATGGC CGCAATAAAA 8340

TTATGAATGA AAAAAAAGnT TCGCGGcTGC GACTTTTTAT AAAATCGTAT ATCACGCCGT 8400

TTACTTTGGT GTTACTAGCA CTAGCCACGA TTTCATTTTT TACAGAATAT GTCTATGCTG 8460

CGCCAGAGGA AAAAGATGTT ACTGGCGTGT TAATTATGTT AGCGATGGTC aTCTTAAGCG 8520

GCACGATGaG TTTTGTCCaA TCAGTCaAAT CaAGCAATGC aGTTGAAAAA TTACAAAATA 8580

TGATTAAAGT TACAGCGACA GTCATTCGTG ACAAGAAGCA AATGGAAATT CCTATTGAGG 8640

AAGTTGTGTG TGGCGACTTA GTCCAACTAT CCGCTGGCGA TATGATTCCa GCCGATTTAC 8700

GTTTAATCCA ATCTAAGGAC TTATTTGTTT CCCAATCATC CTTGACTGGA GAGAGTTTTC 8760

CCATTGAAAA ACACGCGACT CATCAAAAAG ATAGTGATCA AATTGATACA GAATACGACA 8820

ATCTTTTGTT TTTAGGAACA AATGTAATTA GTGGCACTGG TTTGGGCATT GTCATTAAAG 8880

TTGGTAATCA AACTTTATTC GGAAGGATGG CTTCTGATAA CGGAGAAGAG CAGCAGCAGA 8940

CGAGTTTTGA AACAGGAATT AATAAAACAA CGTGGGTGCT GATTCGCTTT ATGTTGGTCA 9000

TTACGCCAAC TGTTTTTCTA ATTAATGGGT TAACAAAAGG TGATTGGGCG GAAGCGTTAA 9060

TGTTTGCGAT TGCCACAGCT GTCGGCTTGA CACCAGAAAT GTTACCTATG ATTGTAACAA 9120

CCAATTTAGT CAAAGGTTCT CGAGAAATGG CTAAAGAAGG CACGATTATG AAAAATGTCA 9180

ATGCCATTCA AAATTTTGGC GGGATGGATG TACTTTGTAC GGATAAAACA GGTACCTTAA 9240

CACAAGATAA AGTAATTTTA GAATACCACT ATAATATTGG GTGCCAAGAA GATCAAAAAG 9300

TCTTGGATTT AGCATTTCTA AACAGTTATT TTCAAACAGG TTTGCGTAAT TTAATGGATA 9360

ACGCCGTTAT TCAAGCGGCG mCACArGAAA GTGATATACA ATCAGATGAT TTTTATAAAG 9420

TAGATGAAAT TCCTTTCGAT TTCAATCGAC GTCGAATGAG TGTGATTATC AAAGAGTTTA 9480

AAACGCGAGA AACACGCTTA ATTACCAAAG GGGCGGTTGA AGAAATGCTC TTGGTCTGCA 9540

CACAGGTACT TTTAAATGGC GAAATTGTGC CCTTAACAGA GACGCTGCGT CAAAAAATTA 9600

CCAAAGACGT TGAAGCTTTA AATCGAGATG GTTTGCGCGT TCTAGCAATT GCCGATAAAA 9660

AAGTCGAAGC GGCTGAATGG GAGTATACAA CTAAAGATGA ATCAGAGTTG ATTTTACAAG 9720

GCTATCTTGC TTTCTTAGAT CCACCAAAAG AAACAGCGGC GGCAGCTATT CACGCCTTGC 9780

ATCAACATAA TGTAGCTGTG AAAGTATTAA CGGGGGACAA TCAGTATGTG ACGCATTCTG 9840

TTTGTAAAGA AGTTGGTCTG GCTGGCGAAA AAATTATTAC AGGAAATGAA CTTCAACAAT 9900

TAAACCAAGA AGAATTAAGA AAAACCGTTC AAGCGTATAA TATTTTCGCC AAAATTACGC 9960

CTGACCaAAA AGTTCGTATT GTAAATGCGT TAACTGAAAA TGGTCAAACT GTTGGCTTTT 10020

TAGGTGATGG AATAAATGAT GCTGGAGCAA TGCGTGCTGC TGATGTAGGA ATCTCTGTTG 10080

ATACAGCTGT CGATGTGGCG AAAGAATCGG CGGATGTAAT TTTATTGAGA AAAGATTTAA 10140

TGGTTTTGGA AAAAGGGATT TTATCTGGAC GGCGCGTGTT TACGAACACG ATGAAGTACG 10200

TCAAATTAAC AGCAAGTTCT AATTTTGGCA ATGTTTTTTC CGTGATCCCA GCAAGTATCT 10260

TTTTACCATT TTTACCGATT GCTCCGATTC AATCGCTATT ATTAAATCTA ATTTACGATA 10320

CTTCGTGTAT GTCAGTTCCT TGGGACAAAG TAGATGAAGA ATACGTAGAA AAACCAAAAA 10380

AATGGGAACC AAAATCAATT GGTAATTTTA TGCGTTGGTT TGGCCCAACG AGTTCTATTT 10440

TTGATATTGT TACCTATTTA TTTATGTATT TCATTGTGTG TCCGGCTATC CTAGGTGGCT 10500

CATTCTTTGA ATTAAATGGA GCAGATCAAT TGCTCTTTAT CGGTATTTTC CATGCAGGGT 10560

GGTTCATTGA GTCCTTATGG TCCCAAATGC TCGTCTTGCA TTTCCTACGA ACAGAAAAAA 10620

TGCCTTTCCT TCAAAGTAGT GCTTCTGGAA tTATGACGTT AGcACtaCAG CAGGGaTTGT 10680

TCTCGGgAAC TGtTTTACCC TTTACCGCTT TCGGTGcAGA ACTAGGATTT GTCGGTTTAT 10740

CACCAaGCTA TTTCTnGTAT TTAATCCCGA CAATTGTTGC TTATTTAGCA CTGGTTGCgT 10800

TCATTAAAGT TTTATACGTC aAACGTTACG GTCaATTACT GTAACTGATT TGTACTATTA 10860

TATATAGAAA AATTTTTTTA CTTTTCTTTC aAGGTTGAGG AGGTGTCGGT TTTTATGACA 10920

GCTCCTCTTT GTTGTTTTAA GTGACTGTGC GAATTTTTTT ATGGATTTAT TTGTCATTTA 10980

CAGTTAGTAT GGCTAGTAGA GACTTTCCAA AAAGAACGAG CTTTTTGGTA ATAAGGAGAT 11040

AAAACGAGCT AATGACCAAA ACAAACCAAC TTTCAACTTC AACGCCGATG TTCGATCGGT 11100

CGGCCTATAT TCATATTCCA TTTTGTGAGC ATATTTGTTA TTATTGCGAT TTTAACAAGG 11160

TCTTTTTAGA AGGACAACCA GTTGATGAAT ATATTCAGAG TTTATTAAAA GAAATTCAAC 11220

TTACGCAAGc ATTGTATCCA GAACAAGAAA TGAAAACcAT CTATATTGGC GGAGGCACGC 11280

CAACTTCATT ATCAGCGAAA CAGTTAGATG TGCTACTAAA AGGGGTTCGC GAACAGCTAA 11340

CGTTTGATGA CCGAAATGAA TTTACGGTGG AAGCAAACCC TGGTGATTTA ACCCAAGAAA 11400

AATTACAAGT CATGAAAAAC TATGGCGTCA ATCGTCTTTC GATGGGCGTT CAGACATTTG 11460

ATGATCGCTT GCTCAAAAAA ATCGGTCGCA AGCACACCGC CGCAGATGTT TATGAAACAA 11520

TGAAATTTTT AGAGAAAGAA AATTTTACCA ATGTCAGTAT TGACTTAATC TATGCTTTAC 11580

CTGGACAAAC ATTGGAAAGT TTTCGCGATA CTTTGACAAG AGCCTTAGCA TTGGACTTGC 11640

CGCACTATTC GCTTTATTCA TTAATTCTTG AAAATAAAAC AATGTTCATG AACTGGGTTC 11700

GTCAAGGACG GTTACAGCTG CCTGAAGAAG AAATCGAAGC ACAAATGTTT GACGAAACGA 11760

TTGAAGCAAT GGAGAAAAAA GGACGTCACC AATATGAAGT CAGTAATTTT GCTTTAACAG 11820

GAAAAGAAAG CCAGCATAAT CTGGCTTATT GGAATAATGA CCACTACTAT GGATTTGGCG 11880

CAGGTGCCAG CGGCTATCTT GGGCAAACTC GTTACAAAAA TCACGGTCCA ATCCAACATT 11940

ATTTGAAACC CTTGCGAGAA AATCAATTGC CAATTGTGGA GACTGAAGAA TTAACTCGTC 12000

TAAATCAAAT AGAAGAAGAG CTATTTTTAG GCTTACGTAA AAAAGTAGGC ATTTCTAAAC 12060

AAAAATTCCA ACAAAAATTT CAGGAACCAA TTGAAGCAAT TTATGGAGAG GTCATTCAAC 12120

GCTTAATCAA AGAAGAATTA TTAATTGAAG AAGCAGATAT CTTACGTTTA ACGAAAAAAG 12180

GGCTATTTGT GGGGAATAAT GTTTTTGAAG CATTTTTGTT AAGTGAAAAA GAGTAAAAAA 12240

ATAAAAAAAT CATCGAAGTG TGACAAAGCA TTTCGATGAT TTTTTTATTA CAAAAGTTGG 12300

TATTGATGGT TTTTGAAGGT GGTTTGCAGC GATTAGCACT CTTGCGTTAA GAGTGCTAAA 12360

AAGTTGCGTA TTTCCCTTGA CAAAAAGGTA AGGACTTGTT ATATTAGTAT ATGTAGTTAG 12420

CACTTAGATG TTAAGAGTGC TAATGAAGGG TGGTAATAmC GATGATTACA GAAAGACAAC 12480

AAAATATCTT GAGACTTATC ATCCAAAATT ACACGAACAC GGGCTTaCCT GTCGGTTCTa 12540

AGAAATTGAT GGaGGATGGc ATTGCCTCTA GTTCTGCCAC AATTCGTAAT GATATGAAAG 12600

CATTAGAGGA ATACGGCTTA TTAGCTAAGA CCCATTCTTC TTCAGGGCGA ATCCCCTCAA 12660

TGGCTGGTTA TCGTTACTAC GTGGATCATc TTTTACmACC mACACAAGTA GAAGAGAACG 12720

AACTTAGAgA ATCCGTCAAT CTTTTGGAAA AGAATtTCAT GAGATTAATG ATATTATTCG 12780

ACAATCAGCT GAAATTCTAT CAGAATTGAC AAGTTATACT GCTTTTTCAT TAGGACCTGA 12840

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TGCTATTATA GTGACAGATA AAGGCAATGT TGAAAACCAA GTATTTGCCA TTCCTGCCGC 12960

TGTTTCTAGC CAAGATCTTG AAAAAATGAC ACAAATCATC AATGATAAGT TGGTTGGACA 13020

ACCTTTGTTG ACCGTTTATC ATCGTTTGCG GACGGAGATT CCGATGATTT TACATCGCTA 13080

TTTCCAAACA CCAGAAGGAA TGATGAACTT ATTCGATGAG ATGTTAGGAC ATGCCTTTGA 13140

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AAATGGTTCT GCAACAACAG AAAATCCAAT TGTTTTTCGT ATCGGCTCAG AAATTGGCAA 13320

CAATCTCTTA GAAGATATGA GCATGATCAC TGCTACGTAT GAAGTATCAG GACATGGCAA 13380

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AGACACGTTT CGACATGAGC TAGCTTCACA ACTAGGTGAC TATTACCGTT TTTTAGGTAA 13500

TTAAGCAAAC CTTGTTAGGA TAAGAAGTAG ATGCATAAAG AGAAAGGAAG TTGCTGAAGT 13560

GAGTAAAAAA GAAGAGAAGC AAGAAGAATT ACAAGAAGAA ATGGAAGCTG TTGATGCTGC 13620

TGGCGTTTCT GAAGTAGAAG TTGAAGCAAC AGAGATTGAA AATCTTAAAG CAGAGCTTtC 13680

CGAAATGGAA GACAAGTTCT TGCGGGCAAG AGCCGAAaTT GCTAATATGA GCmATCGAAa 13740

TAAAAcGrAC GAGAATTATt AGTcGTTcCG CTCACAAGAT TwGGTAAAgA TTTACCACTA 13800

TTGTAATT 13808

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

AATAAAGCAT CGTTACGCTC TTTAATTTTA GCAGCAGAAT TCGCTGTGAT TATTGCTGTA 60

CTTTCACAAT TTACAATTCC ATTGGGGATT GTCCCCTTAA CTGGACAAAC ATTTGCCATC 120

GGCTTAACCG CTACCGTTTT GGGCAAGCGA ACGGGGACCT ACGCTATTTT AATTTACTTC 180

TTATTAGGAT TAATTGGTTT ACCCGTTTAC GCTGGGATGT CTAGTGGGTT CGGTGTACTC 240

TTTGGACCAA CTGGCGGCTA TTTAATCGGA TTTATCTTTA ACGGCTTATT AACTGGTTAT 300

ATTTTAGAAA AAACAACCTT TAACTATACT TGGGCCATTA TCGCAAATAT TGCCGGCGCC 360

TTAGTTACCT TAGTTTTCGG TATGATTTGG TTGAAATATT CCGCAAATCT GCCGTGGcCA 420

AACGCTTTCG CTGGCGGGTT TGCTCCGTTT ATTATTCCTG GTATCATCAA GGCTGTCGCA 480

GCTGCTTATG TTGGTATTTT AATTCGCCAA CGCTTTATGA AACGTTTTTT AGCACACCTT 540

TCTTAAGGGG AAAACTTTTT TCTTTTCCTT GTCTGTAGTA CACTAAAAGG ACAAAGGAGT 600

GAAGTCCATG TCCTCATTAT TAAAACGATT GGTTCAGTTG GTTTTGTTAG TCGTCGCTGT 660

CTTGCTGATT CGACACTATG TTTTCTCCCC TGCTGCGGTG AACGGCTCTT CAATGGAACC 720

AACACTTCAT AACAACGACC GTTTATGGGT GACCTCGATT AAAAAACCAC AGCGCTTTGA 780

TATTATCGCT TTCCCTAGTC CTCGCAACGG CCAACGAGTA GCCAAACGTT TAATTGGTTT 840

ACCTGGCGAA ACAGTCGAGT ATCGCGATGA TACCCTTTAT ATTAATGGTG TATCACTCAG 900

TGAAGATTAC TTAGCAAGTG CTAAACGAAA TGTCTCTAAA AATGAAAATT ATACCCAAGA 960

TTTTACGCTA GAGACCTTAG AAGCCACCCA ATCCCTGACC GTTCCAGAAG GCATGTATTT 1020

TGTCTTGGGG GATAATCGCC CGCGCTCAGA CGACAGTCGT TATTTTGGCT TTGTTAAACA 1080

AGCGAGTGTG GAAGGTGTTT TGACTTTTCG TTATTATCCA TTAGATAAAA TTGGCTTTCC 1140

ATAAAATAGT AAACCGCCCT CAAAAAGTCT AACTTTTTGG GGGCGGTTTA CTATTTTTTT 1200

AAGGTCCAGT GACTAAGTTC CACGTCACCG TTCCTTGATA TTTCTCATTT ATTTTCCCTT 1260

GATTGGCAGG GACTTCTAAT TTCACATTGG CAAAATCAAA ATCTAATTGA TAGACATCAT 1320

TACCTGTAAA TTGGTTATTA AGAATTACTG GTGTAGATGT ACCGTCACTC GTCAAAGTTA 1380

AGGCTTTCGT AACCCCAACT TTATTTGTTA ACTCTGTGAC TTGATTATAG TTTTCGATTG 1440

CTATAACATC CGCACTTCCT AATAATAAAC GCGTACTAGT TGGCAAACTA tCAGcTGACG 1500

CTGTTAACTG TGACAATTGT GCTGTTAACT GCCAATTAGG TTGGCTTGTC TTTATTCGTA 1560

GATATGGATT ACGTGTGCCG CTGCCATAGT AATCAGCTGC TTTTTTCAGT CCGTACTGCT 1620

TAGTGCTACT GTTAATCGTA ATTTTCCCAA AATCAAACAT TGGTGTACTA ATGAAACCTT 1680

CTTCTACTGG TGTTGGCGTA ATCGTTTGAT CTTCTCCTTG AATACGTACA AAGTTACTAG 1740

CTGTCACTGC AGAAAAATTT CCACTAGCTG TCATTTCTGC GGTTAAAAGT TGTCTTGGTT 1800

CTCCCGTAAT TTTCGCTGTG TTCACTGTCA CTaAAGTTCG CCGTTCACAG GAATCTCTAT 1860

ATCTAAGTTA ACTCCTGCTT GCCATTGTTC TGCCGTCACT AGAATAATTT TATTTGGTGT 1920

ATTACCAATG CGAACAGCTA ATTGTGTTGG TGGTGAAATA CCTGCCGCCC ATTTGGCAGT 1980

TGGGGCTAGT TTAACGTTGG TCAATGGAAC TTCACTGGTG TTTTTTAGTC TAACTGTCCA 2040

AACCATAGAA GCTTCATTTG GGATCACTTC TAGTAACCGA CTAACCGTCA TTTCTGCTGT 2100

TGGTTGGACT TCCTCATAGA CCGCTGTCAT GTCATCTTTA TCGTCGTAAG TCACGGCGTA 2160

ACTTGGTGTT TTAGTCGTTG TCAAGGTGCC TGGTTTGGTT TTACCTTTGT ACCAGCCTCT 2220

GAACTTATAG AATTTGTCTC CTGTTGTATA AGTGTCTGGT AAGGCTTTCG TACTAGCGTA 2280

AGTGAAATTA TCACTATCAA TCACTGTTTG TTTTCCTTGC GTGAAGCCTG TTGGCGGTGT 2340

AATTTTAGCG CCGCTTGGAT CCACAAAGTT TTCAGTGACT CGGCGATTTT CTAAATAATA 2400

GTAGATTGTT CCCTCTGGAG AAGCTAGGTT ATAGTTTTTT CCGACTGTCC CTGAATAAAT 2460

TCCCATAGCA TACAACGTGT TATTCGGGTC CCATGTCCAA AAAGCTCGTC TGGTTCTAAA 2520

AAAAGTTCCA GCGTCAGTTA ATTTGAAGGC TTCTGCTCCG TCAGCTTGAG AAACAACCGT 2580

ATATGGCGCT TCTATATTTT TCCGGATCTC TTTGCTCATA GGATACTTTG TTTTGTCTCC 2640

CGTATAAGTA GCTAGCGGTG TAATCGACAT TGTCTTATAT TGTTTAGGAA TTGTATGATT 2700

AACAGACCTT GCACCGTATG TCTTAAGCTT ATCTATCGGG AAATCATATG ACTTGCCAGG 2760

AATCGATAAT TTTTTTAATT TACTCATCAC TTCATCAGTT CCTTGGATTT TCCCTAATAC 2820

TGTTGATTCA GTTTCGTCAC TTTCACCTAA TTCGGCTTCT ACAGAAAAGC CTGCTGTATT 2880

CAATAGGTTA TCTGCCTCAT CAACATAACC AAAGTACACA TCTTTGGCTG GTAAATTATA 2940

CGTTTTCATC ACGACTTCTT CATAGACAAC CGTCAAATCA TCATCATCAT TATAAGTGAC 3000

TGGATAACTG GGAGCTTTAG TCGTCGTCAA GGTGTCTGGT TTGTTTTTAC CTTTGTACCA 3060

GCCTTTGAAC TGATAGGTTT TCGTGCCGAC TTTATAGGTA TCTGGCAAAT CTCCGCTTTG 3120

CTTAAAGGTG TACGAATCAC TAGTAATTAC TGTTTTTTTC CCTTGGGCGA AACcTGACGG 3180

TGCGGTGATT TTAGTACCAT TGGTATCTAC GAAGTTTTCC GTAACaCGAC GATTTTCTAG 3240

GTAAAGATAC ATACGTGCAT TTTCATCTAG TGTATAGaCA CTCGGTTCTA CTCCTTTACC 3300

AGTAATAGTC GCACTTAATA GTGTTGCAAG TCTAACATTT ATAGGCATTG ATGACCAGTA 3360

TATACCGCTC ATCGTAAAC 3379

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

TAGATTGTTT AAAAAAACTA TCGAATAATA GAGATTAAGC TTGCATTTTA GCGGTGTTTC 60

CTGnAAAGTA AGCTTGTGTG GAAACACACC ATCTATCACT TGGTTTAGCG AGTCACCAAC 120

GCTTCACTCA GTGATCAGAC GAATAATAGA GAAAGAGGTG GAACAAATGG CAATTTCACA 180

AGAAAGAAAA AACGAAATCA TTAAAGAATA CGCACGTCAT GAAGGAGATA CTGGTTCTCC 240

AGAAGTACAA ATTGCTGTCT TAACTGAAGA CATTAACCAA TTGAACGAAC ATGCGCGTAC 300

ACACAAAAAA GATCACCATT CTTACCGTGG TTTAATGAAA AAAATCGGTC ACCGTCGTAA 360

CTTGTTAGCT TACTTACGTA AAACTGACAT CCAACGTTAC CGCGAATTGA TCCAACGTTT 420

AGGATTACGT CGTTAATCAT TACGTATAAA GCGAGGTTCA ATCAGAATCT CGCTTTTTAT 480

CTTATTGTCA CTATTGAAGG TCCTCTTTGG AAAGTTTTTA GGAACTACTA ACCAAATGAA 540

AGAGCAGCAA CGACTTGTTA CTTTTTCATT TGTTTAGTAG CCGTCTGACT TTTCCAAAGA 600

GCAAGAGTAA AGGAGAAGAA TTATGACAGA AAAACAAGTC TTTAAAACAA CTTGGGGCGG 660

CCGCCCACTA GAAGTAGAAA TCGGCCAATT AGCCAAACAA GCCAATGGAG CTGTCTTAGT 720

ACGTTACGGC GATACGGTCG TTTTAAGTGC TGCTGTTGCC TCTAAAGAAG CAAAAGATGT 780

AGACTTTTTC CCATTAACTG TAAACTATGA AGAAAAAATG TATGCGGTAG GAAAAATTCC 840

TGGCGGCTTC ATTAAACGTG AAGGTCGTCC AAGTGAACGT GCGACATTAA CCGCTCGTTT 900

AATCGACCGT CCTATTCGTC CAATGTTCTC AGAAGGCTTC CGTAACGAAG TCCAAATCAC 960

GAACATCGTT ATGAGTGTGG AGCAAGACTG TACACCAGAA ATGGCTGCAA TGTTTGGGtC 1020

TTCCTTAGCG TTACAATTTC AGATATTCCG TTTGATGGAC CAATTGCTGG TGTTGACGTT 1080

GGTCGTATTA ATGGCGAATA TGTTTTAAAT CCAACGGTAG AACAAGCGGA ACAAACAGAT 1140

ATTGAATTAA CTGTTGCTGG AACAAAAGAA GCCATCAATA TGGTTGAAAG TGGTGCCAAA 1200

GAAGTATCAG AAGAAGATAT GTTAGGTGCC TTACTTTTCG GTTTTGATGC CATTAAAGAA 1260

CTAGTGGCGT tCCAAGAAGA AATCGTTGCC GCTGTAGTAA ACCGGGGATC TTAA 1314

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

GCCGTTTTGC ATACAGAAGG ACCACTGTTA GTCATGGCTG GTGCTGGTAG TGGAAAAACG 60

CGGGTTTTAA CACACCGAAT TGCCTATCTA ATTGAGGAAA AAGAAGTAAA TCCATGGAAT 120

ATTTTGGCGA TTACGTTTAC CAATAAAGCT GCTAAAGAAA TGAAAGAGCG TGTAAATAAA 180

TTACTGGAAA CGGGTGGCGA AGATGTATGG GTCTCCACTT TTCACTCCAT GTGTGTAAGA 240

ATTTTACGTC GTGATGTGGA TCAGATTGGT TACAACCGTA ATTTTACAAT TATTGACCCA 300

TCGGAACAAA AAACATTAAT GAAACGCATC TTAAACGACT TAAATATTGA TTCAAAAAAA 360

TATGATCCTC GCTCAATTTT AGGTACGATT AGCAATGCCA AAAATGAATT ACAAACGCCT 420

GAAAAAGTTG CTGAAATGCA AGGTTCCTTA TATGAAGAAA TTGTCGCAAA ATGCTATGAA 480

GCCTATCAAA AAGAATTGCG CAAAAACCAA TGTATGGATT TTGATGATTT GATTATGAAT 540

ACGATTCGTT TATTTAATGA ACAACCAGAT ACGTTGGCTT TCTACCAAAA TAAATTTCAC 600

TATATTCATG TGGATGAATA CCAAGATACC AATCATGCAC AATATACCTT AGTCAATTTA 660

TTGGCTGCAC GTTTCAAAAA TCTGTGTGTC GTAGGTGATG CCGACCAAAG TATCTATGGT 720

TGGCGCGGGG CGGATATGCA AAATATCTTG GATTTTGAAA AAGATTATCC AGATGCCAGT 780

GTAATTTTGC TAGAACAAAA TTATCGATCC ACCAAAAACA TTTTGGCGGC TGCGAATGAT 840

GTCATCAAAA ATAACCGTAA CCGCCGCGAG AAAGAACTGT GGACAGAAAA TATAGACGGT 900

GAAAAAATTG TCTATTATCG CGGGGACACA GAACGGGATG AAACACAATT TATTGTGAGC 960

CAAATCCAAA AAGAAATGCG GGAAAATGAC CGAATTTATG GTGATTTTGC GGTATTATAT 1020

CGGACCAATG CTCAATCCCG TGTAGTGGaA GAAATGCTCt TGAAATCTAA TATTCCGTAT 1080

ACCATGGTGG GCGGACmTAA ATTCTACGAC CGTAAAgAAA TTAAAGATAT TTTGGCTwAT 1140

TaAGTTTGAT TGCCAATCCA GATGATcGAT TAGTTTTGAA CGAATTGTCA ATGAACCAAA 1200

ACGAGGGATC nGTAAAAGTC AATTGGAAAA TnAC 1234

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

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AAAGGACCGC CTAAACCAAC AnCGACCTGT CGGAGCGnAC GATCATTTTA GAyCCAtGCC      60
CGTTsCCAAA TCACCCGTCG aGAATCAATC TTTAATTCAT TTCCTTGCTG TAAATGATTA     120
TCTAGTAACG CAGCTAAGGC ATTATTGGCT GTCGTAATCG CATGCATATC ACCAGTAAAA     180
TGCAAATTGA TTTCTTCCAT TGGTAATACT TGTGCGTAAC CGCCACCTGT TGCGCCACCT     240
TTAATCCCCA TCACAGGACC TAATGATGGT TCTCTTAGGG CAATAACTGT TTTTTTATTG     300
ATTTGATTTA ATGCATCTCC TAAACCAATG GTCACGGTTG ACTTTCCTkC TCCTGCTGGT     360
GTTGGATTAA TCGATGTAAC GAGGATTAAT TTACCTTCTG GTTGCGCTTC TAAGGATTGA     420
AGCGTTGGAA AATCTATTTT CGCTTTGTAT TTTCCATAAA GTTCGAGCGA ATCTTCTGAA     480
AGACCGATTG TTTCGGCAAT CTCTTGAATA GGTTTTAATG TTGCTGCTTG TGCAATGTTA     540
ATATCTGTCT TCATAACGGA CCCCTTTTCA ATTCTTTATC GTCTTTGTGA CACATTGTTT     600
CTTTTAAATT ATAGCTTGTA TTGAATAGAA TGGCTAGAAT AACCTTTTTT AAACAACCCA     660
ACCATTGACG TTTGGTAGCC TTTTCTCGTA TAATGAAAGT GTCTTTACAA ATCTAAAAGG     720
AGCGTGAATT GGATGCAAAA AGGAATTGTC AAATGGTTCG ATAACAGAAA AGGTTATGGT     780
TTTATCGTTT ACAACGAAGA AGATGAGATT TTTGTCCACT TCACTGCTAT AGAAGGTGAT     840
GGATTCAAAT CACTTGATGA GAATCAATCT GTAGAGTTCG AGATAATGGA AGGCAATCGT     900
GGGCTACAAG CAGCACATGT CAAAAAAATA GATAACTAAA AAAGCTGAAC CAACAGCGCT     960
TAGCTCCAAA AAGTAAGTAA ACGTAGCGTT TGTTTCAGCT GATTATTTTA AGATTTTGAG    1020
AGTGGGTCAC CAGTCGTTTC GACTTATGAC TCACTCTTGT TTTTTTCTTC TTTTTTATGA    1080
AGGCCCAAAG AATGATCTTC TGCTACCTTC AATTCAGGCT TTTTTACCTT AAGTGCCTCA    1140
AGAAATAACG GAATCGTTTT CTTTTTCATT AAAAAGACTT TTGAGCCTTC CTTAAATTCT    1200
GAGGAAAAAA TTTCGATGCT TTTTTCATTG TAGGTTACTT TTTCTATCTG AGAAAGCGGA    1260
AGTGCTTTTT TGCGAAACCA CAAAACATCT CTGACAATTA AAGATGTTTC TGTCATATTA    1320
AAAGACCGCG CAATTCCTAG ATAAGCAAAC ACAAAAAATG GAACCATCAC CAGATTACTA    1380
ATCAAGTAAG GACCATTATT TTCCAATGCT AAAATTAAAC TAATAAATAA TATACAAAAT    1440
GTGCAAGACC AGTAAATAAT TGTTGgATGC TAATTCTGGg CTGgCCAATA GgAATTTCTG    1500
TTTTTTCATA AAGgTGCCCT CACTACTTCT gGATCAACGC CGCTAAATTT AAATATGTTA    1560
TAATAGTAAC ATACTTTTTT TAAGAACmAA AAGAAATTAG GAGTAATTTT AwGtTAAGaA    1620
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TCACCGACCA ATCGCGGCAA CAATTGCATG TGCCTTTAnG CATTGTTAGT AATCACGAAG    1740
CCGAATTTAA AgTGCTGATT GAAGCTTTAA AAAAAGCGAT tGCCAATGaA GACmATCAAC    1800
aAACCGTTCT TCTCCACTCA GATAGTAAAA TTGTTGTCCm AACmATTGAA AAAAACTATG    1860
CTAAAAATGA AAAGTACCAG CCTTATTTAG CAGAATATCA ACAACTAGAn AAGAATTTTC    1920
CTTTGCTCTT AATCGAATGG CTACCTGAAA GTCAAAACAA AGCGGCCGAT ATGCTTGCAC    1980
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GGCAAGCATT ACAAAAATTT TATCCCAATA AAAAGTAGCA CTGTTTACTT AATGCTTTTC 2040

CTTTATTAAT TTGATAATTA AACACGTGGA GCAAAAATTC CaAGTGATTT TTGCTCCaCg 2100

TTTAAAAACA GATAAAcGGT TCTGTCTCGA CTTCTTCTTA TAGCCaCTTA TTCTTTTGTC 2160

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TGCATGCCAC GTTTGCCTGC AGAAACAATA ATTGCAGAAT ATTGTTGAGC TTCTTCAGCC 2280

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GCTAATTTTT TCAAATCTAA TTCTTGATTA CCAGGAATGA CAGCCACGAC TGGACCTGTT 2460

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ATCCGAACAG TTGACCTGTT ACGCGACTAA TCATCCCTAA CTGTCCCATT GACATAGTAA 2820

CGATTGGAAC GGATGCATAA TGGGTGTACA TTTCATTGGT TGCTGAAAGT AACGTAAGTA 2880

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AATGACACCA AAGAAATAAA TAGCAGCAAA AGTTAGAATC ACTTGCATTG TAGCAGTTTT 5160

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TGATAAGCCA AATGCAAAGA GAATAGCTGT GTAAAACATG CGTCGAAACG GTTTGGCAAA 5280

ACGAAACAAA CGCTGAACAA TCGTTAATTG TTCTTTCATC GGTAATTCTC TGGACCATTC 5340

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ATCAGCGkAA TAAaCGGaTC AAATrGgCAT CTAAAAAGTc GTcGTGAATT TTGAC 6415

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CCTAGGACTG GCCTAAGATG GGGCCCCTCT TTCTAAACCG AAAGGGTCTT ATnGGAAAGG 60

GTAACTCTAT GGTAAATGGA GGTnCnTCTA AATTTCAACC GATTTGGCAA AAAATCCAAT 120

AGCTCAATGT TTGACCAGAA TAAATCAAGT TAGGATTTGC TAATCCGTTT AATGCAGCTA 180

AGGTTTGATA AGTCGTACCA AGCTTAGCTG CAATACTTGA TAAATTATCA CCGTATTGAA 240

CTGTGTAAAT GTTGCTTACT ACTGATCCAT TTACTTTCAA AATTTGGCCA GGGTAAATAA 300

GATTTGGATT TGTCAATCCA TTTAATGCAG CCAATCTTTG ATAGTTTGTT CCGTATTGAT 360

AAGCAATGCT TGATAATGTT TCGCCGTATT GTACCACATG AGTCGCTTCT GGTTGTTTAT 420

CAGGAACAGT TGCCGCATCT GGCAATAATT CAATATTGCC TTTGCTGATC CATGACAAGA 480

TACCTTCaAG CAATACTCTG CTcTCAGTTA CTTCTTGTAC TTTATAGCTG TTTCCTTTTA 540

CCCATTGCGG AATAGtTCGC CAGTTGCCCA AGCATCAACA CTAAATTTCA CTTTAACAGT 600

GTCGCCCACT TTAACATCGG AACTTGGCGT ATTTTCTACT TCTTTACCTT CCTCAATAGC 660

TGGTGTGTTT GTTGCTGGyT GGTTATTCTT TGTATAACCA TTATCAGTAA TACCTGTTAA 720

ATCAACGTTA CCATCTAGCC CTCCTGCAAC GTAGGTTGAC GTGAACTGAA AAATACCGAT 780

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ATACCCTTTG TATCCGTAAA GCATCGGTGT ATATCCAGCC TCTTTGATAT AGTCTAACGC 960

CCATAGCGTT ACATCCGTCG ATTGAACGCC GTCTTCCGCA TCTAAGGCGA CAATTGATCC 1020

CTTTGGTGTT TGAACTTTAG GTAAAAAGTA ATCTAATACT TGCTTTGCAT TTTCGTAGGT 1080

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cATCCTGCAC CTACTTctAC TTACAAGAAA aACCGCTTAG CTTTCGCTAA ACGGTTCTCC 1860

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ATTTTTTAGA ATGGTGACGA CATTTTCAGC GATCATTTTG ACATTTTCAA TGTTCGCTTT 9360

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ACTAGAAATA AATTCTTGTA TATTTTTCCA AATATTTTTA ACAGCATCCC TAAACCCTcG 9840

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TTAATGCTGG TCCTAAACCA CTATTAATCA TTGAATTCCA AGTTTCAGCA TCTACTTTAC 10500

CATTTGAGAA CGATTGGGAC AGCTGGATAA TAGCATTTTC TACCATTTCA GCAGAACCAC 10560

CAAAACCGAG GATACCGTTA TTTAAAGCTG CGAAAATCTG TTCTGATTTA CCTAAATCAT 10620

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AAATTCAAGA TTGCTCCAGA ATTAGAAGCT TTGTATTCAA TTGAATACTC ACCAACTAAT 14280

CCAATCCGTC TTGAATCTGT TGTTTTTGCT AATTCTTCCG CACGCCATTC ACGTAATGGA 14340

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(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACATTGnTGA AAGAATTGTT GACGGAAGAG GATGATCAAT TTAACTTTTT CTCATTTGAT 60

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TTTTGGtACA wATTTtCCtA GTACATCTTC ATGACCTAAG CCATTTAATA AACATAGTAC 1620

ATACGTTTTT TCAGTAATCA TTGGTTGAAT CGCTTTAAAC ATT 1663

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

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CACGGAATGC TTTTTCGTAA GCCCAAGTTA ATTTTTCAAA TTTATAGGCT TGTGGGGTTG 240

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CAAAAATTTG TTCATTATAT GGCAACGAAG TCACTGCATT TCCGTATTCT TGACACTTAA 360

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TCCACTAAAA cGTCAAACcG TATCCAnAGA AGCGATTTAn TnTTGCCATT GGTATACGAG 1560

TAGACGGCAC TAAAGGAGTA CTGAGTT 1587

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

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TGCTGCGTAA ACGTACCAAT TTGCCTTCTA AGTCATGGAC TTGCTTACTT GCGCCAGCTA  13440
ACTTTTCTTC AATGGCTGTT AATTCTTGCG TTTTCGTTTC CCAAATAGCT TTTGCTTCTT  13500
GAATTTCGGT CACAGTTAAA TTGACATCAA TTTCGGTAAG TTCTTCTTTC AAAGCTAAAT  13560
ACTTTTTAGC CGCATCTGCT TGGGCGGCTA GAGGAACTAA TTGGTCTTCC AACTCGTAAA  13620
TGATATCTTG GACACGGCTT AAGTTGTCCT CGGTTTCAAA AAGCTTTTGT TCAGCCTTTT  13680
TCTTTCGTTG TTTGTATTTT AAAACGCCCG CTGCTTCTTC AAAAATCCCT CGACGGTCTT  13740
CAGGTTTACT ATTAAAAATC GCTTCAACTT TCCCTTGTGA AATAATTGAA AAAGATTCTT  13800
TGCCTAACCC TGAATCCATA AATAAATCTT GAATGTCTTT TAAACGGCAC GCTTGTTTAT  13860
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TAATAAAAAA GTCACTTTCG CCCGTTCGTT TTAAACGACG GGTGACACTA ATCTCACTAT 13920

AATCCAATGC TAAATAATGG TCGCTGTTGT CTAACGTCAC GGTAACTTCC GCAATATTTA 13980

GCGGCTTACG ACCTTCCGAA CCGGCAAAGA TAATGTCGTT CATTTTGCCA CCGCGAAGGT 14040

TTTTCGCAGA TTGTTCACCT AATACCCAGC GAACGGCTTC CGTGATATTA CTTTTCCCAC 14100

TTCCATTCGG ACCAACCACT GCTGTCACAT CATCTTCAAA TTCAATAATG GTTTTATCTG 14160

CAAATGATTT AAATCCTGTA ATTTCAATTC GTTTTAAATA CACGAATATT GCTCCTTCCA 14220

GCCTTACTGA GGAATACTTT TCAGTGCCCG CTCAGCGGCA TCCTGTTCAG CTAACTTCTT 14280

CGATTTTCCT TGGCCTAACC CAATGAGTTC ACCATTCATG TAAACTTCAG TGAAAAAGGT 14340

GCGGTCATGA GCAGGGCCTT CTTCTTTAAT TAAGCGATAT TCAATTGAAA CATCGCCTTT 14400

GCGTTGTAAA ACTTCTTGTA ATTGTGTTTT GTGATCCATC TCATGTGAAA AAGCACCGGC 14460

ATCAATTTTC GGAAAAATAA CGTCTTCAAT AAATTTcTTG cTGCGCCAAC TTTTTGGTCT 14520

AAGTAGAGGG CACCTAAAAA GGCTTCAAAT AAGTCACATA ATAATGATGC ACGTGTTCGT 14580

CCGCCCGATG CTTCTTCTCC TTTACCTAAT AAAATGTAGT TGTCGAAGTG ACATTCTTTC 14640

GCAAATTTGG CTAAACTATC TTCCCGAACG ATGgTGCGCG CATCTTCGTT AATTTTCCTT 14700

CTGGAAGTTC TGGGAATTTT AAATACAAAT ATTGTGAAAC AATTAATTCT AAAACTGCAT 14760

CTCCTAAAAA TTCAAGACGT TCATTATCGG ATAATTTTAA ATAGCGATGC TCATTCACAT 14820

AGGATGAATG AGTAAAAGCT TGCTCTAATA GATTGACATC ATGGAAAACA ATGCCGTAAC 14880

GTTCTTTTAA CTCTGTTGTT AACTGATTGT CCATTCTCCA CATTCCTTTA CATTTATTTA 14940

CACCTTGTTT CATTATACTT TTTTTTTCAC TTTTTTTAAA TGGTTCTATT CAGAAAAAGC 15000

CTGTTATTCA CTGTGTTCTC ATTATTTTTT AGAAAAAATA AATAAATCAC CTCTCCAGCT 15060

ATCAAATCAG CCACTGCTAC CCCATAAAAA AAGAGAAAAC GTAGCAACGT TTTCTCGGAA 15120

TTTTTTGAAT AAACGTACCA GCAAGAGACA ATAAAAAAAG CATTCAGTTA TTCACTTTCA 15180

CTAAATATTA ACATCTCATT TAAAGATTGG GATAATTCTT CTTTTTGTCG TCTTTTTAAT 15240

TTTGTTTTAG TCGCATCATG ATTCTTTACT GTGCCTATAT GAACCTGCAC CTCTTTCTTA 15300

TTATTTATAG CAACAATAAA AGGTACAGAA AGCGACTCAT CCCCAGTATA TTTTTGATAA 15360

AAT 15363

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CACTATTTTA TTTATATTAA TGCAACGTtT CTATGTAGAA GGCGTGAcTT CTGGCTCTGT 60

CAAAGGCTAG AAAAActCGT TTGGTTTATA GCCAAACGAT GTTTTTTATT TTTTGGCGTT 120

GTTTTCCTTA CACGTTTTTC TTCGTAGCGC TTGATAATTG GACAAAATTT TCATGACCGC 180

CAAAAAGTGT TGATTGACCT CTTGATAATC CTCTAAGGAA AGAACACTAA GCGTTTCAGA 240

TAGTTGCTGT TTTACTTGAT TTTCTTTTTG CTTAAAGAGC TTCTCGCCTT CTTTTGTCGT 300

ATAAACATTA ACCACGCGGC GATTTTCTTG ATTATGGCGA CGTTGAACAA TCGCTCGTTC 360

TTCTAACCCC GCAATAGAGC GACTCACTTG aACTTTCGAC GTTCCTACTT GGTTGGCTAA 420

CTCCGTCATA CTAATTCCTT CATTTGTTGC CACAATTAAT AAAATTAACA TGTCTAACTT 480

GGTTAATTTT AGATCCTCCA AGTCTAGGTC TTTAAAAAGC AATTGGCTCA TATATGAAAA 540

AATTTCAGTA AAGACACTAA TATCTAAATT TGATGAATGC TTCTCTTTAT CCATATGTTC 600

TCCCTCGTTT CCCACCTAGT GTATACTAAA TTCACTTGAT TATCAAATGG TAATGATTGA 660

TTTTTGTTAA CTATTATGTT ACGTTATACA CTAACTTAAG GTTGTATTGT TGATAAATTG 720

GAAGAAGGAT GCGAAAAATA TGCTAGAACT CAAAGAGATr AAAAAATATT ATACTGTCGG 780

CGGAACGACC ACTAAAGCTT TAGATGGCGT CTCTGTCGCT TTTCGAAAAC AAGAATTTGT 840

AGCCATTCTG GGTCCCAGCG GCTCTGGTAA AACGACGATG TTGAATGTGA TTGGCGGATT 900

GGACAATTAC GATTCTGGTG ACTTAATCAT TAACGGCAAA TCAACAAAAA ATTTTAAAGA 960

AGCCGACTGG GATGCTTATC GGAATAACTC AATTGGTTTT ATTTTTCAAA GTTACAACTT 1020

AATTAGTCAT CAAGGGATTT TGGATAATGT CGAGCTTGGT ATGACACTGA GTGGTATTTC 1080

AAAAGCAGAA AGACGCCAAA AAGCCGAAGA TGCACTCATC CGTGTCGGTT TGAAGGACCA 1140

TATCCATAAA AAACCTTCCC AATTATCTGG CGGTCAAATG CAACGGGTTG CCaTTGCTCG 1200

CGCTTTAcTn AATGaTCCCG ATATTTTACT TTGTGaTGAA CCaACTGGTG CATTGGaTTC 1260

AGAAACCAGT CTGCaAATTA TGGCACTTAT CCAAGAACTT TCGAAAGAAA AATTAGTTAT 1320

TATGGTGACC CACAATCCTG AATTAGCTCA CGAATACGCT GATCGAATTA TTGAATTTTC 1380

AGATGGCCAA ATTCGTcATG ACTCGCGTCC TCATATTGAA CATGAAAAAA AAGAACCTTT 1440

CGAATTGAAA CGCACCAAAA TGAAATTCAC GACTGCGCTG CGTTTATCTT TTAATAATAT 1500

CCGCACTAAA AAAGGGCGAA CTTTTTTAAC CGCCTTTGCT TCAAGTATCG GAATTATCAG 1560

TATTGCGATT GTCCTTTCTC TTTCAACAGG ATTCCAGAAA CAAATTGATA AAACTCAGTC 1620

GGAAACGTTA GCGCAATTTC CGATTACCAT TTCTAAAATA GCGACCGATC AAGATCCAGA 1680

AAGTTTCAAT AATCAGGACA AAAAAGGCAC CTTCCCGAAA GAAAAAGAAG TGACTGCTAA 1740

AATTAGCGAT GCGGACCGTG CGCAACACAC GAATTTAATT GATCAAAAGT TTATTGACTA 1800

TGTCAATCAC ATTGATCCTG AATTAAGTAA TAATATCGGC TATACTCGTC TAGTCAATAT 1860

GrACTTATTA AGAGAAATCA ACGGGAAAGC ACAAGCTGTC AAATTTTCAA aCkmyrCACC 1920

CGACGGcCAA TCAAACGCGA TGGCTTCTAT GATGGCTGCC CAAACTGGTG TCGGCGTTTC 1980

TGCTTTTCCT AAACAACTAG AAAATGGAAA AAACAATTTC TTAAAAGACA ATTACTCGTT 2040

GCTTGAAGGA AATTATCCAG AAAAAGAAAC CGATGTCGTT TTAATCGTCG ATAGTAACAA 2100

TACCACCAAT ATTAATGCTT TAAAAAATCT TGGCTTTGAC GTGAAAGATA ATCAAAAGAT 2160

TGCCTTTTCA GACATTGTTG GCACAAAAAT GAAATTAGCC AATAATAATG CATTTTACAC 2220

CAAATTACCG ACAGGCAACT TCATTCCTAA CCAAGATTTG CAAGCTGTTT ACGATAACCC 2280

AGAAAATACT GAATTAACAA TTTCAGGGAT TTTGCGAATT AAAGATTCTT CAACAATGAA 2340

TCTATTAGCA CCTGGAATTG CTTATAGCGA TGCACTTTCA ACTAATATGA TTGCCAAAAA 2400

CAAAACCTCT GACATTGTTA AAGCGCAAGA AGCCAGCAAC ACTAACGTTA TGACTAACGA 2460

AACATTAGAT GCTTCCGCGA AAGAAAACCT GTTGTCTTAT TTAGGAGCGA ACGAAATCCC 2520

TTCAAGTATT ATGATTTATC CAAACGATTT CAAATCAAAA GATAAAATTC TTGATTATTT 2580

AGATGCTTAT AACAAAGGAA AAGATAAAAA AGACCAAATC ATCTATTCTG ATTTAGCTGG 2640

AACAATGACC CGCTTAACAG GTGGTTTAAT GGATGCCATC ACCTATGTGC TGATTGcATT 2700

TGCTGGGATT TCCCtTGTTA CAAGTATGAT TATGATTGGG ATTATCACCT ATACTTCTGT 2760

CATTGAGCGG ACCAAAGAAA TCGGTATCCT GAAAGCGTTA GGAGCTCGTA AAAAAGATAT 2820

TACCCGGGTG TTCGATGCCG AAACTGCTAT TTTAGGCGTT GCCTCTGGTA TTCTTGGTGT 2880

TGTGATTGCC TTTCTCGCAA CATTTCCGAT CAATGCAGTG CTCTATAACC TGACTGATTT 2940

AGAAAATGTT GCCACCTTAA ATCCAATTCA CGGGATTATT TTGATTGTAA TTAGCACAAT 3000

CTTAACCATG ATTGGTGGCC ATATCCCTGC CCGAATGGCA GCGAAAAAAG ATGCGGCAGT 3060

TGCTTTACGT GCAGAATAAA TAACAAAAAA TAATCCTTTA ATTTCTCTTA AAGGATTATT 3120

TTTTGTTTGT AATTTTTATA AAACCACCGT ATACTAAATG ATTGTGAATG CTTAATAAAA 3180

AGAAACGAGG TAATTTCATG TTAAAAAAAC CATT 3214

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CGCGGCTTGA TTTAGAGGAA GTCCAACAAG AAATTAACgA TGCGAACGAA tTGCAAATGA 60

AGCGAAACAA TCGTGGCAAG CAAAAAAAGA ACAACACAAA GAAGCAACAT CGAAAGAAGA 120

ATAAGGAGCA AAGACTGTTT TCTGAATAAA GGAAAACAGT CTTTTAAAAT ACTAAGAAAT 180

CACGGTTTTT TATGGTAGTT TGCTAATTTT TTGTTATTTT ATCGTAAAAT ACGGTAAACT 240

AAGAAGGAAA CTTTGAGAAA ATAGATAAAT TATTATTTGC TAAAGGAGCA AACTTCTTCT 300

AAAATAAAAA GGaAGTTTAA AAGAAAGTAT GGTAGCAGAT GGAAATACAA TTTTTAGGAA 360

CAGGCGCTGG TGTACCagCA AAACATCGCA ATGTCACAGG aATTGCGTTG aAATTATTAG 420

aTGAACGAAA TGCAGTTTGG CTCTTCGATT GTGGGGAAGG GACTCAATTG CAAATTTTAA 480

AAAGTAGTAT TCGCCCAAGA AAAATTGAAA AGATTTTTAT TACACATTTA CATGGGGATC 540
ATATTTTTGG TTTACCTGGT TTGTTAAGTA GTCGTTCTTT TCAGGGCGGG ACAGAACCTT 600
TAGAAATCTA TGGACCAGTT GGGATTGCTG ACTTTGTCAA GACTTCTTTA CGGGTCTCGC 660
AATCGCGGTT GTCCTATCCA CTGAAATTTA TTGAATaACG AAAGAAAATG ACgTTATTTT 720
TAAAGATAwA CAATTCACTG TTCGCTGTAA TATCTTGGAC CATGGCATCA CGAGCTTTGG 780
CTATCGAATT GAGGAAGCAG CGCATGAAGG AgAwTTmCAA GTAGAGAAAC TTCAAGCTTT 840
AGGGATTCCT TCTGGGCCGT TGTATGGCAA ACTCAAACGT GGTGAAACGA TTGTTTTTGA 900
TGGACAGGAA ATTAATGGAC AAGCGTTTGT GGGAGAGCGT AAACCTGGAC GAATCGTGAC 960
GATTTTAGGA GACACTCGCA AAACCAAAAA TAGTGTAACT TTAGCACGAC GAGCGGATGT 1020
TTTAGTCCAT GAAAGTACGT TTAATAAACA CGAAGCAAAA ATGGCAAAAG CCTACTTCCA 1080
CTCAACCAGT CAACAAGCAG CTGAAGTTGC AAAAGAAGCG CAAGTAAAAC AACTTATTTT 1140
AACGCATATT AGTGCCCGTT ATTTAACCAA AGAGGCCTAT CAGCTTCAAG AAGAAGCCCA 1200
AGAAATTTTC CCCAATACAA AAATCGTAAA AGATATGGAT ATCATTGAGA TTCCATTTGC 1260
CAATGAAGGA GGAGCTTAGA TGGATTTAAC AAATAAAGTC GTTGTCGTAA CTGGAGGTTC 1320
AGCTGGTTTA GGTGAACAAA TTTGTTATGA AGCAGCTAAA CAAGGGGCGG TCGTCGTTGT 1380
CTGCGCCCGC AGAATTAATT TGATTGGTAA AGTTCGCGAG CAGTGTGCTG TTTTAAGCGG 1440
ACGAGAAGCA TTTTCTTATC AATTAGATAT TGCCGATCCA GAAAGTGTTG AACGTGTGGT 1500
TGAAGCTATT TCAGCAGAAG TTGGTCCTAT AGATGTTTTA GTCAACAATG CTGGTTTTGG 1560
CTTGTTTGAA AATTTTGTTG AAATTGACTT GGCTGTTGCA CGCCAAATGT TTGATGTCAA 1620
CGTTCTAGGA ATGATGACGT TTACTCAAAA AGTAGCTATT AAAATGATTG AAGCTGGGCA 1680
AGGACATATT ATCAACGTTG CTTCAATGGC TGGGAAGATG GCTACAGCTA AATCAACCGT 1740
TTATTCTGCA ACGAAATTTG CTGTGTTAGG TTTTTCAAAT GCTTTACGTT TAGAATTGAA 1800
ACCGTTGGGT GTAGCAGTAA CGACTGTCAA TCCAGGACCA ATCCAAACAG AATTCTTTGA 1860
TAAAGCGGAC CCGACAGGCA CATATCTAGC TGCGGTGGAT AAAATTGTTT TGGACCCTAC 1920
GAAATTAGCG AAAGAAGTGG TTGGGAGTAT GGGGACTTCT CGACGTGAGA TTAATCGTCC 1980
ATTTGTCATG GAAGCGGCAG CCCGCTTTTA TACATTGTTT CCACATTTAG GAGATTTCAT 2040
AGCGGGAAAT ATTTTAAATA AAAAATAAAG GAGTCGATCA AGTCATGAAA AATCAATGGC 2100
GTGTTATTTT GGGCCTTGTG TTGGTCTTAA TTGTTGTTAT TTTTGCTGTT TTAAATAATC 2160
AAGCTGTTCC AGTAAACTTT GGTTTTACTA AAATTAGTGG ACCGTTAATC TTAATTATTT 2220
TAGGTTCTGC AATTATTGGC GCACTAGTTG GATTACTAAC CTCCACAACC ACCATTTGGA 2280
ACCAACGTAA GGAATTAAAA GCTGTACAAA AAGAGTTGGA TATTTATAAA AATGATATGG 2340
ATAAATTAGT CAAAGAAGAA ACGGAAAAAG TTCAACGTTC TTTTGATAAT CAATTGGCTG 2400
ATTTGCAAGC CAAACAAGCG GCAGCACCAC AAGTCTCAGA ACCAGTGGTC AACGAACAAA 2460

CGTCAAACAC AGAAGTAGAC GTAACGCCTG TGTCAGGTAG TCGTATTGAT CGTTATGTGA 2520

AACCTCGTGT GAATGAAGAG GAACAAAAAT AAGGAAGAGA CTTTATCACT AAGTTTCTTT 2580

TAAAATAAAA CTGTGATATC TGCTATTTAT CTAACAGATA TCACAGTTTT TTTCTCAGAT 2640

TTAAAAAAAT GCTTTCTTTA GTTTTTGGAA AAATTTTGCT ATAATTACTT GGTTAGGAGT 2700

GACGTCGTGA AAAAATCAAA CTATCAATGG CAGTTACAGA CAAAGACAGA ATTACCTGTA 2760

GAATTTATAG AACAATTAAA AAAAGAAGAA ATTAATCCAT TAATTGGCCA ACTTTTATGG 2820

CACCGCAATA TCCGGACAGA AGAAGCATTA CGTAAGTTTC TACATCCGAC TATCGAAGAT 2880

ATTTATGATC CGTTCTTAAT GCATGATATG GAGAAAGCGG TAGCCCGCAT CCAGCAAGCC 2940

GTCGAAGCGG GTGAACAAAT CCTTGTCTAT GGGGATTATG ATGCAGATGG CATCACTAGT 3000

ACCACGGTTA TGAAAGAAGC AATCGAATTA GTCGGTGGCA TGGTTCAGTA CTTTCTACCG 3060

AATCGTTTTG TTCATGGCTA tGGGCCTAAT AAAGaCGTAT TTGCTGAACA AATTGAACAA 3120

GGAGtCCAAT TAATTGTAAC CGTTGATAAT GGTGTAGCsG GACATGAAGC AATTAACTAC 3180

GCTATGGCAC AAGGAGTAGA TGTAATCGTT ACTGACCATC ATGAATTGCC TGAACAATTA 3240

CCAGAAGCCT ATGCGATTGT CCACCCTAGA CATCCACAAG GTGACTATCC TTTTGGAGAT 3300

TTAGCTGGTG TTGGCGTGGC TTTCAAAGTC GCTACTGCGT TACTTGGTGA ATTGCCAATT 3360

GAGTTATTAG ATTTGGTAGC AATTGGGACG ATTGCTGACT TGGTTTCATT AACCGATGAA 3420

AATAGAACGT TTGTCAAAAT GGGCCTTCAA ATGATTCAAA CTGGTGATCG AATTGGTTTA 3480

GACGTTTTAT TACAAGAAGC GGGTGTGAAA AAGGAAGCTG TTTCAGAAGA ATCAATTGGC 3540

TTTACCATTG GACCTCGTTT AAACGCATTA GGTCGATTAG GGGAAGCCGC ACCAGGTGTT 3600

GAATTGATGA CTACATTTGA TGAAGAACAA GCGCTGGAAA TCGCTAAATA TATTGATCAA 3660

CAAAACAATG AACGAAAAGA CATTGTAACG ACGATTGCCA AAGAAGCCCT GGATTTAATC 3720

GACCCGAATG CGCCGGTCCA TATTTTAGCG AAACAAGGCT GGCATGAAGG CGTCTTAGGG 3780

ATTGTCGCGG GCCGCATTAT GCAAGAAACG GGGAAACCAA CCATTATTTT AGCAATAGAT 3840

GAATCTGGTA CGACTGCTAA AGGCTCTGGA CGCAGCATTA GCGCATTGAA TCTCTATGAG 3900

GCGTTGAACG AAgTGCGTGA GCAATTCACT CATTTTGGTG GGCATCATAT GGCAGCGGGA 3960

ATGACTTTAC CTGTTGAAAA TATTCCTTTT GTTCaAGAAC ATTTGGCACA CTTTATTGAA 4020

AAAAATCAAA TTGATATGGC TAATGGACAA GAGTTGCTCA TTAGTGAGAG CTTAGCGGTT 4080

TCGCAGGCCA CGACTACTTT TATTGATCAA TTGCGTATTT TGGCGCCTTT TGGGACCGAT 4140

AATACTGTTC CAACTTTTGT ATTTAAGGAA ATCACGCCTA CGCAAATTCG GCAAATTGGT 4200

GCAGATAATG CACATCTGAA ATTTCAAATG AATCAAGAAG GGGCACAATT GGATGCAATT 4260

GCTTTTCAAA TGGGGCCTCA AGCGGATGAA CTAGCACAAG GAACCGCCGA TGTGGCAGGC 4320

CAACTTTCCA TCAATGAATG GAATGGTCGT AAGAAACCAC AATTAATGGT GACTGATTTT 4380

GCTGTATTGG GAAGACAATT ATTTGATTTT CGTGGCAAAA ATAATCAAAC GAAACCAATT 4440

CCTTCAGAAG CAACAGCTTA TCTTTTGTTT GATGAAAAAA ATCAAAAATT CATTTCAGAT 4500

CCAACCGCTA ATATTATTGT TTGGTCAAAC CAAGAAGAAT TGGTGGAAGC TGTTTCTCAA 4560

AATCAAATCG AACAACTGGT TTTTGTCGAC TGTCCTGTGG AAGCAATCAC GGTTAAAGAA 4620

ATTGTTGAAG CGACTGAGAT ACAACGTATA TACATGATGT TTATTTCACC AGAAGAAGCT 4680

TATTTAAACG GTATGGCTTC ACGTGAACAA TTTGCAACAT TGTATAAATT TATTTTGCAG 4740

CAAAAAGAAG TAAATCTACG TTCCCAGCTA TCGAAGGTGG CAAATTACTT AAATATCCAA 4800

GAAAAATTAT TAATTTTCAT GATACAGGTG TTTTTGACT TAGGATTTGT TACAATAGAA 4860

AGCGGTGTTT TAAACAGTAT TGAGAAACCC GACAATCGAC CATTGACTGA AAGTCAAGTG 4920

TACCAACAAC GATTGAAAAA AATAAAAACA GAAGAATTTC TACTTTACAG TGATTGTCAA 4980

ACAATACAAC AATGGCTGTG GAATGAGGAG GACAAATAAA AATGGATTTA AGAGATTACA 5040

TTGCAAGCAT TCCAGATTAT CCTGAGAAAG GGATCGTGTT CCGTGACATy TCTCCATTAA 5100

TGGCTAATGG GGATGCCTAT CGTGAAGCAA CGAAACAAAT CGTGGATTAC GCGAAAGAAA 5160

AAAGAATTGA TATGGTTGTA GGACCGGAAG CTCGTGGCTT TATTGTCGGC TGTCCAGTGG 5220

CTTATGAACT AGGGGTTGGC TTTGCTCCGG TTCGTAAAAA AGGAAAACTT CCTCGTGAAA 5280

CCATCGAAGT GACTTATGAC TTAGAATATG GTTCAGATAC ATTAACGTTG CACAAAGATG 5340

CCATCACACC AGGCCAACGT GTTTTGATTT GTGATGACTT GTTAGCAACT GGTGGTACAA 5400

TTAAAGCAAC CATCGAATTA GTCGAACAAT TAGGTGGTAT TGTGGTTGGT TGTGCGTTCC 5460

TAATTGAATT AATGGATTTA CATGGCCGCG ATAAAATTGA TGGCTACGAT ATTGTTACCT 5520

TAATGGAATA CTAATCTAAT TTAATTAGAA AGAGCGAAGG ATTTAATCCT tCGCTCTTTC 5580

TTTGACATAT TTATAAAAAC GGAGCGTAGC TTGGGGGGAA CACACCGTTT TATTATTTAT 5640

TAAGGGAACT TACGATAAAC GTATCTTGCT TGCTGTTGTT TACGTGTACG TGTATAACGC 5700

TTCTCATCCC ATGACATAAA CCAAAGAATA AATAACGGCG TCACGATCAT AAAAGCAAGA 5760

CGTAATCCTA ATGTTCCnAA GAAAATACCT ATAACCAATA CAAAAAATAA AAATGCCAAC 5820

ACGACGAATT 5830

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

TATTTGACTG CTTAAACGTA TAATGAAACG CCGAGTCATT TGTTGGTATC CCTAAACCAT 60

TTTGTAAAAA TTCAATCGCT TCCTGTTTAG TATAAGATTC TGCTTCTAAT TGCGTTCCTA 120

AATGCGGATT TTTTTGATCA ACAAATTGTC TTGCTTTGTC ATTATTAGCA GACTTTTCTA 180

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TAACGACTTC CTGTTGCGAA TTCCTACTTC CTGAACAGCC AGTTAATACA AATAAAATCA      240
CCAACAACCC GAAACACTTA CTCAAAGTTT TCTCCTCCTC TCCCTTTTCA TTAGTGATAC      300
CTGATGATTT CTTTTATATT TTAGCATGCT TGATATAACG AATGGTGCTC AAAAAAGACA      360
GAATCAACAA GTAAAAtTGT CgACTCACCT TTCTCAACTA AtATTAAAAA CCATCTGTCT      420
CAATATTTtC GAATTtCCTG kAAATTACTG ATAAATAAAA aCAGCTCCTT TTGCGtATAC      480
yTATATTATC AGCACCTAAA gGAGGAAmTT TcTTGAAGcA AAAAAAtCTA CTCACTTATC      540
AATCACTTGT AGCCTTGTTG CTaGTATTCA GTCTCTTTAG TTTTGACCCA TCGGTTTCTT      600
TTGCCACCCG TTCTGGAAAA ACGCCTGTTT CAGTTGAACT AGAAATTGGA GGGCTGCCTG      660
GTGATGAATC GGTTGACGAT GCCATTGATC CTGATTTAGA AAATCCTAAC ACTAGTTTTG      720
ACTTGCTCTT TATTCCGAAA GAATTTACTT TTGAAACCCA AGCGATTTCT GGTGATTTAA      780
CGGCAGTTCC TATACGACCT TCTGAAGGCA ATACTCATAC AATGAGACAC TTCGGGATGG      840
GGGATGTTCG CGGAGCcTTA ACTGGTTGGC ATGTCACTGC TGAAATCCCA CACATGCGAA      900
ACGAAGCTCA TTCTTTACTA GGCATCATTA CGTTTCAATT AACAGGCAGC TATGCTCGCT      960
ATGACAAAAC GTTAAGGCGT TTCTTTATGA CAAATACAAT GTATGGACTG GATTTTTCAG     1020
AAGATCCTGC TGCACCCGAC TTCCCGACCA ACCCAATTAT TATCGGTAAC GGTGCGACTT     1080
TAATGAGTAA CGCTGGTGAT AGAAAAGGAC AAGGAATGTG GAGCGGCCGC ATGACCGATA     1140
TTTCTCTTGC AATCCAAACC CCTGTTTCAC AATTATTTCC TGGCGCATAT ACAGGTTCGA     1200
TTATCTGGAA TTTAATCTCT GGACCTGTAT AAAATAAAAA AACGCTTAGA AAACTAGCGG     1260
AATCACTACT CTTCTAAGCG TTTTTTTATA TCATAAGGAC TATTTGCTCC TTCTATTTGT     1320
CTAAGCATGC TTTACCACTT TTCGTTTAAC GAATCACTTG GCCCCAACGG TAATCAAACT     1380
GATACTCTTG ATTACCATTA TTCAGGTTAA TTTTGTATAA ATAACGCGGG ACTTTAATGA     1440
ATAACGCATC CTCTACTTGA AAAGCTTCAA TAGGTACaTT TTCTTTAGTT AAAAGCAACG     1500
GTGTTTGCCA CTCGTATGTT TTTTTCTGCC AATTGTATAA GCCAACTATC GCTkGATTAC     1560
TTkGTCTTTT CTTGTATGAC AGAACATAAT AATTTGCTTC ATCTTTCTTG CCTAATAAAA     1620
CTGGTGCTAT TAGTTGCTCT TCTAGTTTTC CTTGCACTGT TGTACGCTCT TCCGATGACA     1680
GCTCTTGACC AATTTGACTC TCATTTGAAT CTACCGTCCA TTTAGGCGCT TCTTGTGTTT     1740
GAAAGACTTC TTTGAAAGTT GGGTCTTGTT TTAACTGCCA ATTTTTCAAA TCTAATTGAT     1800
AATATCGATT GTtTAATCCA TAAATATAGA GATAGCGATT ATCCATAAAA CGATAATCAA     1860
CGAAATCAGA GCTTAAATAG TCTTTTAATT CAGGGAATTt CyTCACTAAA TCTGCTtCAG     1920
AAAACTGkTT TTTCCtGTTT GnACnAGnAA GAAATGGCC                            1959
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(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GATAACCTGA CGAGCCATAA GATTGATTAT AAAAACCCTC ATAAAGTTAC TTCTGCACAA 60

GTTGGTTCAT ATAGTAAAAC AGAAACAGAT AACCTATTCA TCAATAAATC AGATGCTGAA 120

AACGGCTTAT TGGTAAGAAA AAGTATTGAA ATAACAGACT TAAATAATGC TAAAGAACCT 180

GGCATATACT CGATTCCAGC TACAGGAGTT GAAAACAAGC CGCTACCAAA CTCTGGAAGT 240

TTGTTCGTTA GTAAAGACCC AGGAGGAGTC AGACAACTAT TTCAAACGGA AAGGACTATC 300

GTTATTCGTC AATTTGGTGG TATTCCTTCA AAGTGGACGG ATTGGAAAGA AGTAGCATTT 360

AAACCGAATG TTGTGAATTT AACTGAACCT CAACGTATAG GsGGAACTAA aGAATTTGCG 420

GATATTCCAT TAGTAAATGG TACAGAAtAG CTTTGAAAGA AGATATATTT TTTTATCAAA 480

AGACTGGGCT TGATGAAGTC CaAGCAGAcT ACAAAGCTTC TTTTAGGGAA GAAACAAATA 540

TGTTTCTTAC ACGAGAAGGA AACAGAGTTG ATGCTTATTT ACGAGTTAAT GTGGTGGATG 600

TCACCAAACT AAAAACTGCT TTTGTTCCGA TTTTTCAAAT TCCTGATGGA TTTAAAATTG 660

ATCTTAGCAT GAGGGAGAGT TTCTGGAATG TTCCATTGAC AGTAACTCAA TACACCTACC 720

CACAAGGTAA CTATGGTGCA TTATATGAGA TGAACGTGAA AGGAATCCGA TTCGGAAGTG 780

ACCGTCTTGG TAATCATTAT CTATACGGAA GTTGGCATAC TAATGATCCA AAACCAGATG 840

CTAAATTTAA GTATATGCTT TATGTGAACT TATATAATTT GTCTGAGGGA AGAGATTTTG 900

TTTCAGGTTC ATACAAAGGA GAAATTTATT ATGTAGCTGT TGAAATTGAT GGACAGTTAG 960

GrGAAAAATT AAAAGTATCT GATGGTTTTT ATAAGTATAC GGTAGGAACT AAAATAAATA 1020

AGGcTTCTCA AAATGCATGG GTGATTGGTT ATGATCAGTC AGGAACAGAA GTAACTAGAA 1080

GCAAAATCAA AATATTATAG AGAGTAAGGA GAAAACAAAA AATGAAAAAA ATTTGGAAAT 1140

ATGGACGTAC TGGAGGGCAA GAGCTACAGG TATCTGATGA TTTCCCAATG CAAGTTCCTT 1200

TTACAGATGT AGTTCCTTTA CCAACCGTCA ATTTAGAAGA CCAATTTTTT ATTCCATCTG 1260

AGAATAGATG GAAAGAAATT TCTAACCAAT TAGATAAGGA AAATTTGGAT AATTTAAGTA 1320

TATTATATAA AAACCTTGAA AAGGATAATG AATTATTAAA AGCTAAAGCA GATAATCTTG 1380

CTCTTCTAAA TTCTAAGCTA ATGCTCAATG ACCTTAATAT CCAAAAAGAA AATACCCTCT 1440

TGAAAGCTAA AGCAAATGAC CTAGCTGAGA TTGGTGCGAA ATCAATGTTG TCCATTGTAC 1500

AAATTACTGG GGAAATAGGG AAAATTAATG AGCAACTTAA AGGAGGTGCT AAATAATGTT 1560

TACTTTTGAT GATGTTAAAT TGATGTATGA TTGGGGTCTT TATACTGATG ATGAAGTAAA 1620

GCTATTTGTA CCTACATGCA TTACAGAAGA GGAGTTTAAC GAGATTGTAG GGAAAGAAGG 1680

TTAGTCAGTT GGAGTTAGAG CAAAAAGTAA AAGAACATGA AAAACGTCTT GGTGATCACG 1740

ATAGAGAAAT AGGTCGTTTA GATAGACGAA CGATGACTTT ACAAGAGCAA CTTAATGCAA 1800

ATTTAGTTAG ATTAGATGAG TCAAATAAAT TCTTACGTGA ACAAAATATG AAGCAAATGG 1860

AGCAAAATAG TGAAATTCTA AATGCTATTT TGAATAGAAA CAGTGAAGCg GATGAAAGAA 1920

AAGACGAACT AAAAAAACTT AACACTGAAA ATATATGGAA AGTAATACTA GCTATATyTG 1980

TTTCTAGCGG AGCAATAACT ATTTTATTTA ACTGGTTAAG CACATTTTTA GGAGGCGCTA 2040

AATGAAAATT AATTGGAAAC ATAAATTCAC AAGCAGAAAG TTTTGGGCTG CAGTGACrGG 2100

rGTAtCaTtG CTTTGkTaGC aGTTTTCAAT GTAGATGATT tAmCaTCTGa AAAAGTGGTC 2160

ACTTTAGTAG CAGCTATTGG CTTATTAGCT GCATATATTG TTGGCGAAGG ATTTGTTGAT 2220

TCAAATAGAG ATAATTAAGA AGTCATTCTA AAATGGCTTC TTTTTTTATA TAAAAAATTA 2280

AGAAAGAGGT TTTAAAATGA AAAAGTTTAG TAAGTTTTTA TTATCATTAG TTGTAGTTAC 2340

AGGATTATTG TTACCAACTG CCGCAGATGC TTATCAAGTG GAACAAGATC CTATCGATTT 2400

TGGCGGATAT TTTCCAGGTT ATGCGACTAA CGAATTAATT GTCTTGCACG AGTCAGGAAA 2460

TGGGAACAAC GTTGGCCTAA ACAGTCTAGA CAATGAAACG GCATATATGA AACGCAACTG 2520

GACGAGCGCT TATGTTTCAT ATTTTGTCGG TTCTGGTGGT CGCGTGAAGC AGTTAGCGCC 2580

AGTTGGCCAG ATTCAATGGG GAGCGGGAGC GACAGCCAAT GCAAAAGCAT ATGCACAGAT 2640

CGAACTTGCT CGAACGAATA ATAAAGAAAC ATTCAAGAAA GACTATGCTG CCTATGTCaA 2700

TTTGATTCGT GATTTAGCAA CACAAATTGG TGCaACATTT GACTTGGATG ATGGAACAGG 2760

ATATGGAATT GTGACGCATG ATTGGATCAC AAAAAATTGG TGGGGGGaTC aTACaGATCC 2820

ATACGGATAT TTAGCACAGT GGGGaATTaG CaAAGCmCaA CTAGCACAAG ATTTACAAAC 2880

TGGACTTCCA GAAGATGGTA GCGAAGTTAT TGTAAATCCT GGCAAGCCTA ATAAACCAAA 2940

ATATAAAGTC GGTCAGCACG TTCGCTTCAC AACAATCTAC AAAAATCCAG ATGCGCCAAT 3000

TTCTCAGcaT ATCAATGCAA ACACATTGTG GACTCAAGTT GGaACCATTA CACAAAAAAT 3060

AAATGGcCGT AAAAATCTAT ATCGCATCGA AAACAGCGGC AAACTTTTAG GTTATGCAAA 3120

CGATGGTGAT ATTGCGGAGT TTGGGAAAAC AGCAAACCAA CACCAGCTAA AACATTCACT 3180

ATTGGTGTAA ATGAAGGAAT TGTGTTGCGT ACTGGATCAC CTAGTTTGTA TGCGCCATTT 3240

ACGGCGTGTG GCCAAAAGGT GCACAATTTA GATATGATTC GGTTCGTGTG GCCGATGGCT 3300

ATGTTTGGTT AGGGGGTTCT GATTCAAACG GAACTCGGAT TTGTATCCCA GTTGGCCCAA 3360

ATGATGGGCA ACCCAGACAA TACTGGGGTA CTGGATATTA AGAACAGCTT GAnTTTTCTG 3420

TTAACCCnTA nGTTTAGGAA TAAACTTACA CTTATTTAAA TTTCTCCTGA GTCGCCTTnC 3480

CCCAA 3485

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 914 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

AGAAGGAAAA AAGAACTGAA AAAGCTTAAA AAAAGCTGGG AAAAAAGTGG AGGAAGAGGT 60

AAACCACCAA CTTCTCTATC TACGTTACGA TGTGGTCGAA TACTCCAAGA ATATATTGAG 120

TTTTGCTTAT TTGATATGGA AGAAAATACT CGTTTAGCTA TGTATCAGCC AAAAGAAGGC 180

ATTTATACAC AAAATGAAAC ACAAATAAAA CGAGTGATTG GGTGGCTTGA ACCGAAACAC 240

AATGCTAGAG CGGTAAATGA TGTTATTTTT CACATTTGGA AAGAAGCTAA AATAAAGCCT 300

AAAACGGTCT CAAGATATCT TATACCAGTG AAAAACGGGG TATTTAACCT TAAAACGAAA 360

CAACTAGAAC CGTTTACGCC CAATTATGTA TTCACATCAA AAATTGCAAC CGCATATGTA 420

GAAAATCCGT CGTTACCTAA ATTTAATGAT TGGGATGTAG AGAGCTGGTT GAACGAAATT 480

GCTTGCGGAG ATGCACAAAT AACTACTCTG TTATGGCAGG TAATAAGTGA TGCGATTAAC 540

GGGAACTATT CAAGGAAAAA ATCAATCTGG CTTATGGGTG ATGGATCAAA CGGAAAAGGA 600

ACGTACCAAC AGTTATTATA TAACCTAATT GGTCCACAGA ATATCGCAAC GTTAAAAATA 660

AATCAGTTTA GTGAGCGTTT TAAACTTGCT TTATTAGTAG AAAAAGTGGC AGTTATTGGG 720

GATGATGTAG GAGCrGGAAt TTATATTGAT GATAgTTCGG AATTTAATAG TGtAGTGACT 780

AAkGrGACTA TACTAATTGA AgTTAAAAAT AGAATGCCCT ATAGCGCTCG AATGTATGTG 840

ACTGTTATTC AGTCTACCAA TGAGATGCCT AAAATTCGTA ATAAATCTAA TGGAACGTAT 900

CGCCGTTTGC TTAT 914

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GGCATAGCCT TGAAGAAGCC TATCAAGCGA TTTTGTCGGC GCCAAGTTTT GATGCTTGGA 60

TTAAAACCAC ACGCCCTTTG AAATTAGACA ACAATCAATT GTGGCTAGAA GTCCCTTCTG 120

CAGTTCATCG TGATTACTGG GAAAAAAATC TTTCGGCAAA AATTGTCGAA ACTGGATTTA 180

AATTGACCGG TGCAGAAGTG ATGCCCCATT TTGTTGTTGC CGATGAAAAA GACGCAGCAC 240

TGGCACAAGA ACTCGAAGAA CCTGCCGAAG AAGAAGTTGT TTTTAGTGAA CAAAGTAAAA 300

AAGCGATGCT TAATCCTAAG TACACTTTCG ACACCTTCGT TATTGGTAAA GGAAACCAAA 360

TGGCTCATGC TGCAGCGCTT GTTGTTGCCG AGGATCCAGG TTCGATTTAC AATCCCCTTT 420

TCTTCTATGG TGGTGTAGGG TTAGGGAAAA CCCATTTGAT GCATGCTATT GGTCATCAAA 480

TGTTAGTGAA TCAACCAGAT GCCAAAGTCA AATATGTTAG TAGCGAAACG TTTACGAATG 540

AATTTATCAA CTCAATTCAA ACaAAGACAT CCGAACAATT TCGGAAAGAA TATCGCAATG 600

TTGACTTATT ATTAGTCGAT GATATTCAAT TTTTGGCGGA AAAAGAAGCA ACATTGGAAG 660

AATTTTTCCA TACCTTCAAC GATCTTTACA ATGAAAATAA ACAAATTGTT TtAACAAGTG 720

ATCGCCCGCC GAATGATATT CCmAAATTAC CTGnAACGAT TAGTTTCTCG CTTTGCTTGG 780

GGTTTGTCTG TCGATATCAC CCCGCCTGAT TTAGAAACAC GGATTGCAAT TTTGCGCAAA 840

AAAGCAGATG cCGAGCGTTT AGAAATTCCG GaTGATACAC TAAGTTATAT CgCTGGtCaA 900

ATTGaTTCCA ACATCCGTGA ATTAGAGGGT GCTTTGGTCC GTGGTTCAAG CCCTTTGCCA 960

CCTATTATGG AGAAGGATAT TACCACTAGT TAACCGGCGG AGCCTTGGAA ATCCCTAAAA 1020

nCAGTTGGAG TAAAAAAnCA ATnGCCnATT TAC 1053

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CGATTAGTGC CTAAAGACAA GCTCACGCAA TTAACGAAAC AATTCCTTTA CTTTTCGGAG 60

TCCTTGGGAT TTTATTTATG GTCGGCCAAT AAGAAGCAAG AACGAATAGA ATTACTTTGT 120

CATATTGAAG AGAGTCAATG TCAACAATTT TATAGAAGAA AACAATCATG GGATTTTTAC 180

GAwAAACrAT TACTAGArAT CTTCCGrCTA CCGACCGCTA ATTTAAATTT ACTGCCAGAT 240

AGACGGCACA CTGGCCAATT GATGCATGAT TATTATCAAA AATTGACGCA ACAACTTGGT 300

TACAGAAATG CTCAGTTGcT TAGAACACAA AGCTTTTTAT ACACGAAAGG TTGTCACCTT 360

CTCCAGTTaC CTCCTTGGTT TTACTATCCT GGATTGAAGC TAATACCTTC TTCTGAAGAA 420

GATATTCATT TAAAAATGCT TGTTTGGGAA GCACTAAAAA CCGAAGAAGA GCGTTTAGTG 480

ACCAAACAGG AACTATGGCG TATCTTGGAA GCTATTTTTT TGGAAGAAGG GAACTTTGTT 540

TGGCAGCCAC TGCCGAATAT TGGCTTAAAA AAGCTTTTTA AAATTGTGGG AAATAACTTA 600

TTGAGATGGT TACAAGAATG TTATGTGTTA ATTAAAGTAA ACAATAAGTA CCTAATAACT 660

AGTATTTTCC TAAGAGAAGA TCCTGAAAAG CTCATTCATT GGCTAAAAAA AGTGAAAAAA 720

CAACATTTTT TTAGTCACAC GTGTTAAATT ATGATAGTAT AATGAGTAAA ACGTTTCTTA 780

AAGGAGAGTA AACTATGAGC GAAATTAAAC AATTACCAAC ACGTGATGAA GkTCCAACTC 840

CATTGACTTG GGATTTAACC AAAATTTTTA AAGATGATGC TGCTTTTGAT GTTGCGTATA 900

ATCAGTTGAT AGAAGAGCTA AATCAAGCAG AATCATTTAA AGGTACCTTA GGGGATGGTG 960

CAGAAGCTTT TCTAGCTGCG TTAGAATACG TTTTAGATGT CTATCGAAAA GTGGAAACAT 1020

TATATGTCTA TTCTCATTTA AAAAATGATC AAGACACTAC AAATACAGCT TACCAAGCTT 1080

TATATGCCAG AGCTAGTTCT TTATATGCAC AAGTTAGTGA AGCTGTTTCT TGGTTTGACC 1140

CAGAGGTTTT AACATTAAGT GATGAACAAA TCTGGGGATA TTTTGAAGAG CAGCCGAAAT 1200

TAGCTGTTTA TCGTCACTAT ATTCAAAATA TTTTAGATGA ACGTCCCCAT GTTTTATCGA 1260

TGGAACAAGA AGCTTTACTG GCGGGGGCTA GTGAaATTTT TGGTGCCTCA AGTAATACAT 1320

TTTCAATTTT AAATAATGCA GACTTAGAAT TTCCAACTGT GCAAAATGCT GAAGGCGAAA 1380

CGATTCAACT TTCTCATGGC GTTTATGGTC AGTTAATGGA AAGTGTCGAT CCATCTGTTC 1440

GTGAAGCAGC ATTTAAAGGT TTGTACAAAG TATACAAACA ATTTAGAAAT ACATTAGCCT 1500

CAACTTTAGG TGCACATGTT AAAACACATA ATTATAAAGC AAAAATTAGA AATTATGATT 1560

CTGCTCGAGC AGCCTCTTTA GCAAGTAATC ATATCCCTGA AAGTGTTCAC GAAACATTAG 1620

TAGCTGTAGT AAATAAACAT TTACCTTTGC TACATCGTTA TGTAAAATTA AGAAAAAAAT 1680

TATTAAACGT AGAAGAATTA CACATGTACG ACTTGTATGC GCCTTTGCTA GGTGAAGCAC 1740

CAATTCGTTA CAGCTATGAA GAAGCAAAAG AAAAAGCAAT TGAGGCTTTA AAACCACTAG 1800

GTGAAGACTA TTTATCTATT GTTAAAGAAG CTTTTTCAAG TCGCTGGATT GATGTGATTG 1860

AAAATCAAGG AAAACGAAGC GGCGCATATT CTTCAGGAGC TTATGATACA GCCCCATACA 1920

TTTTAATGAA TTGGCATGAT AGTTTGGATC AACTATTTAC ATTAGTCCAT GAGATGGGCC 1980

ATAGTGTTCA TAGTTACTAT ACAAGAAATA ATCAGCCGTA TGTTTATGGC GACTATTCAA 2040

TTTTCTTAGC TGAGATTGCT TCAACCACAA ATGAAAATAT TTTAACAGAA TATTTATTAC 2100

AAACAGAAAC AGATCCTAAA GTACGTGCGT ATGTCTTAAA TCACTATTTA GACGGCTTTA 2160

AGGGAACCAT TTTCCGTCAA ACGCAATTTG CGGAATTTGA ACATTTTATT CACACGGAAG 2220

ATGCTAAAGG CACGCCATTA ACAAGTGAAT ATTTGAGTGA GTATTATGGC GAGCTCAATG 2280

CTAAATATTA TGGACCAGAA GTAGTTAGAG ACGAAGAAAT CAGTTACGAA TGGGCGAGAA 2340

TTCCACATTT TTATTACAAT TACTATGTTT ATCAATATGC AACTGGCTTC TCAGCCGCTT 2400

CGGCATTGTC TAAACATATT TTAGCTGGAG AAGAGGGAGC TTTAGAGAAT TATCTTAACT 2460

ACTTGAAAGC AGGAAGTAGT GACTTCCCAA TTGAAGTGAT GAAAAAAGCG GGCGTGGATA 2520

TGACACAAGC CGCGTATATC GAAGATGCAA TGAAAGTTTT TGAAGAACGT TTAACGGAAT 2580

TAGAAGCTTT GGTTGAAAAA TTATAGACAA AAAAGTGGGA TATAAGTCCA GATGACTTAT 2640

ATCCCACTTT TTAACTCTTA AGATAATTGG TTAACAGCTT TCGTCGCAGC ATCTTTTTTA 2700

TAATAAATGT AAATGTCCAT TTGGAAAATG ATAATTGGAG CGACGTTTAA ATTCAAAGGT 2760

TGCGTCACCT kGGTTCAGCA ACGGTTCGTT ATGTGGATGA ACACGACAAA GTTGTTTAAT 2820

TTCATCCATG TTTTCAAAAT TTTCGACTAA AATGCCGAAA TCGTTCTCGC AAGTATAGTT 2880

GTA 2883

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

CGTTAACCnA GGGTCTAGCT GTCTGnTAAA GCTAGAACCG AAGGACTTAG AGnCGGATTA 60

CCCCACAAAG TCTTCCCACA AwTTTkGATA CTTTACgAGT kGAAACgCCT GATACATACc 120

ATTyCCAAaC ATTGAAGCCc ATGAGGGCTT TTTCGTTTCc GTTGATAACG TTCcAAACAC 180

TGTGGGTGAA AAATGGCCaT CACGTGTTCT GGGTACTTTT AATTCTAGCG TGCCTACACG 240

TGTCGTAAAr TGCGCTCATA ATAGCCATTT CGTTGACTTT GTCGGTTTTC TGTTCGTTCA 300

TATTCTTTTG CTTGAATATA TTCTGTTCGT TGATTTTCCA TTAGTTGATT AAATACCGTT 360

GTTAAAATAT TTTTAGAAAC GTCATCCTTT ACAGAATATT CAATAATGCT TTGAATCTCT 420

TCGCTTTTCA GTGTAAAATG TACTTGGGTC ATGTAAAAGT CCTCCTGGGT ATGTTTTtGT 480

CGTTAAAAAC ATtGTACCGT AAAAGGACTG TTATATGGCC TTTTTACTTT TACACAATTA 540

TACGGACTTT ATCtATTTcA GCCTGTATCA TAGCTAAACA AATCGAGTTG TGTGTCCGTT 600

TTTGGGCGTT CTGCTAGCTT GTTTAAAGTC TCTTGAATGA ATGTATGTTC TAAGTCAAAA 660

AACTCTGACA GCGCCTTTAT ATAGCTTTCT TTTTCTTCTT TTTTTACTTT AATGATCGAT 720

AGCAACAATG ATTTAACACT AGCAAGTTGA ATGCCACCAT TTCTTCCTGG TTTAATCTTA 780

AAGAAAATTT CCTGATTCGC CTTCAGTACC TTCAGCAATT TATCTAATGT CCGCTCAGGA 840

ATGCCTAGCG CTTCTCTAAT CTCTTTTTTA GTCGTCACCA AATAAGGCTT GTATACATCA 900

CTTTTTTCGC TAATATAAGC CATTAAATCT TCTTTCCATT CTGACAAATG AACACGTTGA 960

CGTTCACTTC TTTTTTTCTT GAATTTAAAC CACCCTTGAC GGACAAATAA ATCTTTACTG 1020

GTTAAATCAC TTGATACCCA AGCTTTGCAA AGAATGGTAA TGTATTCCCT ATTAGCCCCT 1080

TGATAGTTTT CTGAATAGGC ACTTCTAACA AGTTTAATCA CTTCTTTTTC TTCTAAGGGT 1140

TGATCTAATC GATTATTAAA CTCAAACATA TTATATTCGC ACGTTTCGAT TGAATAGCCT 1200

GAACTAAAGT AGGCTAAAGA GAGGGTAAAC ATGACGTTAT TACGCCCTAT TAAACCCTTT 1260

TCTCCTGAAA ATTTCGTTTC GTGCAATAAG AGATTAAACC AGGGTTCATC TACTTGTTTT 1320

TTGCCTTCTG TACCGCTTAA AACCGTTAGA CTTGAACGAG TAAAGCCCTT ATTATCTGTT 1380

TGTTTGAAAG ACCAATCTTG CCATTCTTTG AAAGAATAAC GGTAATTGGG ATCAAAAAAT 1440

TCTACATTGT CCGTTCTTGG TATaCGAGCA wTCCCAAAAT GATTgCACGT TAGATCAACT 1500

GGcAAAGACT TyCCAAAATA TTCTCGGATA TTTTGCgAGA TTATTTgGCT GcTTTGaCAG 1560

ATTtAAATTC TGATTTTGAA GTCACATAAC TGGCGTTTCT AAAACAAAAT ATGcTTGaTA 1620

ACCtTTATCA GATTTGATAA TTAACGTAGG CATAAAACCt AAATCAATAG CTGTTGTTAA 1680

AATAtCGCTT GCTGAAATAG TTTCTTTTGC CGTGTGAATA TCAAAATCAA TAAAGAAGGT 1740

ATTGATTTGT CTTAAATTGT TTTCAGAATG TCCTTTCGTG TATGAACGGT TTTCGTCTGC 1800

ATACGTACCA TAACGATAAA CGTTTGGTGT CCAATGCGTA AATGTATCTT GATTTTCGTG 1860

AATCGCTTCT TCGGAAGTCA GAACAACGCC ACGTCCGCCA ATCATGCTTT TTTTTGAGCG 1920

ATACGCAAAA ATAGCCCCTT TGCTTTTACC TGGCTTGGTA GTGATTGAGC GAATTTTACT 1980

ATTTTTAAAT TTGTACTTTA ACAAGCCGTC ATGAAGCACA GTTTCTACAA CAAAAGGGAT 2040

ATTCATTCAG CTGTTCTCCT TTCTtACGAA AATTAATTAG TTAGAAGCTA CGATCAAAGT 2100

TGAATCACAA CAAAAAAGGC AATCAACTAA GTTTTTCTTA ATTGATTGCC TGGTATCTTC 2160

TTAAAGACTT GAAATTCCCT CAAAAACCCG ATATAATGGG TTTACAGATA TTTAAGTATC 2220

TGATTAATAA AGTAATTAAA TACTTTACCA AATTTCGGGT CTCGACTTCT TTAATTGATT 2280

GGTGGTAATC AATTAAGGCT CGCAACTTAT TTTCTtGGCG GAAAATAAGT TGGTCGTGGC 2340

TCTTTTTTTG TATTCTTTAT TCAGTTCGTT GTTTCGTTAT ATCTAGTATA CCGCTTTTAA 2400

AAAAAATAAG CAACAATTTC GTTAAATATA TTAACGACAA TCATTGCTTC TCTTCTTCTA 2460

TTTGCAACTC TACTTGTTCT AATTCATTAG GAATTAAGTC AATAACTAAG GTTGAGTTTG 2520

TCAATTCTGC AATTCGTTCC AATGTTTTTA ATGTCGGATC TGATTTTCCT GATTCAATCA 2580

ATGAATAATT TGGTTCTGTT GCAAAGTTTT AAATCTACTA TCAAATAAGG TAGAATAATA 2640

GAAAAAGATA GCAGGAGGAA TGACGATGAA TCATTTTAAA GGAAAGCAAT TTCAGCAGGA 2700

TGTGATTATT GTAGCCGTGG GCTACTATCT TCGTTATAAC CTTAGCTATC GTGAAGTTCA 2760

AGAAATCTTA TATGATCGTG GCATTAACGT TTCTCATACG ACGATTTATC GTTGGGTGCA 2820

AGAATATGGC AAACTACTCT ATCAAATTTG GAAAAAGAAA AATAAAAAAT CCTTTTATTC 2880

ATGGAAAATG GATGAAACGT ACATCAAAAT TAAAGGAAAA TGGCATTATT TGTATCGAGC 2940

CATCGATGCA GATGGTTTAA CCTTGGATAT TTGGTTACGT AAAAAACGGG ACACACAAGC 3000

AGCCTATGCT TTTCTTAAGC GGTTAGTGAA GCAGTTTGAT GAACCGAAGT TGTtAGTCAC 3060

AGATAAAGCC CCCTCTATTA CAAGTGCCTT TAAGAAACTA AAAGAATACG GCTTTTATCA 3120

AGGGACAGAA CATCGTACCA TTAAATACCT GAATAATTTG ATTGAACAAG ACCATCGTCC 3180

AGTAAAGAGA CGCAATAAAT TCTATCGAAG TTTACGCACT GCCTCTACCA CGATTAAAGG 3240

CATGGAAGCC ATTCGAGGAT TATATAAGAr AACCCGAAAA GAAGGCACTC TCTTCGGGTT 3300

TTCGGTCTGT ACTGAAATCA AGGTATTATT GGGAATCCCA GCTTAAATCA TAGATACCGT 3360

AAGGGATTTT ATTCTTTATT TAAAACTTTG CAACAGAACC ATTGTGTAAA AGTAAAAAGG 3420

CCATATAACA GTCCTTTtAC GGTACAATGT TTTTAACGAC AAAAACATAC CCAGGAGGAC 3480

TTTTACATGA CCCAAGTACA TTTTACACTG AAAAGCGAAG AGATTCAAAG CATTATTGAA 3540

TATTCTGTAA AGGATGACGT TTCTAAAAAT ATTTTAACAA CGGTATTTAA TCAACTAATG 3600

GAAAATCAAC GAACAGAATA TATTCAAGCA AAAGAATATG AACGAACAGA AAACCGACAA 3660

AGTCAACGAA ATGGCTATTA TGAGCGCAGC TTTACGACAC GTGTAGGCAC GCTAGAATTA 3720

AAAGTACCCA GAACACGTGA TGGCCATTTT TCACCCACAG TGTTT 3765

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7043 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

nnATAAATGT TGAATAAAGT TTGATAnTGT TTTATTATGT TTTCGAGAAG GGGATTTGAG 60

TTTAAAGAAA GGGACAGAAT TTTAATAGTA GATACACGAG GTAAGGAGGA AAACAAAATG 120

CGTGTCATAC TTGGTTCAGA TTTAGATGGA ATAAAATTAA AAGCAGAAAT GAAACAATAC 180

TTATTGCAAG AAAAAGTTGA GGTAATCGAT AAAAGTGAAA GTGCTTCGGA AGACTTTATA 240

GAAGCAACGC TTGCTGTTGC TCATGAAGTT TTAAAGGATA CTGAAAGTTT AGGAATCGTT 300

TTTGATGGTT ATGGGGCAGG TAGTTTTATG ACTGCTGCTA AAATTAAAGG AATGATTGTC 360

GCTGAGTTGT CAGATGAGCG TTCTGCATAT ATGGCGCGAG AACACAACAA TGCTCGGATG 420

ATCACGGTGG GCGCAAAAAT TGTTGGAACG GAACTAGCCA AAAACATAAT AAAAGAATTC 480

TTAACAGGTC ATTATGCAGG CGGGCGTCAT CAAATACGTG TAGATATGTT AAATAAAaTG 540

GCTTAaTAAA TAATAGAAAG GAAGCGTTTT TATGAAAATT GCCATTGGTT GTGATCATAT 600

TGTGACGGAT ACCAAAATAG CAGTTTCTGa TTTTTTGAAA GCAAAGGGAT ATGAAATTTT 660

AGATGTAGGC ACGTATGATT TTACTCGAAC TCACTATCCT ATTTTCGGAA AAAAAGTGGG 720

AGAAGCCGTA ATGAGCAATC AGGCTGATTT GGGTATATGT ATTTGCGGAA CAGGCGTTGG 780

aATTACCAAT GCGGtTAACA AAGTGCCGGG TATCCGTtCT GCTTTAGTTC GCGATATGAC 840

TACAGCGTTG TATGCGAAAG AGGAATTGrA CGCAAATGTT ATTGGTTTCG GTGGGAAAAT 900

AACAGGAGAA TTCTTGATCT GTGATATCGC TGCTGCCTTT ATTGAAGCAC ACTATCATCC 960

AACAGAAGAC AACGAACAAC TAATTGAAAA AATTAATCAA GTTGAAAAAC AACATCCAGA 1020

ACAACAAGAT GCGCACTTTT TCGATGAATT TTTAGATAAA TGGCAACGAG GAGTCTATCA 1080

CGATTAGTAT TTAATCAATG AAGGTTACTT AAGAAAGTGG TCTTAAATAA TAATCATTGG 1140

TATTTGAGTT AAATTCCCCT TCATTAATTT TTATTGCTGT TTTAATGTGG CACTGTAAAG 1200

AGCATTATTA AGAAAAAGAA GTAACAAAGG AACAAATTGA AGGCTATACA GGTAAsCATA 1260

AAAAGTACAC GAGTTCTTTT CTCGTGTACT TTTTATGGTT TCGCTGCTTG TTTTATTTTA 1320

GTAATTATTT TTCTATAAAA ATAGTCCCAG AATTATTAAA ATAATCCCGA TAACTAAACT 1380

GCCGATGCCA GAAGCCGTAC CATATTTTTT ACCTAAATTT ATATCAGTAG TATTTTTAGG 1440

AATCAAGTTT GAGAAAAAAT AAAATTTTTT TACCAAGATT AGATATGCAA CAAGTAAAAG 1500

TAATAATCCT AAGAGAaGAT AACTAAGaTT TTCAGCTAAT AAATCtrGAT GAGCTAATAA 1560

CaATATCCCC AAAAAGAGGC CTACCAATCC ATATTTCATC GTTTTTTCTT TTGCTGACAT 1620

ATAAACATCC CTACTTTACT TTTTAATTTA TTAAGAGCAT AAAACCATAG ATTCGATATA 1680

AGTTCATTTT GTTGTATCCA AAAGAGCATG ACCTGGAATG ACCTATATAA TTAGAAAATT 1740

GGAGTGATAT ATAGTTATTT TACCATAGCT TAAATGAGTT GATTAACTCC GAATAATGTA 1800

CAACTATGTA CACCTATTGT GGGTGGAATG TGTGTTGGGA CTTTGCTAAC CTAATAGTTG 1860

AAAAAATGAA TCAATAAATT TAGAAAAGGG ACTATTCAAA AGAAACTTTT TTGGGAATTG 1920

CTATATTATT TATTTTTTTA AGCGTAATCA ACTAAATGTT TTTATGGATA AAGAAAGTCA 1980

TTGTTCCTTG TCATCAAGCT ACAACAGCCA AATTCATTAG AATTTTTTTA GTGAATGACT 2040

TTAATTTTAG AAAGGTACTG TTGTTAAACA TTCATGCTAT CAAAGGAGTG TGAGGCGAAC 2100

GAAGCAAGTA TTTTCaTTTT ATAAAAGTTG TATTATGGAC TCTTAAAAAG AGGTGATTTA 2160

AAAAATTTTG AAGTGGAAAT GTTAAGAAAG GAGAGAGGAA ATGACTTATT TAGTTCTGGT 2220

CAGTCATGGC GATTTTGCTA GAGGGTTAAA AAATTCATTA GGGATGTTTG CTGGCGATGA 2280

GATAGAGAAA GTCAGAGTGT TTGGCTTACA ACCTGGTGAA TCTACCGATA ATTTTGGTAA 2340

GCGGTTTCTT TGTGAAGTTG AAAAATTACC GCAgGAAACG AGGCTAATCG TTTTGGCTGA 2400

TATTGTAGGT GGGAGTCCAC TTGCTACTAT TTGTAAAGTA TTAGATAAGC AAAAAATGCT 2460

AGAAAATTCT CTGATTGTTG GAGGAGTGAA TTTTCCAATG GCTTTAAATG CGCTTCTATT 2520

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AATTCTAGTT ATTTTAGGTA CCG 7043

(2) INFORMATION FOR SEQ ID NO: 289:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

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TGGGGCAATT AAGTAGTTAT TTTGATGCGG TCGTGAGTGG GGAAGATTTC GAAGAAAGTA 600

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(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

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GCTTTATTCG TAGGAACTAA AAAACAAGCA CAAGAAGCAA TCAAAGATGA AGCAATCCGC 180

GCTGGTCAAT ACTATGTAAA CCATCGTTGG TTAGGTGGTA CGTTAACTAA CTGGGATACA 240

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(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4956 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

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(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

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(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

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TGTAATTTCT AAGTTAAAAT CTGTAACAGA ATAATGTTCT GCATTGTCAT ATTTTTTATA 960

CACATTTCTA AGCGCCATTT CCACCATTTG ATACGTCACT CTTTTCTTTT TGATTTGTTA 1020

CTCATAGTTT AAATGAAAAC GCTATCTTTC GGCAAGGGAG AGTTGCACAA GAAAAAGAAG 1080

ACTTTTTCGT CAAGGTGACA AAGGGCAAAC ACTCTCAGCG GATTTATCGA TAAACTTTTG 1140

TTATAATATA ACAAAGACAG GAGTTGGATA ACATGAAAAT CGCTTTAATC GCTCaTGATC 1200

GTAAAAAAAC ATTAATGATC AAACTAGCAA CCGCTTATAA ACATATTTTA GAAAAACATG 1260

AATTGTATGC AACGGGAACG ACAGGCATGA AAGTGATGGA AGCAACTGGC TTACCCGTGC 1320

ATTGCTTTAA ATCGGGGCCA TTAGGTGGGG ATmAACAGAT TGGCGCAATG ATATCAGAAG 1380

ACAACATTGA TTTAGTTATT TTTTTAAGAG ATCCTCTTTC CGCGCAaCCG CATGAACCAG 1440

ACGTGACGGC TTTGATTCGT CTAAGTGATG TCTATGAAAT TCCTTTAGCG ACCAATATTG 1500

GCAGTGCTGA AATTCTTTTG AGAGGTGTCG AGGCGGGGTT TGCGGACTTC CGTGAGGTTA 1560

TCCATGAAGG GGATCGTCGA CCGTTAGCTT TTTAGAGAAC CTTAATGGTT ATTTTGACTA 1620

TTTTGTGGTA TATTTTATGA GGACTTTTGT CCAAATAAAA TAACAGAGTA GGAGACAAAG 1680

CGTTAAGTGC TAAAAGGATG GGATGTTGCC TTTTGGACGA AGAACATAAA CAGTGTGTTG 1740

CTAGAAAGCA AAGGTTCTTA CTTTGCTTAT CATCAGAACA ACACGnTCAG CTTTTTAATG 1800

TTCGCGGTTT TGTTTnTCGC ATTCGCTGCA TGGTTC 1836

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

TATTTTATTG ACAAAGAAGG GGACGAGTAC AAAGAAGTGT TTGATCGATT GCATGTTTTT 60

TCAGCTGAAG AATTTGAAAG TGAATTGAAA CGATTACTAG AAAAAGATAA ATTCATTAAT 120

TGGGAGTGAG TTTCATGAGA AGAATAGAGA AAGAATTCAA CAAGAAGCTA GCCAGTTACG 180

AAAGAGAGTT AAAAAAATTA GGATGTCTGG ATGATGAAAC AGGGCTTATT CCCATAAGCA 240

AAAGACGATG GCATGTCATT TGGTGGCAAC CTGTTACACT TGCAAAAACA ATCGTGAGAT 300

CTTTTCGATT AACGCTAGAT AATGAAAACT TATGTATTTT AGGAGATGTA GAAATCACTA 360

TTTATCATGA TGGAACATAT GGTATTTCTA AAGAAGCTGT CCCAATTTTT ATTAATGATT 420

TATTGTCTTT AAAAAAGTTA ATTACTATTT TCTATGGAAC ACCTTTTAAC TTAAATTTTG 480

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GTTGAGTTCG CATACGCTCA CCTAAGAGAG GAAAAGAACG AAGTCAAGCT TCGTTCTTTT 720

TTCTACGTCG GAGAACCGAC GTAGTGATTC AGACGCAAAA ACCATTCGTC TGAATCAGGC 780

CCGTTTTTAG GAAGGGCTAG TGTGTTTGAT TTATCAGTTC TCACAGCCGT GTAATTTCTA 840

AGATTCCCTA ATCGTCTATC AGTCACTCGG CGAGTATAAC CTAAAACATA ACCTGTCGGA 900

GGTCAAGGGC AAGTGGCATC GGCAAGCCGA CCCTTGTCCT CCGACAGAAC ATGTTTTCTA 960

GTCGGTTATG CCGAACGACC GATATACGAA AAGGGAATCT AACCAGAATT TCCCCTCTGA 1020

CCTTTGAAAA CTGAAAAGCG AAATCAAACA AACAGGCCTT CGTCTAAAAA CGAGCCTAAT 1080

CAAACCTTAG GGGTTGCACC CCTAACACCC GGCGCCTCAC TCTCTCAACC GAAAAGGTTG 1140

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AAAATACAAT ATGAGCGATA TTCGCAATAT GTATGGTTCG CAGGTAGTTA AAGAAGAACA 1980

AGCCAAACAA AAGACATTAA CAGCAACAGC CTAAGGAGGA AGTACAATGG AACAACAACA 2040

CCCGACTATT CACACATTAA AAATTGAAAC CGAGTTTTTC AAGGCAGTAA AAGAACGGCG 2100

AAAAACATTT GAGATAAGAA AGAACGATCG TAATTTTCAA GTAGGGGATA TTTTAATTCT 2160

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AACGGATTAT GCACAACGTG AAGGTTATGT GGTGCTAGGA ATTGAATTAC ATTAGTAAAA 2280

AATTAGATTA TACGTCCAAA GAGGTTTTAC CTCTTTGGAC yaCCAAATAA AAAGAAAGAA 2340

GGAATCAAGA ATGATTAAAA CAAGTGCAGT AGGAAGATTA ACAAAAAGTT CAGAACTAAG 2400

AGTAACGTCA ACAGGGAAGG CCGTTGCCAA TTTTGCATTA GCTTGCAAAA GAGAAAGACT 2460

TGATAAAGAA GGGAATGCCC AAACGACTTT TATTCAATGT GTAATCTGGG GGAAACCTGC 2520

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TCATTAAAAT TTATCTGAAG GAGGGAGAAA ATGAAAAAGT TAATCGGTAA AAAGTGGCTG 2820

CTgCTTACAG CAGTAGCCAC TTTTTTATTA TCAGGATGCG CAAGTCTTGA ACAAAAAGCA 2880

CAGGATAGTG TAAAAGAAGT TACTGAAAAT GTTACTCAAA CTATTTCAAA CGATCAACGT 2940

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GACTTTAAGA AAGCAAAGAA ACAAGGAAAG AATTTAGAGA AGTTAAAAGA AGTATTAGTA 3840

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CCAGGGCGCA ACGATCGGTT CTGTTGCAAA GTTTTAAATA AAGaATAAAA TCCCTTACGG 4200

TATCTATGAT TTAAGCTGGG ATTCCCAATA ATACCTTGAT TTCAGTACAG ACCGAAAACC 4260

CGAAGAGAGT ACCTTCTTTT CGGGTTTTCT TATATAATCC TCGAATGGCT TCCATGCCTT 4320

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GATGGTCTTG TTCAATCAAA TTATTCAGGT ATTTAATGGT ACGATGTTCT GTCCCTTGAT 4440

AAAAGCCGTA TTCTTTTAGT TTCTTAAAGG GCACTTGTAA TAGAGGGGGC TTTATCTGTG 4500

GACTACAACC TTCGGGTCAT CAAACTGCTT CACTAACCGC TTAAGAAAAG CATAGGCTGC 4560

CTGTGTGTCC CGTTTTTTAC GTAACCAAAT ATCCAAGGTn AAACCAT 4607

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TTCTCGCGGA TTTATTCGGA TTGAACACAA CAAACCCAAA AGGTCAAATG ATGGTTACGT 60

ATGATTTTAC TGCCTGTTTT TCAAAAGATT CAATTATTTT TACAAACGAG CAAAGAAAAA 120

CAAGTTGTCG CAAACCACGA AGATGAAATT AAACAGCTTT ACCAAGGCTT TGAAAAAGAA 180

TTCGGACGTC CACTTTCACC AATTGAATTA GAAATGATTG GTCAGTGGTT GAACACGGAC 240

CATTATTCCC CTGAaTTAaT CCGGTTAGCG TTGCGAGAaG CTGTTTTAAA TCAGGCGTAT 300

AGTTTGAAAT ATATTGAtCG TATTTTACTT GCGTGGGAGC GTAAAAATAT TACCACCAAA 360

GAACAAGTTG CTGCTGATCA GAAAAAaCGA AAAGATTCTA TGATTCAAAA TGAGATTGAA 420

CAACAAGGTC AGACACAAGA ATCGTTGCCA AAGGTTACAT TACACAATTG GTTAAATCCA 480

GAAGACAGTG AATAAAAAGG AGGTGGGCCA TGCTATCAAA AGAGAAAACA ATGGAAGCTA 540

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TTGAAATTAT GTATGAGATG TTTCCAAATG CAGAATGTGA ATTAAAACAT AAGAATCCTT    600
TTGAATTATT AATTGCTGTG ATTTTAAGTG CGCAAGCAAC CGATGTATCG GTAAATAAAG    660
CGACTCCTGG TTTATTCGCA GCTTTTCCAA CACCAGAAGC TTTAGCAGct GCGCCGGTGG    720
AGGAGATTAT TGCTAAAATA AAAACCATTG GCTTATATCG CAATAAAGCA AAAAATATTA    780
AAGCGTGCGC ACAACAACTT TTAGAACGTT TCAATGGAGA AGTTCCGCAA ACCAGAGATG    840
AACTGGTCAG TTTACCTGGC GTGGGGAGAA AAACAGCCAA TGTAGTAATG GGAGATGCTT    900
TCGGCGAACC GGCTTTTGCA GTAGATACAC ATGTGGAACG AGTGTCCAAG CGCCTTAGAA    960
TTTGTAAGCT AAATGCGAAT GTTACTGAAG TTGAGCAAAC CTTAATGCGT AAAGTTCCGA   1020
AAGAACTCTG GGTGAAAACG CACCATACCA TGATTTTCTT TGGGCGTTAT CACTGCCTAG   1080
CAAGAGCGCC TAAATGTGAA GCCTGTCCGC TACTCTATAT GTGTCAAGAA GGCAAAGAAC   1140
GGATGAAAGG GAAATAACAC ATTTTTTCCT AAAAAAGcGA GCCACAAGTC CAACCGACTT   1200
GTGGCTCGCT TTCTTTTTTT GATTTTTAAG AAACGCAACA AATGATTGCG GTTcTTAAAA   1260
ATTGATTTAG TATAGACAGT GTGGtATATA CyAgAAAATt TATTTTTTTG AAGAAAGATA   1320
GGCGATGAAA TGACAGAAAa TGCACCCAAA TTTAAGCmAA TTtCyGCAGA AaTTGAAAAG   1380
AAGATTCGAG ACGGTCTGTA TGTAAGTGCA CAAAAATTAC CTTCAGAATA TGATTTAGCT   1440
AAAGAATATA ACTGCAGTCG CTTGACCATC CGTAAAGCGA TTGATGATTT GATCCGCAAA   1500
AATATTTTGG TAAAACGACA TGGTAAAGGT AGTTATGTGA TGTCGCAAGC GAAAATTCAA   1560
AGTGGTCGCG CTGGCTTACA AGGTTTTACT GAGGCAGCCA AAGCTTACGG GAAAAAAAGC   1620
CAGACAGAAG TCATTTCCTT TGAAGAAGTA GTACATCCCG CTGAGAAAAT TCGGGAGGCG   1680
CTCCAAGTAG GCAAAAATGA GGCAATTTAT GAACTGATTC GCCGCCGAAT GTTAGACGGC   1740
GAACCAATGA CAGTTGAAAA AATTTATTTG CCACAGGCAT ACGTACAAGG CCATACGAAG   1800
CAAGACTTCG AGGGCTCTCT TTTCTGCTTA ATCGAGAAGA ACGTCGAGAT TGCTTATTCG   1860
CATCAAGAAA TTGAAGCAAT CTTAGTTGAA GCGGAAATTT CAGAATTATT GAATGTTCCT   1920
GTGGGCCAAC CACTTTTACA AGTCCACTCT ATCACCTATG CGCTTGATGC AACTCCTATT   1980
TTATATGATG TCTCTTTATA TCGAGCAGAT CGGTACACGT TTAAAAACAC ACTGACCCGC   2040
TATAGCCCGT CTGAAAACAA CCAAGTGGAG CTAGGAGGTT CTTGGAACGA ATGAAGATCA   2100
AAGAAGAAAT AGCCGCTCAA AAAGATTTAT TTTATGAAGA CTTAAACAAA ATTATCGCGA   2160
TTCGAAGTGT GAAAGGGTCG CCTAAAAAAG AGGCACCTTT TGGCGAAGGA CCGAAAAGAG   2220
CCTTGGAAGA AACGCTGAAA CTTGCAGAGC GTTATGGTTT TCAAACTGGG ATTGTCAATG   2280
ACGCAkTggC TATGCGCAAT GGGGAACAGC GGAAGAATAT CTGGGAATTA TTGGTCATTT   2340
AGATGTAGTA CCAGAAGGTT CTGGTTGGTC AGTGCCGCCC TTTcAATTAA CGAAAAAAAA   2400
TCaACGTTTG TATGGTAGAG GAATTCTAGA TAATAAAGGT CCTATCTTGG CTTGCCTGTA   2460
TGGAATGAAA TTACTGAAAG AACTTGGTTA CCAACCAAAG AAAaCCATTC GCTTAATGTT   2520
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TGGCACGGAT GAAGAAAGTG GGAGTGGAGA TATCCCCTTA TATTTAGAGA AGGAAAaCGC 2580

ACCCGTTTTT GGATTTACTC CAGATTGTAA ATATCCAGTA GTTTATGGGG AGCGAGGGAT 2640

TGTTAATTAT GAGATCACAA CGACCATCCC AGATGATTCA AGTGAACAAA TTGGTCAGAT 2700

TATAGGTGAT CAAGCAAAAG ACCACGTACC TGATCAATTA AGTGTGGTGA TTGCGGGAAA 2760

AACAACAGCA ATCACGGGAA AACGTGCTCC TTCCAATGCG CCAGAACTAG GCAAGAACGC 2820

GATTACTTTA TTGGCACAGA AAATTAGCGA GGAACAGTTA GTCAAAGGAA ATTTATTACA 2880

GTATTTCGAC TGGTTAACCG CTAGTTTTCA CGAAAAGCAC TATGGCGAAG GAGTAGCTCT 2940

GGACTTTAAG GATCAGGATA GTGGGCAATT GATTTTAACG CCyTATGyGT TGGAAAAAAG 3000

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AGTAACCACG CAGCTAACGA AGGCACTATT TCCAGAAAGT GAAGTGACCG TCATCCGCCG 3120

CCTCCCTAGT ACGCTGTTTC CAAAAGATGA GCGCAATGTT CAAAAATTAA CCAAGGTTTA 3180

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CTTTATGCCG AATATCGTTG CTTTTGGTCC ATCATTTCCT GGTCAAAAAG GCATTGCGCA 3300

TAACCAAGAT GAATATATGG ATGAAAAAGA TTTACTGCTT AATCTGGAAA TCTATATGCA 3360

AGCGATGATT GCATTAACAG AAGCATAAAA CCAATAGAAG ATACACGTAT GAGAAGAAGA 3420

CAATGTGTTT CGTAGAGGTC GCATACGTGT ATCTTCTATT TTTCTGTATA AAATTTCATT 3480

TTCAGTATAT ACAAAACAGT ATATACTAGT TTATAATGGT GGAGAAATGT AAGCGTTAAC 3540

GAAAGGGCGG ATGGAAAATG ACTTGGGGTG CAATTGCGAC ATGGCGGATG GCACATGATG 3600

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ACGGTTTTGA AAGAAAGAAT ATGTTGACAG AACGCGCTAA TCAATGGTGG CAAAAGCGTT 3960

TAAAAGAAAT TCAGGAAAAT CAGTTGAACC CCTATGATGG GCATGATACT GTCGGCGCTA 4020

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AAAAAGCAGG ACGTGTTGGC GATTCACCAC TGTCAGGTTC TGGTTTTTAT GTTGATAGCG 4140

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AATTGAATAA ATGAGGAGAG TGAAGGAACA TGAGTAAAAA ACAAATTTAT CTTTTTTGTG 4560

ATGCAGGGAT GTCTACAAGT ATTATGGTGA ATAAAATGAT GGAAGTGGTG GAAAAACATC 4620

AAATGCCTTT AATGATTACT GCTTTTCCTA TTGCAAGAGC mCAAGAAGTG GTTGAAGCAG 4680

AGAAGCCTGT TGCtATTTTA TTAGGcCACA AGTCCGTTTT TTTATTAGGn AAAAACCA 4738

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GGGTGCTGCC CCAATGGCGT ATGCACTTTG GACAAAACAT TTAAAGGTGA ACCCAACAAC 60

TTCTAGAAAC TGGGTTGATC GTGATCGTTT TGTACTTTCA GCAGGCCACG GCTCTGCAAT 120

GTTGTACAGC TTATTACATC TATCAGGATA CAACGTAACA ATTGACGATT TGAAAAATTT 180

CCGTCAATGG GATAGTAAAA CACCAGGGCA TCCAGAAGTG CACCACACAG ATGGTGTTGA 240

AGCAACAACA GGACCTCTAG GACAAGGGAT TGCTATGGCT GTTGGTATGG CAATGGCTGA 300

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CGCAATTTGT GGTGATGGTG ATTTAATGGA AGGTGTTTCT CAAGAAGCAA GTTCAATGGC 420

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TGCTCGTTTT AAAGAAACGA TGATTGGCGA AGGCCAAAAA GCTGAAGAGG CTTGGAATGA 840

GATGTTTAAG AACTATGAAC ATGCGCATCC AGAATTAGCC AAACAATTTA AAGAAGCTTT 900

TGCCAACCAA TTACCTGAAG GTTGGGAACA AGAATTACCT AAATATGAAC TAGGAACAAG 960

TGCCGCAAGT CGTGTAACAA GTAAAGAAAC GATTCAAGCT ATTTCAAAAG TTGTTCCAAG 1020

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TGAAGCTGCA GCAAGCTTTG GTTGGGAACG CTATGTAGGG ACGGAAGGCA AAACaATTAC 1800

AATTGATCAC TTCGGCGCTT CTGnCACCTG GCGGTCTAGT TCTTGAAAAA TTCGGCTTTA 1860

CTCCTGAAAA TGTGGTTAAT ACCTATAAaT CaCTATAAaT AAACGATAAA AAACCTGAAT 1920

GCTTGTGATA GCATTCAGGT TTTTTTGCTT CATTTCTTTT TGGGAGCAAA GAGCATAAAG 1980

TGAAAAAATA ATGCGAACAA TTGGAACCCA ATACCAGTTA AAGTAACACC AGACCAACCA 2040

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AACATAAAGA CGGTATTGTT ACGATTGCTG GCTTCTTCTC CCAAATTTTG GACGCGTGTT 2160

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GCCATGACCG CAGCATAAGG AATAATAATT TGGGCGACAA TAGAGAGCAG CCCGATAAAA 2820

AAAGAAGAGA GTGCAAACAG GAGAAAACTT GGTGCAAAAA ATGCAGCACT TAGAGACAGC 2880

GAGGAGAGCG CGGCTACTCG AATGATTAAT TTGCGACGAT CAACGACATC GCCTAATGGA 2940

ACAAGAAAAA GTAAGCCTAG CGCATAGCCT AATTGGGTCA GCATAGTAAC AAAACCAATA 3000

GAACCAATAC TGACTTGAAA GGCCTGAGCA ATTTGGGTGC CAATTGGTTG AATATAATAC 3060

ATATTGGCGA CCACGACCCC GCAAGTTAAC GCTAATAAAA ACGTCACTTG ATTTGTTAAA 3120

CCCGATTGTT GTTTCTTCAT CTAACCACCT ACATTTCTAT GTAATTCATT TTGTAATACA 3180

ACAACTACTC GGCAATAGTT GTTnTGATTA CAAAAACAGA CTTCT 3225

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 682 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

AAGTCCTTGT TTATTGGAAT TTTACGACAG TCGCACCATT ACCACCTTGG TTTTGTGGCG 60

CAAATTCATA GCTTTTCACA CTGCGGTGAT TTTTTAAAAA TTCCGTTATT CCGGTTCTTA 120

ATGCACCTGT TCCTTTGCCG TGAACAATGG TTACTTGTGG ATAGCCCGCT AGAATCGCAG 180

CATCAATGTA TTGGTCAACT TCTGCCAATG CTTCTTCGTA GCGTTTGCCA CGTAAGTCTA 240

GTTGTGTGCC AACATGACTG CTTTCTGCAG AACGAACCGT TGTAACTCTT GGTTTCGCTT 300

CTTTTTGTGG AGCGACAGGC GTCATATCCT CTTCAGATAC GTTCATTTTT AAAATGCCCA 360

ATTGGACTTG CCATTGTCCT TTGCCGTTGT CTTTTAATAA GGTCCCTCGT TGGCCGTAAG 420

TATTGACAAT TACTTCATCG CCAGCTTTTA ATTTTTTCTG TTCTTtCGCC TTCTTCAGCA 480

CTTTGTTTTT AGCAAGCTTG GTTTCyTCAt GGTGTAAnTG AGAAAGTTGT GkTTTCGCAT 540

CAATTAACTG ATGTTCTTTG ACACCACCTT GTTGGCCACT TTCCAATTGC ATTTTGCGAA 600

TATCAGAAAT AATGGTTTCT GCGTTTTCTT CCGCTTCTGC AATAATTTTA TTTGCTTCTT 660

TCCGTGCTTn TTGTAATTCT GT 682

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GCCAGTTGAG GAnTTGGTGT TGGCGCGGAA TACCnTTTnT CAAAAAATAC CAAGGAGAGA 60

ATTAAAAGGA GTTATCCCCT ATTATATTGT CCGATGCTTT CGCGGAGGAA GTTTTTAAAG 120

GCAATCCCGC CGCTGTTTAT GTTTTGGAAA AATGGTTGCC AATGCTGTAT GAAGAATTTT 180

TTTATACTAT TTTTTTGCCA TATTATAAGG GACGGGTTAA AGAAAGAACT TATAATAATA 240

GACTTAGTAT GATAAAAAAT ACTTTTGCCT ATTTTTTTAA AATGAAATTG AAAAGTATAG 300

CTCCTGTTCA TATACAGAAG TGGCAGAATG AGCTGTTGGA ACAGTATGAA AACACGTATG 360

TAAGAAATAT TTATGGACTG TTTCAGATGT CTTTAGATCG AGCTGTTGTG TTAGGAATGA 420

TTTCTTCAAA TCCAGCAAAG ATCGTTGGTA ATGTGAAAAA AAGTAAGAAA GAAATTGATT 480

TTTGGACAAA AGAAGAATTT GAAAAAGTTG TTAAGACTTT TTATGTAGAA GATTATTACC 540

AAAATTTTTC TTTTATTTGT ATCTGGTTAT TATTTATGAC AGGCATGAGA ATAGGTGAGG 600

CTACTGCTTT AACTTGGAAA GATGTGAATT TAGATAGAAG ATATTTAACA GTAAAAAAAT 660

CACTATATTA TAAAAATGCG CAAACTTATG AATTAGTGTC TCCAAAGACT AGAGCCAGTA 720

TTAGGACGAT TTATTTAGAT GAAGATACAG TTCACTATTT AAGAGATTGG AAAAAAAGGC 780
AAGATGATGT TGGAGGAATT GAATTTATTT TATCTTATAA TTCAGTTCCT ACTCAAAAAC 840
ATACAGTAAG ACATATTATT AAACGTCATG CAAAATTGGC AGAGGTACAT GATATTAGGA 900
TTCATGCTTT AAGACATTCT CATGCTTCTT TATTAATAAG TATGGGTACT AATGCTTTGT 960
TGATAAAAGA ACGATTGGGT CATGAAGATG TGCAAACAAC TTTAGGTACT TATGGACACT 1020
TATATCCAAG TAGCTCCACT GaAATAGCTA ATGAATTGAA GGGAATAGTT AATGTTGAGT 1080
TTACTAATCA AAATATGGCT TCGGAGGTTA CTAATCAATT TACTAAAGGA GTAAAAAAAT 1140
AAAGTGTGAT AAAAGTGTGA TAACGCAAAA GAAAACCCTC TATAAATCCT ATTATATAGG 1200
GGTTTATAGA GGGTTGTTTA TTATTCCCAC TCCACAGTTG CAGGTGGTTT TGAAGTAATA 1260
TCGTACACGA TACGGTTTAC ATGTGCAACT TCGTTCACGA TGCGCACAGA GATTTTTTGT 1320
AAAACATCCC AAGGGATACG GGCAAAGTCA GCGGTCATGC CGTCGATAGA AGTCACAGCA 1380
CGGATACCGA CTGTGTAATC GTAGGTACGG CCATCGCCCA TAACGCCTAC TGAGCGGATG 1440
CCAGGTAAGA CAGTAAAGTA CTGCCAAATG TCACGATCTA AGCCAGCTGC TGCGATTTCT 1500
TCACGTAGGA TAGCATCTGA ATCACGAACG ATTTGTAACT TATCTTCTGT AATTTCACCA 1560
AGCACACGAA TACCTAATCC TGGTCCTGGG AATGGTTGGC GCCAAACGAT TGCATCAGGC 1620
ATGCCAAGTT CAGTTCCTAA GGCACGAACT TCGTCTTTGA ATAATGTATT TAAAGGTTCA 1680
ATTAATTCAA ATTGCATGTC TTCAGGAAGA CCACCAACGT TGTGATGTGA TTTAATTGTT 1740
TGCGCAGTTT CTGTACCAGA TTCGATGACA TCTGTGTAAA GAGTTCCTTG TGCTAGGAAT 1800
GAAACGCCTT CTTCCCCAGC AAGTTTAGTT GCTTCGTCAT CAAAAACATA CACAAATTCG 1860
TTACCGATGA TTTTACCTTT TTGTTCAGGG TCAGAAACGC CTGCTAATTT GCTTAAGAAG 1920
CGTTCTTTCG CATCTACTTT AATAATGTTT AAGCCAAATT TACCGCCTAA ACTTTCCATT 1980
ACTTGTTCTG CTTCACCTTT ACGTAATAAT CCATGGTCAA CGAAGATACA AGTTAATTGG 2040
TCGCCAATGG CTTTTTGTAA AAGCACGCCG ACAACACTTG AGTCAACGCC ACCTGATAAA 2100
CCAAGTAAGA CTTTTTTATC GCCTACTTGT TCACGGATTT TAGCGACTTC CATATCGATG 2160
AAGTTTTCCA TGCTCCAGTC ACCAGTACAG CCACACACAT CAAAAGCAAA ATGACGTAAT 2220
AAGTCGTTAC CATATTCTGA ATGACGAACT TCTGGGTGAA ATTGTACGCC GTAGAATTTG 2280
CGGTTGGCAT CTTCGATAGA AGCGATTGGA CAATCGTTGC TTGTCCCAAC TTTTTCGAAT 2340
CCAGGAGCGA TTTCTGTTAC TAAATCACCG TGGCTCATCC AAACGGTTTG TTTCGCAGGT 2400
GTTCCTTGGA ATAATGTCGC ATCACCAAGG ATTTCTAATT CTGCTTTTCC GTATTCACGG 2460
TTTGCGGCAG GTTCTACTTT TCCGCCTAAG TTATGAGTCA TTAATTGCAT ACCGTAGCAG 2520
ATGCCAAGAA TGGGAATTCC TAACTCATAA ATTTCTGGAT CAATGCTAAA AGCATCTTTG 2580
TCATACACGC TGTTTGGTCC ACCTGAGAAG ATGATTCCTT TAGGCGCGAT TTTGCGAATT 2640
TCTTCTGCCG TAGTTCGGTG GCTTAATAAC TCAGAGAATA CGCCAAATTC ACGAATACGA 2700

CGAGTAATCA ATTGGTTAAA CTGACTACCA AAGTCTAAAA CAATAATTTT TTCGACAGAT 2760

GTCAAATCGG CAACGTTAGT CACGTCTATT ACCCCTTATC CATTTAAATT TATCTAAAGA 2820

AAAGGCGGTT AAAAAGTGGT CAGCACCAAG AATTAAGAAA GGATTTTCAA AAATTGTTTT 2880

ACGATTTTTA GAAAATTTTG GCTTAATTCC GCAGGGgCTA CTTTTAAACA GCCGAAAATC 2940

AGGCGGTTAA AAAGTGGTTC ACTTTTGTtC CGTACTCTTC TTTGTCTAGC TATACTTATT 3000

AAAACATTTT ACTCCTTGAA AGTCATGCAT TCTGCTGAAA ATTTTCAAGG ATATTTCTAC 3060

mAAAGATACA GGATATTTCT TAGCTCGTCA ACCCTTAATA TTTACGTAGA TAGATTTGGT 3120

CAATCAAATG ATTTTCCGTT TTATGCAAAA TAATGTCCGC ACGTCCGCGC GTTGGCAAGA 3180

TATATTCCTC CAAGTTCGGT AAGTTCACGG TTTTCCAAAC ATTCCGTGCC ATGGCGAAAG 3240

CATCTTCTCG TTTGCCAATT GCATATTGGT AATAATAATT ATTAGGATCT AAGAAAGCCG 3300

TATCTAATAA GGCCCCAAAA CGTTCTAGGT ACCATTTTTC AATTAAGGCT GGATCGGCAT 3360

CTACAAAAAT AGAAAAATCA AAAAAATCAC TCACATAAAT TTGTTGATTG GCGGGTAACT 3420

GTAATGTGTT AATGCCTTCA ACAATCAGAA TATCTGGTTG TTGTATCAAC TCATATTCGC 3480

CTTCGATAAC ATCGTAGACA CTGTGAGAAT AGACGGGTGC TTTAATTTCG TCTTTGCCGC 3540

TTTTGAtTCG TTTAAGAAAT TAATTAGCTT CTCCATGTCA TAACTTTCAG GAAACCCTTT 3600

TCGGTCCATA ATTCCCTGTT CTTcTAACAC TTTATTGGGA TACAAAAATC CATCCGTkGT 3660

AATGaGTTGA ACGTTTCTTC GTTTAAACGT TCGGGCCAGA ATTCTTTGCA AAAGACGAGC 3720

GGTGGTGCTT TTACCAACGG CGACACTGCC GGCAATTCCA ATGATGAATG GTGGTACAGA 3780

GACATATTCA TGTAGGAATA ATCCTTTGCT AAGTGTTAGC GATTCAAATT CTTTCATGTA 3840

CAAATGAATA AGATGCGTTA AGGGTACATA AATTTCTTGT ACATCTTTTA GTGAAATTTG 3900

GTCGTTCACA CTTTTAATGT TATCCAATTC TGCTTCGGTT AACGGTGCTT TGCCGTCATG 3960

ATAAAACCCA TGCCATTCTT CTCTGGAAAT TGGGTAGTAA TTCATTTTAT CGTCCATTGT 4020

TCCTCCACC 4029

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

AACCGGTGTG ATTACATCAT ACAATACTGA TTCAGATTTG TAAACCGCTT TCTAAAAAAA 60

ATAAATAAAC ATAGTCCATA AAATGGACTA TGTTTACGGC CTTAAAAAAA GGTAGTTATA 120

TTTGTAAAAA TTTACTCACT AATAATCTCA ATCTGATAAA AATCAGAAAG TATGAAACTT 180

TGACTATATT CAATCGGAAC CCCATCGTTT CCTCTAATCA AACGTTTAAT ATTGAATAAT 240

GAAAAGCTAT CTTCTTCACC AAAACTTTTT CTTATTATTC TCAACGGCTC TAGTTCATCT 300

GAATCCTTCG TTAATAAAAT CGTGCTCACC TCCATCGTCA TCGGAAGATT AGCCATATTT 360

CCTTGAAGAC CCaATTCATC GGATAAACTA GCTCCTTCAA TCAGGCGTTT TACTGAATCA 420

TCCCTAAGTT TATCTGCAAA GAGATAGCGA TTTTGAATTT TCCATGGAAA ATCATTCGTT 480

AATGCAATTT GGGTTAGCTT AAGCAACGCT TTGCTGCCTG ATTTGTCGCC TAATATCTGT 540

GCGATCTCTT TATCAGTAAA TTCTTCCGAA ACTAAAGTGA TCGTTTCCTC AACCGACTTT 600

TGTTTTTCGT TATTGGACAT CGATAACTTC TCTGAGAAGA AAACTTTTCT ATGCTTCAAA 660

TTTTTTCTGA CAAAGGTTCC CTCGCCCtGA CGCCGAATTA AATACCCTTC ATTTaCCAGA 720

TCGTTCAAAG CCTTTACTAC TGTTGTATTA CTGACATTAT ACTTTCTTTT TAAATCACCT 780

TCTGAATAAA CTTTCTCACC CGTACTAAAC TCTCCAGATT CAATCTTCTC TATGATATCC 840

CGCTTTATAA TCTCATATTT AGGCAACATA TGATCCTCTC CTAACACGTt AACCGTTAAT 900

CTTCATTGTA AAGAACTTTT ATATTTATGT AAATAGAATG AGTAATAATT ATTTGCTCAA 960

ATTTCGCACA CCAAAATCAT AGCTAAAAGC TTGGCATGAA AGGGCGGAAG TTTTTGGGAA 1020

TTGATTTCAA TAAATTTGAG TTCTTTTTTA GTATAATTAG CTTATAAAAA TACTGACCGG 1080

ATTAAATGAA TGATGrAGCG AATGrCTATC AAAAAACAAn CACCTACAAA AATTTA 1136

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3914 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

AGATCGGTCC nTAATAATTT ATTTTTGCCC TCCAGCGTCG nTAATGTCTC CTGATGAGGA 60

TGTTTAAAAC GATTATTCAG TCCAGCTGrA AyCAAgCyTC TCGCGGATTA AGCTGTTTGA 120

TAAATCTTTT AGTAGACGAC GTTTTACTAC CATGATGACC GACTTTCAAG ATGTCGATTT 180

TCAACTGGGG ATAGCGAGCC AACACTTGTT CTTCTCCTTC GGCTTCCAAG TCACCAGTAA 240

ATAAAAAATG CCGTCCGCCT AATTGTGTGG AAAACACTAT CGAGTCATTA TTGCCCCCAA 300

TACTGCTCTT ATTTGGTGAT AAAATTTGAA AAGAAACGGG CCCATTAATT CGCTTGGGCG 360

CTAAAATTGG CCGACAGTCT GTCCCGCTTT TTTGGAGTTG TTTCAAGACT TGGCGAAACG 420

AAAAATTGGC TTCAGCTGCT CCTTTAGGGA AATAAAGAAC AGAAATTGGA ACCTTCTGCG 480

CAATGGCTAA TAAATCGCCA AAATGGTCTT CATGTGCGTG TGTGATGATC ACTTCATCTA 540

AACGTTTGAC TCCTTGACTT TTGAGAAAAG GAATCACTGA ATATTCTGCT CCTGATCGAC 600

TATTTTTCCG TTGCCGCCAA GCTTCTTTGC CAAAAGACAA CCGCCCCCCT GTATCGATCA 660

GTGTATTTTT TCTGTGAAAA GGCGCTTGGA TAAACAAACT ATCCCCTTGG CCTACATCGA 720

TCATTGCAAC AATGCCAATT GGCGAAAGGT ATTTACTATT TATCAAAACA ATTAGTAGTC 780

CGATTGAGAA AAAAATTTTT TTAGACTTGT CTGCTAAATA AATCATTGAA AATCCGATTA 840

GTAATAACAA ACTAATTTGT ATCCAAGAAT TTAAATAGCC GATGGTCAGC TTCGGATTTA 900

AGTGAACTAG CACCCACTCA AATAAGCCAT TCATTGTTAA AAATAGTGGT TCGAGCAAGG 960

CTGCTAAATA ACGTGCTGGC ATAATAATCA CTAGAAAAAA GCTCAACGTC AAAAGCGGTA 1020

ACAAGAACCG TTCAAAAATT GGTAACAAGA GAAATGTTAA GAAACTTCCT AACAAGGGCC 1080

ATTCATAAAA TGATTGTACT AAAATAGGTA AGGAAGCCAC AGCCAATAGG AAAGAGCCTA 1140

AACAATTTTT AATGAAAGGC GAAGAATAAC CAACCAATGT TTGCTCTAAA AACAGCAGAA 1200

CAAAGGAAAG TAAATAACTA AATTGACCGC CGACTGAAAA AAAGAGGGTT GGCTGAACAA 1260

TCAAGTGCAC TAAGAGAGTT AAACTCCAAC AATCGAGGGC CGGAACCTGC CAATTAAACC 1320

GTCGATTGAA CGTATTGAGG TTTGTTTGTA AAAGCGCCCG CATGACACTA ACTGAGAATC 1380

CTGTTAAACC AGCATATATC AGAGAAAAAC CGCATTGCCA CAAAAAATAA CTTTCTTGCG 1440

TTCGGCGAGC AATTCTTAGC ATTAGCAAGC GAAATAAACG AAGGAAAAAA GAAACATGCA 1500

TCCCTGACAA ACTAAAAAGA TGCAAAATGC CTAATGCTGA AAATTTATCG CTTATTTCaG 1560

CAAATTCTTC aTTACGAAAA CCTAATAGCA ACGCATTCAT ATACATTGCA CTAGTCTCAG 1620

CAAAATTTTT CTGAATATGT ACCATCGCCC ACTTCCGCCA GCCGCTAATG ATTTCTTTAA 1680

ACCGCCAAGA AAAAAAGGAA CGCGGTTGTC CTATCTCCTC AATGAATAAA ATAGCTTCGA 1740

TTCCTTGATT CTTTAAAAAT AGTTGATAAT TGAAGCCATT TTTGTTGGTT TGACCTTGGG 1800

GCGAGTCTAA AATACCTACA GCGGTTGCCT GAATGGTTGT GGTTAGTTGT TGCCATTGCT 1860

GTTTTTCTTT CACACTTTTT AATTGATAAA ATGCCATCAC TTTCTGCCTT TTGCCTTTTA 1920

CGATCCAATT GGCAGGAAAT TTTACTTGAT CACCATCGAC TTGTATTTCA TCTGGTAATA 1980

TCGTTAGCTG TCCTGACAAG CGGACTTCTT TAGGCAACAA AGAGACTGGC TTTAACCACT 2040

GGAAAATCAA TATGCCCCCT ACTATTAAAA AACTGCACAA AAAACCTCCC AATATAACAG 2100

GAAAACTTTT TGTACAGACA ATACGGATAA CAGTGATAGA AAAAAGAAGA GCTCCTAATA 2160

GACTAGGTGC GAAAAAACAC CACAGCCCAC AACTAGTCAG CAGAGCTATG AAGAACCAAT 2220

TATTCCTCAG CTGAGGAAGG ATTGTCCTCA AGTGTGGCAA ATTCTTCTCC CCATTGTAAT 2280

TCGGCAAAAT ATTTTGGTAC TAAAGTCACT TTTTCAACCG TGGCTCCTAC TTGTTCAATT 2340

AAATTTAGGG CGTACGCATC ATTACGGTAA TCCTTTAAAT AATAAATCTT TTTAATCCCT 2400

GCTTGTAAAA TCATCTTTGT ACATTGCAGG CAAGGGAAAT GTGTCACATA AATTTCTGCC 2460

CCTTCTGTAG GGACGCCAAA CTTCGCACAT TGTAAAATTG CATTCATTTC TGCGTGGATT 2520

GTTCGAACGC AATGATTATC AACAACATAA CATCCTTCAT CAATACAATG CGTTCCGCCA 2580

CTGACTGAAC CATTGTAACC TCCTGCAATA ATTCGTTTGT CGCGAACAAT GGTTGCTCCG 2640

ACAGTTAACC GTGTGCAAGT ACTTCTTAAT GATAATAAGA CGCTTTGTCC CATAAAATAT 2700

TGGTCCCATG GAATTCGTTC CATAATAAAC CTCCTTTATT TTTAATGACT CCTGTGTTCG 2760

ATTTGCCAAA TCATTTAATC TTATTACAAA TAGTATGTTA TCCGCATCCC ATAGTCAAGA 2820

ATTCTCAGGA ATTTTCTGTT AAAAGTTAGC CAGTCACTGT CAACATGTCT TTTAAACGTT 2880

CTACTGTnTT CTCTCCAATa CCTGGgAACA TTTTTCaGTT CCTCGACGGT TTTAAACGGT 2940

CCTTGTTCGT CACGAAmACG AATAATCTCT TGTGCTTTTy TCGCACCGAT TCCTGAmATC 3000

GTTTGTAGCT CTGCTTCTGT TGCCGTATTA AGGTTGATTT TTTCCTCCTG ATTTTGCTGA 3060

GCAGGTGCTG ATTCCTGCAG CGTTTCTAAT GATTGTGCCA CTGGnTCTCC TTTTTTGGGC 3120

ACGTAAATAA TCATTTGATC TTTtACTTTT tGrGCGTAAT tGACCTGGGT AGTATCAGCT 3180

TCCTcGtCAC GCCTCCAnTA AAGtAAAGCA TCCCAAATCC GCTGCTGATT TTTTAGTTGA 3240

TAGATTCCTG GTACTTTCAC TGCGCCTTTA ATATCAcATA GATCATTGTT TCTGCCCTTT 3300

CTTTTGTGGC ATCTGTGGCG ACCTCTGTCG TAGTGGTCAA CTTGTTTCTw CmcACATTGT 3360

GGTGTCTACT TGTAGCTCCT TATTAACCAT CAAATAAATG CCCACTAATA GAGTTATCAA 3420

AATGACCATG AACACGCCAC TACCTAGCAA TAGCCACTTT TTAGGTAACT GTTTCAACCA 3480

ATCCATCGTT TGCCCTCCCT TCAAAATATA ATTACGCATT TTTTAACAAA AAAATGCGCC 3540

TGGACCAAAA ATCACTAGTA ATTTTTGGTC CAGGCCTACT TTTATTTTAA TTTCTCTAGA 3600

TAGTTCAAGG CATCTTGAAC CgTTyTTACT GGGACAATTT TCATTTTTGT CCCAATTTTT 3660

TTCGCAGCTT CTTGTGCTTC TTGATAATTC GATTTGATTT TTGGCTCAAC TTTTTTCATT 3720

TCTGAAGTTA TTTCATCATC AGGTGCAAAG AAAATTTCTG CGCCGTTCTC ACTGGCAGTT 3780

ACAACTTTTT TGTCAATGCC TCCGATTCTA CCAACGATTC CTTGACTGTT CATCGTACCT 3840

GTTCCAGCAA TTTCATGACC TTTACGTAAA TCTTTATGAC TTAATTGTTC ATAGGTCTGC 3900

AAAGAAACAT TAAA 3914

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17764 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TCGTGGCAGG AAAAATGTTG GnACTTTATC ATTACGGATT AAAAAAATCn ATGnTCCTGA 60

AAAAGCTGTC ATGACTTCAG GTGGTAATTT TTTAATCGTT CTGGTAACCC ATTGAAACCA 120

CTCCTTCTTT TTTATCATAC CACAACATCC ATTTCTCTAA AAGCGCAGCA CTTACTACTG 180

AATATCTGCT AAAATTTGCC TGATAATCTG CTTTTCAGAC AGTTGTTCAG ATAACCGCTG 240

TTCTCCCGGA AACCCTAAAT AATCTTCTGG TAGCCACCAA CGTTTCATTT CCACGACACC 300

AAATTCTTGA TTCTTGTTTC TCTGGCTATG TCTTTTCAGC GTTTCTTCAA AAGAAATATC 360

AAAATAATAA ACCTGAACGT TTCCTTCAAA GAGATGGATT ATTTCCTGAA AAAAGGAATG 420

ATAAATGGCT TTTTGAAAAA TCCCTTCAAC AATCACATAC TGGCATTCTT GATACCCAAA 480

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AGCTACCAAC TGTTTTAACA AAGCAATACT TAGATTACCT GTTTCATCTT TAACACGAAG     540
CATTTCTCTG CGCACCACAT CTTGAGAAAT CAATAACGAT TGTTCTTTAA GACACTGATG     600
AAGCGCGTTA gcTATCGTTG TTTTACCACT ACCAGAATTA CCACGTAAAA TAATTAATTT     660
CGGTTGCATC TGTTTCCCTC CATTTTCTTG ATTGTTGAAA ACCAGCACAA AAGAGCAAAA     720
AACTTGGAAA AAACTCTCCA AGTTTTGCTG TTATTTTGAT GAATGTTTCG TTGAATCTCG     780
CTGAATGAAT TCCGTTCCGA CAATAATTTT TCTAGGAACT GGGGGGGGAT tCAAGCATAA     840
CTCTTTCATT GTCTCAACGG CTAGCTCACC CATCCATTCA GTATGAACTT aACTGTkGTT     900
AATGTTGGTG AAACATATTT GCGACACTAA TATCCtTAAA ACCAATGATA GAAATATCTT     960
CTGGCACACG AATGGCTGCT TCTTGTAACG CCCGCATTAC ACCAATCGCC AATGTATCAC    1020
TTGcAGCGAA AAAAGCGGTT GGACGAGTGT CCGCTTCTTC AATAAAGTCT TTCATCGCTT    1080
GATAGCCTTC TTCAACAGAA AAAGCTGCTT CGACAACCCA TTCTTGATGA TAAAGGTCCA    1140
GATCTTTTAA GGTTTCTTTA AAAGCGACAA AACGTGGATC AACCAATGCC ACGTGGGACT    1200
CTTTCGTATA TTCTTGCCCA GAAAGCATAC CAATTTTCTG ATGCCCTTGC GCCAAAAATT    1260
CTTGCACAAT TGTTTTAACA CTTCCAGCAA AATCAACAAC AATGGAGTTT TGGCCAAAAG    1320
CCATTGCATC AAAGTCTACA AATAGAAGAG GTGCGCCTAA GGCGGCTAAG GCCGCCACTT    1380
GCTTTTCATC AAATTTTCCT AGGGCAATTG TCCCATCAAA TCTTTTTTGA GACAGGTTTG    1440
TCAGAGATTC TTTGACTAAA AGAAAACCCA ATTCCTCTGC CCGCTTTTCA ACACCTAAAC    1500
GAATCGATAA ATAGTAAATA TCATCCAGTT CTTCTGGATC GCTGAACCAT TGGACAAACC    1560
GAATTTTCTT TTTGCCTGCT TGTTTTTTTC TGGCTCGCTT TTTATAATTT AACGTTTCTG    1620
CTGTTTCAAA TATTTTCTTC TTCGTTTCAT CACTAACTGA TAATGTTTCA TCATAGTTCA    1680
AAACTCTCGA AACTGTCGCC GAAGAAACAC CGACTTGCTC TGCTATATCT TTAATGGTTA    1740
CGATGTTCCT CACCTCAAAC TAATCATTTT CTATACATTG AATAAATCGT TCAAAAGCAC    1800
GACGACCTTC TTCGTCACGT TTAAAGACGC CGGCATCTGT TAAAATTTGA ACAAAAAATTG    1860
TCCCAATTCC TTGTTGGATC ACTTCTTTGA CATTGGCTTC AGTGATGGTT TGCTGACTGA    1920
GTTCATCCGC CCAAGCTCGA TGACTTTCAG CAATTTGATT GGGTTGCTTT AATAAATACT    1980
TTTCGACTTC TCTTAATTCT TGTGCCAGCC TTGGTGGCAA AATAGCTAGT CCCATTACTT    2040
CAATTAAGCC AATATTTTCT TGCTTAATAT GTTGTACTTC TGGATGTGGA TGAAAAATGC    2100
CATCTGGAAA TTCCTCCGAA ACATTATTAT CTCGTAAAAC TAAATCCAAT TCAAATAATG    2160
ACCCTTTGCG TCGGGCAATT GGCGTAATCG TATGATGCGG TGTGCCATCT TTTGAATAGG    2220
CCCGAACTGA GACACGTTCA TCAGAATAAT TGCGCCATTT GGTCAAAATT AATTCGGCCG    2280
CCTCAACTAG TTCCTCTTGA CGATCACTTT GAAGACGAAT CACAGACATC GGCCATTTTA    2340
AAATACCAGC AGTTATCTCA GGATATTTTT TCAAAGAAAA TCTTTTTTCC ATTGGTGCTA    2400
AATCCATTGG AAATGTATGA CGTCCTGCTT GGTAATGATC ATGAGATAAA ATAGAACCAC    2460
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CAACAATTGG CAAATCTGCA TTAGAGCCCA CAAAATATTC AGGGAATAAC TCCGTAATTT 2520

TAAGGAGTCG CTGGAACGTT TTTTTCTCGA TTTTCATTTC TCGATGTTGT TGGTCCAAGA 2580

AAATCGCATG CTCATTATAG TAAGCATATG GCGAATATTG AAAGCCCCAA GCTTCGTCCT 2640

CTAAATTTAG TCGGATAATC CGATGGTTTG TACGTGCTGG ATAATTTACA CGGCCATAAT 2700

AGCCTTCATT CTCCATACAT AACATACACG CTGGATATTT TTTTTGACTC ATTTTCTTTT 2760

CAGCCAAAAT TTTTCGAGCA TCCTTTTCTG GCTTCGATAA GTTAATGGTA ATTTCTAGTT 2820

TACCATAGGG TGAGTCCATT GGGAAAATAA TATTTTTGGC GATTGCTTTC GTTTTAATGT 2880

AGTTATTCGT TTTACATAAC TGATAAAAAT AATCCGTTGC TTTTCGTGGA GACTCTTGAT 2940

AATAATCCAT AAACTTCTGA TTAATGATGG TTGGGGTCGG CGTAATAAAA TCCATTAACT 3000

CCGCTTCTAG TTGTTCTGCT TCCGTAATTG AGTCATCGAT TTGGTGATTG GCTTGTGCAA 3060

TATTTAAAAG ATGTTCCACC ACACGCAACG GTTCTTGCTC ACAAGCAACC GCTTCTGGTT 3120

GTTCAAAAAA ATCACAGCCA ACTAGTTTGG CAATCCGATT CGTCAAATAA TAGCGGTCTG 3180

TTTCCGTCCA ATCGCCATTT TCTATGATTA TCTCTACAAA TGCAGCAATC CATTTACTAC 3240

TTTCTTTCAT CATCTGATGT TCTCCTATTC ATTATAGCCT TGAGGATGTT TCACATGCCA 3300

TTGCCAAGCG GTGGCGATAA TATCCTTGAC CTCAGTTACT TCTGGTTGCC AGCCTAAAAC 3360

TCGTTTGGCT TTTTCACTAG AAGCAATTAA CGTACTAGGA TCCCCTGCTC GGCGTGGGGC 3420

GATTGTCGCA GGAATTTCTT GACCTGTCAC TTCGCGAGCA GCATCTAACA TTTCTTTAAC 3480

AGAATAGCCG TTGTTGCTAC CCAGGTTAAA GACGTCACTT TCGCCGCCAT TTTTCAAGTA 3540

TTCTAAAGCC AAAATATGTG CTGCAATCAA GTCTTCAATG TAAACATAAT CTCGAATGCA 3600

CGTGCCATCT GGTGTATCAT AATCATCCCC AAAAATACTT AGCTCTGCTC GTTGGCCCAA 3660

TGCCACTTGT AAAATAATTG GCACAATATG CGTTTCTGGC GTGTGATCCT CACCAATTGA 3720

GGCATCTTTT TTTGCTCCTG CAACATTAAA ATAACGCAAA GCAACATATT TCATTTCATA 3780

AGCGTTGTCG CACCATTTCA TGATTTTTTC CATCATTAAT TTACTTTCCC CATACGGrTT 3840

TTTAGGATTC GTTGGGGTTT CTTCTGTAAT AGGCATTGCT TTTGGTTCGC CATAAGTGGC 3900

CGCTGTGGAA GAAAAAACAA TGTGTTTCAC CCCGAATTCT TGCATGACTT CCAACGCAAT 3960

TTGAGTGCCG TGAACATTGT TATTGAAATA CATTAACGGT TTCTCCACGG ATTCTCCTAC 4020

TAAAGAATTG GCCGCAAAGT GCAACACCCC TTCAATTGAT TCCTTTTCAA AGACGCTACG 4080

TAAAAAAGCT TTATCACGAA TATCGCCTTC ATAGAAAGTC GCTTGTTCAT GAACTGCTGA 4140

ACGATATCCC GTTAATAAAT TATCAACAAC AATAACGGCA TATCCTTTTG AAATTAATTG 4200

ATCGACGGCA TGTGAGCCAA TGTAGCCTGC GCCACCTAAT ACTAAAATAG ACATAAATAC 4260

GCTCCTTTTA CTCCCTAATT TCTTTTTCTA TTGTACCATT AAATAAGGTC TACTTCTGAA 4320

TTATTTCATT TTGTAAACAG GATTTAATTT GGCCATTTCT CCTTATTCAT TTTTCCTATA 4380

AAAATACAGA AAAGACTTGG TAAATTTTAA CAAATCTCTA AATTAGTCGT AGAGTTTATG 4440

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AAAAATCATT GTAACTATTG GATTTTTTTG CTTTTTTCCG TCATAATAGA AACAAATACA      4500
ATTTGAAAGA AGGAATGAAC GATGAAAAAA TTTGTATCAG GTATGTTAGT CGGTACTGCT      4560
ATCACAGTTG CTGCTTTAGC CGGTGTGGCT ACAACTATTA AAAAaACAGT CATTGATCCA      4620
ATTGAAGAAA AAGAAGATAT GATTGAAGAA AACCGTAAAA AAGCGATGCG TAAGCGTATT      4680
GCACGTTAAA AAATAGCTGT GACGTTGAGA TAAAAAATCT AACGCCAAGA AATCAACAGA      4740
AGCGCTTCTG GCTCTGTTGA TTCTCTTAAG mATAACAAGT GGTCATCCAT CGCTTTGATG      4800
GATGACCACT TGTTATGCTT TCTTTTTTAC CAAAGGAACT GACTATTTTT CTTAACTATT      4860
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TGTCGCCACC TGTCCATCTT TTGTCATGAC TTGATTCGTG GCAGGCACAA TCAAGAGTGC      5040
ACCTGTTTTG ACTATTTGAC CATCGGCTAA TGCCAGTTGA TGGAGCGTAg cTAGCTTATC      5100
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CGCTTCAATT AAAAAGTGAC TATTATACCG ATTTTCCGGA AACAAATTAG CATAAGTAAT      5220
AAATTGACCC GCTTTCATTT CGACACGCAT TTCTGGCCCC AGAATCGTGA CTAATCCCAG      5280
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ATTCAACGGG GTAAACCAAT GCCACAACCA CTTTTGACTC TCGTCATTCG TTAATAATCC      5400
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TTCCCCGTAG CCTTTTTGAT TATTCCCTCG AGGATGAGAA GGAAAACCGC GACCAGAACC      5880
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CCAGTCCAGC CATCATAGCC GCCTTTTAAA ATATAAATAT CAGTATAGCC ATTTTTGCGT    7260
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CCTGGTGTTC CCATACCAAT TCCCACAAAA TCTTCTTTTT TCATATTATA AAGATCTATA    8400
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CATCTTCCGT TCCATGCCAA AACAGCATCG GTCGTTCTTG TAGTCTTTCT GGCGTTTGTG    10380
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GATAAGAAGG TATTCGCTTC TTCAnTGAGT TAGCTTGGAT AAACAGCCCT AAAGTCATCA 17760

CAGA 17764

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GGGATTAACT TGCCTCnTAA GTTTAGTGCA GATTnCGATA CAAAATTAAG TGCTGAAGAA 60

ATAGCTACTC TTGAAAAAAC GGCnCTAGAA ATGAACAAGA ATTTTCCAAC GAGCAAAGAA 120

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TTGGCTAATC TTCAAGCAGT TGCGACTAAr AGTACGACAA ACTATGAAGA AAAAGTACGA    900

CAAACTGCrr CGGCAGAAAC AAACCTTCAA CAAACAAAAG ATCAATTGGC AACAATCAAT    960

GAGTTAATTC AGAATCGAGC TGTTGTTTTA GAAAAAGCGA AAACAAAAGT TGCAGACGCA   1020

CAAGCGATTG AACAAACGTC TGCTAAAGTG CTGAAAGAAA AACAAGAAGC CCAAAAAGCA   1080

GAAGAAAACA CATTGAATAG CTTGAAGGAA GTATTGGATT TAGCAAAAGA AAACTTAAAT   1140

CAAAAACAAG TTGCGCTTAA AACAAGTACA CGTTCATTGG CTCGTTTAGA AAATGCTCAA   1200

CCAACATACG AAAAAGCAGT GAACGAGTTA AACAAAGCAG AAGCGGCAGT GGTCCAAGCA   1260

AAAGAAGCCT ATGAAAATTC TCTGAAATCA TTGGAGGAAC TCAAAGAACA ACAAGCCGTT   1320

GCTACACTTG CTTATACACA AGCACAAGAA GACCTTTCTA ATGCGAAGTT AGAGCTACAG   1380

CAGTACCAAG GCATATTAAG AGACTTAGAG GCACAACAAG CCGAACAGCG CCGACAAGAA   1440

GCGTTGCAAG AGCAAGTAGC AAAAGAGCAA CAACGCCTTG AACGAGAAGC AAAGCAACAA   1500

CAAATGTTAG TAGCAAGTGC TACTTCAGCA GATAAAACAC CTGGTCTCCA ACAGTTATCT   1560

TTTTCTAAAC AAAAAGAACA GCCAAAAGCA CAAACACTAA CACATTCAGA ACCTCGTAAG   1620

ACGAAACAAG TAGCAAAAGC CCAAGAATCC TTACCACATA CAGGAGAACA AAAAAGTATC   1680

TGGTTGACTA TTTTTGGATT ATTCATGGCA GTAGGTGCGA TCAGTTTCAA GAACAAAAGA   1740

CGGAAAAATA GTTAAAAGTA TAATAGGTGA GGAGCGAAAT TTTCGCTCCT TTTTATTTTA   1800

AATACATGAC ATGAAAGGAG AAAACATTGG CAAAGAAGAT AAACCTTGTT TCCATATTTT   1860

GTTCTCACGA AGCACTAGAA CAAATTTATA TTCTATCCTA CCCGTATTGT TTAATTAAGC   1920

AATATCTATT CAAGAGAATC GAAGATATTT TTGGTTCTTT TTTTATTGGA GAAATGACAT   1980

TGCTGTGGCT GAATAGAAGT CGCTTAAAAT AAAGCAGTAG AATCCCCTTA TTGTTTTATT   2040

TGATTATGCA AGGTGCGAAT CCTTGCCAGC AAGTAGGGTT TACGGTAAAT GATCCCGACT   2100
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GCCGGTTAGC GAAAACCGTA TAGAGATTGA GCGGTAGTGT GGCAAGCAAC AGCTCTTATA 2160

CCATTCATAA GCCTACCGCA AAAAGAATGG CAATCTCAAA AAAACAGGAA ACTGAGAGGT 2220

CGCTCCTTTT AGGTTGGCGT GTAgCATCTG GGATGCAACG GACATGAAGG AAGATAAGAG 2280

GTAGGTTCGA CTCCTACCAC GCCAGTAAGT AGCTTTGCTA CGAGAGAAAA AGAATAATAG 2340

GAGGAATAAC AATGAAAAAT TATGATCCAA ATATCCGATG GGGCTTGCAT ACAATCAAAG 2400

TAAGTTTCCA ACGAGGTGTA TACAAAGGAT TTGTTACCTT TGTAAAAAGT GGAAATTGTA 2460

AAGGGTTAGA CGTATTAGGC ATAGACGAAG AAGATTTATA TGACATGAAA TTTAAAGAAA 2520

ATCCAATCAA TTTTAGACTG CTTGGTGAAG ATGATAATGG CGATGAATGG TTCGCAATGA 2580

CTTTGAAGAA TGACAAAAAA GATGAATTGT TAGTTGAAGA TGTGTGGGAA GAGTTAAGTG 2640

AGTACATTGT GAGGATTGAA ATTATTGATT TTGAGGAGGA AAAATAGAGG AGCGAGAAAA 2700

TACTCGCTCC TCTTTTATAT ATAGAGAGGC TACCCAGCAA TGATAACTAG GTAGCCACAG 2760

ACATAAAATT ACTATTAATC TGGGAATAAA TTATTTATAC CATGAAAAGG GTTACTTATC 2820

AAGAAAAAAT ACCAATGAAT AGGAGAATGT GGAATGAAAT AAAGTAATAC ATCTATAAAA 2880

AAGAGAGGAG GAAAAAGTAT GACTTGTGTA CGTGCGCCAT GTCGGAGAAA TCGTTGTTTG 2940

TAAAGAAAAG AATAATAGGA ATTAAAAAAT ATAATTTACG AGGAGAAGGA TTCATGAAGC 3000

AACAAACAGA AGTAAAGAAA CGTTTTAAAA TGTATAAGGC AAAGAAGCAT TGGGTGGTAG 3060

CCCCTATTCT TTTTATAGGT GTGTTAGGAG TTGTAGGATT AGCTACTGAT GATGTACAAG 3120

CTGCGGAATT AGATACGCAA CCAGGAACAA CGACGGTGCA ACCCGATAAC CCCGATCCGC 3180

AGgTAGGTAG TACAACACCT AAGACAGCAG TAACTGAAGA AGCAACAGTA CmAAAAGACA 3240

CTACTTCTCA ACCGACCAAa GTAGAAGAAG TAGCGTCTGA AAAAAATGGA GCTGAACAGA 3300

GTTCAGCTAC TCCAAATGAT ACCACAA 3327

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TTCGCTGGTA CGTTTTTtCA ATACTTAATA ATGCACTAAC GTTATATAAA ATAAACCGAG 60

TTGCATCATC TACACTGATG CCCTCTTGTA AGCAATTGGT TTCAGGTTCA CTTTCAAAAA 120

TAGCCGCAAT ATTATTGATA TAGGTTTTTT TGAAAATTTG ATACAGCGTA CGATTGTAAT 180

CAGGGCCCAT TTCTTGAAAC ATATCGTTCA ACATTAAGAA AAGATTGGTC GGATGTTCAT 240

CTAACAAAAC TTTGATTAAT TGATAAAGTT TTTCTTCTAC TGATGCATTT CCAGAAACAA 300

TTGGGACTAA TTCTTCCTGA ACACGGGACG TTAATTCTTC AATCACAGCT AAATACAGTT 360

CTTTTTTATT TTTAAAATGG TGATAGAGAT TCGGTTGGGT AATGTtCGCT TTTAAAGCAA 420

TTTCACGAGT GGAGGtATTT TgAACCCCTT tGTCATGAAT AATTCAGAAG CGACAGATAA 480

AATAATTTGC CGTGTACGTC TAnATCAGCT 510

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENCTH: 2047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GACATAAGTC GTTTTGACTT ATGTCCTATT TTCGTTTTTT ATTTCCAAAC ATTTTACGAG 60

AATATTTTAA AATTTAGCGT ATACTTAATA TAAGCAAGTT AGGAGGGCTT ATTTATGAAA 120

CCATATGTTT ATGTAATCAG TGATATTCAT GGACAAGCAG ATTTGTTTGA TGCCTTACTC 180

ACAGACTATG ACCCAGTCGA GCATCAGCTA GTTTTAATTG GTGATTTAAA CGACCGTGGT 240

TCGGATTCTA AAGCCTGTTT TCTCAAAGGA AAAGAACTTG TCGAGCAACA CGGCGCTGTT 300

TATTTACGAG GcAATCATGA AGAATATTTT TTGCAGTTTC TTCAAAATCC AGAGGACTGG 360

TTTGCAGGAT ATGTTCGCAA TGGTGGCAAG GAAACAATTG AAAGCCTCTT GCATCCAGGA 420

GCTACTGCAG AATACTCACC AACAGAAATG GCCTTAATGA TCCGTAGTCG CTATCCAGAG 480

TTAATTGATT TTTTAACAAA ACGACCACTT TATTTTGAAT GGCAGCATTA CTTATTTGTG 540

CATGCTGGGG TTGATTTAAC GATGGAAGAT TGGCGGCAAA CAGCACCTAA GGATTTTTTG 600

TGGATTCGCG AACCCTTTCA TCAAGGGAAA AATAATACAG GCAAGACCAT TGTTTTTGGT 660

CATACCATTA CTCCGATGTT ACATGGTGAT ATGCAGACCA CGGACCTTTG GCAAAGTGAT 720

GGAAAAATTG GGATAGATGG TGGTGCTATT TTTGGTGGCT CTGTGCATGG TGTGATTTTT 780

AATGAAAAAG GCATTGTCCA AGATATCGAA TATCAAAAAC GCACCCcTGC GTGGCAACCA 840

GAATTTTGAT TCCTTAATCG TATGAATCAG TTACCTCACT TCTATATTTA GAAGCAAAAA 900

TATGCTAAAA TAGATAAGTA TGCATAAGAA AAGAGGTATC TAGTTAATGG CAGAAGCTTA 960

TAACGAAGAA GTAGTAGCGC TACTTCAAAA AGAATTGACA ACGTATCGTT CAAAACAAAT 1020

AACAACGGTT TTAACTTTAT TAAATGAAGG AAATACAGTT CCTTTTATTG CCCGTTACCG 1080

GAAAGAAATG ACTGGAAGTT TAGATGAAGT CCAAATCCGT GAAATAGAAG AACGTTATCA 1140

TTATTTACAA AACTTGAAAA AGCGGAAAGA AGAAGTTCTC CGTTTAATTG AAGAGCAAGG 1200

AAAACTAACA AAAGAACTCA AAACAGATAT TCAAAAAGCA GTAAAAATGC AACAAGTGGA 1260

AGATTTgTAT CGACCATATA AACAAAAACg TCgGACCAAA GCGACTATCG CGAAAGAAAA 1320

AGGGTTGGAA CCATTAGCAG ATTGGTTGCT CTCTTTACCT GAAAACGCGG ATATCTTAGC 1380

CAAAGCGGCT ACTTTTATTA ATGAAGAAAA AGAAGTTGCA ACCGCCGAGA TAGCCTTGCA 1440

AGGTGCTCAT GAAATTTTAG CAGAACGTAT TAGCGATGAA CCAAAATACC GAATATGGTT 1500

ACGTGATTAT ATGGTTAAGC ATGCGCAATA CGTTAGCGTA GTTAAGGATG AAGAAAAAGA 1560

CGAAAAGCGG ACCTATGAAA TGTATTACGA TTTTGCAGAA CCAGTTAGCA AAATGGTGCC 1620

GCACCGTGTC TTAGCAACGA ATCGTGGTGA AAAAGAAGAC ATTTTAAAGG TTTCCCTTGT 1680

CGCTGATGAA ACaAAAATTA ATGATTATTT CCAACGTCAA CTAATCGGCA AGCAAGCAAC 1740

AAGTTTAGcT GcTCCATACA TTGAGGCTGC TTATTTAGAT AGCTATAAAC GATTCATTGG 1800

ACCAGCGATT GAACGGGAGA TTCGCAATGA ATTAAcAGAA AAAGCTGATG AACAAGCGAT 1860

TGCAATTTTC GGTGAAAATT TACGTAATTT ATTATTACAG TCACCACTTA AAGGAAAAGT 1920

TGTTCTAGGA TTTGACCCGG CTTATCGGAC AGGCTGTAAA TTAGCAGTTG TCGATGAAAC 1980

TGGTAAAGTT TTAGCAATTC CAAGTGATTT ATCCACATAA ACCAGCGACT GCTGCGAAAC 2040

GTGAAGC 2047

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CnCCCGGGGG AAATCAnGAn GAATTTCCCG AAATTGCTCT TTAATTTTTG GAGAATTTCG 60

GCTTATTTCC GAAGGAGTTG GTTCTGTTCC CGCCGTTTAT CAGTTTTTGA GGGTGGAGCA 120

AAAATCCAAA GTGATTTTTG TCCCACGCTC ATTTTTCTTA AATGAAAGTT TTTAAAAAAT 180

TTCCATGATT TTTCAAGTAA AATGAGGTGG GCACTTTTGT TCGATTCCAT TTTTATGTAT 240

AATGAGAAGT GATGGAAAGA GGGAAGTTAA ATGGCACAAA AAAGAGCAAC AAATAAGAAA 300

AAAAGTACGA CAAAGAAAAA GACCAAAAAA CAACAGCAAC AACAAGAACG TTTAAATTAT 360

ATGTTTCTTG GCCTGATTTT TATTTTATTC GGTGTCTTTG GACTCTTTCG CTTAGGGTTT 420

TTAGGCACGT TATTAGCGAA TTGTTTACGC TTAGTTGTAG GTAATACCTT TCCATTTGCA 480

GCGATTTTAC TAATCCTGTA TGGCTTATTA GTCATGATTT ATGGGAAAGA TTTTCCGTTA 540

AAAAGAGGGC GCCCTATTTT TGGGGCTGTT CTGATTTATA TTAGTGTTTT GTTATTTTTC 600

CATGCCTTTA TGTTTCGAAA TGTTAGTGGC AGTCAACCAG ATATTTTAGG TAACACTTGG 660

GAATTTTTGC AAAGCGATCT AAAAGCTAAC CAAGTGACGC AAAACGTAGG GGGCGGTATG 720

ATTGGCGCAC TGCTTTATCA AGGAACGTAC TTTTTGGTGG CACAATTTGG TAGCTATTTA 780

ATTGCCACCT TGCTACTGTT AGCGGGTATT TTCTTGATGA GTATGTGGGA TTTTCAGCmA 840

ATTGTTGATC ATTTCCAAAG TATTCAAGAT CGCCTAAGTC ATGTTTCGGC AAAATCACAG 900

GCGCGACAAG AAGAAAAAGA GGCGAAgCGA gCAGCGAAGA AAGAAGCCAA AGCTGCAGAA 960

CGCCAAGCAA AAATTGAAGC CGCTGCCCAA CAAAAATTAC AAGAGCGGGA ACGCATGGAA 1020

CAAGCGGCAG CCGAGCGCTT AACAAAAACA CCTGTTGAAA CCCACCAACC AATGGTGGAA 1080

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GAACCGGCCG CACCAACGCC TGTTCAAATT GATTCGTTTC AACAGCAAAA TCAGGCGATG   1140
CCTGTACCAC CAATTGCAGC AACAAAACCG CAACGAGAGC AGGAAGAAGA GGCGGCAGAT   1200
GAAGCTGGTG TTCTCGAATT TGAAATTTCT GAAGAAGCGG AAGATCGTGA TTATCAACTA   1260
CCACCAACTG ATTTGTTAGA TACAATTCAA GCAACGGATC AAAGTGGTGA ATATGAAAAA   1320
ATCGAAAAAA ATATTGGCGT CTTAGAACAA ACCTTCmAGA GTTTTGGTGT TGATGCTAAA   1380
GTAGTCAAAG CTAGTTTAGG ACCATCTGTC ACAAAATTTG AAGTTCAACC CGCTGTTGGG   1440
GTAAAAGTTA GCAAAATTGT TAACTTGACG GATGACATTG CTTtAGCGCt TGCGGCCAAA   1500
GACGTTCGTA TGGAGGCTCC GATTCCTGGG AAATCACTAA TCGGGATTGA AGTTCCTAAT   1560
AGTGCAATTA GTACAGTATC CTTTAGAGAT ATTGTTGAGG CACAACCAAG TCATCCAGAT   1620
AAACTATTAG AAGTACCTTT AGgTCGAGAT ATTTCAGGGA TGGTTCAAAC TGCAGATCTA   1680
TCAAAAATGC CGCATTTATT AATTGCGGGA TCGACAGGGa GTGGGAAATC GGTTGCTATC   1740
AATGGCATCA TCACAGGTAT TTTGATGCAA GCGAAACCTC ATGaAGTAAA ATTAATGATG   1800
ATTGACCCGA AAAtGGTAGA ATTGAATGTG TATAACGGGa TTCCTCATTT ATTAACGCCA   1860
GTGGnTTACT AATCCGAGAA AAGCGGCCCA AGCCCtGCAA AAAGTAGTTC AAGAAATGGA   1920
ATTTCGTTAT GAAAAATTTG CAGCAACAGG CGTCCGAAAT ATCACTGGTT ACAATCAACT   1980
AATTCAACAG AAAAATGCGG AAGATGGCGA AAATCGTCCA ATTCTACCAT TTATTGTTGT   2040
CATTGTTGAT GAGTTAGCTG ATTTAATGAT GGTGGCAAGT AACGAAGTAG AAGATGCGAT   2100
TATCCGTTTA GCCCAAATGG CACGGGCAGC AGGTATTCAT ATGATTTTAG CGACACAACG   2160
GCCAAGTGTG GATGTCATTA CAGGAATCAT CAAAGCAAAT GTCCCTTCTC GAATGGCTTT   2220
TGCGGTCTCA AGTGGGACAG ACTCGCGTAC CATTATTGAT ACCAACGGGG CGGAGAAACT   2280
ATTAGGTCGA GGCGATATGC TCTTCTTACC AATGGGAGAA AATAAACCAA TTCGTATCCA   2340
AGGGGCCTTT ATCTCTGATC AAGAAGTCGA ACGAGTGGTT GCGTTTGTAA CGGATCAACA   2400
AGAAGCTGAA TATCAAGAAA GCATGATGCC AACAGATGAA CCGACCACTT CAGGCGGTGG   2460
CGAAGCTCCT CAAGATGAGT TGTTTGAAGA AGCGAAAAAC TTGGTGGTTG AAATGCAAAC   2520
AGCTAGTATT TCATTGCTAC AAAGACGTTT TAGAATTGGC TATAATCGTG CGGCTCGCTT   2580
AGTAGATGAA TTGGAAGCAC ACGGAGTTAT TGGACCATCA GAAGGTAGCA AACCAAGAAA   2640
AGTCTTTCTA CAAGCGGAAT CAGAAGAGGC AGCAACCGAG ACGCCAGAAC AATAAACAAA   2700
AAGAACAAAA ATAGATAAAT TTATCTATTT TTGTTCTTTT TTTATAATTT CAGCAAAGCA   2760
TCATGTTATA ATCATCATTT TCTGGTAAAA TAGAAAGGAA TAGTGCGGTT GGGAGGGAGC   2820
GTATCATGAG AAGAAAAAGC GTGCTTTATT TAGAAGTAGC AGATCAGATT AAAGAAGATA   2880
TTTTGAGTGG CAAGTATCCA GTAGGAACGT TTTTACCAAC AGAAACAGAA TTGGAAGAGC   2940
TGTTTAACGT TAGTAAAATT ACGATTCGGC GGGCAATCGA AATGTTAGCA ACAGAAGAAT   3000
TTGTTGAGAA AAAAAGTGGT CGAGGCACAA CTGTGTTAAG CAATCGTCCC TATAATAAAC   3060
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TATCAAAAGC AGGGACATTC ACTGAATTTT TGAATGAATC AGGTCAGAAA GTAACTAAAA 3120

AAGTTTTACA AGTTGAAAAC TTGACGTTGT CAAAAGAGAT GCCGGCTTAT CAATTTTTAG 3180

GAGAAGAAGT GGTTCATCTT TCACGGTTAT ATCTAATCGA TGAACAACCC TATATTTATT 3240

TTAATTACTA TTTGCCAGCT GCCATGAAAG ACGTATCATT GACTGAATAC AAAGAAGAAT 3300

CCTTGTATCG TTTGATGGAT CGACATGCCA TTGAAATTTA TAAATTTGAA GACCGTTTTG 3360

AAGTTGCAAC TTTGACAGAA GCAGAGCAAA AGATGTTGCA AACAACTGAA ACAACGGGCT 3420

TAAAAAGAAT TCGGCGTTCG TTAAGCCCAA CAGGTCGTTG CGTAGAATAT TCAGAAGCTA 3480

TTTATAATAC GAAGATTCAT CCTTATGTGA TTGAATATGA AGCATAACTT TTAAAAGAAT 3540

AACAGTGCAC TTACAGTAAT GTAAGTTCAT TGTTATTCTT TTCTATTGTC GTTTTTTTTC 3600

GTTTTCGATA CACTAAATGA GTGAGAAGAA TAGGAGTGGA AAATATGTTA GAAGTACAAA 3660

ATTTAAAAAA AGTTTACGGA AACGAAATTA AATATGAAGC CTTAAAAGGG ATTAATTTAA 3720

CTGTCCAAGA TGGTGAATTT ATTGGTATTA TGGGACCTTC TGGAAGTGGG AAAAGTACAC 3780

TTTTAAATTT ATTGGCAACA ATCGATAGTC CAACAGACGG TGAAATACTT TTAAATGGAA 3840

AAAATCCAAA CAATTTGAAT CAAGAACAAA TTGCTAAATT CCGTCGTACA GAATTAGGAT 3900

TTGTTTTTCA AAGCtTTAAT TtAATGCCAA CATTAACTGT TGAAGAAAAT ATTATTTTGC 3960

CATTGACACT TGATGGAGAA AAAGTCTCTG TAATGAAACG ACAATTAGCA GAATTAAGTG 4020

AGCGTTTAGG TATCAATCAT CTGTTGAAAA AACGAATTGC AGAAATTTCT GGTGGACAAG 4080

CACAACGGGT CGCCGTTGCT CGGGCAATGA TTCATCATCC ACAATTATTA TTGGCTGATG 4140

AACCAACAGG AAACTTAGAT ACGAAATCAT CTAAGGATGT GATGGGCTTG TTACAACAAT 4200

TAAATGAAGA AGAAGCGGCG ACTATTTTAA TGGTGACCCA TGATCCGCTA GCCGCAAGTT 4260

ATTGCAAGCG CATCGTCTTT ATTAAAGATG GTGAATTAAT TGATGAAATT GTCCAAAATG 4320

GCAATCAAAA AGAGTTCTAC GATTTAATCA TGGTGAAACT GGCTGAGATT GAAGGTGTCG 4380

ATAATGAATT TTAATCAGTT TGTTATAAGA AACACGATTC GAAATAAGCA TTTATACTTG 4440

GCTTATTTCC TAAGTACAAT GTTTTCTGTG ATGATCTTTT TTACGTTCAC TGGTTTTGTC 4500

TTTCACCCAG CCTTAGCTAA TGGTTTAAAT CCTAAAGCAC AAATGGGAAT GACGGCTGCG 4560

GCAATTATAA TCTATGGTTT CTCTTTCTTA TTCGTTTTAT ACTCGATGGA TGTCTTTATC 4620

CAATCTCGAA AAAAAGAGTT TGGAACCTTG ATGATTCAAG GGATGAGTCC AAAACAGTTA 4680

AAGAAAATGA TTTTTATTGA AAACTTAGTG ATTGGTTTCT TTGCTACAAT TTTTGGTAGC 4740

ATTTTAGGTG TTGGATTTTC ACAGTTTATT TTATGGATTA GCAATTTATT GATGCATCTA 4800

GGTTTAGGTT TTTATTTGCC AGTGATGCCG TTTATCATTA CTGTCATTTC ATTTGCGGTC 4860

TTGTTCTTAG TAATTTCTTT CTTTATTCAA TTCCGCTTGC CAAAAGCGAC ACTTCAAGAG 4920

CTATTAAAAG CAGGAGAAAT GGGTAAAGGT GAAATCAAAA GCTCTAAAGT TAAATCTTTC 4980

TTAGCCGTGT TACTTTTAAT TGTCGGTTAC GGAATTGCTT TAGTTGCTAA GGGACAGTTA 5040

GTTTTAATGG TGATGTTCCC AGTAATTTTC TTAGTTATTT TAGGGACAAA ATTCTTATTT 5100

GmCCAATTGA GTGTTtCTGT CATTGAaCGT TTAAAmCGGA AaCCAAAAaT CTTTTGGAAA 5160

AAAmCCAATA TGGTCGTTTT ATCAGATTTA GCATTCCGCA TGAAAGATAA TGCACGTTCG 5220

TTCTTCTTGG TTTCGGTGAT ATCAACGGTT GCTTTTGCTG CCATTGGAAC GTTATACGGC 5280

GTGAACGAGA TGATTTTTAA AGGAATAAGT TCTGTACCGT ACGAACTGAC ATTGTCTG 5338

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

TGAATTCGAA GAAGAACTCC CTGCAGAACC TATTTCCAAA TTAGGTGATA TTTATCAATT 60

AGGAAGGCAC CGTTTAATGT GCGGGGACAG TACAAATTCT TTAGAAGTAG AAAAATTAAT 120

GGGCAATAAA AAAGCCGATC TTTTGATTAC TGATCCTCCA TACAATGTAG CGTACGAAGG 180

TAAAGGAAAA GAAGCACTAA CTATTAAAAA TGATAGTAAA GAAACGAATG AATTTCATTC 240

ATTTTTATAT GAAGCTTTTA GTGCAGCCAT AAATAATATG AAATTAGGAA GTTCATTCTA 300

TGTGTGGTAT GCCTCATCAG AAGTAGTGAA TTTTCATACT GCTTTAGAAG AAGCTGGGTT 360

TTTAGTAAAA CAAGAATTGA TTTGGAATAA AAATAGTATG GTTTTAAGTC GTCAAGATTA 420

CCATTGGAAA CATGAACCTT GCTTATATGG TTGGGCTTCT GGGGGcAGTC ATTCTTGGTA 480

TTCAGATAGA AAGCAGACTA CTATTCTTAA TTTTGACAGG CCTACAGTTA ATAAGGAACA 540

CCCTACTATG AAGCCAGTTG CACTATTCGA TTATCAAATT AAAAATAGCA GTAAGCAGGG 600

AGACTGTATT TTAGATTTGT tTGGAGGtTC TGGTACTACG TTAATAGCAT GTGAGCAGAA 660

TGaAAGAGAA GCCTATTTAA TGGAGTTAGA TCCAAGATAT GTTGACGTCA TTATAGCTAG 720

ATGGGAAGCA TTCACAGGAG AAGTGGCTGT GAAGATATCA GGTAATGATA CGGCGGTGGT 780

TGATGGTGGC TAGAAATGAT AATTTAAAAC CATTTTCAGA GCGAAGCGTG GATGAAGCTr 840

GAGAGCTTGG AAGAAAAGGC GGTAAAGCAA GCGGAGAAGT TAGACGAAAA AAAGCTGACT 900

TGAAACGAGC TATTTCTATT GTTTTATCAT CAGAAGTACC AAGCTCTAAA ATGGCTAAGA 960

CGCTAAAAGA AATGGGATAT GAGAACACTA ACGAGATGGC CATGGTCTTA TCTATGACGC 1020

AAAAAGCAAT TAAGGGAGAT GTCAAAGCAG CATCCTGGAT TTCCAATATT ATTCAACCTG 1080

CAAAGGTAGA GCATGAAGTT GAAATGAGTG TGGGCGTTGA TGAGAAGCGG AAAGTAGCAG 1140

AAGAATACAT TAGGGGCCTG TTTAATAATG ACACTGGAAA TAGCACAGAA GAGAACAATT 1200

AAGCTTTTAA AAAGTTCAAC GCCCAAAGAA AAACTCAATA AGTTTGTAAA AGGTTATGTT 1260

CCAACTCACT ACAAGAGATT AAGTATATCA ATGGAAAAAG CAATAGAACT AGCCATAATT 1320

GGGGCAACCG AAAGTCTAGC ATATTATGGT GATCGATTAT ATTTTACGCA GGCTCTATTA 1380

ATGGGGGCTG TGGTAAGTGG AGAGTATGAC AACATTATTG TCGTTACCCC TTCACAGTAT 1440

GGTAAAAGCT GGTTGAGTTC GAGAATAGCT GTTTGGCTCG CTGATCACAA TCGGCGTTGT 1500

TACGTGGCGG GTGGTAAAAA AGATACCACT GATATTATCA TGCAACATGT TACAGATACA 1560

CTACAGACTG TTGATGAATC AATTGCAAGA AAATTATTAG AGCCTGTTGA TAAGCTAGAA 1620

AGACTTCAAA CGGGTTTATC CAAAAGAAAG ATTTCTTTCA GTGGCGGAGG ATCGATTGAA 1680

GGGATTTCAT TAGGTGAACA TTTCAAAGGA AACAAATCTG GAAACCAAGC GATTGGTCGT 1740

GGTGGAGATT ATATTATTGA TGAATCAGCG TTCGTCTCAA ATGAAACATA TGCTGAGCTT 1800

GGTCGTAGAA ATTTTGCAAA TGTGGATGGT AAAAACTATC TATCTTTTGA AATATCTAAC 1860

CCACATAATA AAGGTCGATT TTATGACAAA CTAACTCAAG AAAATATTCC AAAAGGCATG 1920

TTGGTTGTAT GGGCAGATGT TAGGACCGCT TTTGAAGAAG ATCGAGTTAA AAGTATTGAA 1980

CAAGTAATAA GTTCTGAATT TTTTCAAAAT AAATCTACAT GCCAACGTTA CTTTTTATGT 2040

GAGCTTCCAG ACGAAAATGA AGATGGAATG TTTGGGACAC CTCAAACAGA AGAAGAACAT 2100

ACCGAAAAAA ATTGGGAGTA TTTCCTTGGT GTAGACAGTG CTTATAAAGG AAAAGATAAA 2160

ATCAAAGCCA CGTTATCAGC ATTAGATGCA CAAGGACAAG TACATGTTAT AGACACTATA 2220

GAAATTGAAA AAGGTGACTG GCAAGACGGT GTGACTAGTA AAAAGATAAT TACTCAATTG 2280

TTGATGATTA TAGAACATTT TGAAGTTAAA GGTGTATGTG TCGACGTAGG TTACGGTGTT 2340

TATATTGTTG AAGGTTTAGC ACATATTAAC GGAGATTTCG AATTACACGG CATAAATTTC 2400

GGTGCTGGTA CAACTAAAGA AAGGGTGGAA AAAAACCACT ACTCGGCAAA ATATGGGGCA 2460

AATAAGCGTG CTGAAATGCA CATTGACTTA CAAGAAAACA TTGATAACAG AAATATATTT 2520

TTCACTGAAA AAGTATATGA AGAAGTTATA GATGAACTAG TTCTTGTAAG TAGCaAGATC 2580

aAGTCTAACG GAAAAACAGC CATTGTTCCA AAGGAAGAAA TCmAAGCTAA GTTGGGCCAC 2640

TCACCAGATA CACTTGATTC AGTTCTGCTA TCGCTACATG CGATTATTCT ATATAAATTA 2700

AACGAACGAT TCTATATCTA TTCTTGATGA AAGGAGGGAA ATGAATGTCT GAAACTGAAT 2760

TAGTTGGGAA AGATGAACTA TTAAAAGCGA TGACTATGTG TAATAGTTGT CCAGATTTTA 2820

ATTTAAACGA TTTAAGAGGT AAGGGTGATA ACAACTATCA GCTTTATGAT TGGTTAATTC 2880

ATAATTTGCC AACAGCACAA TATGTTCTTG GTAAGTTAGT AGAGCTTATT TTTTCTAATA 2940

ACTTAACTAC AGGCGATGAA AAACAAGATG AAATATTGAA TAACTTTTTA TATGGTCAAA 3000

CGAATCCAGA AGGAGTTACC AACTATCACG TACTTGTTCA ATCAATTAAG GAATCAATTG 3060

TATACGGTCG ATCTGGTTTA CGTTTTTTAT CTAAAGATGA TGGATTGATT AACGTAAAGT 3120

GTAATCATTT TGGCGTTGCT CAAATATTGA ATAAAGAACA TTACGGATAT AAAGAATTGA 3180

TTGGTTTCGT TATTGACAAA AAAGGTCGAG CTATTACAGA TGTCGATCTC CGTGAAGGAG 3240

AAATTGATTC AGAAGAATAC TTTAAAAAAG GAATATTTGT TTTTAAAAAC AATGACAATA 3300

TTTTATTGCC ACCCGAAAAA TTCGTTAATT TAAGGGTTGA TACATCTACT CCCAAAGGAT 3360

CGAGTGTCTT TGATTCGGAT ATCCAACGAG TCCTGCTTAT AGCTTCGGTA TATAAACGAC 3420

TACTATATGA TATCGAATAT GATGGCGCAG GAAGATTAAT TTTCTGGGCA GATAATGCCA 3480

ATAGTAATGA AGAAAGCTCA AATAACTTTT TGAACGACAC TGAATCGGCA ACCAAACGAC 3540

GGCAGGATAA ATATAAAAAA GAAGTTGAAG AAATAATGAA GCTCGTAAAA GACAGCAATT 3600

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CGGTGGACGT GAGGTTTATG ATTATGACTC TTTAGAGAAA AAAGTTGAAA TCGATCAAGC 4140

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CaATCGTTAT AAAAAAGAAA aTGATGCTTA TTTAATCGTA ACAGACTATC GTGcCATTAA 4320

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(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

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TCACCTCGGG GCATCCGTGG TTAGCAAT 4888

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

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CATATAAATA AGGGGTTACT TCATCCAATG AAATTTCTTC ACCAGACATA CGTCCGCCAT     960

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AGTCCTCATA ATAAgCTGCT GGgATCATTg CAATTTGATA AAATtGTTTG ATGTATTCcA    1440

AAATCGATAT CATnCAGCTG GTCTGTTTCT AAAGCTTGtC TAAAATCTAC TGCCcCTTTT    1500

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ACCCAAGTTA AAGGCTTTTC CAATTCCCCC ATTTTTAACA TTGAAAACGC GAAAACGTGG 2160

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TTAAAC 2406

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

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(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

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ACTGTTTCTA CTGTTAGTCG TTCGAATTTA AGGTGCAATA AGTCAATACC TTTATCTTCA 3360

AAACGTTGAA TGATTTTGCC AACTAACTTT CGtTCAACGC CATCTGGCTT AATAATTACT 3420

AAACTTGTTT CCTTCATTTT TTCCATCCCT TTCAAAACTT CCTTTTGCCC TTTCCCAAGG 3480

GGTAGCTACA GAATAAAATG AAAGCGGATA CTTTGTCAAT GATAAATTTT CTTTTCCTTT 3540

TGATTAAATA AAAAATTAAA GATTATTCAC AAGATTTGTG AATTGTTCTT TCAGTTCTGT 3600

ATTGCTTGTT TCTTTTAAAA ACAAATAAGG TTGCTCCTCT ACTGGCTGTT CTTTACTCAC 3660

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TGTCGCACTG TCAGAGTATA CTGCCACCAG ACAATAACCC CCTTCGCTGC CTGTTTCTGA 3780

CCAATTTAAC CAAATGGGAT TGTTCCCAAT AGCTGGTTGT ATTTTAGGTT CATAACTCAA 3840

TAAATCATCA GGCACTTGAA TCGTGTAAAA AGCTACAGAG TGACCTGGTT GGTACGCTTG 3900

ATAGTTCTGA TTGCGTTCTT GACCCCAGGT TTCCATGTAT TGTCCTAACT GTTTTGCTTT 3960

TTGCTGATTC CAAATCGTCC CTTCTTCTGT AACTAATTCA GTTAATTCTT GTGTTTGCGT 4020

TGTTTGCTCT AATTCCAACG CCGTGGTTTG ACTAACTTCG GTTGCTGAAA TTGCTCTTGT 4080

TTCTTCAGTA TTTACATTGT TTGTTTGTAC GGTTTGTACT TTCTGTGATT CCTCTTTCGA 4140

TTTTTGCCAA CCACAGCTAG ATAAAACGCT TCCAACAACC GCTATCATAA TAATCCCGTT 4200

TAGTTTCATT CCTTAAACTC CTGTTTTTAT TTTTAtTCnA TCGAAATAAA CCTAAAATCT 4260

CAATCCCTTT CTTTGAATAG TnAAAACCA 4289

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7925 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

AGCTCGGTAC CCCCAATTAT TATTTAAAAG CTATATTGAA TATAGCTTTT AAATAATAAT 60

AACTGAATGA AAAAAAACTG TCCAATAATA TATAGAAATT TCTGAAAAAT CATTTkTAAT 120

GTAAATTATT TTAATAAAAT TAATAAGAAA GGAAAAAAAT ATGCAACTAG AATATCCATT 180

AACGAATCAT ATGAAAAGAA ACATGGTTTT AACTAAAGAA AATCAAGTGA TTGCGTATTA 240

TCGTATTCGG TCAGAAACAG TTGGCTTAAC AGATTTTGAG AAAAAAAGGA AAACAAAGAA 300

AAAAGTAGCT CGAACGTTGA AACGTTTACA AGAGAATGAG GGTTTTGAAA TTGTTCTTTT 360

ACCTGTGAAT GCGGATATTC GAGGGAAAAT GGGAGGTATG CGCCAATTAG TGGACAAAGA 420

AAATCATAGT GTAGCGGTGG ATAAGTTGAT GAAAACTGCT CAGTATCTTG AAAATGAAAT 480

TGGCATGGTC TATGAGTATA TTTGGTTAAT TGGCGTGCCT TTAGTAAAGA AAGAGCGGTC 540

AATTGATATT AAAGAAACAT TTTCTACGGC GTTAAATAAT CTATCTGAAA AAGTGGTTAA 600

AGGACTTGGT TTAGAAGTAG GAGTAGCGGA GGATTGGGAA GAAGCTTATA AAGACCAAGA 660

ACAAGAAGTA TATCAGAATT TGTCAGAATT GTTAGTGGAA CGATTGACAG AAGACGAGTT 720

GTATTACTAC CAAGCCTATC AATTTTTAAA TAATATTCAA CATGAGAAAA AAGAACTTTT 780

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AGAATTGTCT AATGAGTTTG GGAAAAGTTA TATTGCTCAT TTACCATTGG GGGATTGTGG 900

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TGCTCGTGCG AGAACACGAA CAAAGAATAT CATGGAAGAA GCACATTTAG CAGGTTCAAA 1080

ACAAAAAAGA AAAATTGTTG AGGGGCAACA TTCACTTGAT GATTTAGATC AAAAAATTGA 1140

TGATGATATT CCGATTATTG ATTGGAAAGC AGTATTAGTG ATTAGTGGGA ATTCAAAAAA 1200

ACAATTACGT GAGCGAAAGA AAAATTTGAT GAATCGACTA GATAGCTTAG GAATTCCGTT 1260

AATCCGTGCA ACGTTTGATA ATGTCTATCT TTTTCAAGCA ACGTTATTAG GCAACTTTCA 1320

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TTGGTTGGTA TCGGGAGATA CAGGTAACGG GAAATCAGTA TTTTCTAAAT GGTTATTTTT 1620

GTATTCTTCT CTATTAGATG TGAAAGTGTT ATACATTGAT CCAAAAAAAG AAGTTCGCCA 1680

ACAGTTTATG CGAACGATTA ATGATCCAGA ATATCAAAGA AAATACCCAC TTGATGTGGC 1740

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ACGTTTAATT AGTCATTCAG AGAAAGACGT TCATGAAATG GGTCGTTTTT TATTATCTAC 2040

GATTAAAGGA TCGATTTTAG AGTTAGCCTT TTCTCATGGT GAAGTAGAAG GACTTTCTTT 2100

TGAGAAGAAA GTGACCATTT TAGAAATTGA AGATTTAGAT TTACCCACAG ATCGGCACGA 2160

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TTCGTTTAAT AATTTTATGG TATTAATTAC GCAATCGGTC AACGATGTGT TAGATAATGG 2400

CGATGGTACA GGCTTTGGAA CGGTGGTTTG TTTCGATGAA GTGGATAATC GAGAAGGGAT 2460

TTTACGTTAT TTAAAATTAC CAGTCAATGA GATTAATTTA AAATGGGTAT CGAATATGAT 2520

TCAAGGACAA TGTCTCATGA AAGATATGTT TAACCAAGTG AATCGAATCG TGATAGACGT 2580

TATTTTTGAA GAATGGTTAG AACTCTTTGA AACAGTTGAT GATACAGAAG CGTCCGTTAT 2640

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GAAGCTTGAT TATGATAAAC TATTAGAAAA GCCTAACCTG AATGATAAAG AGAAAAAGGA 3360

TTTTAGAGAA AAAAGAAATG CTTATATTGA ACAGCAGGAG AAAGACAATC CTTATTTTTC 3420

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GTTAACAGAT ATTGAAGAAA TAGGACAGAC AGAGTTAGAA TCTGATAGTT TAGATAACTC 4260

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CGCAGAGGAA TATTCAGGTT ATGATAATGT GATTGTGACC AACTTTGATG AATTGGCTAT 4440

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GAGCAGTGCT TAGAGCATTG CTCTTTTTTG TTTTAGGAGG GAAAACAATG TTAATTGTAA 7320

CAAAAGAAGA CCTAATGAAT TTAGGATATG GAAAATATCA AGCGGAAGAT ATAATTAGGA 7380

AAGCAAAGGC AGTAATGGTG TCTAAGGGAT ACGCATATTA CCTAAATAAA CGATTAGGAA 7440

GAGTTCCTGT TGGAGCTGTC GAAAGTGTAT TAGGAATAGA ACTAGAATCT ATAGCAAAAG 7500

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CCGAATGAGC TGTTGGAACn GTATGAAAAC ACGTATGTAA GAAATATTTA TGGACTGTTT 7920

CnGAT 7925

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

TAAAATAwTw TTTATAATAG AaAGTTATCG AAAGGATACC TATGTTTAAA TTATTAAAGA 60

CTTTTCAAAT TGTGTATGAG CAAATGAACT TTTCCAAAGC AGCTACCTGC CTATATATAT 120

CACAACCAGC CGTTTCTAAT CAAATCAAAC AATTAGAAGA AGAATTAGGC TGTTCATTGT 180

TTTTAAGAAA TGGTCGACAA GATGTAGTCC CTACTAGGCA AGCGGAAGTC TTGTATAATC 240

GTTTGCTAAA TTTAGCTGAT GATTGGCAAG AAACATTAAC AGCTCTTCAT CAGGCGAGAT 300

TACCTAAAGA AACTTGCCGA ATTGCTGCGT CTAATACTTT TGCAGTTTAT TATTTGCCGC 360

AACTGATGCA GCATTTACAG ACACAGTATG CAACGATCAA TTTTGTTTTA GAAATGAACA 420

ATTCAGAAGA AGTAGTGGAA AAAGTTGAAA AACATCAAGT TGATTTTGGC TTTATCGAAA 480

AACCATTAAT TACGAAAGGA GCAACTCGTG AAGAAATTAT TCAGGATCAA TTGGTTTTAG 540

CTGGGGACCC TgCCAATcAG AATTGGTTGG TACGTGAAAA GGATTCTGGG GTCTTTCATT 600

ATACCCAACA GTATTTAGAA GAAAGTAATC AAAGCCCAAC ACTCATGACG GTTAAAAACA 660

ATGAAATGAT TGTTAAAATG TTGGAATTGG GCATGGGGCA ATCGTTGCTT TCAAGAAAGG 720

CGATTACTGA AAAAATTCCT TTCCAAACGT TAGGTGAAAA GTATTGGCGT TCCTTTTATT 780

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GATTCTATCA GACGGAAATG AATAAATACT AAAACGTTCT CTTTGTTTAT TTATCAATCT 900

TTGACTACAC TAAAGAAAAC GAAGGAGGGA ACCACAATGC CTAAATTTTC ACCATGTTTA 960

TGGTTTAACA CACAAGCGGA AGAAGCTGCT AACTTCTATA CAACAATCTT TGAAAAAGGT 1020

GCGATTCTAA GTAAAACGAA CTACGTTAAT GAGGAGCATC AACCTCaAGG aACATCATTA 1080

ATGACCATTG AATTTACCTT GGCGAACCAA ACAATCATTG GTTTAAATGG CGGACCAGAA 1140

TTTTCCTTTA CGCCAGCTAG TTCATTTTTT GTTGAATGTA CAACATTACC ACAAACAGAA 1200

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gcAGCCAAAG CTCTATCAGA ATGGTTGGCG ATTTTCGGTC CAGGCGAAAT AATTGAAAAA 1440

GTTGAATATG AAGATGGGAA CATTGCGCAA CACTTTTCAC ATTACAGGAG CAACCGTTTC 1500

GAGTAATGGA TGCACGAGAT AAACATGATT TTGATTTTAC CATGGCCTTC TCCATTTATA 1560

TTGATTGTGA AAATCAGGAG GAAATAGATC GGCTATGGCA ACAAGTGACT GCTAAAGGGA 1620

AAGAATGGCC GTGTGGCTGG ATGGAAGATC AATTTGGAGT CAGTTGGCAA ACAGGCAATC 1680

CTGAACTGAA ACGTTATTTA TCTGACTCAA ATCCAGCTAG AGCAAATGAA GTGACCAAAA 1740

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AGTCCATGCC AATTGTCGAA AAAGCTTCTA TTGTATTAGG AATTAATATG TCTGTGTTAT 2220

TATTAGATGG TATTTTTGCT TTCGTTGGTA AATTCATCAT GTTATCAGAA TGGGAATTAT 2280

TAGCGCCTAT TTTTGAAATA GTGTAAAAAT CATCATAAAG TCCTATATCC AAAAAGAATG 2340

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GAGGAGAATC CTCAATTAGT CTTGATGGAT ATTAATTTAC CTGTTTACGA TGGGTACTAT 2580

nGGTGTCAGA AAAT 2594

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

TGTGCTAAGC GTTTnTTAAC TTTTTTTAnG TAGTTTGGCA GGTTCATTAG GAGnTGGCGC 60

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TCGTGTCGAA CCTATTTATC CAGACGACTT AAAAATGATC ACAGAAGTTA GTTTATTAAA 180

AGAAATGGTT GGTTTATGGC CGTTTATTTT TGTGGTAGCG TTAGGTTGTG TAGCACTTTT 240

TTTCTTAGGA AAAGCCTTTT ATAAAAGTTT CTTTTTATCG AAGAAAAAAC AAACGATTCG 300

TGTGTTAAGT CTTGTTCTTT CGATTGGTCT ATTTTCATAT ATTGGTGATT TTAACAATCC 360

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TATGGACCAA CCAAAGGGCT ATTCAAAAGA AGCTATTTCA GAAATTACTC AGAAGTATCA 540

AAAGTTGGCC GAGGCGAAAA CACTGCCGAG CAATGAGCAA CCAAATATTG TGTTTGTCAT 600

GAGTGAAAGT TTTTCAAATC CAGATCATCT GAAAGGCTTG TCCATTATTG GTAATCCTTT 660

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TGGGGGCGGA ACTGCGAATA TTGAATTTGA AGCCTTAACA AGTTTTcGAT GGAATTAATG 780

AATGCTCAAA TGACTACACC TTATACGATG ATGATTCCTA AGATGACgGA ATTGCCTTCC 840

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AACCGCAGCA AGAATACTAG ACACAGCTAA AACTAAACCA AGAAAGCCAT ATTGGACACT 2280

GCTAAAGCCA AAGTGATTGA TGAAAATAAA CGGAGCTTCT GCATAGTAGC TAAACAATAA 2340

ACCATTAATG CCCCCAATCA ATAAGCCGTA GCACCAAACT TTCGAGTCGA AGGAAAGGCG 2400

TTTCGCCACG GACCAAAAAG GCGCTTTCGT TAAGGTATTT CCTAAGTGAA AGGTTTCTGG 2460

TAAACGATAA AAACTATAGA AAAGTAATAG AACAGCCATG ACAATTAAGG TGCTAAAGAC 2520

ATGCTGATAG CCAAAATAGG TTTGAACAAG TCCGCCGACT AAGGGTCCGA TGGCAGGAGA 2580

TAGCGATAGG GCAGCGCTTG TTTGAGCAAA AATTTTCCCT CTTTGAAGAT CGTTAAAGCT 2640

TTCCCGCATC ATCGATTGGG TAATGACAGA ACCAACGCTT GCACCAAATG CTTGAATTAA 2700

ACGGAAGAAT AACAGCCAAG GAAATGTCGG ACTCAAAAAA AGGCCAATAT TTCCAATTAA 2760

ATAGCATAAA ATTCCTAATA ACATAGCTGG GCGACGTCCA ATCGTATCGG ATAGAATTCC 2820

CCAGAATAAA ACGCCAACGG CAAAGGCAAC AAAATAAATA CTCATGGTTA ATTGTGCCAC 2880

GCTATCGTGA ATGTTAAAAG CAGAACTAAG CGCTGGCAAA ATGGGTGTGA AAATCGACTC 2940

GCTGATTTGT GGAAATCCCA CAAGCAAAAT AATAATTAGT AATGATGGGA CGGTGTTTCG 3000

GGTGTTTTTC ATGATTTTTC TCCTTAAAAG TTTAATCTAA TCAAAAACAC CCATTGTCTT 3060

TTACAACCGC CAAATTTAAA ATAAGTAAAA TAATGTCACC AACTTTCCTT GAAATTTTTT 3120

ATTATACAAA GTCTAAATGA AGCAGCGCTT CTTCTTGACT AAATTCATAA GTGTAGCGAC 3180

CGGATAAACC GGCAAGCTCA CCTGATGCTT GAAATAGTTT ACCTGGGCAG TCTAAAAGAC 3240

CCTGTGTAAa CGTCCCTTTT TCGCAAGCAG TAAAGGTGCC TTTTTTTCCT AAATAAGTTC 3300

CTTCGAAATG GAGGAAACCG ACCACTTGAG CCACAGCTTC AAGCCCATCT GCCATTGAAG 3360

AGCCTTGATA AGTCATTAAG TATTCCACAG AAGcTGTCCC AGATAAGGCG CCTGACAATT 3420

GATAAGTAGC GCTCGCTTGA TTTACTGGGA AATTTTCATT AAGATTGTCA ATCGGTTGTT 3480

CTTGCCAACT AGATACAGTA AATGATGCTT GCTCCATTGC TGTCCCTTCT TTCTTATTAA 3540

TAAGAATAGG GTAGCGGGAA GCGCACTATT TGTCAACAAT CCACCACTTT AACTCTTCAT 3600

TTTTTGCACA AAAGAATGTA ACGCTAAGCG GTTGATGTGA TAAGCAGTTC CTTGTTTTTG 3660

AATAAAGCCG CGCTCTCGAA ATTGTTTGAA GGTATAAATA AGATGGCGAT AACTAACCCC 3720

TAAGTATTCG GCAATCTCAG TATGTTTTTC TTTATAAACA TCTTCGTGAT TAGCGGCAAC 3780

CAATAGCAAT TCCGCTAGCC GATAACTTAG TTCATAGGTC TGATTCGTTG TAAAGTGGTC 3840

CACCCGTTGA AGCATTTTTT TCCCTAGATA ATGGCTGAGT TGCTGCATAA AAAGCACCTT 3900

GTTTTTTAAA ACAGTTTCTG CGTAAGCTAA AGGTACAGCC AAACAACAGG TTTCACCTAA 3960

GGCGATAACG TCCTTGGTTA TCGTTTCCGC TTGAACTAAT GTTAAATCGC CAATTAAATC 4020

ACCTGCCGTT AAAAACTGAA CAATGGATTG GCGGCCATTG CGTTCTGTTT TTAAAATTTT 4080

CGCTTTTCCT TTGATTAAAT AAAAAAGATA ATTTAATGGC TCTGCTTGGT GATGAATGAA 4140

TTCTTGATTT TCAAAATCGA TAATAAAACT GTGTTTTAAA TCAGTTTCAT TAAAAAAAGG 4200

CGTATTTTTA GCTAATTCTT GTTTCGGTGA TCGT 4234

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

TAAGGTTGCA AAGCCAATTT TTTTATTCTT ATCCGTAAAA TATTTTTTGC GTCGATGGTT 60

CACTGAATGA ACTTTGTCTT CAAGGGTTCG TAAAGATAAG CTAATCTTTT GAGAATATTC 120

ATCAACATCA ATAACTTGAA CGGTTACTTT TTGTCCAACG GTTAAGAGTC CATGGATATT 180

TTTGGTAAAG CCAGCTTGTA CTTCCGAAAC ATGAATCAGT CCTTGTGTTT CTTCGTCTAA 240

AGAAACAAAT GCGCCATATG GTTGAAGTCC GGTAATTGTG CCAGAAAGTA CCATACCAAT 300

TTTGTACTTC ATCAAATTTC CTCTTTTCAT ACGATAAATT TCTTTTTCCG TTTCTACTCA 360

TTTAAAATAA TAGCATTTTT TCAACGTTTG TGCATTATTT CTTCCCTAGT TGTTAAAACT 420

ATTGTTTCAT CTTTTAAGCA AAATCTACTA TACTATAGGA AGTAAGACTT TATATAGAAG 480

AAAAGGAGTT ATCTTATGTT TAATTTTAAT GAAACCATTG AGCGTCGCCA CACGAATTGT 540

GTTAAATGGG ACACCGTTGA AGCGAGTTAC CACGAAAAAG ATTTACTACC TTTATGGGTT 600

GCTGATATGG ATTTCAAAGT ACATCAGCCT ATTCTTGATG CCTTGTCACA AGTTATTGAA 660

CAGGGCATTC TAGGATATGC AGTTGCACCT AATGAACTGT ATCAAGCAAT TCAAGATTGG 720

CAACGGCAAC ACCATCAATT GATTGTTGAA AAAGAAGAAA TTTTGTTTAA TAGTGGCGTG 780

GTACCCAGTT TGGCCACAAC CGTTCAAGCG TATACAGCAC CTGCTGATTC TGTCATGATT 840

TGTGATCCAG TCTACCCCCC TTTTGCAGAT GTGGTAAAAC AAAATGAGCG TAGACTCGTG 900

CGCCATTCTT TACTAGAAGT TAACGGACAT TATGAAGTTG ATTTGGTTAA AATGGAACAA 960

CAGATAATCG AAGAAAAGGT GAAACTGTTA CTTTTTTGTA ATCCCCATAA TCCTGGTGGA 1020

CGTGTTTGGA CAAAAGAAGA ATTGCTGGCA ATTGGCCGTT TATGCCAAAA ACACCAAGTA 1080

ACTGTGGTTA GCGATGAAAT TCATCAGGAT TTGATTTTCA AACCGCATAC CTTCACTTCC 1140

TTCACTGTCG CTGATGATGC ATTTAAGGAA TTCACTGTTA CCTTAACCGC AGCAACGAAA 1200

ACCTTTAATT TAGCGGGGAT TAAAAATTCA ATGCTGTTCA TTCCTAATGA AAAACTACGG 1260

CAATCTTTCG TATCTTTACA AGACnAAAAT CATCAAGGCG GCATCaATAC TTTTGGCTAC 1320

GTTGGAACGG CAGCTGCCTA TCAAACAGGG GAGGAATGGC TAACGGCATT ACTTGATTAT 1380

TTAAAAGAAA ATATTGATTT TGCCCTTTCT TTTTTCCGTG AAGAGCTGCC TAGCGTTCGT 1440

GTAATGGAGC CTGAAGGGAC CTATCTTTTA TGGTTAGACT TTAGTTCTTA TTCACTAACG 1500

GATCGAGAAC TTCGCGATAC CTTAATTCAT AAGGGGAAAG TGGTTCTAAA TCCAGGAATT 1560

AGTTTTGGTC CCCAAGGTTC TCAACACATG CGTTTAAACT TAGCTTGTTC AAAAGAAACT 1620

CTCGAAGAAG GCCTTTTACG TATCAAAAAA GCCTTTAATT AAAAACAGCT GTCCTAGTTT 1680

TTAGGACAGC TGTTTTTAAT TCTTTCTTTT GCGTTTAGCT AAATAAACTC TGACGAACCA 1740

GATACCTGAA AATAGAaGTA AAATTTCTCC AATTATGATT GTATAAAATC CTGGTTCATG 1800

AACGATTCCT TGCTGATCTA CATACGTAAA AAACGTTCCT ATAAATGGGA GTATTACTGC 1860

AAACAAAGCC AAGGCCATTG GATATCTGTA TTTTTCTAAC AAATTTGCTT CCTCTCCTTC 1920

TATTCTTTAA CTCAGTATCC TATAAAGACT TAATTAAAAG AAGAGATTTG GATGCTTTTA 1980

AAAAAAAGTT AGTCGTTTTA AGAAAwAAAT AAAGAGTACC AACGAATTTG TCCCTCGTTG 2040

GTACTCTCTT TTTCAATTGG TTAAACTTAT TCACCAATGA TTTCAACTGT GTCCATCACG 2100

ACGTCAAATG TTGGACGGTC TTGGGCATCC CGTTGGACTC CACCAATTTC ATCCACTACA 2160

TCCAtACCaT CAACAACATG ACCAAAAACA GTATGACGGA AGTCTAACCA AGGTGTTCCG 2220

CCTTGtTTGT AAGCTTCAAT AATTTCTTCT GGAAAACCAG CATCTTCTAA CTGACTCATC 2280

ATTTGAGCTG GAACATTTTG ATTAGTAACA ACAAAGAATT GGCTACCATT TGTGTTAGGA 2340

CCAGCATTTG CCATTGACAA TGCGCCACGC AAATTGAAAA CATCCCGAGA AAATTCATCC 2400

TCAAATGCTT CTCCATAAAT ACTTTCGCCG CCCATTCCTG TTCCGGTTGG GTCACCGCCT 2460

TGAATCATAA AATCAGGAAT CACACGATGG AAAATAACGC CATCATAGTA GCCCTTTTTC 2520

GCTAATTCAA CAAAATTTTT AACCGTTTTA GGCGCTTGTT CTGGGAATAA TTGAACAGTG 2580

ATGTCGCCTc GGTTTGTTTT AATGACCGCT TTTGGGCCTT TAGCATTTTC TAAATCTAAT 2640

TG 2642

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGCTTAATT TTCCTTCATT TACATAAAAT TGAAACATAG TGTGACAAGG CGGCAACGCC 60

ATTGAAGGCA CATCTTCTGG ATTCCAAGCG GAAACAATTA AACGGCGAGA ATCAGGATTG 120

GTTTTAATCA TTTCAATCAC ATTAGCTAAT TGATCGATAA AGCTACCATC TTTGGTTTCC 180

CAGTGACGCC ATTGTGCACC ATAAATATTC CCTAATTCAC CATATTTTTC TGCAAACTCT 240

GCATCATTTA AAATGGCATC ACAGAATTTT TGATGTTCTT CTTTGTATTG TTCTGCAAAC 300

GCTGGATCTT GTAAGACACG ATGCCCAAAA TCCGTCATGT CTGGTCCTTG ATAATCTGCG 360

CTTTTTACGT AACGTTCGAA CGCCCATTCA TCCCAAATAT GATTATTTCG CTCTAACAAA 420

TAGCGAATAT TCGTGTCGCC TTTTAAAAAc CACAATAACT CACTTTTAAT CaAGcCAAAC 480

GGTACTCGTT TGGTTGtTAG TAAGGGAAAT CCTTTGGCCA AATCAAAACG CATTTGATAG 540

CCAAATAAAC TATACGTCCC aGTTCCTGTA CGGTCTTCTT TAAAATGACC TTCTTCTAAA 600

ATCTTTTTTC CTAGCGCTAA GTATGCTTCT TCCATCTTAT TCCCTCCGTC TCTTAATCCG 660

CGTATTCACT CAAGTATTCC CAACGATTCA TTTTTTCTTC TAACAATTGT TCCGTTGCTG 720

TTACTGCTTC TTGCAATTCT TGTAAACGAA CAAAATCATC ACCCTGatGA TTCATTTCTT 780

CAGTTAATGT TTCTAATTTC GTTtCTAATT GTGTGATGTC TTCTTCAATT GTtGCCCACT 840

CTTTTTGTTC CATATAAGTC AGCTTTGTTT TttCTTtCTT TtCTGTCGAt GCTCTTTTAC 900

tGGTTtAtGA gsGGTTyTTc TTTGACtTTT CTTGTTCTTT TtGGTTCGCC AAATATTCAC 960

TCATCGTGCC ATAAAATGAT AGGAkCTGAC CATTTCCTTG AAAAACTAAC AATTTAkCCA 1020

TTGTTTTATC CAAGAAATAA CGGTCATGAG AAACCGCAAT TACCGCTCCT TTAAACGTTT 1080

GGATATAATC TTCTAAAATG GTCAACGTAT CAATGTCCAA ATCATTGGTT GGCTCATCCA 1140

ATAATAACAC GTTAGGCTGA CTAATTAATA ATTTTAAGAG ATATAACCGG CGTTTTTCTC 1200

CACCAGACAG TTTGCCAATC AGTGTGCCAT GCATAAAACG AGGAAATAAA AAGCGCTCTA 1260

ACATTTCAGC GACCCCAACG CTGCTTCCAT CACTGCGTTT CACTTCTTCT GCTGCTTCTT 1320

GCAAATAAGC AATCATCCGT TGATTAGGAT CCATTTCTTC GTTTTGCTGG GTATAATAGC 1380

CAATTCGGAC GGtTTCACCG ATACTATATA GACCACTCTC TAAAGGAATG CGTCCAGCTA 1440

AAATATTTAA TAATGTGGAT TTGCCTGCAC CGTTTTTACC AGTAATGCCA ATTCGATCGT 1500

TTGCTTGAAT GAGTAAATTA AAGTCTTTCA AAAGCTGTTT ATGATCAATG GCATAATTTC 1560

CTTCCtTGAT TTCCAGAACT TTTTTCCCTA AACGCTGCGT GGCAAAGTCT GCTTCTAAGG 1620

TGCCATTGGT TTGTACCTGA TGCAAGTtTT CTTTTAAATC CTGAAACCGA TCAATTCTTG 1680

CTTGTTGTTT CGTtCCTCGT GCTTGAACGC cTGCTCGCAT CCaCGCAAGT tCTTGTTTGA 1740

AGAGGCGTTT TCTTTTTTCT TCTTGTTCTA CAGCGACACG TTCACGTTCG GCTTTTTCCA 1800

TCACATACGT TTCATAGTTT CCTTTGTATT CATACAGTTT TCCAAAAGAA AGTTCGAAAA 1860

TCCGATTGGT TACTCGATCT AAAAAGTAGC GGTCATGGGT CACCATTAAA ACCGCGCCAC 1920

GATAGTTATT TAAAAAGTTT TCCAGCCATT CAATCGTTTC ATAATCCAGA TGGkTCGTTG 1980

GTTCATCCAA TAACAGTAAA TCAGGCGCTT CAATTAAGAC TTGCGCCAAG CTTACTCGTT 2040

TTAACTGCCC ACCAGAAAGC TCACCTATTT TCTTTTCCAA TGTTGGAATG CCTAATTTTT 2100

GTAAAATAAT TTTTGCATTG GTATCTGCTG TCCAAGCATC TTGTTTATTC ATGGCTTCTT 2160

CTGCTTGCGT GTAACGTCTT TGAACCCCTT CGTCTAAACC ATTCTCACTT AAAGCAGTAA 2220

CGCTAATTCA TAATTTTTGA CCGCTTTTAT GATCGGGCTG TCTCCCTGAA ACACGGCTTC 2280

TGCAATCGTA ATATTCTCGT CAAATGTTTG ATTCTGGGAA AGGTACCCAA TTTGATAATC 2340

ACTTGGCTGC TGAATCGCAG CAAGATCACC ATCACCGCTA TCTACGCCAG CAATAATATT 2400

TAATAAACTG GTTTTCCCTG TGCCGTTAAT CCCAATTAAA CCAATGCGAT CTTTTTCATG 2460

AATCAAAAAA GAAAGATGAT CAAATAGTGT TTTTTCCCCA TATGTTTTGG TTAAATCTGT 2520

TACTTTTAAT TCTTTCACCG ACACTACCAA CTCCTTCTAT TTTGGTCTTG CTTATTGTAT 2580

CAAAAATTGG ATTATAAAAA AAGTGCATGA GATAAAAATC GTCTTGGTTT CATCTCATAC 2640

ACTATTACTT ATTCTTTATT AAAATTTTTA ACAAATCGTT TCAGCGGAAC ATTATTCACT 2700

TCGCCGCTAA TCGAATAACT CTCTAATAAA TTGACATTTT TTCGTAACTC GTTCGCTTCG 2760

ATAATTGAAA TGCGTTCAGA TTGTTCGTAA TGATCAATCA TCCGTCGTTC TTCTTGGAAG 2820

CCTAATAATA GGTCTTTGAC ATAGTCTGTC TCCGTATGAA CAATATACGA ATCAATAAAT 2880

TCGCCTTTTT CAAACTTATG GGCTAAATCC AAGCGTCCGT CAATGAAGAA ATCAATTAAA 2940

TCATCATCAT AGACACCGCG CAAATTATCT AAACTCTTCA GAATAACTTG AGAATTTCTT 3000

AGAAAAACTT GGCGAATATT TTCTAGTTCT TCATTTCGTA ATTCTTTTTC TTCTTCAGAA 3060

GCTTCACCAC GATTGAAAAA TAGCTTAGGA TGTAAAAGAA TCGAAATGAT TTGTCGAGCA 3120

AATAATAACC AAAAGCCTAC AATCGATAAT AATTGTTTGG CAATCGACCG TTGCATCCGT 3180

GTAATCAAGC GTTGATACAT ACGATAACTT CTGACACTAA TTTCTCCTTG TTTCAGACTT 3240

TCTTCTAAGC CGTCTCGTTC AATGGACACA ATTAACGTCC GCAACTCTTG CACTTCTTGT 3300

TTTCGTTCTG CaCTTAGCTG cTCGGTATAC AATTCTTTTA AACGATCTTG ATAATTTTCA 3360

ATGACCGCAT TCATTTCACC ACGAGGATTC TCTTCATTTT GCTGTTyTAA GACATCAATG 3420

ACATCACGTA ATAAATCAAT TTCGACTGAC TCTTCATTTT CCACTTCCGT CTCTGAATCA 3480

GTTAAAAATG GTAAAACTAG AATCCCGCCA ATCAGAGTCA CCAAAATAAC ACAAGCCGTA 3540

ATAAATAGTA ATAACGGTCG TTCTTTAAAA TGCTCGCCGT TAATCGCTGT TGGCAAAATA 3600

AAGATGGTGG CTAAACTCAC TGTTCCTTTA ACACCGCCAA AAGTTAAAAT CaGCATTTCA 3660

TTCaTTGCGT TTTTAACTTT CTTAAGTTCa TGTTGAAGCG TGTAAACACT GAAAATGGCT 3720

AAGAAACGAA TCAAAAAGAC AACGGCGTTA ATAATTAGAA CAACCAGTAG TAGGAACCAG 3780

TTTGAATATT GTTGGTCAAT CCAAATTGGC GAAAACACTT GAGrAAGTTC AATTCCTAAG 3840

AATAAGAAAa CTAAGGCATT TAAAGTGAaC TCAATCAAaC TCCAAATACT TTCGCCAACA 3900

TTTGACAGCT CAGCTTCAAA AAGCGAAACT TTTTTCAAAC TAGACGCTTG CATAATTCCA 3960

GCAATCACAG CAGCAATAAT TCCAGAAACG CCAATCAACT CTGAAATTAA ATAAGCAATA 4020

AATGGCAAGA GTAATTCAAT CAACAAGTAG CCTGTAACAT CTTTTGCCAC TGCAGTTTCA 4080

AGTAAATGAA CAATTTGCTG TTTTAATAGA ACTAACACGA TTCCGACTAC CGCTCCACCA 4140

ATGCTGGAAA TAACCAAGGT CCCTGCCGCT TCCACCGGCG AAAATGACCC CGTTAATAAA 4200

GCCGCTAATG CAAATTGAAA GGCTGTAACG CCTGATGCAT CATTAATGAG TCCTTCACCA 4260

GATAAAATGT TCATCGAACG TTCAGGAATG TCAATTCGAC CTGATAACGA ACCTACCGCC 4320

ACCGCATCCG TTGGCCCTAA AGCCGCTCCA AAAGCGAAGC AAGCAGCTAA TGGTAAAGTA 4380

GGCAAAATCA TATGCAGGGT CCAGCCGACT CCAACTAAGG TAATTAACAC ACCAAAAAAG 4440

GCCAAGAAAA GAATCATCCC GAAATTTTTC ATCATTGCTT TCAGATTGAT TAGCTCCCCT 4500

TCtCTAAATA AAAGCGGTGC AATAATCATT ACTAAAAACA CTTCAGGCTC AAATTCAATT 4560

TCCTGCCCCA TTTTAGTTaA ACCAATTAGA ACGCCTACAA TAATT 4605

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

TnTACTTCTA CTGTCACnTG CGGTAnTAnT TTCCTTTGTG GATTGTATTT GTTTATGCAC 60

CTATTTGCTT TTCGTTATGG GGACATGGAA ATTGGCTAGG GAAAATGGGA GTACTGGATT 120

ATTCAGGCGG ACTAGTAGTC CATACTACCG CTGGAATAGG AAGTCTTGTT TTAGCAATAA 180

CATCACTAAT ACGTTTAAAG AATTCATTGA TATTTAAATC ACAAGAAATG ATAGCTTTTG 240

TAGGAATGCT GTTTATTACC TTAGGATGGT TCGGATTTAA TATGGCACCT TCTGGAAAAA 300

TCGGTGAAGA AGCCATTCAA GTTTGGTTAA ATACACTTAT TTCAATTTTA GGCGGTAGCA 360

TTAGCTGGAC TTTTACCTAA TGGATTTTAA TAAAAAAAGT ATCTATCTAT TCTATAATGA 420

ATGGAATAAT CGGCGGATTA GTAGGTAGTA CTTGCTCGGT TGGATATGTA wCTCCTGCAT 480

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TTAGTTTATT AATTnCGGTA AtTGkATGtA CCCTTTGtCC AATTGTwATt CACATAATGC     540
ATCTAAGCAT AGCAAATTTT GATGACGCTG CAGATTCTTT TGGGATGAAT GCAGTGGGTG     600
GAATTGCAGG ATCGATTTTA ACTGGTGTCA TGGCAGAAAA AGGGGACTTT TTTCTTCAAT     660
TATTTGGGAC TTTTTTAATC AGTATTTGGA GCCTTAGTTT AAGTCTTTTG ATTCATTATT     720
TATTGAAAAA AATAGTAAAT GATTGTTATT CTCAATGTAT TAAATAAAAA AATTAAAATT     780
ATTCCTAGTG TGTATGAATA TCAAAATAAT AGTCAATAAT AACACTCAGG AAGAAATTTG     840
AAGACTTTAA ATTTTAGTGG AGGTAAATAA TGGAAAATAA AGAAGTTATA ATTATTGGAG     900
CAGGCGCTGC TGGCGTAGGT ATGGGGGTTG CTTTAAAAGA TTTTGGCATA AATAATTTTG     960
CTATTTTAGA GAGAAAGCaG GTAGGTAATA GTTTTATTAA ATGGCCTGAG CAAACAAGAT    1020
TTATCACTCC TTCTTTTACA AGTAATGGAT TTGGGATGCC TGATTTAAAT GCAATAGCAA    1080
TTGATACATC TCCTTCATAT ACTTTAGGTG AGGAACGTTT ATCTGGAAAA GATTATGCTA    1140
AATACCTACA ATTAGTTTCA GAAGAATATA AGTTACCTAT TAAGACAAAT TGTAAAGTTC    1200
AATCTATTAA AAAAGAAAAA ACTGGTTATT TGCTTGAAAC AACAAAAGGA TTTATTTATG    1260
CAGAATATGT AATTTTTGCG ATGGGAGAGT TCTCTTTTCC AAATAAATCT AGTATTAAAG    1320
GTGCTTATAA GAATAGTTTA CATTATGGCG AGATTAATTC TTGGATTGAA ATTAAAGGGG    1380
ATAAGCAGAC GATTATCGGA GGAAATGAGA GTGCGATTGA TGCAGCTATT GAATTAGCTA    1440
AATTAGGTAA ACGAGTTACA ATTTATACAG ATACTTTGGG GTTAAATATA AGAGATGCTG    1500
ACCCGAGCAA AAGgTTAGCA CCACGCACAA GACAGAGATT TTTTGATTTA CGTGTAAACC    1560
AAAAAAAATT AGATAGTATT AAAATATACA CAACTACCAA AGTTAAAAAA ATTGAAAAAA    1620
AGTCTACTAG TTATATATTG ATTACAGAAA ATGGGAAATC ATTACCTGTA GAAAATATAC    1680
CAATTCTTTG TACAGGTTTT AAAAATGGCA CAAAATCTAT TACTGCATCA TTGTTTAAGT    1740
ATAAGGAAAA TGGAGAGGTT CTTTTAAATG ATTTTGATGA ATCGACAATA GCTAAAAATA    1800
TTTTCTTAAC CGGTCCAAAT GTACGTAAAG GTAATACCAT TTTTTGTTAT ATATATAAAT    1860
TTCGCCAACG TTTTGCCGTA ATCGCTAATG AAATTGCCCG ACGAAAACAT ATTACTATTG    1920
ACGAAAAAAA ATTGTCATAC TATAAAAATC AATCTTTTTA TTTAGATGGT TGCTCTGGGT    1980
GTGAAGTAAG ATGTAGTTGT TGACAAATAA GTAATTGTTA CAACTTATTT TATAAATTAA    2040
AAGATTTTTA AATAATTTAA GTCAAGTCCA GACTCCTGTG TAAAATGCTA TACAATGTTT    2100
TTACCATTTC TACTTATCAA AATTGATGTA TTTTCTTGAA GAATAAATCC ATTCATCATG    2160
TAGGTCCATA AGAACGGCTC CAATTAAGCG ATTGGCTGAT GTTTGATTGG GGAAGATGCG    2220
AATAATCTTT TCTCTTCTGC GTACTTCTTG ATTCAGTCGT TCAATTAGAT TGGTACTCTT    2280
TAGTCGATTG TGGGAATTTC CTTGTACGGT ATATTGAAAG GCGTCTTCGA ATCCATCATC    2340
CAATGATGCG CAAGCTTTTG AATATTTTGG TTGATCGATA TAATCATGAA TCAATCGATT    2400
TTTAGCCTCA CGCGCTAAGT TAATATCTGT GAACTTAAAA ATTCCTTTAA CAGCTTCTCT    2460
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GAAAGATTTT GAATTTTTTT TAGGAATGGT GGTAAAGATA TTTCTTAGGA AGTGAACTTG 2520

GCATCyTTGc CAmCTTACGT TGGTGAAGGA TTTTCTAATG GCAGAGACTA ATCCTTTGTG 2580

CGCATCAGAA ATAACGAGTT CCGTAcCTTG TAAACCGCGT CCTTTAgGAw TCmAAAAATG 2640

TkGTCCAGGc TCTCGCTTCG cCACTTGAAT CAGaAGCgAT AATTCACGGC GCAnCTTGGT 2700

ATCCAACGGC AAAGAAGCTT TGAGnG 2726

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

ATAAAAAACT ACAATTTTTT GGTACAAATA GTAATGTTTT TTTAAGTTTA TTCAATACTG 60

TTGGGACAGT AATATTGATA GCTATAGGCA GCTTATTAGT ATTAAAGAAT AGTATAAATT 120

TAGGAAATTT AACAGTATTA ATTTCATTAT CAGGAATAGT AGTATCATCC CTAAATCAAT 180

TTGGGTCGTT TCAAGCGCAA TATGAATCGA TGCAGGTGGC TAGTCATAGG CTTGAATCTA 240

TATTAATAAA TATGGAAAAT GAGAATGTAT GCGGGGAAAt AATTTTAGAC AAGAAAATAG 300

AATCAATAAG ATGTAAACGT GTTTCCATAA AAAAAGGAGA TACTTTATTA CTCGACACTG 360

TTAACTGTGA AATCTATAGA GGGAAAAATC TTTCAATACG AGGTGAAAAT GGTTCAGGTA 420

AATCTACATT AATTAAGTCT TTAGTAAGAT TAGATGATGA CTATAGGGGA CAGATTCTAA 480

TTAATAATAT TGACATAAAA AAAATCAACT TGGACTGTCT ACGATCAAAA TTAGTGTTTG 540

TAGAGCCCAA TCCTAAATTT TTAGAAGGTA CAATTAGAGA TAATTTATTA TTGGGACATA 600

AAGTTCCGAA TAGTATATTT AATAAGTTGA TAAGAGATTT TGAAATAAAC AAAATATTAG 660

ACGATCTACC TTTAGGTATA AACTTtCCTG GAGAAgCTGC AATAAAATGC TTATCTTCTG 720

GACAAAAACA AAAGCTAGCC T 741

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

AGTAAATAAA TGAATACATT GCAATTATTT AAGCAGGCCT TTTTTTCAGT TTCAGAATTA 60

CGGCATGCGA AAAAAATGGC GTTTTGGAAA GTAATTCTCT ATGCTGTTTT TTTAAGTGCT 120

ATTTTAGCAC TACCTATTAC CAAACAAGTC TTTTCTGTGC TACAAGAGGT GCAACAAGAT 180

GGCCAAAAAA TTGCAGAAAA GTTGCCTGAC TTTTCTATTG AAAATGGCAC GTTGCAAACA 240

AAGGCCAAAG AATCTGGCTT TATTTATCAA ACCGACTCGA TTATTTTTAC GTTTGATCCA 300

GATGGAAAAC GTACAGCCGC TGATGTCCAA AAGGATTTAA TTGGTAATGC GTTTGGTTTG 360

GCTTTTTTAC AAGATGAATT TGTAGTCGCC TTACCAAATT CAGGCGCAAC TGAATCAATT 420

CTAGGCACCG ACCAATTTAT CTTCCCCTAT AGTAAAGGAA CCTTAGATGG CGTTAACGCT 480

CAGAGTATCA AGACTGCGCT AAGTGAGGCA GCGATCCCCT GGTGGACAAA ACTCATTGTC 540

TTTTTAGTGG CTATCTACCC TGTTCTAATC GGTTTAGTTT TAGACTTACT GATTGCCGCT 600

ATCGGTGCAT CTCTCTATTC AAAATTACGT TTTTATTCTT TACGTTTGAT TGATTGTTTA 660

AAAATTATTA CGTATTGTGC TACCGTGCCA GTTATCTTAA GTGCTATTTT AAACTTCGTA 720

AATCCGATGT TTAACGATGG CATCCTAGTT ATTTTACTAA GTCTGTTCTT TTTCTTTGTC 780

ACAACCAAAA ACGAACCACG GAATATCCCT GGTTCTTAAA AAAAGGTGTT GTCTTAAAGA 840

CAACACCTTT TTACTATTCT TCAAATTCTT CTTCATCTGT TAATTCAGGT AAGTCAATCG 900

TGGTCACCGC AGATTGGCCA ATTTGCGTTA AATATGCAGC TAATTCATCC ACATTTTCCA 960

CAGGTGAGAC GGCTGCTTCA ATTGCCATTG CTAAATTAAG TCCAGCGACT ACTCGCAATT 1020

GCGGATAAGT GCCCATGGCC ATCATAGCCA CATTACAAGG TGTTCCTCCT TTTAAATCAG 1080

CTAATACAAG CGTCGGGACA TTGCCAGCTT CTTTTAAGAT TGCTGCCAGT TTTGCTTGCG 1140

TGCCGCTCAA GCCATCTTCT GCGGTCATTG ACACAATCGC AGCATCTGCT AATTCCCCGA 1200

CAATCaTTTG aGTAGAAGCT AAGGTTtCTT CTGCCATCCG TCCATGGcTC ATTAAAATTA 1260

ATTTTGGTTT CATCATATCC TCCTAAAAAT ACTGCTGATA AATTTTTGTT CGTGCTTTCa 1320

GAAAGCCACG TTCTTCACGA GTGGGaTGAA TCCGATTCGT TAACAAAATT AGGGCTTCTT 1380

TGGTCTCTTT TTTCATACCA ATCGCCGTTC CAGTAAAGCC AGTATGATAC AAATAGTCTG 1440

CCCCTGCTTG CGTCTTTTTC ACTTCCCAAC CAAATGTACG TCCCCCTTGA TTCATAGACC 1500

AGAGAGCAGT GAACATTTTT TCAGAAAATA ATGGTTTGCC AGACGGGTAG CGATTGTTCA 1560

TAAAACACTG aACAAAAGTG AGTAAATCTG GTAAAGTTGC AAATAAACCT GCACTGCCAA 1620

TTGGCGCTTT TAGTTGATAG GCTTTCGAAT CGTGGACCAC TCCCTGAATA ACGCCGCGTT 1680

GTTTTGTAAT CTCTGTGGGC ACTGCCTGGG CAAAATCGCT GACCGTAAAA CTTGTATGCT 1740

GTAGGTTCAT TGGTTGAAAT ACGTATGTTT GAAAGCTCTC TTCTAATGAG CAGCGATCCA 1800

ATACTTGAAT AATTTCTCCC AATAAGTAAT ACCCTAAATC AGAATAAGTG GTTTTCCCTC 1860

GTTCAGATAA CGAATGCGTT AAAATGATTT CTTGCAAGCT TTTTTTTGTG ACATTTTTCT 1920

TATCGACAAC ATCAGCTGGC AGTCCACTCT GATGCAGTAG AAGCTCCCCA ATCGAACAAG 1980

ATAGTCCTTG ATAATCAGGT AGGATTTCCC CCACAGTGGT TGAAAATGTA AGCTGATTTG 2040

TATCGATTAA TTGTAACATT CGATTTGTTG TCCCAATAAC TTTCGTTAAG GACGCTAAAT 2100

CATACAGGCT AGCTGATGAA ATCTTTTGTC TTGCAAATGG ACCAGTATTA CCTAAAAAGC 2160

CCGTATACTG TTCTGATAAG CTATCTTCTG TGATCGTCCC CCAAGCGACA CCCGGAACGA 2220

CTTGCTGATT AATCAGTCTC TGAATTGTTT CTTGAATTGC GATTTGATTC ATTGTTCACC 2280

ACTTCTATGC TAAAACTTCT GAAATCCGTC CGTCATGTTC TGCTAATAGT TGTTTGGCTT 2340

TTTGAAAATC AACGTGGGCT TTCGCCATTA CAATGGCTGG TGCCACTTCT AGCTGTGCTG 2400

CCTCCAAGTA TTCTTTGGCT TGCGATTCCT CGATTTCTGC TGCTTCTTTA ATGATATTCG 2460

TGGCACGTTG AATTAATTTT TCGTTCGTTG GTTGTACATT GACCATCAAA TTTTGATAGA 2520

TATTCCCTAC TTTAACCATA ATTCCTGTTG AAAACATATT TAACACCATT TTCTGTGCTG 2580

AACCCGCTTT CATTCTAGTT GACCCTGTAA TGACTTCCGG TCCTACAATT GGCGCAATCC 2640

CAATTTCCGC CAATTGATTC ATCGGACTTT GATTATTACA GGTAACTGAA ATGGTTAGAG 2700

CGCCCACTTT TTTTCCGTAT TCAATTGCGG AAACAGCATA TGGTGTCCGA CCACTAGCAG 2760

CAATCGCAAT TACGACATCT CGGGCAGTCA ATTGATGTTG CGTTAAATCT TCGATAGCTA 2820

ATTCTTTCGA GTCTTCAGCG CCTTCAATTG CTTGATACAT TGCTTTTTCA CCACCAGCTA 2880

AAATACCAAA TGCGCGTTCT GGCGACACAC TATATGTGGG TGTTAATTCA ATCGCATCCA 2940

AAGCACCTAA ACGTCCAGAC GTTCCTGCAC CACAATAGAT TAAACGGCCC CCTTTTTTAA 3000

ATCGTTCTGC CGCTGCATCA ATTGCTGCAG CAATCTGCGG AAGCACCTTT TCAATTGCTT 3060

GTGCTACCTT TTGGTCTTCT TGATTTATTA AAGTTACCAT TTCTAATGTT GACACTTGGT 3120

CAATCTTTTT AGTCGCTTCA TTTCTGGCTT CTGTCGTTAA TCCTTCTAAG TTCATTTGCT 3180

TGCACACCCC TACTTCTCTT TTAGACGGCT GACAAGTTGA CTCGTTTCAA TCATATTGCG 3240

TTCAATTTCT GTGTCTAAAT CATCTTGAAT TGAACCTAAA TACAGAACAT CGCCAATTGC 3300

CATTGACGAA GCAATCGATG AAATAGCCCC AACTCGAATG AGGTGCTCAT TATTGGGGAC 3360

TAAAAGAACT TCATCGCTCA ATGATCGCAC GTTTTCTCCA TCGTTACTGG TAATAAAAAT 3420

AACCGTTGCG CCTCTATTTT TGGCAATTTC ACAGGCGATT AAGGCTTCTT TTGTCAAACC 3480

ACTATAGGAG ACCGTGATCA AAATGTCTTG TGCCGTTGCA TAATTTAAAA ACTCCAACAT 3540

CATGTGACTA TCATAATTAA AAATTGCTTG GCGACCAGCG CGGTTAAACT TGTGATAAAG 3600

ATTATAAGTC GTTAAAGAAG AGGCACCAAT TCCAACCAAA TGAATTTTTT CCGCTTTTTT 3660

AACATGCGCG ATTGCTCGTT CCAAGGCTTG TTTATCCACT GTATAAAATA AATCCTCAAT 3720

CGTAGCATTT AATAAAGATT CCACTTTCAT ACAAATAGTA TCCACCGAAT CATCCACCGC 3780

TACAATTGGA TCAATATCTT TTTTACCGTT ACTGGCAGCT TGTACCGCTG CAATGGATAG 3840

TTTTAACTCT TCCCAGCTGT CAAACCCTAA TTGTTTAGAA AAACGGGTAA CTGACGCCGG 3900

AGAAGTTTCG CTATTGCTAG CAATTTCGTT TGCTGTTAAT GAGAGAAGAC GGGTCGGATC 3960

CTTCAGTATA TAGTCTGCGA TTCTCTTATT TACTTTGGAA AAGTCCTTAT ATTTTTGTCT 4020

GATTGAACGG ATTGGCTCCA TCTTCTCATC TCCATTTCTA TTTTATGAAA GTTAAAATTG 4080

CTTCGTTTGG TTCAGAAGGG ATCATCTGTG CGGTAATAGT CACCCCATTA TCTGTTAAAC 4140

GACGAACGGT TTGAATATCT TCATCGGTTA ATGCAACAGA TTTTTTAATT GCTCGACTGC 4200

CTTCTTTTTG AGAAATATTG CCGACATTGA AGCTCTGCAA CGGAACACCG CCATCAATTA 4260

AAGCCGCCAT ATCTGCAATG TCTTTCGTAA TTAAAAAGAC TTTTTCTTCA TCATAATTGC 4320

CTGCTAAAAT TTTTTCAATC GCTTTACGTT TTGATAAAAT GGATAATTTA ACTCCTGCaG 4380

GCTTAGCCAT TTTTAAGGCA CCAATTTGTA ATTGATCTTT GACAGCGGCA TCATTTACTA 4440

CCATGATTCT TTGTGCGCCA ACCGTATTCG TCCAAACGGT TGCAACTTGT CCGTGAATTA 4500

AACGCTCATC TACTCTTGCA TGTACAATTG TCATAATAAA TCTCTCCTAT TATATACTAT 4560

TTTTTTAAAA TAAACCGCCA ACCCAAGCCA ACATTGGTTG TAAATTGCCT AAAACCATGC 4620

CAATtAAAAT TAAAACAAAG ATTAGCCGTG TTGAATTCAT TTTCTTTTTC CCTAGTAACC 4680

AATAGGATAA AAGAACAATC CCTAAAGGAA TTAATGCGGG TAAAATTTTA TCCAACATTT 4740

CTTGAACAGA TAATGTTACA TCTCCCATTT TATAAGTTAA ATCTAATTTG TAAGTAATTA 4800

CCGAAGGAAT CAAACCGCCG ACCACTGTTA ACCCTAAAAT GGCTGCrCCT TGCGTAAACA 4860

ATTTCATTTT ATCCGCAAAT TCTGTCGCAA TTTTTTTCCC TTGATGGTAA CCAATCCAAG 4920

TGAATTTATA GCGAACCCAT AGGACCACTG CTCCGGCAAT TAACGGGATC AGTAACCCAA 4980

CAACCTGGCC CCCTTGCGCC ATGTAAGCTG CAATCGAAAA AACAATCGsA CGrTAAATnG 5040

CGATAAAAAT GGTATCACCA ACACCAGCAA ACGGACCCAT TAGACCTGTT TTCAAACCAG 5100

TAATGGCCGT TTCATCTTCA ATGCCGACTT CTTCTTCCAA AGCCATATCA GCTCCGACAA 5160

TTAAGTGCGA CATGGCTGGC GTTGTATTCA TAAAGCCAAG ATGTGTCTTC AAGGCTTTCT 5220

TCATAGCTAC TGGATCTTCA CTGTATAGTC GCTTTAATGC AGGCATCATC ACCCAAGCGT 5280

AACCAAGTCC TTGCATTTTT TCATAGTTCC AGCCCCACTG ATAGCCAAAA AGATTACGGA 5340

CGTAAACTTT ATTAATATCC TTTTTTGTTA ATTTGTTAGT CATCAATCTC AACCTCCTCA 5400

TCATCTTCGT AAATAACCGT GCCACTTGTT GTAGTGCGCC GCCTTTGTTA TGATTCATCA 5460

CATAAATCGC TGCTAAAGCC AAGCCAACCA GTGCGACACC TAAAACTGAG AAGAATTGGG 5520

CCCCATAAGC AAGTAACACG AACCCAnTAA TAAAaTAAGG CCAGTATGTT TTAATTGGCA 5580

AGTAACGCAT TAAAATAGCA ATCCCCaTCG CTGGTAAAAT AGCGCCTGCT GCTTTTAACC 5640

CATTCATCAC CCAAATAGGA aTCCAATCAT TGATAGCGTT TACAACTTGT TCACCAAAAG 5700

CTAGGCCAAT AAAAACTGGG ATGACACGAG AAATCGTCCA AGGAAAAATT CCTAAAACAT 5760

TGCAGCGCTC GACCCCTTTA TAATTTCCTT CTTCCGCATA ACGATCTGCT TTGTGTTGAA 5820

AAAACGTATT AGCCATTCTG CCTAAAATAT CTAGTTGTGT TAATAATAAC CCAATTGGAA 5880

CCGCAACTCC GATACCATAC TCTGCCCCTT TCCCTGAAAT GATTGCATAA GCCGTTCCCA 5940

TAATGGCCCC TGAAAGAAAG TCTGGGACTG TTGCTCCTCC ATAAGTCGCT ACACCTAATG 6000

TCATCAATTG AAGCGTTGCC CCAATCATCA AACCTGTTTG AACATnAaCC TAAGACTAGG 6060

CCAGTAAACG TTGCAGCAAA CAATGGTGTA TATGGACCAA TCTGAATAGA AATTTGGTCA 6120

AGTACACCAA CAACTGTGTA AAGACATAAA ATCAAAA 6157

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAATCTCAAA TAGCAAtCAG GCTTCAGTGG ATATTTTAAA GACAACTGCT CATAGGGGAT 60

TAACCCCAAG CAACATAAGT ATCGATCCTT CACCCAGTTT TTCGACGAAT GGGGATCAAA 120

TAATGTTATC TAGTGTGACT AGAGAATCAA TGATAAACAA ATCAATTAGG TTTTCTTATG 180

CACCTCAAGA TTTAATAGAA GGTTCTACAA CAGGAACTAA ATCATTTAGT GGCACAATCA 240

ATTTTTTTGA AGTTAGCAAT TTAACTAGTG ATTTAAAACC TAATTTAAAA AAAGTATATT 300

CAGGAGATAA AGTAGAATGG ACTTGGGAAA TAATTAATAC ATCTTCTAAA CAAGCGTCGA 360

ATATTTATTC GGAATTAAAT TTACCTGTTG GATTAATTAT TGATCAAAAC AGTATTATAA 420

AGAACGGAAA TGTAGCAACG ATAAATGATC TTAACGGAAC GAATAACCTA GGAGCATTAG 480

ATTCTAATCA AACAATAAAA TTTACTTTTG AAACTATAGT ATCTGGAAAT TCAGGAGAAT 540

GGCTGGAATT AAACGGAAAA GTAAATTGGG AAGATCATGG GGCTCGTTTT GTGACAAGTT 600

CAAATCAAGT GAAAATAATA GATGATGAAC AAAAGGATAA AGCTGAAGAG ACAGATGAGT 660

TAGAGATTCT TTCAGTACCA CAATCTTTTA AATATGGCAT CCTAAATAAA AGTAATGTCG 720

AACAAATCAT TCATTTGAAC ACnAATAATT ACCAGACAAA TACTTCGGTG GTTACGGATG 780

GATTTTATAC ACGTATGAGA GATGAGCGTC CTAGTCTTAG TGGrTGGrAA CTAACTGCAC 840

AGTTATCyGr TTTTAAAGAk GTTmCAAtTy CAcGGTGTTA aCGAATtCTG GGrTAGCyTT 900

AAAAATGGaA AATATGAAAt TGAATCTATA AAAAATCGAG ATAsTCCACA AGAGAGTATT 960

GATCAAAATC CAACAGGAAC ACCTTCAACT GTTAGCACsA aTGAAACGCT GATATCAGGA 1020

CAAGCAGCAA AAACATTGAT CAATGCACAG GCAAATGAAG GTCACGGTAC GTGGCAACTA 1080

AGGATTCCtT TTGATAAAGT GTCCTTGACT GTACCAGCGA ATACAGGGGA AATAAATAAA 1140

AATTATACAG CGACTTTGAC ATGGTCATTA GATGATACAC CATAGGAGGA GAGTTCTGTT 1200

TATACGAGTA TGGATTGATT CTTGAATCGT ATTCTTGCCT AACTTTCCTC TATTTTGTTA 1260

TTAAGGTATG GTCCATAGGG TGTGGACATT GGTGGGAAAT CAACAGAATT ATTAGTAGAC 1320

TTTGGTTTGA TGTTTATAAC TTAGTGTATG tAGTTGAAGC TGCTTATTAT ATCTTGATTA 1380

TGTTAAGCAG CTTAATATTT yTATCTTATT AAAAAAGGGG GAAGCTCAAT GACAAGAGTA 1440

CTGATAATTG CAAGAAGTCC TTTAGCGGAA CAAGAGTTGG AATGTACACT TCAGCGGTCA 1500

TTCGATGAGG TCTTTTGTTC TTCTGAATTG ATGAAAGAGG TCGAAAAATA CTCGTTAGTT 1560

ACTCAATATT TTTCAGTGGT CATTTTTAGT GATACAATCT CCACCAGTGA AATGGCCACA 1620

TACTTACCAT ATTTTAAGAA ATTGGGCTTG TCTATTCTGC GAAAAGGACA GAAAGAACAA 1680

TTGAAAACAA CAGAATATAC GTATCTAATA GATGAAATTG ACGATTGGTT TGATGAACAA 1740

ACATCACCGA ACGTGCTGAT AGAGAAAATT GTTAAACTTG ATAATAAATC TCAAAAAAAC 1800

AGGATACCTA ACCTTCGTAT AATTGAATCG GTACAAAAAT CAATAGTTAA ACGAGATCAG 1860

GTTATCATTT ATTTTACGAA AAATGAACGT AAATTATTGT ACTATCTATA TAAATCTAAG 1920

GGTAAATGTG TTTCAAGGAG AGAACTGTGT CAATTAATGT GGGGAGAGGA AATAAGCAAT 1980

TCTTCCCTGA GTCAATTATC TACATTAGTA GCACATGTGC GAGAAAAATT aACCCATGTC 2040

GGGTTTGAGG AGTTATGGAT AAAAACGATT TGGGGGAGAG GCTATATTTT AAGTGATGAA 2100

TTTATCGACT ATTTGTCTCA AAATAATACT TtcAGTAAAG GTcGTGTGTc TAAATTaTTG 2160

TAGATTTGGA AATACATTTC GTTAAAAAAG ATTTAAAACA ATATAATAAG TGTTGTGCTA 2220

CATAGTTAGT AATGCAGCGA AAAATTTAAC CGAAGCTAGC GATTGCTAAC TTTGGTTAAA 2280

TTTCAAAAAT ACAACTGGAT TAGAAACTTC TGGATAGTCn ACTTTCnGGT AAGTATTTAT 2340

ATACCAAATC CTTTTATTTT AGnAATGAAT AGGGGATC 2378

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

GATTAAAGCT ATTAATCTCT TGCTGCAGTT CAATAGTTTC TTGAAATTCT TCCGAGTTTT 60

CTCTCAAAGT ATCGTAATAT TTAGTATTGG CTTTCGTTnG GGATTTCTTT GATAACAAGA 120

TTAAGACAAA ACTAAATAAC GTTGGCAAAA TAACAGCTAA TCCCATTTTG ACATTACCAA 180

CCAAAAGCAT CACTGAAATA AAAGGGAAAA ACAGAGCCAT ACCGCCGGAT TTAGGTATTG 240

CATGACTCAT CGCATGCTCA ATACCTTCAA CGTCAGACAT GATAGTTTGA GATAAATCTG 300

ATAAATTATG TTTTGAAAAA TAGGATAATG GTAAATTTGA CAAATCGTCT GCAATTTGCA 360

CTCTTAAATG CGCACTTTCT TTATAAGTAC TATTATATAA GTtTTCATAC TCCCTATCTA 420

ACAACCAATA CATGAAAAGC AAAGTAACAA ACGATACTGC AAAATAAAGC CAACGGGGCT 480

TtGCATTTTC TAAAACTAAT TCGTCTATCA GCATCATTAT AATGAATGCT GGTACCATAT 540

TAATGCAGTA TACAAAAAAA CTAGAAATAG AAGCTTTAGT TAAAGCTTCT GCGCCCTGAT 600

CAGTTAAAGC AAATTTTTTT TTATAAAAAT TTTTCATTGT CAAGCCTCCA ATCATTTGCA 660

TTCTCATAAT TAGTGACCAA TTGTTTATAC ACTCGATGTT TAGCCATTAA TTCATTATGA 720

TTTCCACGTT CTACTATTTT TCCTTCTGAC AAGACAAGAA TTTCATCTAC AGATTTAATG 780

CTGGATAATC GATGAGCTAT CATAATAACT GTTTTTTCTT TCATCAAATA TTGAAAAGCC 840

TTTTGTAGTT CATACTCATT ATCTGGATCA ATAGATGCAC TAGCTTCATC CATAATAACA 900

ATCTTTGCAT CTTTTAAAAT TGCTCTGGcA ATAGCTATAC GTTGTTTTTC TCCTCCTGAC 960

AGATAAACTC CTTTACTACC AATTAAGGTA TGCTCTCTTT CGGGAAATTT TTTTAAAATC 1020

gATTCGCAAC CGGCTAATCT TAGCGCGTCA AATACTTtAC TTGCtGGCGC TgAGGATTTG 1080

CTATAGAAcG TTATCGTAAA TACTCTGATT GAATAGTTTC GTATCTTGAA AGACAAAAGC 1140

AATTGTGTTA ATAATTGTGT CTTTTGAATA GTGATTTAAA GGCTTACCAC CAATTTTAAT 1200

CTGTCCCTTA TCCACATTGT AGAAACCTGA AATTAGTTTA GCTATCGTAC TCTTTCCGCT 1260

TCCTGATTTT CCTACTAATG CATAAATTCT TTTTTGTTCT AAAACTAAGT TGAAATTTTC 1320

TAAAACACAC TCTTCTTTGT ATGAAAAGCT GACATTTTCA AATGCAATGT CACAATTTTT 1380

AATCTGTGTC TCGTTCCCAT ATTTTAGTTG GTCTTGCTTC ATTTCTAAAT AAAGGGAGTC 1440

TAGTGTTTCG ACTGCATATC TTGCTTCAAA CAAGTGCATA CTTACATACA TTATTCTCAT 1500

GAAAGAAACA AAAATAATTC CACTTAAAAA AAACAACATC AACAAGTCAA CAGCTAATAT 1560

CTTGGGAGTG GTAAGAGAAG TTATAAAAAA GGTTATAGGA ACTATCAAAA TGCAAACTAT 1620

GCCAAAAAAT AGCCATTGAA AAAGAACAAA AGGTGTTTTC CCACTCAAAG AATACTTATA 1680

TGCAAACTTA GCATAATCGT TAATTGCTTT ATTCAAGGCT TTAAATGATG TTACTTTAGC 1740

ACCAAATATC TTTATAACTT GAATTCCGCG GATATATTCT ACCGTTTCAG AGCTTAACAC 1800

ATCTAACGAT TCTTGATATT TTTGAATAAA ATTTGTATTC CCTGTCATTT TCTTTAACAA 1860

GAATACACCA ATTACTAACA TGGCGATTAG AACCAATCCA ATTTTAAAGT TAATGAAAAA 1920

GCCTAAGGCA ACTGATAAAA CAGGTGTTAC TATGGCTTGA GCACTATCTG GAATCAAGTG 1980

AGCAATTGCC ATATGTsTTT TAGCCGCGTT GTCATCAATT GTCTTTCGAA TATATCCCGA 2040

AGAATTTAAA TCAAAAAAAC GAAAACTTGC TTTTGTTAAa CCGCTAATTC CCTTTTytCT 2100

CAAATTAGTC TCyAAGCGAA ACCCAAGGAT ATGAGAAAAT AAGCCAGAAA AAATATAAAA 2160

TAAAGCTCCT AAAGTTAACC AAGCAACAGT TTGAACCGCA TAACTCTTAG CTAAATATTC 2220

ATCTCCTACA ATAATTAGAG ACTGAAGAAA TTTGTAAATA CTGTAATATC CATAGACTGT 2280

TAATACGACA GAAAAATCAG AAAATAAAGT GGCTAACCAT CCGTAGTATT TCATTTTAGG 2340

GACATAACTA AATAATTTTT TGTATACTTT CATTTTTTCC TCCCCCGCAT TCAATTTCTT 2400

CTCTTATTCG TTTACAACTG TTAATGCTTT CCGTAATGGC GTAAATTAGA GATGTACAAA 2460

CAGATAGAAG GTAAAmTACG TTCTATTTTT TGTATTTTTT TAAGACTTTT CTTCCAATCA 2520

ATACACCAAT CATAGATAAA CTTGCTACAA CTAACACTGA AATAATTCCC CATATACCCA 2580

CCGCGTAGTG GATCATTGCA TCCATTGTTG CAGCAGATTG TCCTCTATCT ATCCAGTCTT 2640

GACGAAAACG ATCTGTAAAG AACCATATGG GAATCCACTG TCCGGCAGCA CTGCCTAGTT 2700

GCATTAGAAC CCAAGACACA ACTTGAGGAA TTGCTCGATC ATATCCAAAT ACATATAGAA 2760

TAATATCAGC TAAGATCGCC ATACTAATCG AACTGATAAA CCAAGGTAAG TACGCCCCGC 2820

CCATTAACGT AAAAAATAAC AATAAAACAA TTGTGTAAAT AGTAAAAATT CCTTTTCTAG 2880

GGTAGTTATA GCTAATATAA ACAAATATGA TTCCAGATAA TAATCCAAAA ATCCCTGGGG 2940

ATATGCTGTG ACCAAACGCC CCACCAATAC TACTAACCAT TATTGAAAAA AAGTAAATTA 3000

CTAGGGAAAT AACTGTAGCT AAACCAATAA AAATATAATC TTTTGTTTTC ATATATATTT 3060

TCCTCAATTC TATTTCGTTA TGTCATTAAA AATCTGTTCT ATCAAAGTTG AATCTTCTAC 3120

TCTAAGTTTT ATATCTTTTT TTATTCCACC ATTTTTTAAA TAAATAATTC TATTGCATAT 3180

TTtATAAAGA AATTCCGGAT CATGAGTGGC TATGACTACT GCACCCTTTT CTTTTAAATC 3240

TTTAATAAGG TCAGCAATCC TTTCCATATT GATATAATCC AACCCACTTG TAGGTTCATC 3300

AAATAGAAAT AAATTAGTTT TTGACAATGa AGCTATAGAA ACCAATAATC TTTGTtTTTC 3360

TCCACCGGAT AAATCAAACG GTAATkGATC TTTCATTTTA TAAAGTTCCa TTTTTTTAAA 3420

ATTTTTTCTT GCTGATCTTT ACTAACTATT TCATTCCCCA GGGCTAACTC GCTCCTAACT 3480

GATTCTGTGA AAAATTGGTA ATCCcATTTC TTGCATTACT AAAAACGGCG ATGACAAATT 3540

TTTnnnATTT TCGATTATCT TTCCTTTGGT AGGGCGAATA ATCTTCATGA GTATTCTTAG 3600

TAAGGTTGTT TTCCCCaCAC CGTTTTTCCC TACCAAACCA ATAACATCTC CaACTTTGaC 3660

ATCAAAATTT ATGTCTTTTA GAATATTTTC ATAAGTAATT TCTTCAACTT TTAATACATC 3720

TGCACTTGCC TTTTCGATAT AGGGAACTTC AATCGAACTA TTAAAAATGT CAAATTTCCT 3780

TAATGCGTTA TTGTTTTCAG TTTTTAACAA CTGAATAGTT GTAGTTTTTA CAGTTCTATT 3840

TTTAACAAAT AGAACTTGAT CAATTAATTC TTTCAAATAA TAAAAACGAT GTTCAGCTAT 3900

AACAATAGTA AATCCTTTAT TTTTTAAATC ACAAAGTAAG TCAGCAAGTT TCTTAGTCGC 3960

TTGGAAGTCC AAATTTGAAG ACGGTTCATC CAATATAATT AATTTAGAGT TTAGCGATAA 4020

ACTACATCCA ATAGAAATTT TCTGCCGTTC ACCACTTGAT AGCGAAAAAA TGTTTTTATC 4080

TAATATATTT GAAAGATCTA ATAATTCAGC TAATTCATTG ATTCTTTTAT CCATATGCTC 4140

TTTTGTAAAT CCAAAGTTTT CCATCGAAAA TACTAACTCA CTCGTTGTAT TTGTTGTAAA 4200

GAATTGTCCT CTAGGATCTT GACTTACGTA GCCAATATTT TTTGATATAC TTTCTTGTGT 4260

TAAGGATTGT AGCGAGTTAT TTTCAAATAA AATTTCCCCA ACCAATTTTC CGTCATAAAG 4320

TCTTGGAATA AGTCCATTCA TTAACTTTAA TAGTGTGGAT TTCCCACTCC CAGAAGAACC 4380

AGTAATCAAT GTAAGACTAC CTTTTTTTAT TGAAAAATTA AGGTCAACAA GCGCTTGTTC 4440

CTTAACATCC TTATATGAAA AAGAAACATT GTTAAATTCA 4480

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

TACAGATTAC TTGAAAATCT TTACGTTCCA GTTTTATTCT nTCTAAAAAA CGTACTCACT 60

TTTTTTCTTA GACTTCTTTT TTTGATTTTC CTCTTTTAGG TCTTGTCCTT TTTGTCTTCA 120

AAATATTTAA ATAAATCCCT TTCAAAAGTA TTTATAGGTT TTGGACAATA AGGAATATCT 180

TTTTTCTTCA TATAAACACC TCATTAAACT ATTTTATATC ATCACATTAT CAAATTAACA 240

AATGTATTAA AAGAAAGTTT TTTATTAAAA cTTTCTTGGC CTTTTGGGAG ATTTCAGTGC 300

GATTTCTTTT TATTCCAATA CTTTTTTGTT GGTCACTTTC GTATACCCAT TCTAAGCGAT 360

AATCGGCGAC AATGTTTTTA CAACGAATGG TAGGACAAAA CAATGGGAGA AAAAACTTTT 420

TCTACAGCAA TCCCTTGTTT TCACCTACCA CATGTTGTGA ACCCAAAGCA CGCCGACGAA 480

CGCTTAGTTA TACGAAAATG ACCTACCAAA AACAAAAAAA GTGAGGTGAA TAGAAACAAA 540

AAGAAATTGA AATCTCCCAA AAGGTCGTCC ACCTCGGGGG CAACTTTCTG CCGAAAATAG 600

TAGTTGGGCC TATGAACAAA CTAACGTTAC TTTTTGGTAA ATTATTAAAT TAACCGAAAA 660

AACAGCATGG TTTCTCCCCA TCAAAAAGCA AACTGTAAAA ACATATACTT CTATGAGTGG 720

AGAAACTATG CCAATGCTAA ATCAATTTAT CgrTTATCCm CTTgcACGaA CCAAAGACAG 780

CATTGTTAGA AAACAAATTA ACCCgCCcTT ATATACCAAT AAATTATACG GTAATCGTAG 840

TTGGGATACA TTTTACTACT ATGATAATCA ACTGGTTTAT GAAaGCAGTT aTTACTAAGA 900

GGGAaTTTTC TTCTTAGTTA GCGTTAAAAA TAACAAAAAT AAAAGGAACA AGAACAATGA 960

AAACAATAAC TCTCTATGAA ATCTTAGGTG AAGAAGGGTC TGACAAATAT ATTTCTGTAT 1020

TCAAATCTTT AATTGCTTCC AATTTTACAG AGAATGAAGA CATTTTATCA AGGTGTCAGC 1080

TATTTATACA CAATAATGTC AGTGCTGAAG AAAATTTATA AAGATGAACC AGAAAAACTG 1140

AAAGAGACGG CAAGCGCAAA CTTAGAATTT TATAACACGA ATCCACAAAT GTTGACATTT 1200

ATTACCAGCA TGCAGTTAGC GATGTATGAT AATGATCAAA GTGTCTCAGA TACACGCAGC 1260

ATTAAGATGG CACTTATGGG ACTCCTATCA GGAATCGGAA ACTCGATTGC TCGATTTGGG 1320

ATTGCCTCCT TATTTTCAAC AATATTTGCA GGATTAGCGA TGAATGGTCT GGGATTTGCT 1380

CTGATGTTTT TTTGGTTATC GATGTTAATC TCAATGCTAG TCATCAAATT ATTAATGGGA 1440

GGGATATTTA GGGTTTAAAC TTGGAACGAG TGTGATCGAA ACCTTAAGTG ATAAAATTGG 1500

TAAAATTTCT TCAGCAGCAA ATATTGGCGG AGTGGCTGTT ATTGCGGCAT TAAATACTTC 1560

TTTTGTTAAG GCAAATATCG CCATTAAGTA TTCACATAAT GTAGAATCTG GTGAAAAACA 1620

AGTAATTGCT ATTCAAGATA TTTTAGATAA GATTACGCCC AAAATGCTTC CAGTCATTTT 1680

AACTATTTTA GTTTTTTATT TGATCAAAAA AAGAAAATGG AACACGTATC AATTGTTATT 1740

TTTTTTATTC GTGATTGGGA TTCTAGCCTC TGACTTAGGG ATTTTAGCAT AGTAAGTGAG 1800

TGTAGTAAGG GACAGGGTTT TCGATTTCGA GTAAACCTTG TTTCCTTATT TATAAGTTTT 1860

CTGAGTGATG GGCATAATAT TTTTTCAGTT AACGGAAATA AAATTTGAAA GCGAGAACAC 1920

GATGAATCTT CAAAAAATCG AAAACTACCA ACTAAAGTTT TATCAGAAAG ATTTACTTTC 1980

AGGATATTTG GAAAAACATT CAAAACTTTT GGAACCACTT TTTGAACGTA CTTATTTTCT 2040

ATTAAAAGAT CAGATTATTT ACAATGATGC GAkGGATATG GAAGCCTGTT CTATTCCGTA 2100

TTCTCTAAAA GAAAATACAC GGAATCGATA ACATGGAGAT GACCCAGAAT gGCTCTTtAT 2160

GTTGAATTGA CAAAGTTTtC TTCTAGATTT ATCACAGGCA TACGCGTTAA TAAAAGAAAA 2220

ATGCTATTTA CAAAAATGGT GCAGTCTGCT TCTTGATTTT ATTCAAGAGG AAGGCGAACC 2280

AAATTCTACT AATAGGAATG TTTGGCGACA CCTTGATGTT GGAATTCGAG TGATGAACTG 2340

GATGAAGAGT TTGACTTATA TTTCTATTGC TGATTATAAA CAATTGGGAA TTGATAAAGT 2400

GTTGCGAAAC GCTTTGCTGG TTAATCTCGA GTATTTGGAG AGGAGCTATA TCGATAAGTA 2460

CAGACTTAGT AATTGGGGAG TATTGGTAAC GGGTGGAATG GCTGCTATGG ATCTATTTCT 2520

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GACTTTCAAA CmAACATCAA AAAGACCCCC TCATTCTAGT ATCACTAACT AGAATGGGGG 6600

CyCTTtTATT TTTTgAGACA GAAGTCGCTA AAGAAAAGAT ATTCCAAATC CGTAATTGAT 6660

GGTATACTAA AACGTAACAA ATAAAGGAGG nnAGACAATT GATGCTTAGC GTCTTAACAG 6720

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5069 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

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TCTTATCGTG GAAGAATTAG TCCCGGAATC ATTTGAAGGA ATCGATTTAG CATTATTTAG 240

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(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

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ATAATTATAG ATTCATCACA GATACATTGC TTTTTTCGAA GAAACTATAA AAAATGAGAG 4860
TCTAGGTTAT TTGAGAATAT CAATTGAGCA AGTACAAATA ACTCCAAATT TAGTAATATT 4920
CCTAATTGAT TATTGGTGAG TAATTAAAAA GGAATACTCA AGCTACATGT ATAGCATAGA 4980
AAATCAGCAT TCAATCAGAC AATTAGGATT GAATGCTGAC TTTTTTGTTA TATTGATATT 5040
TTCAATTATC TTCTTTATTT TCTTCTAGTT TTTCGAAAAA TAGGTATTCT CTGATCGTTG 5100
TATTAGTGGA AAGGGGATAA AGGAGCATAT TGATCGTGCA ACAAAACAAC AATGAGATAT 5160
CTACACAACA CCAATTTGAT GCCTACTGTA AAAAAGTATT ACGCAATGAA GCTAAGTCTA 5220
TTCGAAAACG AAACGATAAA ATAAAAGAAA ATGAGGAACC ATTAAATGAT TTAAATGAAG 5280
GTAAGTATTC ACAAACTCAT TTAGATGAGC AAGATGTTTA TTTCTTATTT GGAATGGAGA 5340

TATTAATTTC AGATCAGAAG TTATCAGCAG CAATTGATCA GTTATCGGAT ACAAGGAAAA 5400

AGATTGTTTT ACTTTATTAT TTTGCAGGTT TTAATGATAC TGAGATCGGT AAAATTTTCA 5460

ACATGAGTAC AAGTGGTATC TGGTATCAAC GAACGAAAGC GGTTGAACAA TTGAAAATGG 5520

AATATGGCTT ATGGTAGACA AACAAAGGAA CCAACATTAC CCATTAGTTC CTATATCTAT 5580

TATCTTATCT GCTTTGAAAG AAGACCCAAT TTCAATCAAA ATGATACTTA AACATTACCA 5640

CGGTTATATA ACTAAGTTAT GTTTAAAAAA TGGtTTTAAT GaGGTGGGGC AATTTaTTAC 5700

CTATGTAGAT GAATaTrTGC TAAGACAGCT AGAAATTAAA TTGATAGAGG CTATATTGAA 5760

ATTTAAAGTT AACTAATTAA AAAGTCCCCT TTCCACTTTT GCTATCTAAA AGAATCTTCT 5820

AATATTTGAG AGATATGTTT TTTAGTTAGA AAACCTATTG ATCATTGAAA ATTAAATAAA 5880

TTCTATCAGT ACGTTAACAC TTCAAGGAGC aTATTTTAGT TGCGCCaTGA TCTCTTATTG 5940

TAAAGAAGGA GCGATTAAAA TTCTGAAATA GTTTTTATAG TCAATAAAAA GCGATGATTT 6000

GAAGTTGAAA TAATGATACT TCCGTAAGGC TCGCCGTAAA CTTGGGGAGA GGTGAAATTC 6060

CTATGTACTT TTGACAAAAG TGGCTGATAG ATTAATTATT GTTAATAGAA AGGAAGAGAC 6120

AATCATGTCG AAGAATAACA ATAAAAGTAA TTCATCAGAG TTAGAAAAAT ATTTGTTTCA 6180

TCCAGAAAAG ATAGAGGATT CTAATAATAA AATGAAGAGG ATAAATCAAC TACCATTAGT 6240

TTTAACGAAT AAAGATTTAA AAGAACAATT TCAAATAAG 6279

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GCGTTCATGG AAnCCAGAAG AGACTTGtTT CAGCAACAGA TAAAACAGGT CAAGATGTCC 60

CATTCGArAA AATCACTGTT TCAGGTCAAG TTGATACTAG CAAAGCAGGC GTTTATCCAA 120

TCATATACAG TTACGAAGGT AAAGAAGAAA CAGCCCaTGT GGCCGTCAAA CCCGACCAAT 180

CTAAGTTAGA GGTTAAAGAT ACAACGATTT ATGTTGGTGA TTCGTGGAAA CCAGAAGATA 240

ATTTCGTTTC AGCGACAGAT CGTGATGGTC ATGCTATATC CTTTGATAAG GTTCAAGTAA 300

AAGGGGAAGT TGATACAAAG AAAACAGGAG AGTACCAGAT TTCCTATACC ACTGAGCCAG 360

TTAATGAAAC CAAACCAGCT GTGCAGTCAC GACTTTTCTC AATGTTTTCA AACGAAACAC 420

CTCGTCAATT AACGACAGTA GCAACTGTTC ATGTGATTGA TCGTAATCCT ACACCGCTAC 480

CAGATAAAAA TGAGAACAAC CAGACTAGTT CTTCAACGAA TCAAACCACG ATAAAAAGTA 540

GTCAGTATGT CACACACATT GTGAAACCTG ACAAGCAAGG ACGTtATCCC AAAACGGGAG 600

aACAAACTAA TGGTCTATAT CGTGTGCTAG GACTTGTTGT ATTACTTATT GTGATTATTA 660

GTGGTATAGT CATCAAGAAG AAACGAAAAT AATTAAATGA GCGTGGGGCA AAAGTTTAAA 720

GTAACTTTTG TTCCACGCTT AAAAGATGAA TAAGTGCATG AATGAGGGTA GCTGTTTCCT 780

TGGAAAATAG GAAGTTTTAC AAGTGACTTT TATTTTAAGA ACACCTATTA GCAGGTTTTT 840

CTGTTAAGAT AGTTATTTTT ATGAAATAGT TTGGAGGAAT AATAAACGAG ATGAACCAGC 900

GAACTATTTA TTATGGTAGT ATCGGCACAG CCTTATTTCT TTCTTCAGGA ATGTTGATTG 960

CTTCAGTGAA TAGCTATGCA AACGAAGCGA CAACACCAGG CAAATACACC GTGACTTATG 1020

AAGTGGATGG CAAAATTGAA ACAGCAACCA TTACGGTCAA AGAAAATCAA ACGGAACTTA 1080

AATTAAAAGA CACGTTTTTA GGAGTTAATC AAGCATGGTC ACCATTAGAC AATGTCGTTT 1140

TTCTAAAAGA TAAAGAGGGT CGCCCTTTAA ATTTAGAAAA TGTAATTATA GAAAATAATG 1200

TAAATACTCA AAAAGTAGGC CTTTATTTTG TAACCTTCCG TTACGAGTCA TACCTTTCTA 1260

TTGCGAAkGT GTATGTCAAC CCTACTAATT TTGCTGCaGA GGGGaATaTG cTTGCaGaGc 1320

TTCCtTATAG TCAAGCAATG ATTGGCCCAG AAAGATCaAT TATTGCCtCG AGACaGGACA 1380

AGGAGCAACA AACAAAACAG GAGAAAAAGA AAAATAAAAT TGAACAGGAA CGAGTAAATA 1440

AAAAGGTGCT GTTAAATGAT GAGTTGTTGA AAAAAATAGA TACGATAGCC CCAGTGGAAA 1500

TTACTGGAGG AGCGGCAAGT GGGTCCTCTC AATTTGGCAC CACTTTAAGC TTCCTGTCAG 1560

GCTCACTTTT GTATGGAACA AGGAGAGTTT AAATGGAATT CTTGTTATTA GATGATCGGG 1620

AAAATTTAAA ATTAGCGATT ATTAGAAAGT TAGAGCAACA ATATTCATTT TCTGAACGAA 1680

AAGATCGTTT ATGTAAGCAA TTAGCTATTT CTCCTTATTT GCTAGAACGG AACATAACAG 1740

AAATCAATGC AGATTTGCAA CGCTTTGGTC TGATTAATGA GATGGAAATC AGTGAAAAAA 1800

ATAATGAAAT TTTGTTATCT CAAAGCCTTC GTATTTCTTC AAGTATTATT GAAGAATATT 1860

ATTTAAAAGA CTCGTTAGAA TTTAATCTAT TAAAAACGAT TTTCTTTCAT CAGTTTACCT 1920

CAATCAAAAA ATACGGTGAA AAGCACGGGA TGAGTCGAAC GGTTGTATAT AAAATTGTTG 1980

ACCATATCCG GAAAGAATTA GGTCAATACG GTATTAAGTT ATCCAAAAAT TTACAACTTA 2040

GCGGCAATGA AATGGCGATT AGACAATATT TTACTATGCT TTATTACCGA ATTTACAAAG 2100

ATTCTGAAGA ATTATATAAT CAAACAGATC TTCsCsCAGT GAACCAATTA TTGGCTCAAT 2160

TGAAAGGCTC TTATGAAAAT ATCACTAATT TTCATTTATT TAAACATTAT GTATTGGTGG 2220

CGTTAGAACG AACGCAAAGA AAAGCTAATT ATTTTTTATC CCAAGAAGAA AATCCATTCG 2280

CTTTTGATGA AGAAAGTTCG ATTtATCAAG AAATTCAAAG TTGGATCAAC GAAGgAnTGA 2340

AGGCGACTCA TGCAGAGAAA AACGCAGAAA TTCAAGgAaT TATCGGCAAT TTAgGTCTAT 2400

CAtGAACTTA TTTCGacATT TGCTGAGTcT CACAATGAGG CAATTACGGC TACGAAAACA 2460

TTATTCTTTT CTTATATGCC GTTTACAATT TCGGACGAAG AATTTTATCA AGAAATTGTT 2520

CCGATTATTT ATCAACATCG TTTTATTACG CCGTTCATCG ATATCACCTT ACGAATTATG 2580

GATTTAGAAT TTTTTCAGGA ACGCTACCCA ATTGTTTTTA ATAGCTGTCG TCAGTTTTTA 2640

TTTGCGTTGG ATTGCTCGGC GTTTGAGTTT AGTAAGCTTT CTTTATTTTT TGATTTGCTA 2700

TTAGTGTTAT CCCGTCTTTA TGACCAAAGG AATGAAAAAA GCACGATCAA TCTTTATGTG 2760

AATTTTACGC AAGGAGAAAA ATATACTCAG TTTATCAAAG AACAAATCAA AATATTCGAA 2820

TCTTTCAGCA TTCACTTTCA TTCAGCGATT CGACCAGATA CTGATTTAGT AGTTTCGGAT 2880

TATTTACCAA AAACGTTATT TTCAGTAAAa TGTTTAATTT GGCTAGCGCC CCCGCGAGCC 2940

AGTGACTGGC AAAATTTTGG CAACGAAATT GTCCGAATTA ATAAAGAGCT ACAACAAACG 3000

AAACAAAGAA AAAGCGAATA AAAACAGTCG CAACGTGTTT TAGTTGCGAC TGTTTTTTGT 3060

TACTGAATGT TTATAGTAAA CTTTCTCATT ATCACTGATG TAAAAAATTT TAAATAAAAG 3120

CCAAATAGGA TTGAAGAAAA AGAAAAAATT GCTAGTGAAG GACCaATTCT CTAAAGTTTT 3180

TCTCAAATAT AGTAGAATTC CTTTCTTTTC TTCTGTGAGA AAGATATAAT AAAAAACGTA 3240

TGAACAAAGG AAAAGGGATG ACGAATGAAT AGAAAAGAGA AAACAAATTT AGATAGTCGA 3300

ATTGATTACG GCGTGATATT ACCAGTTTTT CTTTTATCAC TAATTGGTAT GCTATCGCTT 3360

TACGTAGCGC TTTACAATGA TCCAAGCAAA CCTAAAATTG GTAGCTTGTT AATGAAACAA 3420

GGACTGTGGT ATTTAGTCGG AGGATTAAGT ATTGTCATTA TTATGCATTT TAGCTCAAAA 3480

TTACTCTGGC GGTTAACGCC CGTTTTTTAT GCACTTGGAT TAGTATTAAT GGGATTAmTA 3540

CTGAAATTCT ATGACCCCGT GCTAGCAGAG CAAACAGGTT CTAAAAACTG GATTCGCTTT 3600

GGTGGCACCA CATTCCAACC ATCGGAATTG ATGAAGATTG CGTTTATTTT GATGTTGGCC 3660

TATATAGTGA CCATGCATAA TGTTAAATAT GTGGACCGAA CACTCAAAAG CGACTTTTGG 3720

CTAATCGCTA AAATGCTATT AGTGGCGATT CCGGTAATTG TTTTAGTACT TTTACAAAAA 3780

GACTTCGGGA CGATGTTAGT TTTCTTAGCC ATTTTTGGGG GAGTTTTCTT AATGTCTGGC 3840

ATTACTTGGA AAATTATTGT GCCAGTTTTT ATTTTAGCTG CTCTAGTGGG GGCAGGAACT 3900

ATTTACTTGA TTACAACAGA AACAGGTAGA GATTTATTGT CTAAGTTAGG GGTCGAAGCC 3960

TATAAATTTG ATCGGATTGA TTTATGGCTA AATCCTTTCC ATACAGATCC AGACCGCTCA 4020

TTCCAACCAG CGCTAGCATT AACAGCAATT GGTTCTGGGG GCCTTTTCGG AAAAGGCTTT 4080

AACGTGAGTG ATGTGTATGT CCCTGTTCGT GAGTCAGATA TGATTTTTAC AGTTGTTGGT 4140

GAAAACTTTG GCTTTATTGG TGGCTGTTTC ATTATTTTGT TGTATTTTAT TTTAATCTAC 4200

CGCATGATTC GCGTTTGTTT TGATACAAAT AATGAATTCT ATGCCTACAT TGCCACAGGA 4260

ATTATCATGA TGATTTTGTT CCATGTTTTT GAAAACATTG GAGCGAATAT TGGTTTACTA 4320

CCATTAACTG GGATTCCATT ACCGTTTATT AGTCAAGGTG GTTCTTCCAT TTTAGGTAAC 4380

ATGATTGGGG TGGGCTTAAT TATGTCCATG CGTTACCAAC AAGAAACGGT TCGTACCAGA 4440

AGTGGTCGTT AAAGAAAGAA GAAAGAAGGG GTAGAAATGT ACACACTTTA TGAATATCCT 4500

AAATGCTCAA CTTGTAAAAA AGCGAAAnCG wGGTTAGACC AACAAGGCGT TAAATACCAA 4560

GCAATTGATA TTAAAGCAAC ACCGCCTAGT AGTGAACAAT TAGCAAAATG GATGAAAGAG 4620

ACCGGCTTGC CTGTTCGTCG TTTTTTTAAC ACAAGCGGGG TTTTATATAG AGAACAAGGC 4680

TTAAAAGATC TTGTTGACAG TTTTTCTATT GAAGAAGCAA GTCAGCGTTT AGCTGCGGAT 4740

GGCATGTTGA TTAAGCGTCC AATTCTCTTA AAAGACAATA CATTTCTAAC GAATGGTTTT 4800

AAAGAAGCAG ATTACGAAGG AGTGCTTGGA AAATGAGTGA AATGAAACAA ATCGATCAAT 4860

TATGGATCTT ACCAACAGAA GCAGGTTATA AAATTGGTTT AACCGCCGAA GCCCAAGAGG 4920

ATTTAGGGAA GATTACTTTT GCGACATTTC CCAAAGTCGG ACAAACATTA GCTAAAGGTG 4980

ATTCTTTAAT TGAATTAGAA GCAGAAAAAG CAGTCAGTGA ATTCAGTAGT CCATTATCTG 5040

GTAAGGTAGT TGCGATTAAT GAAGCGGCTG ATCAAGAGCC AAGTGCATTA GATGAAGAAA 5100

ATGCCTGGAT TGCTGTTTTA GCAGATGTTG AACCAACAGA ATTTGAAAAT CTTTAGTCTT 5160

ACGTTGACAA GGCCAATGaT TATTGcTATA ATTTTCTCAA TCTAATCAAA AGAAAGCTTT 5220

GaAAAGAAGA GTACATGTTa AGGACGTTTG AAGAGAGCCC kGTTTGCTGA GAaTGGGtAA 5280

CAGATTTaAG ATGGrAGATG GtCyTTGrGc aGAGTAAGTG AGCGAaGCAG 5330

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TGACAGrGaC AATTkGTkGA AgCTTTCAGG AATATTGGCT ACACTTGCTC CGAATAATTG 60

TAAAAAAGTA TCGTTAAAAA TAACACCTTT TAACCCTAGG AACAATCCTG TTGCTGCAAT 120

TACTGGAACA ATTGGAATGA ATATTTCACT TAAAATGCGC ATTGTTTTGC GCATGCCTGT 180

TTCATTATTT TTTAAAATTG CTGTTTGCTC TGCTTTTGaC ACAACATTGa TTCCAAGTTT 240

TTCTATTTCA TCATACACTT TAGTCACAAT ACCAGTTCCT AAAATCACTT GGTATTGACC 300

ACCATTATAA AAAACCCCCT TGACTAAATC GATTTTTTCT AGTTGTTTAC CATCTACTTG 360

TTCATGGTCC TTCAAAATAA AACGTAACCG CGTTTGACAA tGGGTGACCG ATATAATGTT 420

ATCCATACCG ATTAATTGAA TAATGTCTTT GGCTGCCTGC TGATAATTTT CTGCCATGTk 480

ATACTCCTCC TAGCTACTCA TTGATAGTAG nCAGTAGTCC TTGATAGCTn TTGAATAATG 540

nCCCnGC 547

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

CCTTGTTCAT TTGACACCGA CGTATTTAAG TCGTTTATTA AAAGAGGAGT TTGGTATTCC 60

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CTTTAGTCAA TTTTATCGAC AATTAAAAAT CACATGGGCT AAACAGCTTC TTTTGGAGAC    120
AGATAAAACA ATTGCCCAAA TCAGTGAAGA TTTAGGGTTT GTTGAAGATA GCTATTTTGT    180
CCGGATCTTT AAACAAGAAA CGGGTGAAAC ACCCCTTAAA TACCGTAAAA GAAAGAACAG    240
AGCATAAAAA AACAACGACT CCTAGAAGTC GTTGTTTTTT TACACCTTTT GCTCTTGCTG    300
TGGCTAATGC AACAAGTGCA AAAGGCGCAT TATATCTGTC GTGCGACAAA GTGATACTAT    360
TAAATATGAA TTGGTAAACC TAAAGCCAAT TCAGCTGTAT CCATAGTAAT TTCGCCCAAT    420
GATGGGTGTG GGTGGATTGT TAAAGCAATG TCTTCTGCAT TCATGCCAGA TTCAATAGCT    480
AAAGCTAATT CAGAAATCAT GTCACTTGCA CCGACACCGG CAATTTGTGC ACCGATGATG    540
ACATTGTCTT CTACAGTTGT AACTAAACGC ATGAATCCTT CAGTTTTATC TAAAGAGATT    600
GCACGGCCGT TACCAGCAAA TGGGAATTTG TAGCCTTTTG CTTCGATTCC CGCTTCTTTT    660
GCTTCTGCAA CAGTCATACC AACGCTTGCC AATTCTGGAT CAGTAAAGGC AACAGCTGGC    720
ATTGCTTTGT AATCAACTGC AACTTTCTTA CCAGAAATTG CTTCAGCAGC AATTTTTGCT    780
TCGTAGCTTG CTTTATGCGC TAACGCAGCA CCTGGTACGA TGTCGCCGAT TGCGAAGATG    840
TTTTTCACGT TAGTACGTCC TTGGTTGTCA ACTGGGATTA AACCACGTTC GCCAATTTCA    900
ACGCCCGCTT GTTCTAAGCC TAAGTCGTCT GTGTTTGGAC GACGTCCAAC AGTGACCATT    960
ACGTAATCTG CTTCAACACT TTCTTCTTTT CCGTTAACTT CATATTTAAC AGTGACGCTA   1020
TCGCCATTGT CAACAGCTTC TTTAGCCATT GCAGAAGTCA CGATTGTTAC GTTTTTCTTC   1080
TTGAAGTGGT CTGTGACAAC TTTAACCATA TCTTTTTCAT AAGTTGGTAA AATTGATGGG   1140
CTACCTTCTA AAATTGTTAC TTCTGAACCT AAGTTAGCAT AAGCGCCACC TAATTCAGCA   1200
CCGATGACAC CGCCACCGAT AATAACGAAT TTTTTAGGAA CTTCTTTTAA GTTTAAACCG   1260
CCTGTAGAAT CTAACACGCG TCCGCCAAAT TTGAATCCTG GGATTTCAAT TGGACGAGAA   1320
CCTGTTGCTA CAATAGCATT ATTGAATGAG TAAGTTTGTG CTGAGTCTGG GTGAATAACA   1380
CGCAATGTAT TTTCGTCAAC GAAGAATGcT TCGCCTTCAA TAATTTCTAC TTTGTGTTTT   1440
TTCAATAACA TGCCAACGCC GCCTGTTAAT GATTTTACAA CTGTGTTATC TTTCCAGTCT   1500
TGTGTTTTTG CAAAGTCTAA TTCGACTCCT TTAGCTGTTA CACCAAAAGT TGAAGAATCT   1560
TGTGCTTCTT GGTAATGATG TCCAGCAGCA ATTAAAGCTT TTGAAGGAAT ACATCCAACG   1620
TTTAAACAAA CGCCTCCGAT GTATTCACGT TCGATAATCG CAACTTTTTG ACCCATTTCT   1680
GCGGCACGAA TTGCGGCAAC GTATCCTCCA GGACCAGCTC CGATTACGAC TGTATCTAGT   1740
TCAATGGCGA AATCTCCTAC TACCATTTGT TAATCATCCT TCCATTAATA GTAATTCTGG   1800
ATCAGCTAAT AAGCGTTTAA TGTTGTTCAT TGCTTTTTGA GCAGTTGCGC CGTCAACGAT   1860
ACGGTGGTCA AAGCTTAATG ATAATTTCAT CATGCGTCCC ACAACGATTT CGCCGTCTGC   1920
ATTAACAACT GGTTCTTGTG CAATTGTACC AACGCCTAAA ATAGCAACTT CAGGGTAGTT   1980
GATTACTGGT GTAAACCAGC CGCCACCGAC TGAACCAATG TTACTAATTG TGATTGTACC   2040
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ATCACGCATA TCTTGTGCAG TTAATTTACC TTCGATAGCC AATGCTGCTT TTTCGTTGAT    2100
TTCATCAGCG ATAGCAAACA TGCTCTTCGT ATTAGCATTT TTAACATTTG GTACATATAA    2160
GCCATGATCT GTATCAGTAG CGATACCAAT GTTAAAGTAA TTTTTGTAAA CAATTTCTTG    2220
TGCTGCGTCA TCGATTGATG CATTCAAGAT TGGGAATTTT TGAACAGTTG AAGTCAATGC    2280
TTTTACAACG TATGGTAAGA ATGTTAATTT TGTACCATTT GCAGCAGCAA CATCTTTAAA    2340
TTTCTTACGG TGATCCCATA ATTTAGAAAC TTCTACTTCA TCATGTAATG TTACGTGAGG    2400
AGCAGTGTGT TTGCTGTTAA CCATTGCTTT AGCAATTGCT TTACGTGTTG GTGTCATTTT    2460
TTCACGTGTT TCCATTTCGC CTAAATCAGA AGTAAAGGCT TTTGGCGCTG CTTTAGGTGC    2520
AGCTGCTTCC GCTTTAGGTG CTGCTTCTGT TGCGGCAGCT TCAGTAGCTG GGGCTGCTTG    2580
AGAACCACCA GAGACAAAGG CATCAATATC CGCTTTAATG ACACGGCCAC CTTTACCAGT    2640
TGCAGTTACT TGTGTAATAT CAACGTCTTT TTCACGCGCA TACTGACGAA CAGATGGCAT    2700
TGCTAAAACG CGTTTGTTTG GATCAGCGGC TGCAACTACG CCTGTTGAAG CGGCTGGAGC    2760
TGATGCTTCC GCTTTAGGAG CGTCAGTAGC TGGTGCTGCG ACTGACGGTG CTGCTGAATT    2820
ATGACCAGGT GCGTCAATTT CAACTAACAC GTCACCCACA TTGGCAACTG TTCCTTCTGG    2880
TACAACGATA TTTTTTACAG TACCTGTTAC TGGTGATGGA ATTTCTTCTA CTGATTTGTC    2940
ATTTTGkACT TCTAATAATG AATCATCTTC ATwAATTGTG tCGCCCGCTT TAACGAACCA    3000
TTTAACGATt TnCnTTCGGC AATTCCTTCA CCGATGTCTG GTAATTgAAT TGGAAAAATC    3060
CGCCAGCTGC TTCGGTTGTT GGTACAGCAG CAGGTTGTGC TGGTGTTTGT TCTTGTGCAG    3120
GAGCTGCTGG TGCTGCATCG TTATCTTCGT GACCAGGTGC gTCGATTtCG AyTAACACGT    3180
CACCAACGTT TGCAACTGTT CCTTCTGGTA CAACGATATT TTTTACAGTA CCTGTTACTG    3240
GTGATGGAAT TTCTTCCACT GATTTGTCAT TTTGTACTTC TAATAACGTA TCGTCTTCGT    3300
TGATTGTATC GCCAGGTTTT ACAAACCATT TAACGATTtT CCTTCGGCAA TCCCTTCACC    3360
GATATCCGGT AATTTAAACT GATAAGCCAT TTTTTAAGTC TTCCCTTCTT CGTTGGATCT    3420
GTCTATTTTC TTAGGAGCAA AACGCGGGGA AACGACTATA GTAGCTGAAC ATTTCATGCC    3480
TATAGCCGTA ATCCACCTGT TTAATTCTTC GTTTATCTAC TTCGAATAAC TATTAAAATT    3540
CGACGATTTC TCTAGCTTTT GCTTCGATAT CTTTCGCATT TGGTAACCAG ATATTTTCTG    3600
CTTGTCCGAA TGGGAAGATT GTATCTGGAG CAGATACACG TCCGATTGGT GCTTCTAATG    3660
ATAATACGGC ACGTTCAGAA ATTTCAGAAA CAACCATAGC GCCAACGCCA GCTTGTTTTT    3720
GTGCTTCTTG AaCGACAACC ACACGGCCAG TTTTTTCAAC AGAGTTAATA ATTGTTTCCA    3780
CATCTAAAGG AGCCACTGTA CGTAAGTCAA TGATTTCTGC TGAAATATTG TCTTTCGCTA    3840
AGCTATCAGC TGCTTTAATC GCTTCACGAA CCATAGCACC GTAAGTGATG ATTGATACGT    3900
CTGTTCCTTC ACGAGTTACA GCCGCTTTAT CTAAAGGCAC TTCATAAGCT TCGTCTGGCA    3960
CTTCCTCACG GAATGAACGG TATAATTTCA TGTGCTCTAA GTAAACAACT GGATCGTTGC    4020
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TACGAATAGA TGAAATTAAT AGTCCTTTTG CATCGTAAGG GTTTGATGGA ATAACAACAC 4080

GAACACCTGG TGATTGTGCG ATTAATCCTT CTAAGTTATC TGAGTGAAGT TCTGGTGTAT 4140

GAACACCACC ACCAAATGGG GCACGAACAG TAATTGGCAT ATTACGAGTT CCACCCATAC 4200

GGTAACGCGT ACGAGCCATT TGACCAACGA TTTCGTCAAA TACTTCAAAA ACGAAACCAA 4260

AGAATTGGAT TTCAGGAACT GGACGGTAAc CTTGCAAGGC AAGACCGAAA GCCAATCCAC 4320

CGATACCAGA TTCAGCTAAA GGTGTATCGA AGACGCGGTC TTCACCAAAT TTTTCTTGTA 4380

AACCTTCAGT tGCACGGAAA ACCCCACCGT TGTTACCAAC GTCTTCACCG AAGATTAAGA 4440

CATTTTCGTC TTTCTCTAAT TCAAGAGCTA AGGCATCTGT AATTGCTTGG ATCATAGTTT 4500

TTTGTGCCAT TTTTATTTCG ACTCCTTCGC TTCATAAAAT GCAATTTGTT CTTTAATTGT 4560

TTGAGGTTGA ACTTCAAACA TATTTTTCAA GAAATCAGAA ACTTTTTGTT TTGGCGCTTT 4620

ATCCGCTTCT GCAATCGCTA CTTTGATTTC TTCTTTTGTT TTTTCAATAA TTTCTTCTTC 4680

TTTTGCTTCA GACCATAAGC CTTTATCTGT TAGATATTTA CGGAAACGAG TCAATGGATC 4740

TTTTTGTACC CATTCGTCAT CCATTTCTTT TGAACGGTAA CGTGTTGGAT CGTCTCCAGA 4800

TAAAGTATGT GGACCATAAC GATAAGTTAA TGTTTCAATT AAAACTGGAC CGTTTCCTGC 4860

AGCTGACCAA TCGCGTGCTT CTTTTGCAAT TGCGTAAACT GCTAATGGAT CCATACCATC 4920

AACTTGAATA CCAGGAATTC CTGCTGCAAC AGCTTTTTGA GCTAAAGTTT TAGCCGCTGT 4980

TTGTTTTTCA CGAGGTGTAG AAATCGCAAA ACCATTGTTT TGGATAATGA AGACACCGTT 5040

TGCTTGGTAA GCACCAGCAA AGTTAATTGC TTCATAGAAG TCCCCTTGTG AAGAACCGCC 5100

GTCACCAGTA TAAGTGAAGA CAACATTTTC TTTTCCACGT TTTTTCAATC CTAAAGCAAC 5160

ACCAGCTGCT TGGATGTATT GAGCACCAAT GATAATTTGT GGTGGTAATG CATTTAAATC 5220

TTCCGCGTAG TAGTTCCCTG cTACGTGACC ACGAGACCAT AAGAAAGCTT CTCTTAATGG 5280

TAAACCATGT TGTACTAATT GAGGTACATC cACGGTAACC TGGTAGTAAG TAGTCTTCTT 5340

TTTCCATTGC AAAT 5354

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CGTAATCTTT TAAAATGACA AGTTTAGAAC AGAGAGATGA GTGCGGACAC TTATTTTTCT 60

GTTCTTTTTC TTTCTGmAAA AGTCTTTGAA ACTTATCATT TCGGAAGGTT TTCTTTTGAG 120

AATATGATAG AATGAAGCTG AGGTGAGCGA akgGnCAAAA AAAATCAATT TACCGAaGCC 180

GTTATTTTCA GAAAAAGGAA AACGGGCGGT CCTTTTATTA CACGCTTATT CTGGCAGCAG 240

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TAATGATGTA CGGATGTTAA gCAGACGTTT AGAAAnAGAA AATTATACTG TCTATTCGCC     300
TAATTTTTCA GGACATGGCA CGCTAGTTCC TGAAGATATT TTAGATCAAA CAACGGAACA     360
ATGGTGGCAA GATACACAAG AAGCAGTCGC TTTTTTGAGA GAAAGAGGCT ACCAAGAAAT     420
TGCCATTTTT GGTTTATCAA TGGGCGGGAT TTTCAGTATG CATGCATTAA CGGAACAATT     480
AACAGGATTA ATTGGTGGTG GATTTTTCTG TTCACCGATC TACCCTGTCG AAAATAAAGT     540
CCCaGAAAaT TTTGTATTAt ACGCAGAAAA CGTGATGAAA ATCGCAGAAG TTCCTGCAGA     600
GGAACAACAA AGCCGGTTGC AATCGATTGA GCAACGAGTC AAACAACAAT TAGGAGCGAT     660
TGAAACGATT GCTAGTCAGA CGGCTGACAA ACTAAACAAA ATCCACGCAC CTCTTTTCTT     720
AGCGCAAgcT GGcAAAGATG AAATGATTGA GCCAATGGGC GTCTATCAAA CGGCCCAAGC     780
ACTAACACAA GCACGTGTGA CCTTACAATG GTACCCAAAC AGCGGACATG TCATTaCGGT     840
GAGTGGAGAA CACAAACAAT TAGAGCAAGA TGTGGTGCAA TTTTTAGCAA CACTACCTTG     900
GAATGAGGAG AAATAATGAC AAAACAAACA ATTAAAGAGC AAATTTTACA TTTCATGGAA     960
AGCCAAAAAA AGAAAAGCTT TTCAATGGAA GAAATTGCAC AAGGCTTGAA TTTAGAAAAA    1020
AGTTCAGATT TTAAAATTTT AGTGCAAACC ATTGCACAAA TGGAACGAGA AAAGTCAGTT    1080
AGTTTCAACA AAAAAGGCAA AGTCCTGTTA CCAATGAAAG ACTTATTAAT AGAAGGAACG    1140
TTTCGTGCAA ATGAACGAGG CTTTGGTTTT GTAACCATCG ATCCTGAAGA ACCAGATGTT    1200
TATATTCCGA AAGAGGCAAC GAACTTTGCA ATGGATGGAG ATACGGTTTT AATCGACGTG    1260
ATCCAACATG CGGATCCTTT TTCAGATCGC GGCGCAGAAG GTAAAGTCAA AGAAATTAAA    1320
GAGCGAGCAG TGAGCCAAGT TGTCGGAGAA TTTGTGGCAT ATAGTGAAGA AGAAATGGCA    1380
GAAATGGGAC TGTATGGCTA CATGATTCCC AAAGATAAGA AATTGAATCA GTATACTGTA    1440
TCAATTGCAC CTGAAGGGAT TAAGCCAGTA GATGGTAGCA TTGTCATTGC TGAAATTACC    1500
TATTATCCAG ATCAAGAATA TCCaACGAGT ATGGAAGGAC TAGTCAAACA AGTGATTGGT    1560
CATAAAAATG ATCCAGGAAT GGATATTTTA TCAATCGTGG TGGCTCATGG AATTCCCACA    1620
GCATTTCCTG ATGAAGTTTT GGCTGAAGCG GACCAAGTAC CAGAAACTAT TGCAGAAAGC    1680
GATTTAGTCG GTCGTCGGGA TTTACGTGAT CAGTTGATTG TGACGATTGA TGGAGAAGAT    1740
GCGAAAGATT TAGATGATGC AGTAACGGTA CAAAAGTTAG CAAATGGCAA TTTCTTTTTA    1800
GGGGTGCATA TTGCAGATGT TTCTTATTAT GTAACTGAAG GAAGCCAATT GGATATGGAA    1860
GCGTATGAAC GTGGTACAAG TGTCTATTTG ACAGACCGAG TTGTGCCAAT GATTCCGCAG    1920
CGATTATCAA ATGGGATTTG TTCGCTAAAC CCACATGTTC CACGTTTAAC CATGAGTTGT    1980
GAGATGGAAA TTACACCAGA AGGAGAAGTT ATTTCGCATG AAATTTTCCA AAGTGTAATC    2040
CAAACAACGG AGCGAATGAC CTATACAGCA GTCAATGAAA TTTTAGAAGA GCAAAAACCT    2100
GAAACGTTAG AACGCTACAA AGAACTAGTT CCCATGTTTA AAGAGATGGG TGAGCTGCAC    2160
CATATATTAG AAGAGATGCG TATGCGCCGT GGTGCGATTT CTTTTGAAGA TCGTGAAGCC    2220
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AAAGTCCTAG TTGATGAAAA TGGTCATCCC AAAGATATTC TTTTACGCAC GCGTGGTGTG 2280

GGTGAACGAT TAATTGAATC CTTTATGTTG GCAGCGAATG AAACTGTGGC GCGTCATTAT 2340

CATGACTTAA AACTGCCATT TATTTATCGG ATTCATGAAC AACCAAAAGA AGAAAAAATG 2400

CAACGTTTCT TTGACTTTGC TGCAGTACTT GGCATTCTTG TTAAAGGAAC AAAAGAAAAC 2460

ATTTCACCGA AAGATTTACA AAAAGTTTTA GAGCAAGTTG AAAATAAGCC GGAAGAAGTG 2520

GTTATCAATA CGATGTTGCT AAGAAGTATG CAACAAGCGA AATACTCAGA AGACAACTAC 2580

GGACACTATG GGTTGGCTGC TGAATATTAT ACGCATTTCA CTTCACCAAT ACGTCGTTAT 2640

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CAAGAAAAAT GGAACGAAGC ATTACCAGAA ATTGCCAATC ATAGTTCAAG TATGGAACGT 2760

CGCGCAGTTG ATGCAGAGCG TGAAGTGGAC GCCATGAAGA AAGCCGAATT TATGGTAGAT 2820

AAAGTGGGAG AAACGTATGA CGGGATTATC AGCTCAGTCA CAAAATTTGG TATCTTTGTG 2880

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CACTTTATTG AAAATCATAT GGCGTTAGTT GGTGAACGGA CGGGAATGAC TTTGAAAATT 3000

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ATCGATACGG TTGAAGCTGG GCTTGTTTTA CAAGGAACAG AAATCAAATC TATTCGAAAT 3420

GGTCGTATCA ATTTAAAAGA TGGTTTTGCA CGAATTCGAA ACGGAGAAGC CTTTTTGTAT 3480

AATGTTCATA TTAGTCCATA TGAACAAGGC AATATTTTTA ATCATGACCC ATTACGTACC 3540

AGAAAATTAT TATTACACAA AAAACAAATT AATAAGTTAA TCGGCGAAAC CAAAAATACA 3600

GGTATCACAT TAGTACCTTT GAAGGTCTAT ATTAAAGACG GCTATGCCAA AGTTTTGATT 3660

GGTTTAGCTA AAGGGAAAAA GCAGTACGAC AAGCGTGAAG ACTTGAAACG TAAGGAAGTT 3720

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TTTCGCATAT TTGCTTGCCT TTCTTCGGAT TAGGTGTAAA ATCTGGTAAG TGTTGAGTAA 3840

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TAACATTAGG CTTGCGTTTG TACGGAAACA TTTTTGCCGG CGAAGTTCTA TTGGGCTTAA 4620

TTGCTGGAAC CGTAGCAAGC GTCGGATTAT GGGTTATCCC ACTAGCAATT CCGCTAGAAA 4680

TGATTTGGGT AGCATTCTCA ATCTTTATTG GATGTATCCA aGCGTTTATC TTTGTGACAC 4740

TTTCAATGGT TTATATGTCA CACAAAATTG AAACAGAAGA ATAATCAAGA AATACGAAGG 4800

ACAAAAATTA TCTTTTAGGA GGATTTTACA CAATGGAAGG ATTAAATTTT ATCGCAGCAG 4860

CAATTGCAAT TTTCGGTTCA GCTATCGGAG CCGCTATCGG TAACGGACAA GTTATTTCAA 4920

AAACAATCGA GTCAATGACT CGTCAACCAG AAATGTCTGG TCAATTAAGA ACAACAATGT 4980

TTATCGGGGT CGCTTTAATC GAAGCTGTGC CAATTTTAGG TGTCGTTGTT TCTTTATTAC 5040

TTTTATTCAG ATAAGCAATA AAATGGAGGC AGGACGCTGA TTATTATCGG GACCGTCACT 5100

GCTTTCTTCT ATCTTTAGCC TTTTCAATAG CTGGTGATAA AGCAGTTGAA GAAGCTAAAT 5160

CGATTTTTGC AGGAAAGGAA GTTGAGACTT CATGCTACTT ACTACATTGG TAGTCGGTGA 5220

AaCGGCTCCT AGTACCACAC TAGGCACGAT GATTGTTGTC AGTGGTGCAT TTTTAATCTT 5280

GATGCTCTTA TTAAAGAAAT ATGCATGGGG AGCAATCGTA GATATTTTGA CACAACGTGA 5340

AGAAAAAATT GCCAACGATT TAGACTCTGC AGAACAATCT CGCGTAgcAG CAGCGAAAAT 5400

GGAAAAAGAA CGTCAACAAC AATTACTTTC TTCCAGATCA GAAGCAGCTG AAATTATTAA 5460

AAACGCGAAA GAAAGTGGAG AACAGACTCG CCAAAAAACA TTAAAAGAAA CAACTGCGGA 5520

AGTTAcTCgc TTACGCGAAA AAGCTCGGAC AGATATTTCT CAAGAACGTG AAGAAGCATT 5580

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TAAAGAATTA ACACCAGATG CACATGAAGC ATTGATTGAT TCTTATATTG AAAGTTTAGG 5700

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AGTTGGCAGT TGAAAAGaAC CAAGCTGaAG CAmTTTATCA AGAATTATTG ACGCTTCGcG 5820

AAGTCTATCA CCAAGTACCT GGTATTGGCG ATATTTTAAG TGATGATCGC TTAGAGCCTT 5880

ATGAAAAAGA CAGCATCATG GnAAAACTAG TAACAGGTTT TAGTGAAATG ATGCCAAAnT 5940

TTTTGCGAGT GGTTTACGAA TATCGTnGCA TGTACGATCT GCTCTTGATG ATTGAnGGAT 6000

ATGAA 6005

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

TTCGTTGCAA CAGAGTTTTC ATTTTTCTTA GGAATTCCAG TAATGTTTGG AGCAAGTTTT 60

TTAAAAATCT TTAAATTCTT GGCCAAAGGA AATACGTTTG GGTCAGAAGA AATCATTATT 120

TTAATAACTG GCTCTATTGT TGCCTTCGTT GTTTCCATCA TTGCGATTAA ATTCTTATTG 180

AATTACTTGA AGAAAAACGA TTTTACAGTT TTCGGTTGGT ATCGCGTAAT TTTAGGTGCG 240

ATTTTAATTG GCTACTGGTT ATTCTCATAA AAATAAAACC GTTGCTTTCA ACAGTGAAAG 300

CAACGGTTTT ATTTTTTTAA ATCACCAAAC GTTATTCGCT CAATCCCCTG TTCTTCAAAC 360

CACTGACGAA CACGAGGATC ACAAATCGTT GCTAATTCTT TGCAGCGTAA AGTGGTATAT 420

GAAGAATTAT CTAACACAAA TTGATCCAAA TACCCAACAT CAAAATGCAT CTCAGCAATT 480

GCCGATTCCG GCATCCGTAA TAAACCAAAG TCATCTTCTA AAAAATTCTC CACTGATACG 540

CCTTCGTGaA TaTAAGATAG CGCCCCAGAC TCTAACAAAT GTGTTACCTG GAAATAACCT 600

TGTTGcGGkG GaTAwTCtTT TTcCCCCACT nATAATTnCA GGG 643

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

TTTGGCAAAC TCTTCATTAT ACATGTTAAT AAGCGCATTA ATATGCGGCT GAATAATTTC 60

TTCAAATAAC GCTTCCTTAG AAGTAAAATG TTTATAAAAA GCACCCGTAG TTACGCCTGC 120

GGTCAAGCAC AGTTGCCTTA TCTTAGTTTG CTGAAATCCT TCTTTTTCAA AATGGCTTAG 180

TCCACTTTCT ATTAATTTTT GGTGAGTTGT AATATAATCT CTGGTTTCTA TGGGTACTTC 240

CTCCTAATAA GATGAATTAA CTATATTATC TTACACAGGA CTTGAAGTTT CAATCGTTAA 300

CGTCTATTAC TGAACTCATT CCTTAGAGCT AAACTAATGA GAAAGAGCAA AATAACTGAT 360

ACAAAAAGCA ATCCTACAAG AATTAATAGA CTCATCTAAA TCATTCACCT TTTCTAAAAT 420

AATCCGAGAA AGATTTAAAA AAATTATATC CAGCTATTAG GATAAGTCCT ATCATAATCA 480

CTCCAATAGC CATTTTCTTA TCCTCCCTAA AAATAAAGTC TTTTACTTAA AACCTTTTTT 540

GTAATCGTCA ATAAATTTTT TCCCTTTATC AGTTAATTGA AATCCTATAT CTAAATAGTC 600

CTCATATCTA AGTTTAGCCA GCATCTCACT TACAGATGCT GGACTAACAC TTAGAACTTT 660

TGCTAAATCA TTATTTTTTA ATTTCTTTTT TCTTTTTGAT AATTCCTGAA TTGCTAGTAA 720

ATAAATTAGT ATAGTAGTTG TTTTAATTTG TACCATACCT ACCCTCCAAA TTATTTCGAA 780

AGGCCTTCAG CAATTTTATC CAGGTTCCAT TTCATCATCG CATAGTAACT ATCACCATCT 840

TGTCCTTTTT CTGCAATTGA ATCAGTAAAA ATCGTTGAAT AGATAGGAAT ATTGGTATCT 900

TTTGATACTG TTTTCATCGG TCTATCGTCC ACACTACTTT CTACGAATAA GGAGGGAACT 960

TTTGTTGTGC GTAATTTTTC AACTAAGTGT TTTATTTGAT CTGGTGTTCC TTCTTCTTCA 1020

GTGTTGaTTT CCCAAATGTA AGCAGAAGGC ACATTATACG CTTTCGAGAA ATATTTaAAG 1080

CATCCTTCAC TTGTAACAAT CATTTTTTTA TCATTCGGAA TTGAAGCAAA TTTAGATTTA 1140

GCTTCTTTGT CTAGAGAATC CAACTTTTCA ATATACTTAT CTAGATTTTC TTTATAGAAT 1200

TTTTTATTAT CAGGATCTTT TTCCGCTAAC CATTTTTCAA TATTTTTAGC GTAAATAATA 1260

CCGTTTTCTA AATTTAACCA AGCATGGGGA TCTTCCTTCC CTTTCTCACT CTGACCCTCT 1320

AAGTAAATAA CATCTATGCC ATCACTTGCT GCAAAATAGT CTTTGTTTTC CTCTTTGTTC 1380

GCATkTTTTA CTAATTTTGT AAACCAAGCA TTTCCTCCAG TkTCCAAGTT AACACCGTTA 1440

TAAAAAATCA AATCTGCTTT TGAAGTTTTT TGAACATCTT CAGGCAAaGG TTCATATTCG 1500

TGGGGATCTT cCCAATAGGT ACGATACTGT GTAAATCAAT TTTATCTTTT GCTATATTTT 1560

CAGTAATATC TGCTAAAATC GAATTAGTAA CTACTACCTT TAATTTTTCG TTCGAAGCCA 1620

CTGTATCTTT GTCTTTACTA TTTGTTGAAC ATGCCCCGAA TATAAAAAGA GCAATCAACA 1680

TTCCCAGACT TCCCACTACT ACTTTCCATT TTCTCATCAT AACGATCTCT CCTTCTTTCT 1740

TAAAAATTTT TGTTTTGGTG AGATTAGAAA ACTAATTACA AATAAGGATG CCGCTGTTAA 1800

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TGAACTTGCT CCGACTGTTG CAGAAATAAA TATCATAGTT TTCAAGCTAT TTGCATATAA 1920

ATATGCTGTA GCTGCTGGCG TAATTAACAT TGCAACAATT AATATAGTTC CTACACTTTG 1980

CATAGCTGTT ACTGCTACTA AAGTTAATAG AACCATCAAT AGATAATGAT AAAAATTGAC 2040

ATTCATCCCC ATTGCTTTTG CCATTAATGG ATCAAAAGAA GTGATTAATA ATTCTTTAAA 2100

AAATAGAACT ACTATAACCA ACACTAAAAC AGAAACGCCA ATTGTAATCC ACTTATCAAT 2160

ATCTTGTACA GCTAAAATAT TTCCAAACAA GATATGAAAT AAATCGGTTG AGCTATTTGC 2220

AACACCTATA AGGATAACTC CTAGTGCTAA AAAAGAACTG AAAGTAATAC CAATTGCTGT 2280

ATCTCCTTTT ATTACACTAT TGCTTTTTaT AAAaGTAATA ATGnTAGrAG CTAATAGACC 2340

AAATACAATC GCACCAATAA AAAAGTTAAT GCCTAAAATA TAAGAAATTG CTACTCCTGG 2400

CAAAACAGCA TGAGAAATAG CtCGCCCATA AGAGACATTC CTCTTAAAAT AATAAAACAA 2460

CCTACTGTTC CAGAAACAAT CCCTATAACT ACAGATGTAA TTAGAGCATT CTGTAAAAAG 2520

TGAAAGTCAT ACAGACCATT AATAAAATTT TGAAGCATAT TATTCCCCCT CTCCAATAAA 2580

TATAGTATCT CCATAGGCTT TTTTTAAATT CTCTTCATTA AATACAGATT CTACACTTCC 2640

GTGAGCAATT AGATTTCGAT TCAAAAGAAT AATATTATCA AAATACTtCT TTACCyTGcT 2700

TAAwTCATGA TGCACAATTA GCACTGTTTT TCCCTGATGT TTCAATTCTT TTAACGTATC 2760

CATAATTATT CGTTCACTAA CTAAGTCTAT CCCTACAAAT GGTTCATCTA AAAATATAAA 2820

ATCCGCATTT TGAGCAAGAC ATCTTGCTAA AAGTACACGT TGAAATTGTC CTCCAGATAA 2880

TTCTCCTATT TGATGATTAG AATATTTTCC CATATCGACC TTTTCCAAAG CCTTTGAAAC 2940

TTTTTGCCAT TCTGCATTTT TAATTCTTTG AAAAACTTTC ATTCCGGCAT ATGTTCCCAT 3000

AGATACACAT TCTTTTACTT TTATTGGAAA AGTAAAATCA ATATCAGCTT TTTGTTCTAC 3060

ATATGCAATC TTTACCAGTT TTTTATTGAT ATCTTcATTA TTAATGGAGA CCTCTCCCTG 3120

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AAAAATACCT GTTAAAGCAC CTTCTTGTAT TTTTAACGAA ATCTCGTTCA ATGCTAAAAA 3240

ATCGTTATAA CAAACmnGTA AGCTTTTTCA CTTCTAACAT AACTTTCTCC TTCTAAATGA 3300

TAATGATTAT CACGATTGTA TGGtACACaA AAATAATAtT TaGtCAaGCC TAAAATTTTa 3360

AATTgGGATT TTnCgGTgGT TGGA 3384

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

AnAATATAAA TCCTGAGTAG TTGCACTGAG AAAGCCAAGG ATTAAAACTT CAAAGGAAAA 60

GCCTGGGACA TCAATCATTT TGGATTTTTG TTCCAGGCTT AAAAATGATA AAGGGTGGGA 120

GCAGAAGCAA CTACTAACAA ATAAGACTTT TCTTTACGAC AAATAATGCG GATCGGTCTT 180

AGTCGTGCTA ATGTTGTCGC GGATTTTTTT CAAGGAATCG GCATTTTGAT CAAAATTGTG 240

ATACATCGTA TTTGTATATA AAATATCCAT TACCGTTAAG TAACTGATCC GTGAAGCCAA 300

GGATTCCGCA CGAAACAAGC CTTCTTCGGT GACGACAATA ATTGCTTCGT CGGACAAGCC 360

TGCCAACTCT GAACCGCTGT TACCAGTTAA CGTAATCATT TTTGCGTTGG TTTTTTTAAC 420

TTGTCGTGCT AGGTTGATTG ATTCTTTGGT TTTGCCTGAA TGGGAAAAAA TAAACACGCA 480

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GCACCGATAG TTAGTCCGAA TGAATTTATG GAAACTATCA AAAGCCACAA TCGAGGACCC 600

GCCTTGCCCA AAAAAATGAA GCGTTTTGGC AGAGTACATC AAAGCCAACA CGTTATCTAA 660

CAGCTCCTTT GTTAAGAACT GTGTGGCGTT ACTGAGGGAA TAAATATTGG CTTGTAAGAC 720

TTTTTTAGCA ATGGTAATAC TATCATCATC TGGTGAAATA TCATCGGCGC CATTCACGCT 780

ATTGACGTTT TGAAAAGTCG GCTGATAATT AGAATTTCTG GCGATATCAA TTTTAAATTC 840

TTGGAACCCA GAATAGCCAA TCTTTTTTAC AAATTGATAC ACGGaAGATT GGGaGACGCC 900

AATTTCGTTG GCAAGACTTT CTAACGTCAT TTGTGTCAAT AATGaTTCAG AATGAACAAA 960

GTAATCGGAA ATTTTCTTTT CTGTGAGGCT CAAATTCGGT TTTTTGaTCC GAATCCGTTG 1020

ATCCAAATAG TGGkTTTTCa TTAACACGTT CCTCCAATCT TATTTTTTTA AAAATAAAAT 1080

GAATGCCTTT TCATTGTTGG TATAGACTGA TTATAGTGGA AAAAGAGGAC AAATACAATT 1140

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AAAAACGTTT TACCTTTTGA GTAGGCAAGA TTTTTGCTAA AAAATAAAAA ATATTTTTTA 1380

ATTAGTGTAA TCGTTTACAT TATTTTTTTT ATCCTTTATG aTTGaAGTAT CAAAAGAGGC 1440

AGGTGaAAGA AAAATGGACA TTGGCTTTAT TGGACTtGGG AAAATGGGTT tGAACATGGC 1500

ATTAAATGTT CACGAACAAG GCTGGCCCAT TATTGGCTTT GATGTAACAA AGGAAGCAAG 1560

AGCGACTGCT AGAGAACAAG GTCTTTCCGT TGTAGATTCG TTGTCAGAAT TATTGAAAGC 1620

GCTTAACAAA AGGAAGGTGA TTTTTTTAAG TACCCCCGCT GGTCAGATTA CCAATCAATT 1680

AGTGGCAGAA TTGGTAGAGC AATTAGCACC AGAGGATATC ATTGTGGATA GTGGCAATTC 1740

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TGATTGTGGT ACTTCTGGTG GCATCAAAGG AGCGCGGGAA GGAGCGTGTT TAATGGTTGG 1860

CGGTGCGCcT GAAGCTGTCA AAGTGTTAAC CCCATTTTTT GAAGATTTAG CTTGTGAACA 1920

AGGGTATCTT TATGCTGGGA AATCAGGAGC TGGTCACTAT TTGAAAATGG TGCATAACGG 1980

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TCGCTTGATG GGCTTAGCGA AAGAGGTTTT TGCGGAAAAT CCTACGTTAG CCAATCTAGA 2160

AGGGAAAGTG GCAGCAAATG GCGAAgcnAA ATGGATGATT GAAGAAGCAT TGCGTTTGGA 2220

GATGCCCGTC CCAACTACGG CGTTGTCCTT ATTTACTCGA AATGAAAGTA TGCTAGCAAA 2280

TCATTTTTCA AACAAAGTGG TCGCTTCTTT GCGACAAGGA TTTGGCGGGC ATGAAGTCGT 2340

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GAAGCATTTT ACAGTCGACA GTGAAATTGG TGGCAAAGAG TTAGCGGAAC GTTTACAAGG 2520

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AGATGAATTG TTGCTGATTT CTCGCCATGG TATTGGGTAT AACAACATCG ATTTAGACGC 2640

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CAAAACTGTG GGTGTCATTG GTGTTGGGAA CACAGGAAGT TGTGTCGTGG AGACGTTACG 2880

AAACGGATTT CGCTGTGACG TGTTAGCGTA TGATCCCTAT AAATCCGCCA CTTATCTGCA 2940

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AAGTTATGGA GCCAAAAAAG TAGACTTAGA TACGTTGCTA GCTTCAGCAG ACATCATTTG    3000
TTTATGTGCC AATTTAACTG AAGAAAGTTA TCACATGATT GGCTCGGCGG AAATTGCCAA    3060
GATGAAAGAC GGCGTCTATC TTTCCAATAG CGCACGAGGC GCCTTGATTG ATGAAGAAGC    3120
CATGATCGCC GGTTTACAAT CGGGCAAAAT TGCTGGGCTT GGGACAGATG TTTTAGAAGA    3180
GGAACCAGGT CGGAAAAATC ATCCTTATCT TGCGTTTGAA AATGTAGTAA TGACGCCGCA    3240
CACCTCCGCT TATACCATGG AATGCCTGCA AGCGATGGGA GAAAAATGCG TGCAAGATGT    3300
GGAAGACGTG GTGCAAGGTA TTTTACCTCA ACGGGCAGTG CAAGAAGTCA GTCGTTACGT    3360
TAGTTAAGAA GGAGGAGGAG CATGTTAACT GATTTAAAAG TGAAAGTTGG ACCGCAATTT    3420
TATCGTTACC ACGAAGGCGC CTTAGCTTCG GTGCCGTCAC TTTTCAAGGA ATATCACGCC    3480
CAACGAATTT TGGTGGTGCA TGGCACCGTA TCCTTTGAAA AAGCTCAGCC ATTTTTACCA    3540
TTCTTGGCAG ATTCAGAGTA TCAATTCTTC TATCACACTT ACACAGGAGA ATGTAGTTAT    3600
TTTGGCGCCG AACAAATTTC ACAGCAAATA AAGGAACACC AGATTGACTT TCTTCTGGGA    3660
GTCGGCGGCG GTAAGTTAGC CGATTTAGTG GGCTACAGCG CCCATTTAAA CAATCTGAAT    3720
TTTGGCTTGG TCCCCACTTT GGCTAGTAAC TGTGCGCCGT GGACACCGTT AGCTGTGATG    3780
TATCAAGAAA ATGGCGCGGC CGAAGGCAAA ACGGAACATT TCTTTCGCCA AGCTGCGTTT    3840
TTAATCACCG ATCCTAAGTT GCTTCTGGAT GCGCCCCGTG ATTATTTTGT CGCTGGTTTA    3900
GCTGATACGT TAGCGAAATG GTATGAATCA GAGACCATTT TACGCCAAGC CCATTTGCAA    3960
GGGGAACCCT TTTTACAATT AGCGGGAGCG ACCGCCAAGC TTTCGCAAGA AGCGATTATG    4020
CGGGACTCAA AAGCAGCCTT AGCAGCGATG GATGAGGGCA AACTCACGCC TGAATTTGTC    4080
CATCTTTCAG AAATTGTTTT CGCTGTTTCT GGATTAGTCG GCGGCTTCGG CGACAAATAC    4140
GCCCGCAATG CAGCAGCACA CGCCATGCAT GATGCTATGA GTAAATTTTT ACCCAAAAGT    4200
CATGACTATT TACACGGCGA AAAAGTAGCT TACGGCATCT TCTATCAATT AGCATTGGAA    4260
AAAAGGTGGG CCATCATAGA CGCATTAATC CCTTTTTATC AAGAGCTAAA CTTGCCCATG    4320
TCGTTACGAC AAATGGGCCT TTACCCAAAA GAAGAAGCAG TACTCGATGC AATGGTTCAA    4380
TTTATTGATT CAAAAGAAAA GGTTCATTTA ATTCCTATTG AGATTTCGGA AGAACGTTTA    4440
CGTCAAGGGA TTAAAGAGCT AGAAAAGTAT ATCCAAAACC AAGGATAAGA AGGAGGAACT    4500
ATGGAAACGT TAAGTGTTTT ACAAAGTTTG ATAATGGCGC TTTGGGTGGC AGCAATTATG    4560
TCCAGATGGC TTGGAGGAGG AGCAACGTTA ACGTTGCGTT TCTCGCCCTT AATGACAGGG    4620
TTAGTAGCAG GTTTAGTGAT GGGCGATGTC CCGAAAGCGA TGATTGTCAC CGCAGCATTA    4680
CAAATGATTT ACATGGGTGT TTTTTCACCA GGTGGCTCTA TGCCAGCAGA ACCATCAATT    4740
GCGGCAGCGA TTGCTGTGCC AGTTGCGTTG CTAGGGAATT TGAAGCCGGA AGCGGCTATT    4800
GCCGTAGCGG TTCCTGTCGG TCTTTTAGGA AGTTATTTAT ATCAATTCCG TTTCTTTATT    4860
AACACGTTTT TAGGGAAGTA TACCGATCGT GCGGTGGCTG AACTAAATTC TAAAAAAATT    4920
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GCCCGCTCAA TTATCTGGTA TCCAACGATT GCCTCATTTA TTTTATTCGT TCCATTAGTC 4980

TTTTTTGCTC TTTATTTAGG GGCACCAGTC ATTGCCGATA TTATTAAAGC ATTAGAAGGA 5040

ACCGTTGTGA TTCACGTGTT AGAAGTAGTC GGTGGTGGTT TAGCCGCAAT TGGGATTGCG 5100

ACAACGGTCT ATGTCATTGG TCGAAAAGAT TTCTTGGTTT TCTTTTTCCT TGCATACTTC 5160

ATGAGTATCG TCTTTAAGTC ATTGGAAATT ACCATGGTAA CGTATGCCAT CTTTGGCGTA 5220

ATTATTGCGT TAATTTTTGT GCAAGTCCAA AAAGGCAAAC CTGTAGCAGA AAGTGCTGGT 5280

TCCGCCAGTG CCACCACTGA TTTTGATGAT GATGACGATT ACGATGACGG GTTTTAAAAG 5340

AAAAAGGAGG AACTGAAATG ACGGAAACAA CAGAAAAAGT CGTGCCGAAA ACAACGAATT 5400

TAGCACCAGA AGAAATTACC AATAAAGATG TTACAAAAGC CTATCTCCGT TGGCATTTTG 5460

CCAATGAAAT TCCCCATTCC TTTGAACGTT ACTTGGCGCC TTCGTTATTG TACGCAATGA 5520

TGCCACTTTT AAAGAAATTA TATAAAGACG ATGAACAATT AAAAGCCGCT TATATGCGTC 5580

AACTGCTGTT TTTCAATACG CAATTAAGTT GGGGCGGCGG GGTCATTACT GGGCTGATGG 5640

CTTCCATGGA ACAAGAGCGG GCCAAAGAAG AACATGAAGG CCGCGAAATC ATGATGCAAG 5700

ATGATTTAAT GTATAACACC AAAGCTGGCT TGATGGGCGC GTTAGCGGGG ATTGGTGATG 5760

CGATTGACTC AGGTACGGTT CAATATATTT TTATTGCGAT TGCGGTGCCG TGGGCGCAAC 5820

AAGGTAGCGC ATTAGGTGCG ATTTTCCCAT TTGTGGCGTT TGCCCTTTAT CAAGTACTGT 5880

TAGGTGTGTT CTTTGCGAGA CAATCCTTTA AAATGGGGCG GAATGCCACA GGCTTAATGC 5940

AAAGTGCGGG GATTCAAAAA GCCATTGAAA TGTTATCTGT TTTAGGGTTG TTCATGATGG 6000

GGATTTTAGC TGGTAATTAT GTCAAAGTTT CTTCAACCCT TCAATTTAAA CTTTCTGGCC 6060

GTGAGTTTGT GGTTCAAGAT ATCCTTGATC AGATTGTCCC AGGACTCTTA CCGCTAGCTG 6120

TTGTAATGGG CGTGTATTGG TTCTATACGA AAAAAGGCTT GAAAGTTACG CAAGCATTAT 6180

TGTGGTTAAC AGGTATCTTA ATTGTCTTAG CAACAGTCGG TATTTTATAA AAAGAAAAGG 6240

ACGTGAATCA GATGGGCGTA GTAAATTTAG CAAGAGTAGA TGAACGATTA ATTCATGGAC 6300

AAGTGATGGT GACCTTGTCC CAAAAAAGTG GCGTTAATTC CATTTTCGTT GTCGATGAAG 6360

TGGTGGCAAA GGATAAATTT ATGCGTGATT TATACAAAAG TGCAGGCAGT CGGACAGGAC 6420

AAAAAACCAT TGTCATTACG CCGGAAAAAG CTAAATTTTA TTGGGATGAA TACCAATTCA 6480

AAGAGTACAA CTGTATTTTA ATCGCTAAAA CCGTCTCTGT AATTTATGAC TTAGTAAAAC 6540

ACGGAGTCCC TATGAAGGAG TTAAACATCG GCGGTATTGC ACAGAAGAAT CCAGAAAAAG 6600

ATTTATTAGT AACCAAATCA GTTTATTTAA ACAAAGAAGA TGCCGAAAAA TTAAAAGAAC 6660

TACATGAGGT GTATGGCGTA GAAGATATTT ATTTCCAAGC AACGCCTTCT GCACCAAAAA 6720

CTAGTTTAAA AGAGGTTTTA GGCAAATTTA ATTTATAAAA AAGGCCAGTC GCTTGAGTCA 6780

TTGCATGACT GTTTGAAGTA ATGACTCAAG CCACTGAACT GAAGGAGGAA CTTTTATGTT 6840

AGGGATTGTG ATTGCTACAC ATGGTGCACT AAGTGACGGT GCGAAAGACG CAGCTACCGT 6900

GATTATGGGC GCAACCGAAA ATATCGAAAC CGTTAATCTA AATAGTGGAG ACGATGTCCA 6960

AGCACTAGGC GGACAAATTA AAACAGCGAT TGAGAACGTC CAACAAGGGG ATGGCGTGTT 7020

GGTCATGGTT GACTTATTAA GTGCGAGTCC TTACAATCAG GCAGTTTTGG TGATTAACGA 7080

ACTCGAACCA gCTCTACAAA AGAAAATCTT tGTGGTGAGT GGTACCAACC TACCAATGGT 7140

CTTAGAAGCG ATAAACCATC AATTATTGGG CACACCGATT GCTGAAnCGG CGCAAGCGAT 7200

TGTTGCGCAA GGC 7213

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ATCCAAAAAG AAAGGAAGTG CCTTATGGCT AAAAAATCAA AAATTGCTAA AGCAAAAAAA 60

CAACAAGCAA TGATTGCAAA ATATGCGCCT ATTCGCCAAG CCTTAAAAGA AGCTGGCGAT 120

TATGAAGGTC TTAGCAAATT GCCAAAAGAT GCTCATCCAA GTCGCTTAAA ACTCCGCGAT 180

CAAACAGATG GGCGCCCACG TGGCTACATG CGTAAATTTG GCATGTCTCG GATTCGTTTC 240

CGTGAATTGG CTCACCAAGG CTTGATTCCT GGCGTCAAAA AAGCAAGCTG GTAACTCATT 300

ATTTCGATAA AGACAACTAG CGAGGACAGT CGCCTTTGGG CTGACCTCGC AGCCCCCTTT 360

ATCTTTTATA CGCAATTAAA AAAATCAAAT TGGAGGACGG TaCTATGCGC CAAACCATTA 420

CGTTAGCTTG CGCTGAAACT GGCGAGCGCC TTTaCTTAAC ArGTAAAAAC ArACGAAATA 480

CACCAGAAAr AtTACAGCTG AAAAAAtATT CaCCAAAACT aCGGcGcCGs GsACTTTTcA 540

CkGAAGTCnA ATraCCGGGG GGAA 564

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

CAAGAATCGT GTGGAACAAA AAGCGGAAGA CGGCGACGCA AAAGCTCAAA AATTGCTTAA 60

GGTATTGCAA GACCCCAATA ACTTTTTATC CACAATCCAA GTAGGGATTA CTTTGGTTAA 120

TATCCTATCT GGTGCTTCAT TAGCAGAGAC TTTATCTAGT CGTTTGGCCC CTGTATTAGG 180

TGGCGGCGCg CAGCTAAGAG TCTTGCCAGT ATCATTATCT TAGCTTTGTT AACGTACGTT 240

TCTATTGTAT TTGGTGAATT ATACCCTAAA CGAATTGCTA TGAATAAATC AGAAGAAGTC 300

GCTCAATTGA CTTCTGGTGC AGTCCGCTTT TTAGGAGTTA TCGCGCGTCC CTTCGTTTGG 360

TTGCTATCGG CTTCGACCGA TTTATTATCC AAAATCACAC CAATGACTTT CGATGATGCT 420

GATTCGAAGA TGACACGAGA TGAAATGCGC TACATGCTTG AAACAGAAGG TGTTTTGGAA 480

AACGAAGAAC TAGAAATGTT ACAAGGTGTC TTTTCATTAG ATACAAAAGT GGCACGAGAA 540

GTAATGGTTC CTCGGACAGA CGCATTCATG GTTGATATCC AAGATGATGT CCAAGAAAAC 600

ATCAATTTAA TTTTAGGAGA AAATTATTCT CGGATTCCTG TTTaTAGTGA AGACAAAGAT 660

AAAATTGTTG GTATTTTACA TACCAAAACG TTACTAAAAG CTGCACGTAA TTTAGGCTTT 720

GAAAACATTG AATTAGGCGC GATTATCCAA GAACCATTAT TTGTCCCAGA AACCATTTTT 780

ATTGATGATT TACTTTATGA GTTAAAACGA ACACAAAACC AAATGGCGAT TTTACTAGAT 840

GAATATGGCG GTGTTGTCGG TTTAGCAACA CTGGAAGATT TACTAGAAGA AATCGTTGGT 900

GAAATTGACG ATGAAACAGA T 921

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

TGAACGTCCT ATTAGTTATA GACGAATTTG AGGACCAAAA AGTTTCAATT TTTTCAATTT 60

AGTTAGTTGT TTATTTAATA AAAAATAAAA GGTTGCTAGA GGATGAAAGG AGTATAATTT 120

ATTTATCTAG AAGAGTAATC GGAATGAGAA AGGGCTGTGG AAATGGATCA TCAACAGGTG 180

TTGAAAAATG AAATTAAACA ATATTTAGTG AGTAAAAACT GTGAGAAGAC GTATTATCAT 240

TGTATGGAAG TTGGAGAGTA TGCCTATCmA CTCGGTGAAA AATATTTAAC TAGTCCaGAA 300

AAAGTAAGTA TTGCmGGaTa TTTACATGAT ATCTCTGCGG TTTATCCAAA TAATCAGrGA 360

ATTAGTGTCG CACAAAAATA TGGGATTGAA TTAAACGAAA CAGAAATGGC CTTTCCAATG 420

ATAATTCATC AAAAAATTTC TAAGTCTATT GCGAAAATGG ATTTTGGTAT TGAAGACAAT 480

GAAATTTTAT CAGCTATTGA ATGCCATACA ACATTGAAGA AAAACTATTC GGACATAGAT 540

TTAGTTTTGT TTGTCGCTGA TAAAATAAAA TGGGATCAAG AAGGGAAGCC ACCATACTTA 600

GATGGTTTAT TACAAGCTTT AAATTGTTCT TTAGAAAATG CCGCATATTT CTATATCGAT 660

TATATTTTGA AaCACGATAT TaAAGTCGTG CATCCTTGGT TATGGGATGC TTACAATCAA 720

CTTAATTTGA TAATTAAATA ACAAATAAAT ATAGCCGTTT TTAGTCGAGT TTTGCTGGTG 780

AGAAAAGGTG AAAAGTAGTA CAGTATTCTT GTCAGAAAGA AGGGATTCCC AATGAAAAAA 840

ATAATCTTGA TAGGTCTTTT ATTGAGTATT TTATCAGGAT GTTCTTCCAA CAAAAGTGGT 900

GATAGCACTG CAAGCAAATC AAGCAAGCCG ACAGCAACAT CAGAAATGAA AGCACAACAG 960

TAGCCAAGCG AGTCAAATGA GCACGGAGTC AAAATCTAGT ACAACTCAAA GTAATTCTTC 1020

TGCTTCTACT AAAACTGAAA ATCAGTTGTG GTCTGTGCAA AAAAAAGCAC AGTTACAACA 1080

ATTTATGGCT GACTGGGGGC AACGGATGAA CCAAACGTAT AAAGAATATA TACCAGGAAA 1140

TTTAATCAAT TTTAATGGCG TCCAAGCGCC TGATGGTCTA GTAGGAAATG TTACTATGCA 1200

ACCAGCGATT GGTCAGCATC CCATTTATTT AGAATGGTCT GAAAaTGGAC AAGTGAAGGA 1260

TGGATATGCG TTAGTTGCTG TTTACTCTGA TGCAGAAACG CAACCAGAAA TGCAAAAGCA 1320

TTTGTATTTA TTCACCATCG TTAACAATCA GCCCTTAGTT TTAGTGACGA TGCAAAATCA 1380

AGGAGATCCT TATGGCTATC TGTATTTTGG AGCAACAGAT AATGCAGAGT TGAGGGCTGG 1440

CTTTGAAAAA ATTGTAGGTG CCCCGTCAAT TACTAAAGAA CAAATCCCAA tATTTCAGTC 1500

AATCCgTGkc tCaAAgAGGa GCGGnTGnAT TTTA 1534

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

TTGATTTGGC AAATATTTCA GGAAAAGCGG GTAAAGAGCT TGGTAATTTT GGCATGATGA 60

TTCAAGACTT AACGAAAACA GTGCCCTATT TAACGATTAC AGAATTGGTG AAAGAAACTT 120

TACAACGTAG TGGTTATCGG GAAGCTTTGA TGGCGCAAAA TAATTTAGAG TCTCAAGCTC 180

GCTTAGAAAA CTTGGACGAA TTTTTATCTG TGACACAAGA ATTTGATAAA CGTTTTGAAG 240

CGCAAAACAA CGACGATCCA AATGGCGAAG AAACAAAATT GGCGGATTTC TTAACAGATT 300

TAGCCTTGGT TTCTGATTTA GATAATTTAG AAGAGAGCTC TTCGCAGGTA ACCTTAATGA 360

CGTTGCATGC GGCCAAAGGG CTGGAATTTC CAGTGGTCTT TTTAATGGGC TTAGAAGAAG 420

GGGTTTTCCC ATTATCACGT GCCATGCTAG AAGAAAGTGA ACTGGAAGAA GAACGGCGCT 480

TGGcTTATGT TGGtATCACA CGAGCGGAAG AAGCCTTGTT CTTAACGAAT GCTTATTCGA 540

GAACATTATA TGGTCGCACG CAATATAATC GACCAAGTCG CTTTTTAGAA GAAATTGAGG 600

CGGAgCGTTT AATGAAACAA GGGGCGGCAg CCAAtTTACA GAAAGCTCCA GCGCGCACCT 660

TTGATCCTAA AGTATTTAAG CCCAGCGCAA GTAAACCAGC TTATACACAA CCAGCTACAA 720

AATCAGTTAG CAACAAAGTG GCAAGTGGTG GCGAAAAAGT TTCTTGGCAA GCAGGTGATA 780

AGGTCCAACA TAAAGCATGG GGCGTTGGTA CAGTCGTTCG TGTAGGCGGT TCGGCCAAAG 840

ACTTAGAGTT GGACATTGCT TTCCCAGAAA AAGGCATTAA ACGGTTGTTA GCGGCATTTG 900

CACCAATTGA AAAAATTTAA CATGCAAAAT AGGTCAGCGA TTTAATGAGA AATCATCATT 960

AGTTAAATTC TTTTTATTTT CTATCTTAGT GTAAATGTGT TAAAAAGACG ATAGGAGCAT 1020

TACGCTTATG AGGAGGAGTT CTACGATGGA ACAACAACCA TTAACATTAA CGGCGGCGAC 1080

AACTCGTGCG CAAGAATTAA GAAAACAACT CAATCAATAT TCCCATGAAT ATTATGTCAA 1140

AGATCAACCA TCCGTAGAAG ATTATGTTTA CGATCGTTTG TATAAAGAGT TAGTCGATAT 1200

TGAAACGGAG TTTCCTGATT TAATCACGCC AGATTCGCCG ACACAACGTG TAGGTGGCAA 1260

AGTTTTATCT GGTTTTGAAA AAgcTCCGCA TGACATTCCA ATGTATAGTT TAAATGATGG 1320

GTTTAGCAAG GAAGACATTT TTGCTTTTGA TGAACGTGTT CGTAAGGCGA TTGGTAAACC 1380

CGTTGCTTAC TGTTGTGAGT TAAAAATTGA TGGGTTAGCA ATTTCATTAC GTTATGAAAA 1440

CGGGGTGTTT GTACGCGGAg CAACACGAGG CGATGGAACG GTTGGTGAAA ACATTACAGA 1500

GAACTTACGA ACGGTTCGCT CTGTACCGAT GCGTTTAACG GAGCCCATTT CAGTGGAAGT 1560

TCGTGGCGAG TGCTACATGC CTAAACAATC CTTTGTCGCA TTGAATGAAG AACGTGAAGA 1620

AAATGGCCAA GATATTTTTG CCAATCCTCG GAATGCAGCG GCGGGAAGCT TGCGCCAACT 1680

AGATACAAAA ATTGTGGCTA AACGGAACTT AAATACGTTT TTATACACAG TTGCTGACTT 1740

TGGACCAATG AAAGCGAAGA CGCAGTTTGA GGCATTAGAA GAGCTTTCTG CAATTGGTTT 1800

TAGAACCAAT CCCGAACGGC AATTATGTCA GTCAATTGAT GAAGTTTGGG CCTACATTGA 1860

AGAATACCAT GAAAAGCGGA gcACTTTGCC ATACGAAATC GATGGAATTG TGATTAAAGT 1920

GAACGAATTT GCGTTGCAAG ATGAATTAGG TTTCACTGTC AAAGCACCTC GCTGGGCGAT 1980

TGCCTACAAA TTTCCACCAG AAGAAGCAGA AACAGTAGTG GAAGATATTG AATGGACAAT 2040

TGGGCGCACG GGGGTGGTCA CTCCTACTGC GGTCATGGCT CCTGTACGAG TCGCGGGAAC 2100

CACGGTTAGT CGGGCAAGTT TGCATAATGC AGATTTTATT CAAATGAAAG ATATCCGTTT 2160

AAATGATCAT GTTATTATTT ACAAAGCCGG CGATATTwTC CCaGAAGTAG CGCAAGTGCT 2220

AGTTGAAAAA CGTGCAGCCG ATAGTCAGCC TTATGAAaTG CCGACACaTT GTCCaATTTG 2280

TCaTAGTGAG TTGGTGCATT TAGATGAGGA AGTGGCGTTA CGTTGTATTA ATCCAAAATG 2340

CCCTGCGCAA ATTAAAGAAG GGCTGAATCA CTTTGTCTCA CGAAACGCAA TGAACATTGA 2400

TGGCTTGGGG CCACGAGTGT TAGCACAAAT GTATGACAAA GGATTAGTGA AAGACGTAGC 2460

GGATCTGTAT TTCTTAACAG AAGAACAATT AATGACTTTG GATAAAATCA AAGAAAAATC 2520

AGCAAACAAC ATTTATACTG CCATTCAAGG GAGTAAAGAA AACTCTGTCG AACGTTTGAT 2580

TTTTGGCTTA GGGATTCGCC ATGTGGGGGC GAAAGCGGCG AAAATTTTAG CGGAGCATTT 2640

TGGTGATTTA CCAACCTTAA GTCGTGCAAC CGCGGAAGAA ATTGTGGCTT TGGATTCAAT 2700

TGGCGAAACA ATCGCAGACA GCGTTGTGAC GTATTTTGAA AATGAGGAAG TTCATGAATT 2760

AATGGCTGAA CTGGAAAAAG CCCAAGTGAA CTTGACATAT AAAGGTCTCC GGACAGAACA 2820

ATTAGCAGAA GTGGAGTCAC CTTTCAAAGA CAAAACAGTT GTTTTAACAG GAAAATTAGC 2880

GCAGTACACT CGCGAAGAAG CCAAAGAAAA AATTGAAAAT CTTGGTGGAA AAGTTACAGG 2940

GAGTGTTTCG AAAAAAACTG ACATTGTGGT TGCTGGCGAA GATGCAGGCA GTAAATTAAC 3000

CAAAGCTGAA AGCTTAGGCG TGACCGTTTG GAATGAACAA GAAATGGTCG ATGCGTTAGA 3060

TGCAAGTCAT TTTTAAGAAG AAAAATTAAC GTTGTCAGAT TTTATGTAGT AATTTGATGG 3120

TATGCTTATT TTAGTCATAA AAGTTATATG AACGAGGACT TTCTGAGTTG AGAAAGGAGG 3180

TTGATGCTTA TGCGCAATTC TTCTTATCTT AATGAAAGGA GCAATGTTTT TGTCCGTTGA 3240

AGCAGCGTTG GGACTGATGA TTGGTTTTGC AACACTTGTT GTGACCATTA TCTTCGTTAT 3300

CTTAGCGCTT GTCTTAGACA ACAAAAATAA CCGTTCATAA GCTTTGAGGA GCTGAACGGT 3360

TAAGCGTTTG AAATAAAACC AATAACTCAG TAAGCCGCTA GTTCTTATAA CTAGTAGTGG 3420

CTACTAGAGA GGTATGTTCC TGCATATCTC TCTTTTCATT TTCATAATAA CATGTTTCCG 3480

TCATTTTTGC GAGCGACAAA TTATCAATGA AATTCAAGGT TTCATCTAAA ATATCCGACC 3540

ATTTTATGGT AGAATAGGAA CAGAGTGAAC AGCTGTGCTA AGCTGTTTAA AGAAATACAA 3600

TCCAATTGAT TAATCTGAAA ATGAAAATTT CAGTAAATGA TAGAAAGAAG GGTATCTATG 3660

GCAATTACAG AAGAACAAGT CAAACATGTC GCTAAATTAT CAAAATTATC TTTCTCCGAA 3720

GAAGAATTAG CGGACTTTAC CAATCAACTA GATAAAATTA TTGATATGGT GGAATTACTA 3780

GAAGAAGTAG ATACAACCGG GGTTCCTTTT ACTTCAAATG TGAATGAATC AATCAATGTC 3840

ATGCGTGAAG ACGTAGCGAC ACCAGGAATG GACCGTAAAG AATTAATGCG GAATGTTCCG 3900

GAATCAGAGA ATGGTTACAT TAAAGTGCCT GCAATTATGG ATAACGGGGA GGCAGGAGCC 3960

TAATGGAAAA ATTATACGAC AAATCGTTAA CAGAGTTACA TGATTTATTG GTCTCAAAAG 4020

AAATCACTGC AGTTGATTTA ACCGAAGAAA CATTAAATCG TATTCAAGAT ACAGAAGAAC 4080

AACTAGGTTC TTTTATCACA GTTAGTGAAG AAAAAGCAAT GGCATTAGCC AAAGCGATTG 4140

ACTTAAAAGG CATCACTGAA AGTAATCCAT TAGCTGGGAT TCCTATTGGG ATTAAAGACA 4200

ACATTGTCAC AAAAGATATT TTAACAACAG CTGGcTCAAA AATGTTACAC AATTTTGACC 4260

CAATTTATGA TGCGACCGTG ATGGATaAAG TCTATCAAGC AGATATGATT CCTGTCGGAA 4320

AATTGAAcAT gGATGAAtTT GCCaTGGGCG GAAGTACGGA AACGTCTTAC TTCAAGAAAA 4380

CAAAAAATGC TTGGGATCAA ACCAAAGTTC CTGGCGGTTC TTCTGGTGGT TCAGCTTCtG 4440

CTGTCGCAGC CGGACAAGTC CCAGTTTCTT TAGGGAGCGA TACAGGAGGT AGTATCCGCC 4500

AACCAGCCGC ATTCAACGGT ATTGTGGGcT TGAAAcCAAC TTATGGACGT GTGTCTCGTT 4560

TTGGTTTGAT TGCTTTTGCT TCAAGTTTAG ACCAAATTGG TCCaTTGACA CGAAATGTTA 4620

AAGACAATGC CTTAGCTTTA AATGCAATTA GTGGTTATGA CGAAAAAGAC GGCACTTCTG 4680

CAGGCGTTTC TGTTCCTGAT TTTACGGCAG ATTTAACTGG CGACATCAAA GGCATGAAAA 4740

TTGCTTTACC AAAAGAATAC TTAGGTGAAG GGGTACAACC TGATGTTCGT GAAGCGGTAT 4800

TAAAAGCAGC AGAAACGTTC AAAGCTTTAG GCGCAACAGT GGAAGAAGTT AGCTTACCAC 4860

ATTCTAAATA TGGGATTGCC GCTTACTATA TTATTGCCTC TTCAGAAGCA AGTTCAAACT 4920

TACAACGCTT TGATGGCATT CGTTATGGTT ACCGTTCCGA AAATGTCCAA AATCTAGAAG 4980

ACGTCTATGT TAATTCGCGT TCCGAAGGCT TTGGTACTGA AGTCAAACGT CGGATTATGT 5040

TAGGAACCTT CTCTTTAAGT GCTGGTTATT ATGATGCGCA CTTTAAAAAG GCTGGTCAAG 5100

TCCGTACACT AATCAAACAA GATTTTGAGA ATGTCTTTGC GGATTATGAC TTAATCATTG 5160

GCCCATCAAC ACCAACTGTT GCTTTTGGTT TGGGTGAAAA TATCAATGAC CCAATCACGA 5220

TGTATATGTA TGATATTTTA ACTGTTCCTG TTAACTTAGC TGGGTTACCA GGCATGTCAA 5280

TTCCAGCAGG CTTCTCAGAA GGATTGCCAG TTGGTTTACA AATTATTGGA AAACATTTTG 5340

ACGAACATAC AATGTATAAA GCAGCCTATG CTTTTGAACA AGCGACAGAT TTCCATACGA 5400

AAAAACCAGT CATTTTAGGG GGGAACGATT AATGAACTTT GAAACTGTCA TTGGATTAGA 5460

AGTCCACGTA GAATTGAAAA CCAACTCTAA AATTTTCTCC TCTGCGCCAG CGCATTTCGG 5520

AGCAGAACCA AACAGCAACA CAAACGTGGT TGACTGGAGT TACCCAGGTG TTTTACCTGT 5580

GATGAATAAA GGTGCTTTAG AATTTGGCAT GAAAGCAGCA CTTGCCTTGA ACTGTGAAAT 5640

TTCAAAAGAA ACACATTTTG ACCGTAAAAA CTATTTTTAC CCAGATAACC CGAAAGCATA 5700

CCAAATTTCT CAATTTGATC AACCAATCGG ACATGATGGT TGGATTGAAA TTGAAGTCGA 5760

AGGCAAAAAG AAAAAAATTC GCATTGAACG TGTGCATTTA GAAGAAGATG CTGGGAAAAA 5820

TATTCACGGC ACAGATGGCT ATTCTTATGT AGACTTGAAT CGTCAAGGCA CGCCTTTAAT 5880

TGAAATCGTT TCTGAAGCAG ACATGCGTTC ACCAGAAGAA GCGTATGCTT ATTTAGAAGC 5940

GTTGCGTTCA ATTATCCAAT TTACAGAAGT TTCTGATGTG AAAATGGAAG AAGGTTCTAT 6000

GCGTTGTGAT GCCAATATTT CTTTACGTCC GTATGGTCAA GAAGAATTTG GTACTAAAGC 6060

GGAATTAAAG AACTTGAACT CTATGAACTT TGTAAAAAAA GGTTTAGCTT ATGAAGAAAA 6120

ACGCCAGGCC AAAGTCCTAT TATCTGGTGG CGAAATTCAA CAAGAAACAC GCCGCTTTGA 6180

TGAAGCAACT AGTACAACGT TGCTTATGCG TGTTAAAGAA GGCTCAAGTG ACTACCGTTA 6240

CTTCCCaGAG CCAGATGTTC CTCGTTTTTC AATTGATGAT GAATGGATTG AAAAAGTTCG 6300

CGCTAGTTTG CCAGAAaTGC CAGcCTCACG TCGTGCCCGT TATATCAGTG AATTAGGGTT 6360

ACCTGAATAC GACGCAATGG TCTTGACTTT AACGAAAGAA ATGTCAGATT TCTTTGAAGC 6420

AACTTTAGCA AACGGTGCAG ATGCGAAACA AGCATCAAAC TGGTTAATGG GCGAAGTTTC 6480

TGCTTACTTA AACAGTGAAA AAGTTGAATT AGCCGATACT AAACTGACAC CAGAAAATCT 6540

AGCGGGTATG ATTACTTTGA TTAACGATGG CACAATCAGC TCGAAAATTG CGAAGAAAGT 6600

GTTCAAAGAG TTAATTGAAA ACGGTGGAGA TGCTAAAGAA GTTGTCGAAG CAAAAGGCCT 6660

TGTTCAATTA TCTGATCCAG CGCAATTATT ACCAATGATT AACGAAGTTT TAGACAACAA 6720

CCAACAATCA ATTGATGACT TTAAAAACGG AAAAGACCGT GCAGTTGGTT TCCTTGTTGG 6780

ACaAATTATG AAAGCAACTC GTGGACAAGC AAACCCAGGT GTGGTTAACA AGTTATTGCA 6840

AGAAGAGCTT TCAAAACGAT AAGAAAGTAG CAGGCAAACC ATGAAAAAAG CTAGAGTGAT 6900

TTATAATCCA ACGTCAGGAA AAGAGTTAAT CAAAAAGAAC TTAGCCGATA TTTTATCTAT 6960

TTTAGAAGAA TGTGGTTATG AAGCCAGTGC ATTTGCGACC ACACCAGAAG AAAATTCAGC 7020

ACGCAATGaA GCACATCGTG cTGCGCGGGC AGGATTTGAT TTACTAGTAG CTGCAGGTGG 7080

AGATGGGACC ATTAATGAAG TCGTGAATGG GATTGCTCCG TTGAAGCGGC GCCCTAAAAT 7140
GGCTATTATT CCTGCTGGAA CGACGAATGA CTATGCACGG GCCTTGAAGA TTCCTCGTGA 7200
TAATATCGTT AAGGCAGCAG AAGTGATTAA AAAAAATCAA ACTGTCAAAA TGGATATTGG 7260
CCAAGCCGGC AAAAATTACT TTATCAATAT TGCGGCGGGT GGTCATTTAA CGGAACTGAC 7320
TTATGAAGTT CCGTCAGAGT TGAAAAGTAT TTTTGGTTAC TTAGCGTACT TAGCCmAAGG 7380
AGCCGAAATG TTGCCGCGAG TGAAGCCGAT TAAAATGCGC ATGACGTATG ATGAAGGTGT 7440
GTACGAAGGC AATGCATCAA TGTTTTTCCT AGGGCTGACT AACTCGGTGG GTGGTTTTGA 7500
GCAAATCGTA CCAGATGCTA AATTAGACGA TGGTAAGTTT TCATTAAksA TTGTAAAAAC 7560
AGCCAATATT TTTGAGATTC TTCATTTAGT TGCGTTAATG TTAAATGGTG GAAAGCATGT 7620
TGAAGATCAT CGACTGATCT ATACAAAGAC CAGCTATTTA CATGCAGAAA CGTTAGAAAA 7680
GAACAATAAA ATGATGATTA ATTTAGATGG TGAATATGGA GGCGATGCTC CAATGACCTT 7740
TAAAAATATG CATCAACACA TTGAAATTTT TGCAAATGGT GATGCACTGC CGTCCAATGC 7800
AATTATGGGT TCTGTCTTAA CTGGTAGCGA TGAGATTGTC GTAGAATCAG AAGACGAAGA 7860
GGAAGAAGCA TATAmCGAAG CCAGCAAAGA ATTTGTCAAA GAAGTTGAAC GACTAACAGA 7920
CGAAGATATT GATGGCGATG GAAAGATTGC GGAAAAAGAA AAGCACTAGG TAGTCCGTGA 7980
ATAGCTAATG AAAGATTTAG TTGATAAGAT CTTTCATTGG CTATTTTTTG ACTAAGGGAA 8040
AGGGTCTCAT TCTTTTATTT ACCCAAAAAG CTCAAACGGA ATTGCTAAAT CGCCATGrAA 8100
ATTCGTTGTT GCTTTTCTTA GGTATTTTCA TTAGAATGAG TGAAGTGTAT TAAAAAGAAG 8160
GAGCGGACTT ATGAAAAATT ATCCCAGTAA AGAAAAATGA CGTCATTGAA GTAGAAATCA 8220
TTGACTTGAC GCATGAAGGT TTAGGCGTGG CAAAAGTGGA CCATTATCCA TTATTTATTG 8280
AAAATGCCTT ACCAGGTGAA AAACTTGAAA TCAAAGTCTT AAAAACAGGC AAAAGTTTTG 8340
GTTATGGGAA AGTATTGACT GTCCTAAAAA GCAGTGAACA GCGTGTGCCC GTGAAAGATG 8400
AAAACTTTAC AAAAGTCGGG ATTAGTCCGT TGCAACATTt AGCGTACGGs GcCCAmCTAT 8460
CATTTAAAAC mCAmCAAGTA GAAAATGTTA TGCAACGTGT CGCTAAATTG CAAGAAGTCC 8520
CTGTTTTACC AACAATTGGG ATGAACGATC CGTGGCATTA CCGGAACAAA GCACAAATTC 8580
CCGTGCGTAA AATTGACAAC CAACTACAAA CAGGTTTTTT CCGGAAAAAT AGCCATGATT 8640
TAATTCCGAT GGAACATTTC TATATTCAAG ACCCAGAAAT TGATGCAGCA ATTGTTAAAA 8700
TCCGTGACAT TATGCGTAAA TATAGCGTAA AACCTTATAA CGAATCTGAT AATACAGGGA 8760
ACTTACGCCA TATTGTCGTT CGTCGTGGCT ACCATACTGG GGAGATGATG GTTGTTCTAA 8820
TTACGAGAAC ACCGAAATTA TTCCCAATTA GTAAAATTGT GCCAGATATT TTGGAAGCTA 8880
TTCCGGAAGT AGTCAGCATT GTACAAAATG TAAATCCAAA ACGAACCAAT GTCATTTTTG 8940
GCGACGAAAC CATCTTATTA CATGGGTCTG AAAAAATTAC AGATACTATT TTTGATTTGA 9000
AATTTGAAAT TTCCGCGCGT TCATTTTATC aAGTAAATCC ACaACaAACA GAAGTGATGT 9060

ATCmAAAAGT TAAAGAGTAT GCGGCTTTAA GAGGCAATGA AATTGTGGgT GGaTGCCTAT 9120

TGCgGGaTTG GaACGAnTGG cTTAACTTTA GCCCAAGATG CCAAGCCAGT TTACGGTATT 9180

GAAGTAAnTG GAGGAAGCGG TCCAAGATGC CG 9212

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCCTGGGAAA TTGGnCCATT AAAATGGAAA TnAAGAATTC TACAGCATTA CTGTGTAAAA 60

GGACATATTT AGCAACATCG CAATGATGAT TCCGATTAAG GCACTATAAG CGGCATGACC 120

AACTGCTGAT AGGTCTTTCT TCGTAAAGAC ACCTACTAAT GACATCGCGC CAAAGGTAGC 180

TGCTGCACTT AAAAATGCGC CGGCCACTGT TCCACCAGTA TACATTAATA ACGTCACGGA 240

TAAAGTGACA CCATTTAATA ATGCATACGC AACAAATCCT GCAATCGCAA TGGTTGGATT 300

TTTCTGTGCT TTTGCGCCTA GATATAAAmC TAAGCCaATT TCAACAAGCC AAATCATCCA 360

AAAAGCTAAG CTTGATTGGA ATAAAGTAGC TAGAACAGGT AAAAAGACAG TTGTCATTGC 420

ATAAGCCATG ATTGCGCTAA TACCAATTCC TAACGCTAAA AATCCGTAAA TTTTGGCATA 480

AAATTTATTC AAACCTGTGC CAGTTTGGAT ATACTCTTGA TTATTCATAA GTnAAAGTCC 540

CTTCTTTCTC TGTTAGTTCA TCAATCGTCA CTTGGGGTGG TTGAACCATC ACCACTGCAT 600

CTAACACGCG ATTTTCTTGC TCATTAACAG CCTCAACTGA AATGGTAATC ACATCTTTCA 660

TTTTGTCGAC TTTGATTACT TCTAATTGGA AAGTCAATGT TTCGTAATGA AAAACGGGTT 720

CCACAAAGTT CaCAGAGAAA TTCaCAACAT GTGaACCTGG TCCTGGTAAA TGTTTAGAAA 780

TCGCACTAGT GATAATTCCC ATCAGCATAA TTGATGGTAC GATTGGTTTT TCATATTCTG 840

TTTTTTGGGC ATAATCATGT TGGATATATA AAGGATTCgC ATCATTGGTC AAGCCCAAAT 900

AAAGTAATAA GTCCTTGTCT TCAATTGACT CTGTCAAGGA CAACGAATCT CCCTCTTCGA 960

TATCTTCGAT GGTTTTGCCT AATTTTCTCG GTTTTCCGAT ATTCAAATTA GTACACCTCC 1020

GTTATTGATA AGATAATTGT ACCAAAATGT ACTTAAAAGG CAAGCTAAAA AGTAGTCTTT 1080

AAAGGATGTT TAAACAAAAC CAACTTATCT AcCATGCtAG CATTCTAAAA AAAACAACGG 1140

aACAGGaGCA GCTTCTTATT TtTTGAAGCC AGATACCCCT GGnCCCGATT TTGGTTATGT 1200

CCCCTATAAA ACGGTCnAGT nGGGTACCTA 1230

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

GTCACAAAAG AnGTTTCAGT CAATACTGAA ACTGGTTTAA CACAACAAGA GGCCCAACAA 60

CGGCTGAAAG AAAATGGCCG CAATCAATTT GAAGAGGCTA AGAAGGATTC TGTGTTAAAG 120

AAATTTATTC ACAGTTTATC TGATTTTACA ACGATTATTT TATTAGTTGC TGCGGCAATT 180

TCGTTTTATA CAGCAATCGT AACAGAACAT GGCGAATATT TTGAAGGAAT CTTAATTATT 240

GCAATTGTGA TTATCAATGC TGTTTTAGCC ATTGTTCAAG AAGGAAATGC TGAAAAATCT 300

CTGGCGGCTT TACAAGACAT GAACAAGCAA AGTAGTGCAG TCTTACGAGA TGGCAAGGTA 360

ATCGAAGTCG ATGCTGAAGA ACTAGTAGTA GGAGATGTTC TAGTTCTTGA AGCTGGTTCT 420

ATGATTACAG CCGATGCACG ACTTATTCAA GCTTCTCAAA TGCGCGTAGA AGAGTCmGCA 480

CTAACaGGTG AAAGTGAACC TGTTGaAAAA GATCCTACAT ACGTGGGGcA TGACGATGAT 540

GGCTTAGGaG ATCAAATAAA TATGATTTTC AAAgGCTGTA CCGTTGTGAA TGGCCGCGGA 600

CGAGCAGTAG TAACTGCAAC AGGAATGnAT ACGGAATGGG TAaAtTGCTG GGTTACTGAA 660

TAACAGCGAT CAGCAAAAAc aCCATTACAa AAACGCTTGa ATCmATTrGG CmAACGTATT 720

aGTTTgTTAG CCtTAGGGGC TGCAGCAATT GTTTTCATTA TTGGTGAACT GCAAGGAGAA 780

CCGCTTCTTG AAATGTTTAT GACAGCCGTt TCCTTAGCGG TGGCAGCTGT ACCAGAAACA 840

CTAACCGTGA TTGTAACGTT AACCTTAGCA TATGGTGTTC AAAAAATGGC nAAGAAACAT 900

GCGATTATTT CGTTCGATTG 920

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

AATACTATAA AACCTTTTTA TACATTTGTA CACAAAAAAC CTCACTTTCT GAGGnAGATT 60

TTATTATTTA GCATTGCCAA AAAGTCAAAA GCAAGAGCCC CCAAAACTTC TTTGTTAGGG 120

TTGcCTTGAA AATAAAGAAA AACAAAAAGC CGAAAACGCT AAAGACGTTT TCAGCTTTTT 180

GTTTTTTaAT GGrATAAATG GcTCTTTTGT GCTAAAGCCG CAAATTTTTT CGATCTGTGT 240

TCCAGATGTG GATAAAGAAT TGCACCGCCA ATACTAAAGA CGACTGAAAT CCCCACCATA 300

ATCCAAATGG CAAACCAAGC ATTTGGCCAG TAAATGCCTC CTGCTGATTC CCTTAGCAAG 360

TTCACGGCAT GCGTAAACGG CAAGAACGGA TTAATCATTT GGAAGAATTT ACCTGAGACT 420

TGAATTGGGT AGTTCCCACC CCCACCAGAG ATGGACAGTA CCAAGATTAT TATCGCAATT 480

CCTTTCCCTA CATTGCCAAA GAGAGCAACA AGCACATAAA CCATTATCAT AAACGTAATG 540

GCAATCAATA CCGCAAACCA GACGCTATAC GCTGGATTAC GAACATCTAC GCCTAACGCA 600

AAATAATTAC CTAAGGTTAC AATCAGTGCT TGACCAATCC CCATGACAAT GAAGGTAAAC 660

ATCCGTGCTG AAAATTGTTC CCGTTTAGAG AAGCGTTTTT TATCTTTTCC TTCAAGATAA 720

ACATCCGTTG TCGCAACACT TGAGAATAAT ACAGCACCAA CCCATAAACA CAAAGCTGTA 780

TAGAATGGCG TACTTGCCGA ACCATTATTA GCAATCGGAT AAACAGCATG TTCTTTGACT 840

TCAACTGGTT GTGTAAAGAA GTCACTTTCT TTATTGGCAT CTAATTTTAG TAATTTAAGA 900

ATTTCGCCTA AATCAACTTC TTTTTCACCT TTACGGATTG CATTCGCTGC TTTGTGTAAT 960

CCTGTTTTGA TATTTGGCCA ATCATTAATA ATTAGCTCGT TGGCTTTGTC CAAGGCCGCT 1020

TCAACATCTG GCATTTTCTC ATTGACTGTT TTCAAGGTAT TCGTTAAATC TTTTCGGATA 1080

CCTGGATAGT CATTTTGCAT AAAGGCTGCC GCTTTGCTGA CTTTATCTTG AATGACTGGT 1140

AAATCGTTTT TATACAAATC AGCACCACGA TTAATGCCAT TGACAATGGT TTCCATATTG 1200

CCATTCAACA TCGTATTCGC ATCATGAATT TCTTGTTTAA TTGCCGGCAT TTCGGCTTGA 1260

TATTTTTCTA ATAAAGAAAT CGCATTAGTG ACCGTTTGAC TTGTTGAGCT CAATAAACCT 1320

TCAAAGTCAA TTTGTTGCGC TTTGTTTAGT TGACCTTGAG CGkTTTGGgA TGGTAGCAAT 1380

TAATTTGTCT AAAATCGTTT TTACTGTGTT TTCAATTGCA TCAGGGGTAA TACTATTGAC 1440

GGTTGCTCTA CTTGTTGAGC TcTGCTTGAA TAGCATTTAA AtCTGCATCA GTTACCGCAT 1500

TCACATCAAT GTTATCAACA TCAGTTTTTA ATCTAACTAC AATACCATCA ATCGTATTCA 1560

ATCTATTTAT TGTGTCTTGT AAATCAGTGT TACCTGTGGC TTCTTGTATT TGCGTAAACA 1620

GTTGAATCAG CTGTTGGATA TTTTCATGTT GTTTTCCTAG GCTTTCAGAC AGTTGTTGCT 1680

TAATTGCTTC TCTTTCTTCA ACTGGTAAAC GATGATTTTT TAAATCTTCT AGTGCTGTAT 1740

TTACACCAGC GCTAATTGTT CCAATTGCTT TTAAAATCGT CCCCACACTT TGAGTAATTC 1800

CAGGTAACGC CTTTTCCAAT TGAGTGGCGC CATCTAATGT GACATTCCCT AAATCATTGG 1860

CTTGATCACC TAGTTTACGA ATATCTGGTA ACGCCGTTTG AACTTGTTGA ATGATTTCTA 1920

ATCCTTGTTT TGCTTCTTGG ATTCCTTCGC TCATTGTTTG TTCCACAGAG GCAAAGTCTT 1980

CATCAATCAT AGCAATTTGT CGGCCAGCGT TTTGAATTTC TGGAATTTTT TCTTGTAACG 2040

TCAAAATAAC ACTAGCTTGT TCTTTGATGC TTGGCATTTT ACCATTTAGC TCAACAATCT 2100

TCTCTCCTAA AGCATCAACT TCAGGTAAAT ATTTCATCGC ATCGTTGGCT TTCGCTAATT 2160

TTTCTTTTAG CTCAGGCATC TTACCATGTA AGTCTGTGAC TTGTTTTGCG TACGTATCAA 2220

TGGTTCCAAT GTTGGCATCT GTATCTAAAA TCATGctCTT AACTTTTtGA ATGCTAACCA 2280

nGTTTTTATC AATAtCATAG cCAATAayCA TkGAAgGTTT gaTaACGtAc TACTTGcCGG 2340

tTTwAAATGG AAATCCTTCC CGAAAATTTT GGTGGAACCG G 2381

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13154 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GCCAGATTAT CGTTCCTTAA AAGGTGTCTA TCAAGGAATC CAGCAACCGG aATACTTATT 60

GAGCCGGACT TGCTTAAAAA CAGAGCCAGA AAAGTTTTAT CAATTCGTTA AAACGCTCTA 120

TCATCCAGAC GCACAACCTA ATATCATTCA CCAGAAAATG GCCCAATTAG AGCAAATGAA 180

ACGGGGAAAA ATTGTTTCAC AAAATATTGA TGGGCTTCAT CGAAAAGCAG GTAGCCAAGA 240

AGTGGTGGAC TTTCATGGTA ATTTATATGA ATGTTATTGC CAAACTTGTG GTGCAACGGt 300

TCCTTGGCAA GACTATTTGC TTAGTGATCG GCACGCTGAT TGTCATGGAC AAATCCGTCC 360

AGCTATTACT TTGTATGAAG AAGGACTATC CGAAGAGGCA ATTGAAAAAG CCATTCAGGC 420

CGTTGCTTCT GCCGACTTAA TCGTGATTGT CGGCACGAGT TTTcAAGTGC ATCCATTTTG 480

CGATTTGATT CATTATAAAC AACCAACGGC AACTATTTTA GCCATTAATC AAACGCCGCT 540

ATTTTTACAA CAACCTTATT ATTTTTTAGA AGCGAAAGCC GAAACGATAT TTGCAGAATT 600

AACGATAAAG GAGTAACGGA ATGGAAGAAT TTAAATCAGA AAAAGAAAAA ATGATCGCAG 660

GTGCACTATA TTTTGCCTCA GATCCTGAAT TAGTGGCTGA TCGCAAAAAA GCCCGTGAAC 720

AAATGGCGTT AATTAACCAA CAACCAGACA CTTATATTCG TCGTCAATTA ATAGAAGAAA 780

CGTTTGGAAA AGTGGGTGTC GGGACGTACA TCGAACCGAT GATTCAATTT GATTATGGCT 840

ACAACATTTC TGTGGGAAAA AATTTCTATG CCAATTTTAA TAACGTTTTT TTAGATGTTT 900

GTCCAATCGA AATTGGCGAT AACTGTATGT TTGGACCCAA TGTGCAACTT TATACAGCCG 960

AGCATCCATT ACAAGCGGCC AAGCGTAATA GCGGAATGGA ATCAGGGAAA CGAATTATCA 1020

TTGGCAACAA TGTTTGGATT GGCGGTGGAG CGATTGTCCT TCCTGGCGTA ACATTAGGCG 1080

ATAATGTAGT GGTGGCAGCA GGTGCTGTTG TGACCAAATC GTTTCCAGAA AACTGTGTGA 1140

TCGCAGGTAA TCCAGCACGG ATAATTAAAG AATTGACTGA AGATGACGCC CCAACAACTT 1200

CTTTAGAACA ACAACGAGCA AAGATTAACC AAATCGATAA GGAACTGGTC CGTTTATTAG 1260

AACAGCGGAT GGACGTCGTC GCAGAGATTG CTGCAGTGAA AAAGAAAGCA GGTCATGCGG 1320

TTTTTGATTC TGAAAGAGAA CAACAAGTAT TAGAAACTAT TCTGAATCAT GTTGAAAATG 1380

CCGAGTATGA AGAAACATTA TCTGAGACTT TCCAGGGAAT TATGGACGCC TCTAAACGTT 1440

TCCAAGAAAA ACATTTAGGA GAGTGAGGCG AAGGTCGTGG ATGGAGAAAT CAGAAGAAGA 1500

GAGATTGTTA AAAGATTAAG AGAGACCGAA AAGCCAATTA GTGCCACTCG TTTTGCAAAA 1560

GCTTTTGATG TCAGCAGACA AATTATTGTA GGAGATGTCG CTCTATTACG GGCGACAGGG 1620

GTCGAAATTG TCGCAACAGC TCGAGGGTAT ATGTTGGAAC AACCTTTAGA AGGAATTGAA 1680

CGGAAAATTG CTTGTCAACA TACACCTGAA CAAACGAGAG AAGAATTGTC AGTCATTGTT 1740

GCCAAAGGTG GAGAAGTGGT AGATGTGAGT ATTGCACATC CGCTTTATGG GGAATTAATC 1800

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GGCAGTTTGC GCATTCAATC AGAGAAAGAT ATTGATAAAT TTATGGACAA GTATCAAAAA    1860
GAGCATGCTA CATTACTATC AGTTTTAACA GGAGGCGTCC ATCTGCATAC TATTCGCTGT    1920
GCAGACGAAG AAACTTTCCA AGAAATCAAA GAGGCACTTC GAAAAAAAAG TATTTTGTTT    1980
GAAGGATAAC GAGAAAAAGA GAGGACGTTG ATGTTTGTTC AAGCCCTTTC TTTTTTTTCT    2040
TAGAAAATTA CCAAAAAAAG ATAGAAGAAT TTGTGAATTT TCTTCTATTT TTTTAACTTT    2100
TTGCTAGAAA TTTTTTATGA AACAGTATAC TATTAAAAAA GGAGCCATTT AAACAATAAC    2160
TATGTCAATT ATATATGTTG GTACATAAAA aTAAATGGAG AAAAATAAAA AAGGAGAATG    2220
AGTATGAAAA AACAATTTGC CCTGTTCTCT ACCTTATTAC TTTTAGGTTC ATCAATGCCA    2280
GTAGGTGCAT TTGCAGAAGG TAATAACTTG GTAGCTGAAA ATAGTTCTGT CGCAGAAACA    2340
ACCGCAGAAG CAACAACTGC TGAAGCCACT GAAACGACAG CGACTAGTGA AACAACAGAA    2400
GCGACAGAAG AATCAACAAC TGAAACAGAA AGTTCAACCG AATCAAGTGA ATCTGCAACC    2460
ACGGAGTCCA CGGAAACGTC AGGAACCGAA ACGACAGATT CCACAACGGA TTCTACATCC    2520
ACAAGTACGA CAGAATCGAC TACTGACTCC ACCTCGACGA GTACAACAGA GTCAACCACA    2580
GATTCTACGT CAACAAGTAC AACTGAATCA AGTACCACGC CAACGACCAC ACCAAGTTCT    2640
TCTAAAGAAC AGCCAAAACC TGGCACGAGT ACTTCTGAaT CAAAACAGCC GGCGAAACCA    2700
GTGACACCAA CAGCGCCAGC TGAAAAGCCA GTAGAACAAC CAGCAGCGTC AACACCGCAG    2760
CCTGAAATAG TCCCACCAGT TACAAATGAA ACGGTTGGGT TAGTGGAAGA CGATGAGACG    2820
TTTACGGTCA GCAAAACGAA GAAGACAGAA GAGTTTATTC AAGAAATCGG TGAATCTGCT    2880
CGGAAAGTGG CCAAGGACAA AAACTTATAT GCTAGTGTGA TGATTGCTCA AGCAATTTTA    2940
GAAAGTGGCA GCGGCAATAG TAAATTAAGC CAGAAACCAA ACTACAATTT GTTTGGTATT    3000
AAAGGCGATT ACAAAGGTCA ATCTGTTTCT TTTATTACCT ATGAAGACAA TGGTTTCGGT    3060
AACCTATACA CAGTAGAAGC AAAATTCCGT CAATATCCAA CGTATAAAGA ATCAATGGAA    3120
GATTATGCGA AATTATTGAA AAATGGTTTA GATTCCAATA AAGATTTCTA TCATGGTGTC    3180
TGGAAAACGG AAGCCAAATC ATACAAAGAA GCGACACGTT TCCTAACAGG AAAATACGCA    3240
ACGGACAAAG ATTACCATAA GAAATTAAAT GCGTTAATTA AAACATACGA TTTAACTTAT    3300
TATGATAAAG AAAAAGCAAC CGTTGAACCA ATGGAATCAA ATTTCCCAGC CTATAATGGC    3360
AAAAACTATG ACACCTTTAA TAGTTATGCT TGGGGCAACT GTACACAATA TGTCTACAAC    3420
CGTATTACGC AATTAGGTAA ACGTGTGGAC TTAACAATGG GGAATGGTCA AGATTGGGGC    3480
GAAACAGGTC GTGCACGCGG GTACAAAGTA AGTCGTACAC CAAAAGCAGg TGCAGCGGTT    3540
TCCTTCCCAG CTGGTGTTTT AGGCGCAGAC AATACTTATG GTCATGTCGC ATTTGTGGaA    3600
AAAGTCTTTA AAGATGGTAG CATCTTAATT TCTGaAATGA ACGTGAAGGG ATTAAACGTT    3660
GTTTCGACAC GTACAATCTC AGCCGATGAA ACACATTTGA TGAACTATAT CGTTCCAAAA    3720
GATAAATAAA AAAATCAGCT CTTTGTCAAT AAGAACGAAT GAGTTGGAAA AwTCAAAGCT    3780
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AGCACTGAAG AAGCAATTTT AATTCTTCAG TGCTAGCTTT TTTTTGTGGC AAAAGTTCTC 3840

TCCAATAAAG TTTAATACAT TCAGATATTG CCAGGAGGCT TCAGGTCGGG ATGAGTTAGC 3900

AACAGTCGCT GAGAGCTATA TTTTTTTTAG GTAGAATCAT TTACTTTTAG GTGGAAGATG 3960

TCTTATAATT GTAAGCGGAT ACAAAAATAA AAAAAGAGGT GGGTAAATGA GTAAAAAAGA 4020

AATAAATCAA GTAGTTGCCA GTAGCTATCA ATTGTATATT AATGGAGAGT GGACAACAGG 4080

TAGTGGTAAC AAAATGATTG CTAGTTACAA TCCTAGTAAT GGCGAAAAAT TAGCAGAATT 4140

TGTAGATGCC ACAAATGCAG ATGTGGATCG AGCTGTAGAA GCAGCCCAAG AAGCGTTTCA 4200

GACATGGAAA GATGTTGACG TTGTAACAAG AAGCAATCTT TTGTTGAAAA TTGCTGATTT 4260

GATTGAAGAA AATCAAGAAC ATTTGGCTAT GGTGGAGACT TTAGATAATG GAAAACCGCT 4320

TCGGGAAACG CAATCGATTG ATGTCCCTGC CAGTGcAGAC CATTTTCGGT ATTTTGCTAG 4380

TGTGATTCGT GGAGAAGAAG GATCTGTCAA AGAATTTGAT AAGGATACGT TATCCATTGT 4440

TGTGAAAGAA CCCATCGGTG TTGTGGGTCA AATTATTCCG TGGAATTTCC CCTTATTAAT 4500

GGGTGCTTGG AAATTAGCAC CAGCGTTGGC AGCAGGTAAC ACGGTTGTGA TTCATCCGTC 4560

CTCGAGCACA TCATTAAGTC TGTTGGAATT GTTTAAAATT TTTGATCAAG TCTTGCCGAA 4620

AGGAGTAGTG AATTTAATCA CCGGTCGTGG TTCTGATTCA GGAAATTATA TGTTGGCACA 4680

TCCAGGGTTT GATAAGCTAG CTTTTACAGG CTCAACAGAG GTGGGGTACA CTGTCGCTAA 4740

AGCGGCGGCC GACCGCCTAA TTCCAGCCAC TTTAGAACTT GGCGGAAAAT CAGCCAACAT 4800

TATTTTTGAA GATGCCAATT GGGAACGTGC ATTAGAAGGC GTGCAGTTAG GGATTTTATT 4860

CAATCAAGGG CAAGTTTGTT GTGCTGGGTC TCGTGTGTTC GTTCAGTCAG GTATTTATGA 4920

TCAATTTGTA GAAGCTTTAA AGGAAAAGTT TGAACAAGTG AACGTTGGTT TCCCGTGGGA 4980

AAAAGATGTT GAAATGGGCG CTCAGATCAA TGAGCATCAA TgGAAGAAAT TTTAAAATAT 5040

GTCGAAATTG GTGTGAAGGA AGGAGcTACG CTGATTACTG GTGGGCAACG TTTAACAGAA 5100

AATGGGCTAG ACAAGGGGGC GTTTTTAGCA CCTACGTTAT TAGCGAATGG TACGAATGCA 5160

ATGTGTGTGG CCCAAGAAGA AATCTTTGGT CCTGTTGCAA CAGTGATTAA ATTTGAAACG 5220

GAAGAAGAAG TCATTCGTTT AGCTAATGAT TCTGAATATG GTCTAGGTGG TGCCGTCTTT 5280

TCTCAAGATA TCAATGTGGC ATTACGGGTT GCTCGTGGTG TACGGACAGG TCGAATGTGG 5340

GTCAACACAT ACAATCAATT GCCTGCGGGC GCGCCATTTG GCGGTTATAA AAAATCAGGA 5400

ATTGGTCGAG AAACGCATAA ATCAATGCTA GATGCTTATA CGCAAATGAA AAATATTTAC 5460

ATTGTGACAA AAGAAGAAGC AGATGGACTG TATTAAGTAG TGTAGTGAAT TCTAGATAAT 5520

AAACTTATTT TTGGTTATTG TTATTTTTCG AGCTAAACAA AACAATAATT TTTTTAAAAA 5580

GTTGAGTGAT GAGTAAAGTA AAACAGATTA AAAGTAAAGC CTGGTACAAA AATCACTTTG 5640

GATTTTTGTA CCAGGCTTTA AAGCGGAGTA ACAATAGTGT TCACTCTTGG TTGTTTTTAA 5700

TTTTTGACTA TTGTAGAAGG AGTTATTTTG CTTCTTCTGC TTCAAATTTA GCAAAAGCTG 5760

TTTCAATAAC TTCTTTTAAT GCAGAAGCAG AAGCTTCCAT TTTTTCTTGT TCAGCaTCTG 5820

TTAATGGAAT TTCAATGACT TGTTTAACTC CtTGGCGGTT GATGATCGCT GGTGcACCGA 5880

TATAAATATC GTTTTGACCA TATTCACCTT CTAAATAAAC AGATAATGGT AACACAGAGT 5940

TTTCATCGTT TAGGATAGCT TTAGTGATAC GCGCTAGTGC AACCGCGATT CCATAGAAAG 6000

TAGCTCCTTT TTTCTCGATG ATTGTGTAAG CAGCGTCGCG TACGTTGAAG AATAAATTAA 6060

CCATTGCTTC TTCATCGACG TCAGGATTAT TTTTCACCCA TTCGTAAATT TGTAAGCCAG 6120

CGACATTCGC ATGTGACCAA ACTGGGAATT CTGTATCTCC GTGTTCCCCT AAGATGTAGG 6180

CATGGACATT TCGTGCATCA ACGTCAACTA ATTCGGCAAT TGCTTGACGG AAACGAGCAG 6240

AATCTAGTGA AGTTCCTGAA CCGATTACTC GTTCTTTCGG GAAGCCAGAG AATTTCCAAG 6300

TTGAATAAGT CAAAATATCA ACTGGGTTTG CGGCAACTAA GAAGATACCG TTGAAACCAG 6360

AATCAACAAT TGTTGTAACG ATTTCTTTAT TAATTTTCAA GTTTTTATGA ACTAAGTCTA 6420

AACGAGTTTC GCCTGGTTTT TGAGGCGCAC CAGCTGTTAA GACAACTAAG TCTGCATCAT 6480

GGCAATCGTC ATAAGTAGCA GCATAGATTT TTTTAGGAGA AGTAAATGCT AATGCGTGAG 6540

ATAAGTCCAA CGCGTCTCCT TCAGTTTTTG GTACATTAAT ATCAATAATC CCAACTTCTT 6600

GAGCAATATT CTGAGTTACT AAAGCAAAGG CATAGCTAGA ACcTACGGCA CCGTCCCCGA 6660

CTAAAATTAC TTTTTGGTGA TCTTTATTCC CTGCGGCTGC AGTCATGTGT ACCATTCCTT 6720

CCTCTACATT CTTTTTCGTG AGCAACGAGT TTTTATTTCC TGTTGCTAAA GTGATAGTAA 6780

CATGGTTTGT AAAAAATGTC ACGAACTTTG ATTGTAAAAA TGATACAGTT TTCAGACCTG 6840

TTTCAAAATG GTAGCTCTTA CATGTGCGTA ATTTCACTAT CTTACGCATA TTTAAATTTC 6900

TAAAAATTTT TTTACATCTT TCTTAATCTT CAAAGACTGC GAGTTTTTTT ATTTCTATGG 6960

TATAATGAAT AAAACTGGGT AGCGCATACG CTTCCCAGCC ATTTTGTGTT GGCAAGCTTA 7020

TAATCCAAGG AGAATGAAAG ATGAAAGTAA TCGTAGGACT GGGAAATCCC GGTAGTAAAT 7080

ACAAAGAAAC AAAACACAAC ATTGGCTTTA- TTACGCTAGA TGAAATTGCG TATCGGCAAA 7140

ATGTTTCGTT TAATAATAGT AATTTTGAAG CAGATATTGC AGAGTTTTTT ATAGGGACTG 7200

AGAAAGTATT GTTAGTGAAA CCATTAACAT TTATGAATGA ATCAGGTCGC TCTGTTGGTC 7260

CGTTGTTGAC CTACTTTGGG GTAGATGAGG AAGATTTGAT TGTTATTTAT GATGACTTAG 7320

ACTTAGAGAT CGGTAAAATT CGTTTACGGC AAAAAGGTAG TGCTGGCGGC CACAATGGGA 7380

TAAAAAGTCT GATTGCCCAT TTAGGAACAA ATGTCTTTCC TAGAATTAAA ATTGGCATTG 7440

GtCGGCCCTC aAAAAATGAT ACAGTTATCC ACCATGTACT AAGTACTTTT CCCAAAGAAA 7500

CACACGAAGA GATGTTACTT GCTGTAAAAA AAGCAGCCGA TGCCGCTTTA TATGCATGCG 7560

AAGGACATAC GTTTGTTGAA ACAATGAATC AATTTAATGG AAAATAGCAG AAAGGAGGGC 7620

CCTTGTTTGA ATATTATCGA ACGAATTAGC CAAACAGAAA TTGCTAAATC ATGGCGCAGT 7680

CAACTAATGA CAACAGGAAC GCGCCAACTA ATTACTGGGT TATCAGGCTC TGCTAAAACA 7740

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TTACTGATGG CAGGCGCTTT ACAAAAGACG CATCAAAAAA TTGTTATTGC GGTCCCAAAC     7800
CTATACTATG CCAATCAATT AGTAGATGAT TTTTTAAATA TTTTACCTTC AGAACAAGTT     7860
CATCTATTTC CAGTAGATGA AGTGTTATCC GCCGAAATGG CCTTTTCTTC ACCAGAAGCG     7920
CGCGCAGATC GAGTGAGTGC GTTAAATTTC CTGATGACAG CGAATGCAGG AATCGTGGTC     7980
GTACCAGTAG CTGGACTACG AAAATATTTG CCAACGAAAG AAACGTGGCA AAATGCGCAA     8040
CTTTATTGGG AAATCGGGAC AGAAGTAGAA CCTGAGATCC TCGCGCAACG CTTAGTGTTA     8100
ATGGGCTATG AACGCCAAGC AATGGTCGGA AAGCCTGGCG AATTTAGTAT TCGCGGAAGC     8160
ATTGTTGATG TCTATCCGCT AAATGCCGAA TACCCTGTTC GGGTGGAACT GTTTGATGTT     8220
GAAATTGACT CAATCCGTTA TTTTGAAGCA GATACCCAAC GTTCATTAGA AAATCTTGAA     8280
GAAGTAACGA TTTCACCAAT GACTGATTTA GTATTCTCAA AGGCAGATAT GAATCATGGC     8340
ATGACGAGGT TACAAGATGC TCTAGAAAAA CGTTTAGCGA CAgCTAAAGA TCAAACGGAG     8400
ACCGATTTTT TAGAAGAATA TTTTGGTCAG TTGCTGTCTT CTTGGGAACA AGGGATTCCT     8460
ACAGAAAATG CTCACTATTA TACAGATTTT CTGTACCAAC AAAAAACTAC GCTGTTAGAT     8520
TATTTACCAG AAAATAGTTT GCTTTTTGTG GATGATTATT CTCGTATGAT GGAAACGGAG     8580
CGAGAAATCG CTAGAGAGGA AGCGGAATGG CAAACCCTGA AAATTGAAGA AATGCGCGTG     8640
TTTTCTGAAC AAACTTTTGG CGTAGACTTT CATGATCAAT TGCGAAAAAC TGCACGAAAT     8700
ACGACCTTCT TTTCACTTTT TCAAAAAGGA ATGGGGAATC TTCGTTTCCA AGAAGTCCAT     8760
AATTTCCAAT ATCGTTCAAT GCAACAATTC TTCGGTCAAA TGCCGTTGCT AAAAGCGGAA     8820
GTGGACCGTT GGCAAAAGCA AAACCAAACG GTCGTTGTTT TTGTTCCTAC GAAAGAACGG     8880
ATTCAAAAAG TCGAAGAGCT ATTTCAGGAC TTTGACATAC CTAGCGTAGT AAGCAATTGG     8940
GATCAGTTGT TAGATGGGCA TGTCCAAATT GTCCAAGGGG CATTACAAAC AGGGTTTGAA     9000
TTGCCTAAAA ACAAGCTCGT GGCGATTACG GAAAAAGAAA TTTTTCATAC AACGACCAAA     9060
AAACGGGCAC GTCGTCAAAC AATCTCTAAT GCGGAACGTT TGAAAAGTTA TAGCGACTTA     9120
AAAACGGGCG ATTATGTCGT TCATGCGAAT CACGGGATTG GTAAATATAT TGGTATGGAA     9180
ACCTTAGAAG TTGATGGGGT CCATCAAGAT TACATGACTA TCTTGTACCA AAATGATGAC     9240
AAGTTATTTA TTCCAGTAAC ACAATTGAAC TTGATTCAAA AGTTCGTTGC TTCCGAGTCT     9300
AAAACGCCGA AAATTAACAA GCTAGGCGGC AGTGAATGGA CGAAAACTAA ACGAAAAGTT     9360
GCTTCGAAAA TTGAAGATAT CGCGGATGAT TTAATCTTAC TTTATGCGAC AAGAGAGTCG     9420
GAAAAAGGCT ATGCTTTTCC GCCAGATGAT GCGTATCAAA AAGAATTTGA AGAGGCTTTT     9480
CCGTATTCTG AAACAGATGA TCAATTACGT AGTGCCGCCG AAATTAAACA CGACATGGAA     9540
AAATCTCGAC CAATGGATCG TTTGTTAGTT GGCGATGTAG GGTTTGGTAA AACAGAAGTG     9600
GCTTTACGAG CGGCTTTCAA AGCTGTTAGC AACAATAAAC AGGTTGCCTT TTTAGTGCCA     9660
ACAACTATTT TAGCGCAACA ACATTATGAA ACGATTCAAG AGCGGTTTGA GGGCTTTCCT     9720
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GTAGAAATTG GTTTATTAAG TCGTTTCCGC ACGAAAAAAC AGCAAAATGA AACAATTGAA      9780
AAAATTAAAC ATGGCCAAGT AGATATTGTG ATTGGTACCC ATCGTTTATT GTCGCAAGAT      9840
ATTAATTTTA GTGATTTAGG CTTGTTGATT ATTGATGAGG AACAACGGTT TGGAGTGAAA      9900
CATAAAGAAC GACTAAAACA ATTGCGTTCA CAAGTGGATG TCTTGACGTT AACAGCAACG      9960
CCAATCCCAA GGACCCTTCA TATGTCGATG TTAGGTGTCC GTGATTTATC CGTCATCGAA     10020
ACCCCACCAG AGAATCGTTA TCCGATCCAA ACGTATGTCA TGGAAAATAA TCCTGGGGCG     10080
ATTCGGGAAG CGATTGAGCG AGAAATGGCC CGAGATGGTC AAGTCTTTTA TTTATACAAT     10140
CGAGTAGATA CGATTGAACG AAAAGTTGAA GAGTTACAAG CACTAGTTCC AGATGCACGA     10200
ATTGCGTATG CACATGGGCA AATGACAGAA GTACAACTGG AGAATACTTT GTTTGATTTT     10260
ATTGAAGGAC AATATGATAT ATTAGTCACT ACAACAATTA TTGAAACAGG AGTAGATATT     10320
CCTAATGCTA ATACCTTGTT TGTAGAAAAT GCGGACTACA TGGGCTTATC TACGTTGTAT     10380
CAATTACGTG GTCGTGTGGG GCGTAgcAAT CGAGTGGCCT ATGCTTATTT TATGTACGAA     10440
CAGCAAAAAA TCCTAAACGA AtTAGTGAGA AACGTTTAGA AGCAATTAAA GACTTTACGG     10500
AATTAGGTTC TGGGTTCAAA ATTGCGATGC GTGACCTTTC CATTCGAGGG GCCGGGAACC     10560
TTCTTGGTGC CCAACAACAC GGcTTCATTG ATTCGGTTGG GTTTGATATG TACTCGCAGA     10620
TGTTATCTGA GGCAGTTGCT CGTAAACAAG GAAAAATATT CCAAGACCAA AAAACGTCTG     10680
TTGAAATTGA TTTGGGCATT GATGCTTATA TTCCAGGAAC GTACATTACA GACGAACGAC     10740
AAAAAATTGA AATTTATAAA CGGATTCGTC AATTAGAAAA TATGGATATG TACGAAGAAT     10800
TAGAAGCGGA CTTGTTAGAC CGCTTTGGAG AGTATCCTGA CGAAGTGGCG CATTTATTAA     10860
CCACTGGCCG TATCAAAATG GaTGGCGACC GTGCCTTGTT AGAAAGTATT CGTAAACGCG     10920
ATCAAAAAGT CAAGTTTGTG TTAAGTAAAA TTGGCACAAA AACATACTCT GTGGAGCAGT     10980
TGTTTGAAGC GTTATCGGCA ACCAGCTTAA AAGCGGATCT AGCAGTTGAG AAAGAACAAA     11040
TGACTATTTC CTTGAAGTTG CCGAAAGATT GTAAAGAAGC TGTTTGGATT CAAGAAATTG     11100
CTGCTTTTAC AACCGCATTG CGACAAGAAA AATACAAACA TTCGCAAGGA ACGGATTCCC     11160
TTTAAAAGGA GGCCTAGAAG ATGGCACAAA AAGAAATGCA ACGAATGATG CAAGGTGCCG     11220
TTGTGTTAAC CATTGCTTCC TTCATTGCAA AAGTGTTGAG TGCGTTTTAT CGCGTTCCTT     11280
TTCAGAACTT TGTAGGGGAT GAAGGATTTT ACGTGTATCA GCAAGTTTAT CCAATCTATG     11340
GGATTGCGAT GACATTAGCA TTGTCAGGCT TACCGCAATT TATTTCCAAA ATTGTTGCTG     11400
AACAACCAGA TATTCGGAGT CAAAAACAAG TGTTGCGCCA ACTATATCCC TATGTGTTAT     11460
GGTTAGCGAT TGCTTGTTGG GCCTTCTTTT TCTTTGGTAG TCAAGAAATT GCTATTAGTA     11520
TGGGGGATGC TGCACTCCAA CCATTAATGG AAGTTGTTTC CTTTACCTTT TTACTCGTTC     11580
CAATTCTTTC TTTCTATCGT GGGAATTTTC aAGGTCATTT GTTGATGGTG CCTAGTGGTA     11640
TTTCACAGGT GATGGAACAG TTTGTGCGTG TCGGGGTTAT TCTAGTAGCT GCGTTGTCCT     11700
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ATCATTACTT TGGTGGCTCC ATTTACCAAA CGGGGACGGT GGCCATGAGT GGTGCGTTGG 11760

CTGGCGGTAT CTTAGCGGTA CTTGTCTTAT GGTACTACAA TCGAAAAATT CTTAGTGGAA 11820

GTACGGAATA CTTGCATCAA TGGAAGATTA TGCCTCAAAC CACAGGACTA TTTAAACGTT 11880

TAATGATTGA GGGTGGTTTG GTCTCTTTAT ATAGTGCTTT TCTGATTCTA TTTCAATTAA 11940

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TCCAAGGTGT GCATCACCGA AGTCAAGCGT TTTTCGTTAC AGTTTTAGGT GTTGCAGTGG 12660

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TGTGATGCGG TTAGATAAAT TTTtAAAAGT TTCTCGCATT ATTAAAAGAA GaACAGTTGC 12840

CAAAGAAGTC GCTGATAAAG GCCGGATTCA AATCAACGGA GTCTTAGCCA AATCTTCTAG 12900

TACTGTGAAG ATTGGTGACC TTGTCAAAAT TCAATTTGGG AACAGAATTT TAGAAGTAGA 12960

AGTCCTGCAA CTGAATGACT CTACGAAAAA gAAGATGCCA CAAAAATGTA TGAAATAAAA 13020

TCAGAAACAC GTGTCTCTGA AGAATAAACA GGTGAGGATG GAGCGCTTGG CAAGTTCATT 13080

GAAAAGATGA ATATTCCAAG CGCTTCATCC TTTCAGCGTT TTAATGAAAC AGACGCGCCG 13140

CTTTTGAAAA AAAT 13154

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TCGTCGTTGC TGAATGCGAC AGCAGTTGGG CCTGTAAAAG ACTCGTCTAA GCCGTCTAAA 60

CCAACTTTTT TAGCTGCACG AGAAAGGATT GAGTTTTTGA TGACTTTCAT TTCTACGCCT 120

GCATCACGTA ATTGTTTACG TAAGTTAGTG ACTTCTTCAA CTGTTAAACC ACGGTAGTCC 180

ACGATTACAA CTGATGCTGC TGATTCAAAT TTCTCAGCGG CTGCTTGAAC TAGGGTTTCT 240

TTTTTAGCGA TTGCTGCTTC ACTCATTTAT TTCACCTCCT GATTTTGATG GTGGAGTTGG 300

ACTTGGTTTA CGTTAkGTAA AGTAGAAGAA TCaAATGAAA CTTcGCTnAC TTCGTTCGCC 360

AAGTATTGTT TTACATCGGC TTTTTTTCAA AAAGTCGTGT AAAACAACAA AACTCCATGC 420

CACCGTrGAC ATAGAGGGaC CGAATTGTAT ATAACTCaAC AATTGTCCTC GGTAGGaAAT 480

TmAAGACTTG CGTCACCTAC TGTCTTCGGG ACAGTTAATT ATTAACCC 528

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

GGGGAAGCCA AGCAAGAACA GAAGCGACGG GTTATGGAAC GGTTTATTTT GTTAAACATT 60

TATTAGcAGA TAAAAACGAT ACGTTTGAAG GCAAAAAAGT CGCTGTTTCT GGTAGTGGGA 120

ATGTCGCAAT TTATGCCATG GAAAAAGCAA CTGAGCTAGG CGCCACAGTA ATCACATGTT 180

CCGATTCGTC TGGTTTTGTC TATGATCCAG AAGGAATTGA TGTGGCGTTA GTAAAAGAAC 240

TAAAAGAAAA AAATCGTGAG CGCATTTCAA AATATGTTGA AACACGTAAA GGCGCAACTT 300

ATTATGATAA AGAATCTGTT TGGAATTTCG AAACAGCGTA TGACATTGCG TTACCATGTG 360

CAaCACAAAA TGAAATCmAC gAAAAGCAAG CCGCTATTTT AGTGAAAAAC GGAGTGAAAG 420

TCGTGGCAGA AGGCGCAAAT ATGCCTTGTA CACTAGAAGC AGTCGCCGTT TTTGCTAAAT 480

CAGCTGTAAT TTATTGTCCA GGCAAAGCCG CTAATGCAGG TGGTGTTGCG GTTTCTGCAT 540

TAGAGATGAG CCAAAATGCT GAACGTTTAG CTTGGTCCTT TGAAAAAGTT GACGGTATGC 600

TAGATCAAAT TATGCAAAAC ATTTATGAGA CTTGTCGTGA TACAGCTAAC GAATATCAGG 660

CACGAGATAA CTTTGTTTTA GGTGCGAATA TTGCTGGCTT TGAAAAAGTA GCGGCAGCGA 720

TGCTAAGTCA AGGACTCGTT TAATAACAAA AAATGCTAGG ATTTCCTAGC ATTTTTTATT 780

GATTTGTTTG ATTAAGAGAA TAAATATCTC TAATTAAATA GTTAAAATTA AACAATTGGT 840

CTATCCAAAA GAATTTGCTT GAAAAAATGT CTAAAAACAC GTAAAGTATA CATGTAGTAA 900

GTTTACTTTC GAGGaGGAAA AGGAATGTCA CACmTTCmAT TaGATTATTC CAAATTaGCA 960

CCATTTGTTG CTGACCATGA ATTGGAATAC aTGcAAcACm AGTCACTGCA GTGGgACAAa 1020

GCATTACGTG AAGGtACAGG AGCTGGtAAT GATTTTACTG GcTGGaTtGA TTTACCgaAA 1080

ACTATGACAA AGAAGAATTC GCGCGCmTTw AAAAAGCAGC AGCAAAAaTT CAATCTGACT 1140

CTGAGGTATT AGTAGTCATT GGTATCGGTG GTTCATATTT AGGTGCCCGT GCAGCAATTG 1200

AATTTTTGAC ACATTCATTT AATAATCTAT TATCCAAAGA AGAACGGAAA GCGCCACAAA 1260

TCTTCTTTGC TGGAAATAGC ATCAGCTCAA CTTATTTAGC TGATTTAATC AATGTGATTG 1320

GTGATCGTGA TTTTTCTGTG AACGTTATTT CAAAATCTGG AACTACGACA GAACCAGCGA 1380

TTGCTTTCCG CGTCTTTAAA GAGTTATTAA TTAATAAATA TGGCAAAGAA GAAGCCAATA 1440

AACGTATTTA TGCGACAACT GACCGTGCTA AAGGAGCAGT AAAAGTTGAA GCTGATGCGG 1500

AAGGTTGGGA AACATTTGTG ATTCCTGATG ATGTGGGCGG CCGTTTCACT GTTTTAACGC 1560

CAGTAGGTCT TTTACCAATC GCTGTTAGCG GTGCGGATAT TGATCGTTTA ATGGAAGGTG 1620

CAAATGATGC CCGTAAAGAA TACGGCGCAA CGAGCGACTT AAAAGAAAAC CAAGCCTATC 1680

AATATGCTGC GTTACGTAAC ATTTTATATC GCAAAGGCAA AACAACTGAA ATGTTAATTA 1740

ACTATGAGCC TGGCATGCAC TATTTCTCTG AATGGTGGAA ACAATTATAC GGTGAATCAG 1800

AAGGAAAAGA TGGCAAAGGT ATTTTCCCAG CAGCCGCAGA CTTTTCAACT GACTTACATT 1860

CCATGGGTCA ATATGTTCAA GAAGGTATGC GTAACTTATT TGAAACAGTG GTTAAAATTG 1920

AAAATCCACG CCATAGCATT TCAATTCCAG AACAAAATGA AGACTTAGAT GGCCTAGGCT 1980

ATTTACAAGG AAAAGAAATT GAcTTCGTCA ATACAAAAGC GTTCGAAGGT ACGTTGCTTG 2040

CTCACACAGA TGGTGGTGTG CCAAACATGA TCGTTAAAGT GCCAACAATG GATGCTTATT 2100

CATTAGGTTA TGTTATGTAC TTCTTCGAAA TTGCAGTGGG CATCTCAGGT TACTTAAATG 2160

GGGTTAATCC ATTTGACCAA CCAGGTGTTG AAGCTTACAA ACGCAACATG TTCGCTTTAT 2220

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TGATACATTT GGTGATACAT TTATAAAAAA ATCAGGTAAC GTTTTAGTTA CykGATTTTT 2400

kGTGTgCATT kGATATAATt CGAGTTTATT TACAGCTCGT TCTTTCACTT CAGGAGAGAC 2460

ATGTGCATAT ATCTCAGTCG TTTTAACATT CTTATGACCA gmATGTCTTT AATGTCCTCA 2520

AGTGGAACTC CTGCTTGTCG TAAACGAGCA GCATTAGTAT GGCGACCGTC ATGAATTCTG 2580

ATTTTTGGTA AGTTTGCTTT TTGAATGATA CGGTGCCAAG CTGTGTCAAC GGATCGTTGA 2640

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aTATyATCTC TAAAATCAAA GTTAAACCAT CGTAAGGCCA TTACTTCGCC TTTCCGCAAG 2940

CCTAAGTCGA AAATGATTAA AAAAAATACA TACCACATAA AATCGTCAAA ATTTCTAGCG 3000

GTGTCAAGAA ATAGATTTTC CTGCTCTAAA GTGTAGAATT CTAGTTTCTT TTCTTTATTT 3060

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CCATTTGAAA CGAaGTATTC CCAACGTTCT TGACCATTTT TCAATTTATA AGATTTTATA 3600

GAAGCCATTA ATCTTCACTC CTGAACATAG ATTTTGGAAG GGTATAAAGT TTAGGTTTAT 3660

ACCAGCCTTT TTCATAGAAC TTATCCATTT TTAATTCTTT TTCTTTCCAT GAAAATAAGG 3720

GGAGTGTGAC CATATTATCA GTTTCAATGT CTTTTTTTAG TTTTAATTGA TCCTTCAGCA 3780

CATCTTGATA TTCTTCTTCA CTATAATATG GGTTtGTTAA TATTGGATAA ATTGTTACTT 3840

CTGGAACATC TCTTTTCAAT CTTTCTCTCA ATTCATATGG TGTCATCATT ATAGTCAATC 3900

CTTTCGTAGT TTTACTGTTT AAATAAAATT AGTAACATAA AATAGAAGAT TTATATTAAA 3960

AATCATTTAT TTTTTCAGTA TTCAGCTCAA TGGATAAGAA CGTATGTnCT TTTTGGTTTT 4020

AAAAGAAAAG CCCATAGGCT AATCTTACTT AGCGGATTTA AACGTACATC CGCAATTATT 4080

ACACnCCATG TGTTTTTnTT ACCCnTTTTT CCAGCGAAAC CAGCTA 4126

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13884 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACGATTTAG GCGTTAAATT AAAAATCGAA GAACTAGGCT TTGATGCTCT GTTAGGGGCC 60

TTAAAAACTG GCAAGATTGA CATGGTCATC TCTGGCATGT CGCCAACGCC TGAACGATTA 120

AAAGAAGTAG CTTTTTCTCA ACCATATATG AACGTTCAAC AAAGAGTCAT TGTTCGGAAA 180

GAAGACAAAG ATAAATTTCA TTCCACTAAA GATTTCGAAG GCGTTCGTGC AGGTGCCCAA 240

AAGCAAACGA CACAAGAAGA ATTAATTAAA ACCGAATTAA CCGGTGCTGT CCCTACTTCT 300

CTTCAAAAAA TTCCAGATTT AATTATGAAT CTAAAAAATA ATAAATTAGA TGCAGTCGTT 360

ATGGAAGAAC CGGTTGGCGA ACTATGgTTT CTCAAAATGA GGATTTAGCT TTTGCTGATG 420

TTACCTTTGA AAAAGGCTCA AAAGATACTG CCGTTGCTTT TCCTAAAGAT GCGCCCGTTT 480

TGACGGAGAA AGTAAATGCC TCTATTAAAC AAATTAATGA TCAAAAATTA ATGGACGGTT 540

ATAAAAAAGA AGCCAATCAA TTAATGTTCC AAAAAGATCA AAGCTTTTTA CAAAAGTATG 600

GAAAGTTCTA CCTTAACGGT GCAGGCTATA CCATTTTCCT AGCTTTCATT GGTGTTTTGT 660

TTGGTGCCAT TTTAGGGGCA TTACTTGCCT TAATGAAGTT AGCCAATTCC AAAATTTTAC 720

GTGGCATTGC CATTGCTTAT ATTGAATATG TTCGTGGCAC TCCTTTGCTT GTTCAAATTT 780

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TTATTGTCTA TTTCGGGACA GGCGTTCTTG GCTTAGACTT ATCAAAAGTA GCAGCTGGTT     840
GTATTGCCCT TTCTTTAAAC AGTGGTGCAT ATGTAGCAGA AATTATcGTG CTGGTATTCA     900
GGCAGTTAAT AAAGGACAAT TGGAAGCTGC TCGTTCTTTG GGAATGAATC AAAACCAAGC     960
AATGCGATAC ATCATTTTCC CACAAGCTAT TAAAAATATT TTACCAGCGT TAGGCAATGA    1020
ATTTGTTACA GTAATTAAAG AATCTTCCGT TGTTTCAGTC ATTGGTGTTT CAGAACTAAT    1080
TTTCCAAGCT GGCAACGTTC AAGGAGCAAG TTTTAAACCC TTCTTACCTT ATTTAATTGT    1140
ATCGTTAATT TATTTCGTCC TAACCTTTAC TATCTCACGT CTATTAGGTG TTGCTGAAAG    1200
GAGAATGAGT ACTAGTGATT AACATTAAAA ACTTACAGAA AACATTCGGA AAAAATGAAG    1260
TACTTAAAGG AATTGACTTA GAAATTGAAG CTGGTGAAGT TGTCGTAATT ATTGGCCCTT    1320
CTGGTAGTGG TAAAAGTACT TTTTTACGTT GCTTGAACTT ATTAGAAACA CCAACTGGTG    1380
GCAGCGTTGA ATTTGAAGGA AAAAATTTAT TAGATAAAAA TACCAACATT GATCAACTTC    1440
GTCAAAAAAT GGGAATGGTA TTCCAAAATT TCAATCTTTT CCCGCATAAA AATGTCTTGG    1500
AAAACTTAAC GATTAGTCCT GTTAAAGTAA AAAAAGAAGC CGCTTCTGAA GCCACAGAAC    1560
ATGCTCTTTC TTTACTGGAA CAAGTTGGTT TATCAGATAA AAAAGAAAAT TATCCCTCTC    1620
AACTTTCTGG TGGGCAACAA CAACGGGTAG CGATTGCTCG TGCTTTAGCC ATGCGCCCTG    1680
ACGTGATGCT GTTCGATGAA CCAACTTCTG CCTTAGACCC TGAAATGGTG GGCGAAGTGC    1740
TATCCGTTAT GAAAAATTTA GCTATTGAAG GGATGACAAT GGTAGTGGTT ACCCACGAAA    1800
TGGGCTTCGC AAAAGAAGTC GCGGACCGTG TCATTTTTAT GGATGCAGGA ATCATTCAAG    1860
AAGAAGGCAC ACCTGAAGAA ATTTTTGATG CGCCACAAAA CCCAAGAACA CAAGATTTTC    1920
TAAGAAAAGT TTTATAAAAA GGAGCACCTA GTATGGATCG CAAGAATATC GCAACACGTT    1980
ACCAACAACC TACTGAAAAT TTACTCATGG ATATTGCAAC ATTGGCGAAA AAGACCCCAA    2040
ATTTAATCGA TTTATCGATT GGTGACCCTG ACTTAATTAC CGATGAGCGG ATTATCGAAC    2100
AAGCAGCTAA CGATGCCAAA AATGGGCATA CAAAATATAC CGCTTCTGAT GGTAGCGAGG    2160
CATTCATTGA GGCGGTCATT CAGTTTTATC AGTCACATTA TCAATTATCT TTTCAACCGA    2220
ATCAAGTCCG GGCCACAGTT GGCGCTCTAC ACGGGATGTA CCTTGCCTTA CAAGTGATTC    2280
TAAATCCTGG AGATGAAGTG ATTATTCATG AACCTTATTT CTCTCCTTAT AAAGACCAAG    2340
TCCTTTTAGC AGATGGCGTT CCGGTCTTTT TACCAACCTA TGAAGAAGAT GGTTTCCAAA    2400
TTGATGTAGC TCTTTTGAAA GAAAAAATCA CGCCTAAAAC CAAAGCGATT ATTCTTAATT    2460
CACCGAATAA CCCGACAGGC GCTGTTTTCT CTGAAGAAAC TTTCAGAGAA ATTGCACAGG    2520
TAGCGATTGA ACACAACTTA TACATTCTTT CAGATGAAGT TTATGAAGCC TTTTGTTTCC    2580
AAGAAACGTT TACTCCCATG GCTACGTTTG CTCCAGAAAA TACTATCACT TTTGGCAGCT    2640
TTTCAAAAGC CTTTGCAATG ACTGGTTGGC GTATTGGTTA TATGATTGCC CCAGACTATA    2700
TTAACGAAGT AGCCAAATTA ATTAATGAAG GCGTTACGTA TTCTGCGCCT ACGTTGTCAC    2760
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AGCAAGCAGG AATCTATGCG TTACAACATT TTGACGAATT TGTAGACCCA ATCGTTGAAG 2820

TGTTCCAAAC ACGTTTAGAG TATGTGGCAC AACGAGTAGC AAAGATTCCT TTCCTTTCGC 2880

TTCATCCAGT CAAAGGAAGT ATATACGCCT TCATTAACAT TCAAAAAACC GGACTAACTT 2940

CCGTTCCTTT TGTGGAAAAG CTTTTAAAAG AGACACAAGT ATTAGTGATT CCTGGAAAAG 3000

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CAAGTATGTT TAAAATTACC CCATGAGAAA ATAAGGGAAC AATGGATTCT GGATCACTTT 3360

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CAGCCTCTGC TAATTTCCCT GTAAAAACAG CAAGTTTTTC AGTCATTTGT TTGCCTCCTT 3480

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TGCCGACAAC CAAAACAATT CCTACCAACA AAGTTAAATC CAAAAGTAAG GTCACTCGTT 4320

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TTACCATAAT CTTTTTCAAT GCTCAGTTTC TCGTTTGAAA CAAAACGTGT GAAGTCCTTA 4740

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CCAAAAATAA TCAAGTTATG ATTTTCTAAT GCCGCATTTT TAGGCGCTTT TTTATAATAC 4860

GTAATCTCAC CGACATTACT TTCGGCATAA TTACCAATTA AGTTAAATAG ATTGGTCAAC 4920

ACTTTAAAAT AGTTATCGTC CATTTTTTCT GGTAATAAAA TCGCTAAATC AGCAAAAGAA 4980

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ACTGGTAAAT TGACAAAGTA CGTTTGTTCT TGGTGATAAG CCCCTTCTAG TTTGTCCCCC 5400

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TCATCAACTG TTGTCTCTTC TTTATCTGTT TGGGTCATTA ATTCATAGTT TGCTAAATAA 5520

CGTCCCGCAC GAACAAGTAA GTCCTCATCT TTAGAAGTAG CTACTAAAAC ATGCTTATCT 5580

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TTATACTGAT CTGGTAATTT ATCATAGCTG GCAATAATCA ACTGATAGGG TGCTGACTGT 5700

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TTGAATGATG CTtTTTTTAC GTCCCAATAA TCAATTTTTG TAAAATACAT GGTGCTACGG 6240

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AAGTACTGAA AATAAATAAC AAAATCGCTA ACAACCACAA GGAATTGCTA AATCCTTGCA 6660

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GCGGATAATT AAAATTCAAT AACGCTTCAA CTGTTCGCAC AATGACAATT CCTTCATTAT 7500

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CAACTAATAA ATTTAGATAA ATTCCTGTCA TTAAAAAGAA GCGAAAAACT AATCTGGGTT 9480

CGTTyCTCTT GAGTCCTCTG TATAAACCAA CGCCATATAA aCCAAACAGA ATCACGCCTA 9540

ATAATAGATA GAAAGCAAAG TTTTTAGGAA AAAAACTGGC TTTAATACGG TTATACACCA 9600

TAAAAAATTT AGATTGtTCC AGCGGTGCAC GCCCCGTCGT TTTCTCAAAA TTCCCCACAT 9660

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GAACGATAAA AGCCGCTAAC GTTGTAAAAC CAATCAACGC AATTAAAAAG GCCGTCATTG 10020

ACAATCGTTG ATAACGTTGT GACAAGTAGA CAAAAAATCC TAATCCAGCA ATAATTACGC 10080

CAATAATCAG CAAATATTCT TGGCGTGTTG TTCCTATTAA AAGTACTACT GCTTGTGCCA 10140

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CGTAGCTATC ACCATTGACA CGATAAAGAC TATTTGAATT TAACACACGA AAATACTCGC 10620

CATTATCTCC CAAGCCATTA ATCGGATAAA CGAATAACAA AATGCTTGTC ACTAACCCAA 10680

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TCCCTAAAAC GGCCAAAAGA CTTGGAGAAA TATAACGACT CAACCATTCA AAAGCCGAGT    10740
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GCCATTAAGT TATTATAGGA ATAGACTTGT TTCGTAACTT TATCACCAAA TCCTCCATAA    10860
ATCGGACTGC TTGAATCCAT AATTTGAAAA TTATTAAGTA CTGTAATTGC CGCACGATAC    10920
AACTCTTTGT CATTTTCGGC AACACCAATT AAAGCCGCTA TCGCATAACT AGCTGCAGAT    10980
TGATTTTTAT CCACGGGCGA TCCATTTAAA TCATACGAGT TAAAAAGCGT TCCTTGCTGA    11040
ACTTGTTTTC GCACAAAATC AATACTAGTC TGCTTCGCCA TACCCACTTC ACTTAAATGG    11100
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AGCGTAATTA AGTCAATATA AAACAAAGAA GTTTCTGAAG ACTGTTGTTT TGATTTACTA    11340
TCGTAAAAAT CAATTAGAAT ATTATCTTTC ATAGAGGTTT TCATAAAACT CTTGCCTAAT    11400
TTTTTAATTT CTTGATCATA CTGATCTGTT TTAAAATGAC CCCCTGCTTC AATTAATGAA    11460
CGAATGATCC GTAAATCATC AATCGAGGCA TTGACATTGT ATTTATTGCC TTGCTCGTCA    11520
ATTCGATAAC TAAATTGGAC GCCGTCGTAA AAGGTGTCTT TCGTCTGCTT GTAAAAATTA    11580
TCAAAACGTC CCTGCGTATC AAAAGCTAAA TTACGCAAAT ATAGACCCGA AGACTCACTT    11640
AGCAATTCAT GTCCTGTGGC GACATCTTTG CGTTCAGCAT CTGGTAAATA ATTGGTTAAA    11700
AAGCCGCCGT CTGTTTTGAG CCGGGTTTCA ATAAAAAACT TCAACAAATC TTTGCGTTCA    11760
GCTGTTTCTT TkGTGTGAAA TTCATGTTTT GTTAAAAAAT GTTGTTTGtC TGTCGACATT    11820
AAGCGTTGAA TTTTTGGATT CACTTTTTCC ACCTCTACTT TATAGGATTT TTCTCTAAAC    11880
AAAAGAAAAT ATCCTCCCAG AAGCACCACG AATACCCCAA TAAAAATCCA AAGTTTTCTC    11940
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CGCACACGTT CCATAATTCG TCTGGCTTTT AGCGGCTCTT GTTCTCCTCG TTGCGTCACG    12180
GTTAAATGCT CTTCTAAAGC TTTTAAATCT AGATTGGAAG AGAAAAAAGT AACTAATTGT    12240
TCTTGCATTC GGTATTGCAA GATTACGCTT AAAACGTCGT CACGAATCCA ACTAGTCATG    12300
GATTCCGCAC CAATGTCATC AATCATTAAT ATAGGGGATT TTTTTACTGC ATCGAGCTTT    12360
TCACCAACTT GATCGCGACC AATGGCTTGC TTCATTTCTA CTGTAAATGT TGGAAAATGA    12420
ACAATTGTCG TAGTAAATCC ACGTTCTGCT AAAGCATTAG CCATCGCACC TAATAAGAAA    12480
GATTTTCCTA CACCGAAGGG gCCTTGTAAA TAGAGCCCTT TATGAAATTC TTTTGGTGTC    12540
GCAGGATATT CTCTTAAAAA TTGCATTGCT TCTGcTAACG CTTTGGCTCG ACCTTGAGAA    12600
GATGGATCGA AATCTCGTAA ATTTGCTTCT CGGACATCTT TTGGCATGTC CATTGCCCTT    12660
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ACTCGATTAC GAATTTCTTC TTCCTTCTGA CGGGCGATTA AATCAGCCGT TGGGACATAC 12720

GTTACAtCAA TGTAATGAAA ATtCAACATT AATCTtGGCT CATAGCCAGG GGCAATCATt 12780

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TATTAATCAC ACTAGTCGGT AAGCCTGATT TGGCAACCAA ATATTTCACT AATGAACGTT 13380

CTTGTGGTGT CGTATAGCCG CCTCGACTAT TTTTTAAAGC TTCTAAATAT TGAATAGGCG 13440

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CCTCATCTTC AGGCAGTTGT AAACCTAAAC GGTGCAAACC TTCCACAAAA TAGTGCCAAT 13800

CAAAAGAATC CGTTGATACA GAAATTTTCT TCGATTTTTC TTTTTGAGAA AAAGTTTCTT 13860

GAATCGTTGT CAATCGGTTC GCTT 13884

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

ATTAATACCT GTATTAATGT CTTTTACAAC TTGAAATTTG ATTTTTTCCA TGGCGACATG 60

CTTCTTATCC CAGTATTTTG GATTTTTAGC AATCGTCCAT TTATCTGAAA TACCAACACC 120

GTTTAAATCA GTTAATGTAA ATGCTCCATT CGTTACAATG TTTTCTTTTG TTGTTCCATA 180

TTCTTTACCG TACTCTTTTA CTGCGTTTTG TTGGACTGGA AAATAAGCAG TCAATGCTAG 240

CAAATCTGTA AAATAAGGTG TAGGTTCTTC TAATTCGATT TCTATTGTTT TGTTTCCCTT 300

AGATTTTACA CCAAGTGTTT CTTTTTGTTG CTTTCCGATA CTAATCTCTT TTGCATTTTT 360

TATAGCAGCA AACAGTTCTA CGTTTGGCGA GGCAGTTTTA GGATCAAGAA CTCTTTGCCA 420

TGCCGTTACA AAATCATCAG CAGTAATATC TGTwCCATCG GCCCATTTTG CACCGTCTCG 480

AATCACAATT GTATATGTTT TACCAyyATT GGATATTTTT GGTTGCCCAG CTGCAATTGC 540

TGGTTGTGGT TGATTTTTTT CATCTAATCG GTACAACCCT TCCATTACGT TGGCCAACAA 600

TGTAAyACTT GTTTGATCCA CTGCTGTTGC TGGrTCTAAA CTTTGAACTG GTGTACCTGC 660

CGATAAAGTT GCTATTTGTT CTACCTTAGT TTCATTTGTT TTTTTTGAAT CTTCTGTTGA 720

TTTATTTACT CCACAACTTG CAAATACnAA CAACACnAAT ACTAAAACAC CAACTnTTTT 780

AAGC 784

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3907 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CCCTTnATTA TTCCTATTTT TTGGnGnTAA AAATCAGAAA TTACTTGTAG GATAAGCTGT 60

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CAATATATCG ATAATTCTTT TTACAAACGG AGGGGAATTT GAACAGAAAC GATTGCGGCA 180

ACCATACTTA TTAGTAAGGG TATTAAAATG CATAACATTG TTTTCTTGTC AATAAATAGA 240

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TCCTTCTTCT TTCAGCTCTT TGATCGCTTT TAATGAAGGA GCATATTTAT CTGTTACAAT 1080

GGAACGTGGT TGACCGTAGA CTCTGATTAG ACGCTTGAAA AAGGCTTTAG TAGAGACAGT 1140

ATCACGATGG TTTCGTAGCC ACATATCTAA CGTATTGCCC TTCGAATCAA TGGCTCGATA 1200

AAGATACCGA TCTTGACCTT TCACTTTGAC ATAGGTCTCA TCAATCCGCC AGGATTTTGA 1260

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AATAGAATTG ATAGTAAAGT TTAATGACGG TGGCTATCCA ATCGAAAGTG AGGTGGTGCG 1680

TATGAACGTA CTTCCAAAAT CtATAGAAAG GAGAAGCCTT TTGTCCGTTT CGGAAAGTTT 1740

GCAACTAATG CyTGCGTTTG GTGGGTTTAC ATTGACCCTA tCcACAACCA TTGTTGCCAy 1800

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TCGTTAATCG TGTTTTTATG GTGGGGGAAT TCTTGCGAGA ACTCGCAAGA ATTGTCTCCT 3900

TTnnGTn 3907

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TAAAGAGTCA AACAGAACGC TTTTTTAGCT GCTTCTTTAT TGCTATACTA CAGAGGGAAA 60

AAACGAAAAG GAGTATGAAA AATGTTTTTT AAAGAAATTC ATCATGTGGC AATCAATGCC 120

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GAAAATCATC GTCCCGAAAA AAACGATATT AAATTAGATT TAAAATTAGG CAGCCAAGAA 240

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TTACGTCATT TAGCTTTTAA AGTTGAACAT ATTGAAGAAG TGATTGCyTT TTTAAATGaG 360

CaAGGAATTG gAAACAGAAC CGCTACGAGT AGaTGaTTTT aCGGGTAAAA AAtGAcCTTC 420

tTTTTGAtCC AGATGGACTA CCyTTAgAaC yTCCwgGAAT AATAAATAAA GGGAGAGnAA 480

nC 482

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

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GAGATTTCCC ATTTCTTTAA GAAAGTAAGA CCCCTGAGAG ATGATTAGGT AGATAGGTTG    240
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AAAAATAATT AAGGAGGAAT GAGAATGAAA TTAAAAAACG AGCAACAACA ATCGTGGCTT 14100

AGCTTAGCAT TTGTTTGGGC GGGCGCAATG ATTAGCGTGC CAGGATTAAT TATTGGAGGA 14160

ACGTTAGTTG CAGGCATGCC TTTATGGGAA GCTTTGTTAA CAGGATTTAT TGGTTACGGT 14220

ATTATTGTTA TTTTAATGAT TTTACAAGGA ATTCAAAGTT CCGACTTACA AGAACCTTCT 14280

GTCAAAGTCG CTTCTCAAGT GTTTGGCATT CAAGGTTCGC AAAAGATCAT TTCTATTATT 14340

CTAGCGATTG CTTGCTTAGG TTGGTTTGGT TTGCAAGCCA ATGTCAGCGG CGGCGCCTTC 14400

ACAAACTTTT TAAAAATTTA CGGCATTGAT TTACCTGTGT CGCTTTCTTC CTTAATCTGG 14460

GGAATTATCA TGCTTATTTC GGCTCTTTAT GGCATAAAAA TATTGAAAAT TCTGAATTAT 14520

TTTGCGGTTC CTGTGTTAGT TCTGGTTTGT CTTTATGGCT TGGTGGCTTC GTTAAGAAAC 14580

AACGGTTGGG CGGCTGTTAG TCAATATACC CCTCAAACAG CAGGAAGCTT TATGTCAGGT 14640

CTTTCAATGA CTGTCGGTTC TTTTGCATTA GGCGCAGTAA TTGCTGGAGA TTACTCTCAA 14700

TATGTTTCTT CTCGTAAAGA TGTGGTCAAA GCGGCCACCT TAGGGATTTT ACCGACAGGC 14760

TTGTTGATGA TTGGCGTTGG TGCGGTCTTG ACCATTGCAT CGAACACCGC AGATATCACG 14820

GAAGTTTTTA TGAATCTCGG TTTTCCAGTT TTAGGAATTA TTGCGCTAAT TTTAGCAACT 14880

TGGACCACGA ATGCCGTGAA TGCTTTTTCT GGCGGACTGG CCTTGATTAA TGTCTTTGAT 14940

ATTCCAAAAG AAAAAGAAAA AGTCGCTGTC GGTGCGGCCG GCGCGATTGG AACCTTATTA 15000

GCAGTTGTGG GGATTTTAAA TTACTTTACG CCGATTATGT CCGTCCTTTC TGCGATGGTG 15060

CCACCAGTGG CTGGTGTAAT GATTGCTGCC TATTGGTTGA TTAACAAAGG CGATCGAACC 15120

AAATGGCAGC CAACGCCTGG CGTGAATAAA TTAGGTGTTT TTTCATGGCT AATTGGTGCT 15180

GCAGTGGGGG GCATTCCGGT GATTATGAGT TTCTTTCCCA ATGCCCCTCA ATTGCCTAAC 15240

CAACCGCTAA TTGGCATTGT TTTATCGTTT GTTATTTATT ATTTCGGTGC AAAACGTCAA 15300

CAGACGAACA CCGAATCATT AGAAATGGAA TGAAGAAGAG GAGTGTCGGA GAATGCGTTA 15360

TTTAGATGCA GAAGCAATTG AGAATATAGC CACAGGAGCA GCTTTTTTAG GGACAGGAGG 15420

TGGCGGTGAT CCCTACATTG GTAAAATGAT GGCTTTGTCC GCCATCGAAG AAAACGGACC 15480

TGTCAAACTG GTTTCTCCAG AAGAAATTGC CGCGGAGGAT TTTTTCCTAC CCGCCGCAAT 15540

GATGGGTGCC CCATCTGTCG CAATTGAAAA ATTTCCCAAA GGCGACGAAT TCGTCCGTGT 15600

CTTTGAGAAG TTAGGAAAAT ATTTAGACCA AGAAACGATT GCGGGAACCT TTCCAATGGA 15660

AGCTGGGTGC GTCAATTCAA TGATTCCAAT TGTTGTTGCA GCGAAgcTAG gCATTCCCTT 15720

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CGCCAGTGCT TTAGTGAGCA TTTATCCCGC GACAGGCAAA CAATTACAAG ACTATGGGAT 15960

TCACAACATC GTGACATTAT CAGAAGAAAT TGGCAAAGTG ATTCGAGGTA CCTATGCAGA 16020

TGAACAAGAA AAACGCCAAG CATTAGTAGA AGTTACGGAT GGCTTTGAAT TGTTCCAAGG 16080

AAAAATTCTA GATGTGGAAC GAGAAGTAAA AGGTGGCTTC AATTTGGGAC GTGTCAAATT 16140

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AGGGATTGCC GGTGCCTTAA ATAAAGTCTT GGCAGAATCA GCAGTGGACC CAACCAAAGT 16620

CACACATGCA ATGTTGGGCA CGACCCAATG TACGAATGCC ATTGTTGAAC GAAAAAAATT 16680

AGCAAAAGTT GGGGTCCTTC GTTTGGGCTA TCCAGCAACC GCTTCGGTCT TGCCTTACAC 16740

AGCTTGGCCC AAGGATTTAG TGGCCACTCT TTCAGAAACA TATGCTTTAG CACATGGCGG 16800

CTACGAATAT GATGGACAAC CATTGACTGC ACTGGACGAA GAAGAATTAC GTGGGATTTT 16860

GGCCTCTTGG CGAGGAGAAG TAGAGGCAAT CGCAGTAATT GGCGTTTTTT CTTCTTTAAA 16920

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CGGCATGGAT TGGTTGATGT TGGTTTAAAA CAAGTGTTAA CTTCATCAGC AATCCCACAT 18480

GAAATAGCTG ACAAAGCTAG TAGTCGATAT GTCAATGGTC ATACGTACTT AATGATTGAA 18540

ACCAAAGGCG CAATTTTAAC GCCAGCGAAA GTTTTATCAG AAGCTTCAGT TCCTAAAAAG 18600

GCATTATTTA GAAATCGTGG GAGCTTATTA AATAAGCAGT ATAATTTATT TGACAAACCA 18660

GAAGATTTAA ATGAGTATTA TGATGCCAAT CAACCGCCAT TCTTATTACT AACTTATGGC 18720

GGATCGAATC ATCAATTACG TTTTGTTCGA TTAGGGTTAC CAGATATTGG AGTTGGTCGT 18780

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CGTAAGGACC TACATTTGAC TTTTACGTCA ACCGCTGACG AACTGATAAG GAGAGGACTA 18900

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ATATGTGCAA GAAGTGTATA AAGTATTAGC AACATATGTG AACTTTCCCA AAGTTTGTTT 19260

ACCAGAATTA ATTGAAAAGA GTATTTATGA AATCACAGAA GAAGAAATTG TGAAAAAGGC 19320

TGAGGAATTA CGGAAAATTT GGGGCTTAGA CTTGATTTCG CCAGTCCCTA ATCTCATTCA 19380

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TTGAAGTGAT AAAACGGTAT CTTCACGAAG CAACCTACGT TTTTATTAAT GGTGACTTTG 20280

ACCGACTAAG TTATTTAGAA ATTGGGATTG CACTTTCCTT AGGCAAAACA CTTTACGTCA 20340

TTACAATGAA CCCAAACGTA ACGAAAGAAG ATTTAGGAAT TCCCTTCGAC AATGCTACGA 20400

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ACTAAACAAA AGTAAGTAAT ACGACTGTCT TTTTTTGCTA TTTTTTGCGA TAATAAGGGA 20520

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GGCGCCGCAC ATTTTAATCG CGACAGGTGG TCGTCCGAAA AAACTAGGTA TTCCAGGAGA 21000

AGAATATGCC TTAGATTCAA ACGGCTTCTT TGCGTTAGAA GAAATGCCAA AACGTGTGGT 21060

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AATCACGACA GATGCCGTGA TTTTCGGGAC AGGCCGTCAG CCGAACACGG ATCAATTAGG 21360

CTTAGAAAAT ACGAAAGTAG CCCTTGATGA AAAAGGCTAC GTCAAAGTAG ATAAATTCCA 21420

AAATACCACG CAAAATGGCA TCTACGCAGT CGGCGATGTC ATTGGTAAAA TCGACTTAAC 21480

GCCAGTCGCG ATTGCCGCTG GTCGGCGCCT GTCTGAACGC TTATTTAACG GACAAACCGA 21540

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TCGCTCTAGC TTTACACCAA TGTATTTTGC TTTAGGAGAA TACCGTCAAA AATGCGACAT 21720

GAAATTAATC TGTGTCGGCA AAGAAGAAAA AATTGTCGGT TTGCATGGCA TCGGCATCGG 21780

TGTTGACGAA ATGCTACAAG GCTTTGCAGT CGCTATTAAA ATGGGCGCGA CCAAAGCTGA 21840

TTTTGATAAT ACTGTTGCGA TTCATCCAAC AGGCTCAGAA GAATTTGTAA CAATGCGATA 21900

AAAGGCGAAT AAACCCCAAA AAAGAGCGTT GCTGATGCAA CGCTCTTTTT TGAATACACG 21960

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GTGGCTTCTT CAAAACTTTA TGAAACGGAT CCTTACGGCT ATACAGACCA AGATGATTTT 22620

TTGAACGCCG TATTGAAGAT TGATACTAGC TATACCGCTG AAGAGTTATT GGCTGTTACC 22680

CAAGGGATTG AGCAAGCAAT GAAACGTAAA AAATTAATTC ACTGGGGTCC GCGGATTATT 22740

GATATTGATA TTTTATTATT AGGGGGGCAG TCAGTCACGT TGCCCCACTT ACAAGTTCCT 22800

CATCAAGAAT TAACAAAACG GTCATTTGTT TTGATTCCCT TAAGTGATGT TTACGCAGAG 22860

GAACAACTAT TGGGCGCGCC AATAGCTACG TGGATTCAGC GCAGTGGCAA TCAAGAAGAA 22920

GTGCGAGTAA GCGAAAAGGA ATGGTAGAGA TGGAGCAGGA 22960

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2966 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

ATAAAGGAAG AtGCCTTCAC CGATTCCACC AGCTAAAACA GGAGTGACGA TATwgAAAAG 60

GCTATGTTTC CAACCGrGAC CtAACAgTGT TCCaACAAGG GTCCCAACGC CCATTGCTAA 120

AATCATTCCT AATGCCATCG GGACAATCAT GCGCATTAAA CCTTGGACTA AAATTTTGCG 180

GTTCATTCCa AGGATACTTC CACAGACCAA ACATGCAATA TAGAAATAGA GAAAGTTTGC 240

TTGTTTCATT AAAATATCTG TTGAGTCTAA GACATTTTGG TTGAGTAAAT TGAAAAAGAC 300

CATAATTGAT GGTACTAATA AAGATAAAAT TGCTGGACCG CCAAAATGTT TCAAAATAGG 360

AATATTTCCA CCAATTGTTC CAAGTAACCA ACCCATTGTT AAAATTACGG CAAAACCACC 420

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TAACATATTG ACTGGTAGTT GTTCTAATAG AGCCGTAACA AGAATAATGC TAGCTGTTAC     480
AAGATAAACA GGTAACGTAA CCGAACCAAT CCTCGTTTTG GTTAATTTGT TGCGCCAATC     540
TGTTTCATTA GCAGCTGTTG CGGGcAATTT CTTTTCCATG CTATTTCCTC CTATAACTTT     600
AATCTATATT CATCATAATG TAAACGTTTT CTGTAGAGTA GATTATTTAA TTAATTTAAC     660
TAAAGAAAAG TTTTTTAACC AAATCTTCCT ATGCTATACT TTATTTGAAG AGAAAAGAGG     720
GATGGAATGA AGCGTGGCGG GAAATTATGG TGTTTCTTAT CAGTGATTTT TATTGCAACA     780
TTAATTATTA TGATTACTTT CTTTTACGGA GTAACGACGG TTCAAACAAT TAAAGAAGTT     840
CGTAAAAACC AAGAGCAAGC ACTTTTAGCC GTCGGGGAAC AGTTGGCTAT TGAACCGAAT     900
GTTATTGAAG CCTTAAAGAA TGATCACTAT TCAGATGAAT TGGAAGCGTA TACGGTTCGT     960
TTAGGTGAAA TCCATCAGTT GGATTTTATC GTGATTATGA ATATGCAGGG GATTCGTTTA    1020
ACACATCCTG ATCGCCAAAA AATAGGTAAG CATTTTGAAG GgGCGATGAA GTGCGAGCAT    1080
TAAAAGGGGA GGAACATTTG TCTGTTAGTC AAGGGAGTTT AGGAGAATCA TTACGAgGTT    1140
TTGTCCCAGT CTATGATCAA GGAAAACAAA TTGGGGTTGT gGCAATGGGC ATaAAATGAC    1200
CTCGCTTTCA CAATTGATTG AACGAACmAA AAATGATTAC ACAGTGAGTG TCCTTTTAAG    1260
TGTTGGTTTT GGCTTTATAT aGCCATCGTG GtTTCnTATT ATTTAAAAAA caACTTCACG    1320
ATTTAGAGCC AAGAGAAATT GCTCGTCTAT TAGAAGAGCG AaACGCCATG CTTGAGGAAA    1380
CGAAAGACGC AATCCTTGTG ATTGATACCG ATCAAAATAT TTTATTAGCA AATATTGAGG    1440
CGACTAAAAT GTATCATAAT ATAACAAATA GTGAAGAAAA TTTACTAGGA AAGAAACTTT    1500
CAGCATTGGT TTTATCTCCT GAAAAATTAG TCGTACATTC AAAAACAGAG CAATTCTATC    1560
GTCAAAATGG CCAGGATTAT TTCGTCTCAA TCGCCCCGAT TAATGTCCGT AAAAAAACAA    1620
TTGGGCATGT TATCTTTCTG AAAAATGCGA CAGAAACGTT TATTGTCGCA GAACAGCTTG    1680
TCAGCACaAC AACaTATGCT TCGGCATTAC AAAGTCAATC ACACGAATTT ATGAATAAGA    1740
TGCATGTCAT TTATGGCTTA GTCGATTTAG AAGATTATGA GGCGCTAAAA CATTATCTAG    1800
CCGATTTATT GAAACCAGAA AAGGAATTTG CACAGCGCTT AGCTATTTTG GTCAGAAATC    1860
CTATTCTAGC AGGTTTTTTA AGTGGGGAAA GAATCAAGTT TGCAGAAATT AAAACACAAT    1920
TAGCTATTGA AATTTATCCA GAAATTCCAC CAAATAAACG AGATGAAGAT ACGCAAAATT    1980
TGATTGCTAT CTACCGTTAT ATTCATCGTT TCCTGATGGA GCAAACGTTG CCAGAAGAGA    2040
TCATTGAAAC CATTGATTAT CAGCCAGGAA GTTTGACGAC GACTTATTCG TTTGCTTATC    2100
CAAAAGAACA ACTGGAACGC TTTGAGCAAG AGTTTTTCAC TTCTTATTTG GCAAGATTAT    2160
TAGAGAATGC GGAAGCGACA TTGACTTGGG AAAACCAACA AAACAATTGG CTTGTCCTTC    2220
GCATAAATGT TCATTACGAA GGAGCAGAGG AAAATGAACC TATTGATTAT TGAAGACGAT    2280
CCTATGGTTG CATATATACA TCAAAAATAT CTTGAAAAAT TAATTCACCA ACCGACTATT    2340
TTTACGGTTG CAACAATTGC TGAAGGTCTA CTACTAACGA AAGAAAAACA ACCAGCACTT    2400
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GTTTTATTAG ATGTTCATTT AAAAGATGGC AATGGCTTGA CCTATCTGGC AACAATTAGA 2460

GATGAAAAAA TTGATACAGA AGTTATCCTG ATTACGGCTG CCAACGAGTT GGAAAATGTT 2520

AAACGAAGCT TACATTTAGG CGTTTTAGAC TATTTAGTTA AACCCTTTTC TTTTGAGCGA 2580

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CCTTTTAGAA AGTAAAAATA GCTATTTAAA AGTGGGGCGT CCCTATCAAT CGTTCnGAGA 2940

ATTTAGTATT TTTTAATTTT TAGGAA 2966

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

AAATTATTTA AAATTCAGAC TCATTAGTAG ATCAGATTAA TATCTAACTT TAATGCTCAA 60

AAGTGCTGAT GATGAATAAG CCATCATGAC AGAATTTAGC GGCATCATAA AAATTATTCA 120

GATCAAACGT CAACTATGAT TATAGCAGAA AAACAATGGG TTCAAAATTG AGATAAGAAA 180

CCAGCTAGAC TGTCrACGTA AAATGATAGG CTAAAAAAAG TGATGTGTGC TTGmTACrAT 240

TTTTATACAG TATTTCrTGA TGTrATAAAy AAATTkTCTA TTAAaaTaTG TtnACTAaaA 300

AGACAAACTT TTTGGGGGCA CTACATATaC CTTGTTGGTC TTTTnTATAT TCCAATTGTT 360

ATTAGGTATG TAGCAGGACA TTTAAGGTAT ATTTTGATTT GTGTTCTGGG TCAGCGCACC 420

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GATGGTCCAA TTTTAAAGAA TAATATAGCA CAGGAGAATA TGAATGAAAA AAGGAAAGTT 540

ACCATTAATG ATATAGGGAG AAATwTAGTG TATTTArGGA ATTTGAGTAA CGGTAAaTAG 600

TTGATGAATA TATACTTTTT TAGTrGAAAA AAAACACTGA TAGGAGGTAT AATATTGAAA 660

AAGAGAATAT GTATCACTAC TGGAGTTGCA ATGTTATTAG GATTATCACC GATATTAACA 720

ACAGGGGCTA CAGTATACGC AAATGAAGAG AGTAACTACG TATAAGTAAA TTCTACAACA 780

AAAGAGCTAG AGCAACGGAT GGAGGCGCTA GCCAATCAAT ACAAAGGAGT TTCTCTATTT 840

GAAACCGAAT TCAATAAAGA AAATATGACT CCTGTTCAAT TAGAATTATA TAACAAAGTT 900

TTAGATCTAC AATATGATAT TGCTTTACAA AATGGAAGTG CAAAAGGGAT GTcTAGAGAG 960

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GGACATGGTT TGATTTCTGT TGACGTCTTA GAAACAGTTT TAGATACTGC GCTTAATGTT 1080

GTATTAATTA TCGGAAGTTT TGGGTCAATG TCTGCAATGG TTAAAGAATT GGGTCAAGAA 1140

GGCGCAAAAA ACTAATTACA AGATAAAGCA GTTGGATTAA TTATTAGTGT GATTCTAAGT 1200

TCTGGAAAGC AAGCTGCAAA ATTATTAGAT TCTATTGACA AAATACCCAA TAATGGCTAC 1260

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TTAAAATTAT CTTGATATCC ATATTTTTAT TTGTAATCTC TTACAAAGGT TATATGGATA 1560

AAAAATATTT CCCAnGAAGA 1580

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 632 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AAGATATGGT AAAAATTAAG GCTAAATCTT CGCATCTTTT TGCATATCAG CTGTAGAAAC 60

AAATTGTAGA TTTGTTTTTT TACCATCATT AAGCTTTATT TCTTTTTCyT CaATtATCAA 120

rGAATTACTA TCaCTTTCtA AATTAACATT TATATTATCT TTGATTTGTA TTTCATTCTT 180

ATTATTTTTt TCTTTTATGA ATACTTTTAT TTCACTACTC TTGGAATAAA ACTCCAAaGT 240

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ATGAACTAAT ATAATTATTA TTCCAAGAAC AGAAAATATT TGTATGAACA TTTTTGGAAA 420

TATCTTTAAT TTTTTCATTT TCTCTCCAAT TTATATCCTA CATTTCTTAT AGTAGTTATA 480

CAGTCTAATT GTAATTTTTT TCTAAGTTCT TTTAtATATA CATCTATTAC TCGATCATAA 540

GGAGkTTCyT CGCTATCTTT CCATACATAA TCaATAATTT GCATTCtTGT TAACACTTGT 600

CCAATAATAA CCAATAAACA TTTAATACTC CA 632

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

AGTGCCTTAT GCCAGAGTTT CaTCCmyTGG ccAAAaCTkG GAACGGCAAA TTCAAGAGTT 60

AAAAAAATTA GGAGCGAAAA AAATATTTGT AGAGAAAAAA TCTGGCGCAA GTATTGaACA 120

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ACGACTAATT TTTACAGAAG CTATCTATTT TGTGAGAGAA TCCGATATTT TTATGGTAGA     180
AGCCATTGAC CGATTAGGCA GAAATTACGA TGAAATTATT CAGACGGTTA ATTTATTGAA     240
AAATAAAAAT GTTCGACTCA TAATTACAAG CCTTCCTATT ATGGCTGAAG TGGTTGGTAA     300
TCCATTATTT GATCGTTTTA TTAAAGATTT GATAGTCCAG ATTTTGGCAA TGATTGCGGA     360
ACAAGAAAGA ACAGAATCTA AGCGACGACT AGAACAAGGA ATTAAAATTG CAAAAATGAA     420
CGGTGTTTAT CAAGGACGTC CTGAATTATA TAGTCCAACA GCAAAAGATC TCCAAAAAAG     480
AGCTGTCTAT AGAAATATTA TAGAAGAGTT ACAAAAAGGC ACTGCTATTT CAAAGATTGC     540
AAAAAAATAT GGAATTAATC GACAAACAGT TTATAGAATA AAAAAAGACT ATGAGTCAAA     600
TCAAGCAGAT TCTTAATGAA TCATAAAAGA AATAAGAGGG CTTATTTGGT GAAAAmCAGA     660
AAGGAGTAGT TATTCTGCAA ATTATTAAAG ATACAAAAAA CACGTAGAAA AAGAAAATAA     720
GCCAATGGTT ATTTTTGATA TGATGTCAGT AAAAGTGGAA AAATTATTAT TAGAGTTGTC     780
AGAAGAAGTA TTTCGAGTGT GTCCTAAAAC AAAGAAAGAA TTTAGAAAAA TGGTTTCAAG     840
ATATAGCTTT AGAAATGGAG AGAATAAGAT GGTTGTTCTA AAAAAATATG ATTACTGGGA     900
AATATAAATT ACTACGTGGA ATAAGGCAAA TATGGTTGCT TATGTTGATT GTGACCAATT     960
GGCTAGAAGA GAGTTAGGAA AATATAATCA TCTTATGTAT AGTAATTGTA AAAAATATAA    1020
ATTAATTAAG AGCGTTTGCG TAGAAATAAG CGCAGAAAAA AATAAAAAAA GGTGAAACCT    1080
TGATAAAATA GTAATAGGCA ACAACTAACT CCTCAATATT AATATAATAG TGTCAATTAA    1140
AATGCATAAA TTAATCCCTA AATTGTTAGT TATTACCTTC ATAATAAATA GAATTGTGAA    1200
ATTTATTGTC TAAGGTGAAT AGTTGTGAGA AGAGAGTACG ATTATCAGAA AATTGAAAAA    1260
CAAGTGTTTA CCAATGGCTG TGAACTAGAA TCCAAAATAC GTACTACGTG AACAATGTGT    1320
AGTATGTATT TTGGTGTTTT CTTAATAACT AATTTTGAAT AATCATTCAA TTCTTTTATC    1380
AATAATTGAA CGTAAGACTT TTTCTCTTAA ATCCAATGAA TTAATCTTGT TATTTTGTTC    1440
ATATTCATGT ACTAACAAAT CACAAATATA AAGTTGTGAA ATTTTTCCAG CTAAAGAACC    1500
ACCATTTAAA AATTCTTCGA TTGCTGTTTG TAAAACTAAA TCTGCAGATT TTCCTATCGG    1560
TGAATGAATA TAATTCGTTA TAGCAAGTAT TTTTGCTCCA TTATTTTTTG CAATTTTTAA    1620
TGAGTCATAA GTATCTTTTG TTTTTCCAGA TAAAGAAAAG ATAATAACTA AATCTCTATC    1680
TGTTAACAAA GAAGCAACTT GAGCTTGATA ATGAGGaTCT AATACAGCTT TAGCTTGTAT    1740
TCCTACCCTC AAAAACATAC TTTCCAAATC AAGACTAGTA TTcCACTAGA TCCTACACCA    1800
AAAATATATA nGcTGCtTGC tGatTAATAA GTTGGGATGG CTTTGGTnAA TTGCCTCCAT    1860
TAATTAAA                                                             1868
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(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3274 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TTCTAATCTT GAAAAAAACA GACATTTTTC CTGATGTCTG AATTATTAAC CAAAATACTT 60

TGAAAGTCAA ACTATTTTTC TTATTTTTTG AGAAAAAGTG CTGGAAACCG CATGAAATAA 120

TAGTTTGATA ATCAAAATAA ACTCGGAGGT ACAGTATGAA AAGAGTGGTC ATAACCGGCA 180

TGGGTGCCGT AACACCATTA GGCAATACCG TAAAAGAATT TTGGCATAAT CTAGTGGATG 240

GCAAGCTAGG AATTGGCAAA ATTACTAAAT TTGATtCTGA AGATACTGGG GTGGCTTTGG 300

CTGGTGAAGT GAAAGAGTTT GACCCAAGTG CTGTTTTAGA ACGCAAAGAG CAAAAAAGAA 360

TGGACTTATT TTCTCAATAT GGCTTGGTCG CTGCTTTAGA AGCGTGGGAA ATGAGTGGTT 420

TAACAGAAGC AACGATTGAC CCGACTCGTT TAGGTGTGAT TGTCGGTAGT GGGATTGGCG 480

GGATGACTAC CTTACAAGAC CAAGTACGGG TAATGGATAA AAAAGGCGCA AAACGCGTAA 540

CACCATTTTT CGTGCCCATG GTAATTGCTA ATATGGCAGC GGGAAATATT TCGATTCGTC 600

TAGGTGCAAA AGGACCTTCT CAAACTATCG TGACTGCTTG TGCTTCTGCG ACGAATGCGA 660

TTGGTGAAGC TTTTCGCACG ATTAAATATG GTTTAGCGGA CATGATGGTA ACTGGGGGGA 720

CAGAAGCCAC AGTATGTGAA ATTGGGATTG CAGGCTTTGC AGCATTGAAT GCTTTAAATA 780

CAACAGAAGA TGCGACTCGG GcTTCGATTC CTTTTGATAA AGAACGAAAA GGTTTTGTGA 840

TGGGTGAAGG CGCAGGAATG CTGGTTTTAG AAGAACTCGA GCATGCACAG AAACGTGGCG 900

CAACTATCTA CGGCGAAATT GTTGGATATG GCAGCAACTG TGATGCTAGC CACATGACCG 960

CTCCTTTAAA AGACGGTAGT GGCGCGGCAG CTGCGATGGA AATGGCGATT GCAGAAGCAG 1020

GGATTACACC GGAACAAATT GGGTATATCA ATGCTCATGG TACGTCAACC CCAGCGAATG 1080

ACGCTGCGGA AACAACGGCC ATCAAACGTG TCTTTGGTGA GCGAGCATCG CAAATTCCAA 1140

TTTCAAGTAC AAAGAGTATG ACTGGACATT TATTGGGCGC GGCTGGCGGT ATCGAAGCGA 1200

TCGCTTGTGT GCAAACATTG CAAGAAGGAA AAGCTCATCC GACAGTAGGC TACCAAGTTG 1260

CTGATCCAGA TTGTGATTTA GATTATGTCA CAGAAGGTGC ACGTGACATT ACAGCGGACT 1320

ATACAATTAG TAATTCGTTT GGCTTTGGTG GCCATAATGG TGTAATTTGC TTGAAGAAAT 1380

GGGAGGAAAA CTAGTATGAA AAAAGTAATG ACTGCAACAG AAATTATGGA AATGATTCCT 1440

AATCGCTATC CGATTTGTTA TATTGATTAT GTGGATGAAA TTATTCCAAA TGAAAAGATT 1500

ATTGCAACAA AAAATGTGAC AATTAACGAA GAATTTTTCC AAGGACATTT CCCTGGAAAT 1560

CCAACAATGC CAGGCGTTTT GATTATTGAA GCATTGGCAC AAGTAGGTTC GATTTTAATC 1620

TTAAAAATGG ATCAATTTGA AGGTGAAACA GCCTATATTG GCGGTATCAA CAAAGCCAAA 1680

TTCCGTCAAA AAGTGGTCCC TGGTGATGTC TTGAAATTAC ATTTTGAAAT CGTCAAATTA 1740

CGTGACTTTG TCGGCATCGG CAAAGCGACT GCTTACGTGG AAGATAAAAA GGTCTGCGAA 1800

TGTGAATTGA CGTTTATTGT GGGACGATAA GAATCAATCA ATTTTGGATA CGTTAGTTTC 1860

CCTAAGAAAA GGAATAAGTC ACAATGGCTT ATTCCTTTTT AAATTTATAT AAATAACACT 1920

AACGCAAAAA AACATGCTAT AATCATAAAA AGCTTATGTG AAGGTGGTAA GCTTATGAGT 1980

AAAACAATTT ACAGGAGGGT TTTTCTTTTG GATATTTCAG TAGAGTTTTC GGGACATAAA 2040

TTGGCGAATG TGTTAATGAA CGCATCAGGC ATTCATTGTA TGACAATTAA GGAAATGGAC 2100

GAGTTAGCGG CTTCTCAAGC AGGTGCTTTT GTCGCTAAGA CGGCAACACC TAATCCTCGT 2160

CAGGGCAATG AGGAGCCTCG GTATTTTGAT ACACCATTAG GAAGTATTAA CTCAATGGGC 2220

TTGCCTAATT TAGGGATTGA TTATTATTTA GATTATCAGA TTGCACGTCA AAAGGAATTT 2280

CCTGAGGAGT TACGCTTTTT ATCTGTATCT GGTATGAATT ATGAGGAAAA TATCGCTATT 2340

TTAAAAAAAG TGCAAGAAAG TGAATACACA GGAGTGACAG AATTTAATTT GTCTTGTCCC 2400

AATTTGCCTG GTAAACCGCA AATTGCTTAT GATTTTGAAT TAACAGAAAA GCTTTTAACA 2460

GAAGTTTTCC AATTTTTTAC TAAACCATTA GGTGTAAAAT TACCCCCATT TTTTGATATT 2520

GCACATTTTG ACGCAATGGC TGAAATTTTA AATAAATTCC CTTTAGTATA CGTGAATAGT 2580

ATTAATAGCA TCGGTAATGG TyTaTATATT GACAGTGACA AGGAmGAAGT GGTcATTAAA 2640

CCAAAAGGAG GCTTCGGTGG ACTGGGCGGC GAATATGTCA AACCAACAGC GTTAGCCAAT 2700

GTTCGTGCGT TTGCGCAACG TTTGAAACCA GAAtCAAAtT ATTGGAACGG GCGGTATTAC 2760

ATGTGGAAAa GATGTTTTTG AGCATCTTTT ATGTGGTGCG ACATTAGTAC AAGTCGGCAC 2820

ACaATTGCAT CAAGAAGGTC CACAAGTTTT TGAGCGTCTA GCCaAAGAAT TACAAGAAAT 2880

CATGGCAGCA AAAGGTTATG AAAGTATTGA AGAATTTCGT GGGAAATTGA AAGAGATGTA 2940

ACAAAAAAAC CGTCAAGAAA TTTTCTTGAC GGTTTTTTGT TATTTCACAG CCTTAACATT 3000

TTCCATAAAG GCTTCCAAAT ATTCAGGTTG TGTTAATTGT TGGTTACAGG TGTCGCTATC 3060

ATGGCAAATG TAATTGCCTT TTTTCGTGTA GGTTCCGTCG CCGCCTGATT TGGTGGTAGC 3120

TAGGAACATA GACACATTCG TGATTGTTTG ACAGATGGAG CAAACACCTT TAACAATGGT 3180

GGGTGAAAGG GTGCCGTGGA CGCCGATTAA TTTATTTTCT CGATAAGCTA AGATAAATAT 3240

TTTCTGAGTC CCAGCGTCGT TCCAACCGAC ATAG 3274

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4760 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TnGGAAACCC AGACTTATTA ACTTTTAnGA TTTTCCACTT nGCATTCGTA GAACCTTTAC 60

TCAACCAATC TAATCGAGTC TtTCAATAAG CAAATTAAAA GATACAGCCG TAGAAAAGAG 120

CAGTTTCAAA ATGAAGAATC ACTAGAACGC TTTCTAGTCA GCATTTTTGA TACATACAAT 180

CAAAAATTTC TAAACAGAAG CCATAAAGGT TTTCAACAGG TAACCGATAC ATTAGTTTCA 240

ATGTTTACTG AGTAACTAAT TATTTTGCAG GAGGACAATT TATTTACACA AAATTATTGA 300

CGCTCCCGTT AACTTTTGAA TCCCTAATTG ACTAGCTGCA TAAAATAGTA AATATTTTAT 360

CGGATTTTGC GCTAAATAAA TAATAATACT AGATTTTCTT AAAAAGTCAC TTCCAGGAAT 420

ACGTATATTT TCTAAATTAA AACTTAAAAT AACCACTAAC ACAGCAACTA TTGGTAACGT 480

AAAATAATTT TGTGCATCAT AAAAAACACC TAATTGTTGC GCAAATTTCA CTTCCTTTAG 540

TCCTACATAA GAAAAAATAA CAATACCTAA AACTAAGAaT AAATTATTTA AAGGCTTTTC 600

AAATACATAG TTTGCTAAAA AATAGCCTAT AATCACATAA CAAATCGTAG ArATCATCGA 660

AAAgATATAG AACCATAAAA AGGCACTTGT TTAATCCATT CAATGTCAAA GTACCACTTA 720

CCATAAGTAG AAGTAAATAC TCCTATCAGA AAGCTAACAA TTCCAATTGT TAATAATACT 780

TTCTCACCAA AATAACTTCG GATGTAATAA ATAATAAATA CACTCATTAC TAATGCGATT 840

AAATACCAAG AAACACCTAT TCTGGGGACA TAGCCTAATA ATATGCTCAG TATAAATGAT 900

ATTTTTCCTC TTAAATCCAT TTCCCCTTTA ACAAAATTcA TAATAGATAC GATAAAGAAG 960

GGAATGTAAA aGATCAACCA CGAAAGATAT ACTTTTAAGA TTCTTTTTAT ATAATTGAAT 1020

AGTATTTTTT TATCTTTTTC TTTTTCTCTA AAAGAAATTT TTTTAAACAA AAAATATCCA 1080

GATACTATGA AAAAAAACGG AACAGAAAAG CGGGCTAATA TTTTCAAATC ACTACCCAAA 1140

ATAGATTTAG AGGGAAAGGT ATGAATTCCA ACTACACTTA ATGCAGCAAT AAATTTGAAG 1200

GCATCCAATA CATCATTGTT TTTAGTCATT TTTCCCCTCT CTATTCTCCC ATTTTTCTTC 1260

AGATTTCATG ATAGATAATT CTTGCAATAA TGTTTTAATG CGATTTTCGT GTTTTGAAAT 1320

CAACACAGAA TTTTTAATTT CCATGATTAA CAGGACAATC ACCGCAACTG ATAATAAGAA 1380

GTTTGATGTT GTTTCAAACC CAAAGGcCAT TGCTAACCAT TCTGCCACAT GCGGGnAAAT 1440

aGCaAAAnTA ATTAaGACmA TTGAGATTAA TAmCCAAATC AAAGCATTTT TTAGGAGAAA 1500

AATATTTTTA TTAATCCCtC GAATAATGTA TAAGAAAAAG CCAATTGCAA ATAAAAATAA 1560

AGCTAGCCAT AACACGGTTG GTAGCATTAG TCTCCCTCCT TCATAAAGGC AGCAATCAGA 1620

ATTGCTGAGC CGACTTCCAG CATATACTTC ACAGAAGCCA AGGCACGAAT CGAAGAAACA 1680

CCACCAAGCC GTTCCATCAT ATTGACAGGT CTTTCAACAA TCACAAAGCG TTTTTTAATT 1740

AAGTGAACAA TCGATTCTGG CTCGGGATAA TTTGTCGGAT AACGCTTTGC AAAAAAAGCA 1800

ATCACTTTCC GATTTCCCGC TCGATAACCA GAAGTCACAT CATAAATTGT TTTACCAGAA 1860

GCCATTCGAA TGCAAAAAGA TAACAAACGA ATACCAAAAC GGCGCATTTT CGTACTTTGA 1920

AAAGACGCTT CGTTTCCAGG AATGAAACGA GAGCCAATCG AAAAATCACA TTTACCCTCT 1980

GCTAATGGTT CCAGTAAAAT AGGTAAACTA TTGATATCAT GTTGACCATC ACCATCAAAC 2040

TGAACCGCAA CATCATACTC ATTTTCTAAG GCATATTTAT AGCCGGTCTG TACCGCCCCG 2100

CCaATACCTA AATTCaACAC TAAATGAATG GCATTAATTT GGTTGGCTTC TAAAATTTGT 2160

TTGGTTCCAT CTGTCGAGCC ATCATTAATT ACCACATAAT CCAATTCATG TTGAAAATGC 2220

GTAACTTCCT GTTTAAATGT TTCAATGGAA GCAATCGTCC GCAAAATGTT TTCTTCCTCA 2280

TTGTAAGCAG GAATGATTAA AAGTACCTTC ATAAAGAGAA ACACCTTTCC ACTTTTTCTC 2340

TAACAAAACC CCTCACTTAC ACAAAACAAT TTATTGTTGA ACATTTTCTA ACATTTGTGC 2400

TAAGGCTTCT TGCCAAGTAG GAATTTTAAA GCCTAACGCT TCTGTTTTAC TTAAATCCAT 2460

GACAGAATAT TGTGGTCTTT GCGCCTTTTG TGGAAATTGA GTTGAATCCA CTGGCAATAC 2520

TTCCACTTCA GTATCTTTTA AAATTTCTTT AGCAAACTGA TnACcAGCTA CAGCTGTTTT 2580

CATTAGACAA ATGATAAACA CCAAATGGCG CTTTTTCTGC AATAACAAAT GCCATAAATT 2640

CGGCTAACGT TCTTGTCCAA GTTGGGCGGC CAAACTGATC GTCCACTACC TTTAGTTGGT 2700

CTCTTGTTTC CGCTAATTTT TGCATGGTAA AGACAAAGTT ATGACCGTAT TGACCAAATA 2760

CCCATGATGT TCGAATAATA TAATAGTCGT CCAGGATTTC TTGGACCGCT TGTTCACCTA 2820

ATAACTTCGT CCGACCATAC TCATTTAAAG GATTCGGTTG ATCATCAATC GCATAGACGC 2880

CTTCTTTTTT AGTTCCATCA AAAATATAAT CTGTACTTAC GTAAACAAGT GTCGCCCCCA 2940

CTGCTTTAGc AcTTCTGCAA CATGACGTGT GCCATCTACA TTCACTTTTT CATCTAATTC 3000

CTTGCCTTCG TCTTCTGCTT TATCAACAGC TGTATAAGCA GCACAATGAT AAATGACGCT 3060

TGGTTGAATT TCTTTCACTT TTGCCAACGT ACTATCCGCA TCAGTAATAT CTAATTCTGT 3120

GGAATCCGTT GAAACATACT CAATTCCTTG TTCGTCTAAT AGGTGACGTA ATTCTGTGCC 3180

CAATTGGCCA TTTCCACCAG TAATTAAAAT CATTTTTTTC GCTCCTTCTT GAAAAAAAGG 3240

CAGGGCAAAG TAGCTTTTGT ACTTTGCCAT CGCCTTTCGA CTGTTATCTC ACATGTCAGA 3300

AAAAATTACT GACCATTTTG TGCATATTTT GCTTCAACAG CTTCTTTATC TGCACGCCAC 3360

CAGTCTTCAT TTTCTGTATA CCACTTGATT GTTTCTGCCA AGCCTTCACG GAAATTCGTG 3420

AATTCTGGTT CCCAACCTAA TTCTTCGCGT AATCTGGTTG AGTCAATCGC ATAACGTAAG 3480

TCATGTCCTG CACGATCGTT GACATGCTCA TAGGCATCAA CAGGTTGTCC CATTAATTCT 3540

AAAATTAATT CCATCACTGT TTTATTGTCT TCTTCACCAT CGGCTCCAAT TAAATATGTT 3600

TCGCCAATTT GCCCTTTTGT TAAAATTGCC CAAACAGCCG AAGAATGGtC GTTTGTATGA 3660

ATCCAGTCAC GAACATTTTT ACCAGCACCA TAAAGTTTTG GTGTAATGCC ACTTAAGACA 3720

TTGGTAATTT GACGAGGAAT AAATTTTTCA ATATGTTGaT ATGGcCCATA GTTATTTGAA 3780

CAATTTGAAA TTGTTGCTTG TAAGTTGAAA GAACGAACCC ACGCTTTGAC TAACAAGTCA 3840

GATCCTGCTT TTGTTGAAGA ATAAGGACTT GAAGGATTGT AAGGCGTTTC GGCAGTGAAT 3900

TTTTCCCcTT CGCCTTCTCC ATGTCCTGGT AAATCTTCTC TTAAAGGTAA ATCGCCATAA 3960

ACTTCATCAG TCGATACATG GTGGTAACGA ACATTGTTTT TACGGCAAGC TTCGATCAAT 4020

GTGTACGTCC CAATCAGATT GGTTTGTACA AATGGGAATG GGTCGTTTAA TGAGTTGTCG 4080

TTATGCGATT CAGCAGCATA GTGAACAACC GCATCTGTTT CAGCGACTAA ACGATTAACT 4140

AATTCAGCAT CAGCGATATC TCCTACGACT AATTCCACGC GATCACTTGG TAGACCTTCA 4200

AGATTTTTTT CATTTCCTGC ATACGTTAAT TTATCTAATA CAGTTACATG AACTTCTGGA 4260

TGATTCTTTA CAACATAATG AACAAAATTT GAGCCGATAA AACCAGCTCC ACCTGTTACG 4320

ATGATTTTTT TCATAATTGA AACTCTCCTA CTTTTTTCTT AAATTTCGCC ATAGATAAAC 4380

GGATTTTCCG CTTCAAATTC TTTTAAGGTT GGATGTTTTT GATCCTTTTC TGACGTAATC 4440

GCTTTTTCTG GCGCAATTGG CCAATCAATA GctAACGCTG GATCGTTAAA AGCAATACCG 4500

CCGTCTGCTG CCGCATTGTA GTAATTGTCA CACTTGTACA TAAAGTTCAC GTTCGGTGTC 4560

AAAGTGACAA AACCATGGGC AAAACCTTTT GGTACTAAAA GCTGACGGTG ATtATGTTCT 4620

GATAAAATGT AGCCTTCCCA TTGACCATAG GTTGGACTCC CTTTACGAAT ATCAACAATC 4680

ACATCTAATA CCGCACCTGT TACAACGCGA ATTAGTTTTG TTTGCGCmTT CGCCTTTTTG 4740

AAAATGCAAT CCACGCAAGA 4760

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1028 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

AACCGGGAAA GnTCTAAAGA TTCTTTCAAC TTACAGGAAT TTTTTTAGGC TTTTCTTGGC 60

AGTTTCnATG AAAATGCCAA GTAAACCTAG AAGGGATGGT AACTGATTAA TTGAAAAGGT 120

AGGGAAAGAG CCTGGATGTT GAATAAAGTC GACCTGAAAA AAGGGTTAAG TACAGAAGAA 180

GTTGCCAAGC AGAAAGAGTT AGGCCTTCAA AATAATTATG AGGAAAATGT AGCAAAATCT 240

ACAAAAGATA TTATTTTTGA TAACGTCaTG ACGTTATTCA ACTTTTTAAA CTTTGCAATC 300

GCTGTTTGTT TACTATTTGT CGGAGCGTAT TCCAATCTGG CTTTCTTAGC GATTATTATT 360

GTGAACATGT CAATCGGGAT TTTCCAAGAA ATTCATGCCC GTAATTTAGT TCAAAAATTA 420

TCTATTGTGG CAAAAGAAAA TGTTCATGTT GTTCGAAATG GCGTACAACA AGAAATTGAT 480

ACAAAAGAAC TAGTTATGGA AGATATTGTT ATTATCTCTG CAGGGGAACA AGTTCCTTCT 540

GATATGGAAG TTATTGACGG TAAAGTCGAA GCGAATGAAG CGTTGTTAAC AGGTGAATCA 600

GATTTAATTG AAAAGGAAAT CGGCGATACC TTGCTTTCTG GAAGTTTCAT TGTTAGCGGA 660

CAAGCCTATG CCCGTGTTAT CCACGTTGGT GCCGAAAACT ATGCTGTGAA AATCACCCAA 720

GAAGCTAAAG TGCATAAACC AATTCAATCA GAGTTAGTCA ATTCGATTCG TAAAGTCTCT 780

AAATTTACAA GTTGGGTGAT TATTCCTCTA GGGATTATTT aTTTGTTGAA GCTTTTTGGC 840

TAAGAGaTGC TGGCATTAAA ACATCTGTTG TTGCTTCTTC AGCTGCTTTG TTAGGGATGT 900

TACCAAAAGG ATTAGTACTA TTAATTAGTA TTGCGCTGAC AACAGGTGTC ATTAAGTTAG 960

CCAAAAAACG TATTCTAGTA CAAGATATGT ACTCAATTGA AACATTGGCC CATGTGGACA 1020

CTTTGnTT 1028

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

GCGgTGGCTT AGGACTCGCT ATGCTACTAG AGAGACCTCA GCAAAAAAAA AACAGCCGAT 60

TTTATCAAAT GAGTCCTGAG GAACGCCTGG CTTCTCTTCT TAATGAAGGC CAGATTTCTG 120

CTGATACAAA AAAAGAATTT GAAAATACGG CTTTATCTTC GCAGATTGCC AATCATATGA 180

TTGAAAATCA AATCAGTGAA ACAGAAGTGC CGATGGGCGT TGGCTTACAT TTAACAGTGG 240

ACGAAACTGA TTATTTGGTA CCAATGGCGA CAGAAGAGCC CTCAGTTATT GCGGCTTTGA 300

GTAATGGTGC AAAAATAGCA CAAGGATTTA AAACAGTGAA TCAACAACGC TTAATGCGTG 360

GACAAATCGT TTTTTACGAT GTTGCAGATC CCGAGTCATT GATTGATAAA CTACAAGTAA 420

GAGAAGCGGA AGTTTTTCAA CAAGCAGAGT TAAGTTATCC ATCTATCGTT AAACGGGGCG 480

GCGGCTTAAG AGATTTGCAA TATCGTACTT TTGATGAATC ATTTGTATCT GTCGACTTTT 540

TAGTAGATGT TAAGGATGCA ATGGGGGCAA ATATCGTTAA CGCTATGTTG GAAGGTGTGG 600

CCGAGTTGTT CCGTGAATGG TTTGCGGAgc AAAAGATTTT ATTCAGTATT TTAAGTAATT 660

ATGCCACGGA GTCGGTTGTT ACGATGAAAA CGGCTATTCC AGTTTCACGT TTAAGTAAGG 720

GGAGCAaTGG CCGGGAAATT GCTGAAAAAA TTGTTTTAGC TTCACGCTAT GCTTCATTAG 780

ATCCTTATCG GGCAGTCACG CATAACAAAG GAATCATGAA TGGCATTGAA GCTGTAGTTT 840

TAGCTACAGG AAATGATACA CGCGCTGTTA GCGCTTCTTG TCATGCTTTT GCGGTGAAGG 900

AAGGTCGCTA CCAAGGCTTG ACTAGTTGGA CGCTGGATGG CGAACAACTA ATTGGTGAAA 960

TTTCAGTTCC GCTTGCTTTA GCCACGGTTG GCGGTGCCAC AAAAGTCTTA CCTAAATCTC 1020

AAGCAGCTGC TGATTTGTTA GCAGTGACGG ATGCAAAAGA ACTAAGTCGA GTAGTAGCGG 1080

CTGTTGGTTT GGCACAAAAt TTAgCgGCGT TACGGGCCTT AGTCTCTGAA GGAATTCAAA 1140

AAGGACACAT GGCTCTACAA GCACGTTCTT TAGCGATGAC GGTCGGAGCT ACTGGTAAAG 1200

AAGTTGAGGC AGTCGCTCAA CAATTAAAAC GTCAAAAAAC GATGAACCAA GACCGAGCCA 1260

TGGCTATTTT AAaTGATTTA AGAAaCAwTA AAAAAcAGTT CAGCAGAAAT TATTCTGCTG 1320

AaCTAtTTTT TTTCACATTA gGTAGCCGTT TCAGGcCACg AATTGGTTTT ACTTTTAAGA 1380

CATCTAAGAA GAAAGTGAAA ACAGGGATTC CTACAATAAG TCCCCATACA CCAAAAAGaC 1440

GCTCACTAAC TAATAAAATG ACAAACGTAT AAAAGATTGG TAACTCTGTT TTACTAGACA 1500

TGAATTTAGG ATTTAGCACG TAAGATTCAA ATAAATGGAC GATTGTAATT AAAGCTAAGA 1560

TATAAATCAC ATCGTTCAAG CCACCTTGGG AATAAGCGAT GAAACTTAGC GGAATGCAGG 1620

AAATAATCAC ACCAGCAACT GGGACTAAGC TCAAAATGAA GATCATAATG GCTAAACTAG 1680

GTAGCTGAGT AAAGCCGATT ATCGCCAAGG CCAAGGTAGT AATGACTGTA TTCACCACAG 1740

CAATGAAAAA CTGAGCTTCC aTTACGaCAC CaAATGTGTT GACGAACTTG TTGGCAAAAT 1800

aATaGATATC cTGmnaAAAC CmATCmAAAT CACtTTTTAA AAwTAACTTr GAAAAATCAG 1860

CCaTTTGCTT CTTCTCAATC ATAAAGAAGA AACTTAAAAT AAAGGACATG ACAAATGATA 1920

AGCCGACAGC GCCAATATCT TGAATGTAGC GTAAAATCAT TGAAGCACCA TTCTGGAGTT 1980

GAGAGAGTAA GTTAGATTTT TCCAAGTATT GATCAATAAA TTGCAATACT TGATTTGTAT 2040

CTGTATGTGG ACTTTGATAA AAATCAACTA CAGAATTAAT CATTTGAGTC GTTTGGTTAA 2100

CTAGAACGGG AACATATTTA GTAATCGCTA AATAGATTAG AAAAACAACC AATGCATAGG 2160

TTAAGAGAAC GATGACAATC GTCGGGATTT TCATATAGCG TTGAACAAAA TGGACCAAAC 2220

GAACAGCTAA ATAGGTAAAG ATAAATGTTA AAAGAATTGT TGTAATCATA CTTCTGGATA 2280

AATAAAGCAC AAAAATAwTC AAAGCAAGGA CGCAAAAACG TCGCAAACGT TCATTTTGGA 2340

TAAATTTTGG TTACAAACTC ATAGGGGAAA CTCCTTCTTT ACTGGATAnT CAATCCTGTT 2400

AAGAATAACA TAACCATACC GATGGCAGCT AGGCCGCAAA CAATAATATG GCGGCGTTTG 2460

TACATCACTA CAATGGCGAT GAACTCTCGA ATAAACGCGT TAGGTAAAAA ATAAAAAGCG 2520

GTTTTTGCAC CAATGCCATC AGCTTTTAAG CCAGCCATTC GAGCGAAAAG ACCCGCCCGG 2580

AAAAGGTGAT AATTGTTTGT AGTAAAAATG GCTTGAAATT AGCATTTCCA AAATCCTCAA 2640

TCATTGTTTC TTTGGAAAAA CGCATATTTT CTAGTGTGTT TTTTGAATGA GCTTCTACTA 2700

AAATATCATC ATCAGGAATA CCTTGTGTCA AAGCATACAT TTTCATCGC 2749

(2) INFORMATION FOR SEQ-ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GGACGCGATT GATTTTTACG AAGGAATGTA TAAAAACnCG GCAAcGaATT yCAcTCAAaT 60

TGACTGGCAT AACTATCaGC GGGCAAATTG GCGCGAGGTA GAAACAAAAG GCGACACGTT 120

GACATTGCAT TTTGCCAACG CGGGCGGTGC TGGGGGCTCA TACACACAAT TCACGAAAGT 180

TGGTACGAAT ACTGTTGTTG TATCATTTGA TGGCAATGCT GCTTATCCCG ATAACCCAAG 240

TAGCGTTTTA CTCGTGCAAA ATAGTGATTA TAAAGTTTTA AGGACTTTGA ATCAGTAATA 300

GGGGAAATAT ATCGTTTACT TAAACATAGG CAAAGGCGGG TTGCTTACCT TTTTATAAGT 360

AACCTACCTT TGCCTATGTG CTATTTTTTG GGATAGAGGT GCTCAGAGTA GGGGATGTTT 420

TTATGGGAAA TTTTTATGCT AGATCTCTGT TTGACTAGGC TCAAATAGAT CTGAATCAAT 480

CGTTGAAGTG aTATCTGTTT ATATAAAGAT AGGCTAAATC GTCAATTTTT TACAAATCGT 540

CGTtCATGTT AAAATAAATG GaGAAATGTT TTAGTAwTCA TAGTAAGTAT TTtATCGTAG 600

AATAAAAGAT ATACTAACAA nnGGAGCGAT GAAAATGCTA AAAGAAGAAA GATTAAAGGC 660

GATAGTCTCT CTAGTAGATC AAAAAGGGGC AATCAAAGTT ACTGAAATTA TGGAACGATT 720

AAATGTTTCG GATATTGACT GTTCGTAGAG ATTnTGACAG AATTTGGAAG CCAGCGGGGC 780

GTTTTnAAAC GAG 793

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CAGTTGGCAG TGTTTCGCTA CATGACAAAG ATATTCCGTT ACAGACAAAA ATTTATTATG 60

AAGTGAAATC TTCCGAACGT CCAGCTAACT ATGGCGGAAT TACCAAAGAA TGGGGCATGA 120

ATGATGTCTT GGACACGACC CATGATCGTT TCACAGGGAA ATGGCACGCT ATTACGAATT 180

ATGACCTTAA AGTAGGGGAT AAAACGTTAA AAGCAGGAAC AGATATTTCT GCCTACATTC 240

TTTTAGAAAA CAAAGACAAT AAAGACTTAA CGTTTACGAT GAATCAAGCA CTATTGGCCG 300

CCTTAAATGA AGGAAGCAAT AAAGTAGGCA AACAAGCTTG GTCTGTGTAT CTGGAAGTCG 360

AACGGATTAA AACAGGTGAC GTAGAAAACA CGCAAACAGA AAACTACAAC AAAGAGCTGA 420

TGCGTTCTAA TACsGTGGTG ACrCATACGC CTGATGATCC AAAACCAACC AAAGCCGTTC 480

ATAACAArAA AGGGGAAGAy ATTAATCATG GAAAAGTGGC TCGTGGTGAT GTTCTTTCTT 540

ATGAAATGAC TTGGGACTTA AAAGGGTACG ATAAGGACTT TGCCTTTGAT ACAGTCGATC 600

TTGCGACAGG CGTTTCTTTC TTCGATGATT ACGATGAAAC GAAGGTGACA CCAATCAAAG 660

ACTTACTTCG TGTCAAAGAT TCTAAAGGGG AAGACATTAC GAACCAGTTC ACGATCTCTT 720

GGGATGATGC CAAAGGCACG GTGACGATTT CTGCCAAAGA CCCACAAGCC TTTATTTTGG 780

CGCATGGTGG GCAAGAATTA CGTGTAACTT TACCAACAAA AGTTAAAGCC AATGTTTCTG 840

GTGATGTGTA TAATTTAGCG GAACAAAATA CATTTGGTCA ACGAATTAAA ACCAATACCG 900

TTGTCAACCA TATTCCAAAA GTGAACCCTA AAAAAGACGT GGTTATTAAA GTCGGTGATA 960

AACAAAGTCA AAATGGTGCC ACAATCAAAT TAGGGGAGAA ATTCTTCTAT GAATTTACAA 1020

GTAGTGACAT TCCTGCAGAA TACGCTGGTA TTGTGGAAGA ATGGTCGATT AGCGATAAAC 1080

TAGACGTCAA ACATGACAAT TTAGTGGCCA nGGTCTGTGT TTGCCAATTC TAmkTTTGTy 1140

TTAGCAGACG GAACCAAAGT GAATAAAGGG GACGACATTT CGAAACTATT CACGATGACC 1200

TTTGAACAAG GGGTAGTGAA AATCACGGcC AGTCAAGCCT TTTTGGATGC GATGAATCTA 1260

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AAAGAAAACA AAAACGTTGC GCACTCATGG AAAGCGTTCA TTGGTGTAGA ACGAATTGCG    1320
GCAGGAGACG TTTACAACAC GATTGAAGAA TCTTTCAATA ATGAAACGAT CAAGACTAAT    1380
ACGGTAGTGA CGCATACGCC AGAAAAACCA CAAACACCAC CAGAAAAAAC AGTGATCGTG    1440
CCACCAACAC CAAAAACACC ACAAGCACCA GTAGaGCCAT TAGTGGTAGA AAAGGCAAGT    1500
GTAGAGCCAG AATTGCCACA AACAgGCGAA AAmCAAAtGT CTTATTAACG GTAGCTGGAg    1560
TTTAGCTGCn ATGCTTGGCT TAGCAGcTTA GgCTTtAAaC GTAGAAAAGA AACAAAATAA    1620
TTGAAGACGA mArGAaGGAC GAaCTGATTG TCCTTCTTTT TTTAGTTATG GAGGGGAAaC    1680
ATTGGAAGCA GTAGTAGTnG AAgAGAGGCA AAGGGGATGA AAGAAATTGC CATCCAAGAA    1740
AAAGATTTGA CCTTACAGTG GAGAGGAAAC ACAGGTAAGT TAGTTAAAGT TCGATTrAAr    1800
AATACACGTG CAATGGAAAT GTGGTACAAC AAACAAATTA CCGAAGAAAA CATTCAAGAG    1860
ATCACCACGT TGAATATyAT TAAAAATGGA AAATCTTTGG CATTAGAAGT ATATCCAGAA    1920
AAAAGTATCT ATGTGAAACC AAATTTAGGC AGAATCAATG TGCCTGTCTT TTTTATCAAA    1980
ACACCTATTA ACAGAGGAGT ATTTGAAGAG ATTTTCGGCG AAACGTTAAA AGCATAAGTA    2040
AAGGAGAAAG AAAAGCCAAT GTATGTATCT TTTGTTCTAA GTTGTTTGCT TGGATTTTCT    2100
GCCTACAGTC TATTAAATAG GCTAAATTCG TTGGAATTTG TGGATGTTTG GTTAGACAAA    2160
GAAACACAAA AATCACACT AAAACGCTGT TTTTATGATA CGTCTTTCAA GAAACAAACA    2220
CTAAAAGAGT TAGAACGAGT ATATTTCCAA TTAAAAGAAA TAATCAACGT GCAAATAAAC    2280
AAGCGGTCTT TAAATACGAA TGACATACGT AATGTACGAG AACTAGAGGA AAAACAACAA    2340
GAAATAAAAC GATTCATGTT AGACGTTTTA GAAGATGCTT ATTGGAAAGA ATTAGCAAAT    2400
ATGCCAGAAG ACCAACGACA CTTAGACGAT TGGGATTTCT TTTGAAATTG GTTACTGAAA    2460
GGAAGCGATG GATTACAATT TGTTTGATTT TTAACCAGCC ATGCTAAGTT TTTCCGTTTC    2520
GGTTCCTTTG GTTTTTTTGT TAGCGATAAT AAAAAAATGA TGCCTGACAC AAAAATATAG    2580
GAGGGAAAAA ATGATTATTT TATCAGGACT TTTTATTTTA GGGATAGGAA TAGTTGGAGG    2640
TTATCAGCTA GCCACGTTAC CTAAATTAAT TGAAATGAAA CAGCACAAAG CAATACAGAA    2700
CCATTTCAAT GTTAAAGGAA ATGAGTACAC CTATTATCAA GAAGACAGTG AAAATTACAT    2760
TTTATCCTTG GAAGATACAG AATATCGAAT TAAATTTTCC AAGAACACCC CGTTAAAAGT    2820
GGTATTCACT GAAATTTTAG AACCTATGTA AGGGTGAGTT TATGTATATC TCTTTTGATT    2880
TAGAAGCAAC ACAAGCAGAA AAAATAGCTy TACCwGTCCA TCAACGATTT TCGCTyGTTC    2940
AAGGTCTTTT GyTACTTGAA CAAGCCAATC AAGAAGTTTT GGCCACAAAA CAAGGAGGCA    3000
CGATAGCCTA TTTTTTATAT ACAGGAAAAG AACAAGAACT ACCTATTTTA GAAGCGGAAC    3060
TTTTATTACC GGTCAAACAA AAGGATATGT TAGACGTATT rCTTGAACCA GTCACAAATG    3120
ATCCAACGCT TGATCCAATA GAAGTAAAAA ACTTCTTACA GTTAGTTAAT CAATCGTTGC    3180
CAAAGAAGCA ACGAGCTAAA AGTAACAAAA AArGTACAGA AAAGAAGGmA ACTAyTGATA    3240
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CAAAACCAGT GAAGAAAAAg TTTTTTTgTC CGTTAGTCTT ATCACACTTr TTGGATTGAT 3300

TCTACTTATG AGTGGTTTTT TATTAGGGAA AACCAATTCT ACACCTTAyC AAGAAAAAGA 3360

ATTAGAGGTr AAAAAAGAAC TCAATACCTT AACAGAACAA GTCAATGAkC AAAATAAAGT 3420

AGAAACATTT ACTCGATTCT TTCTAACTAA TTACTATTCA GGAAAAACAG ATGCCAAAAC 3480

CAGACAAGCA GTTTTAAAAA AGTTTGTAAA AAAAGAAAyC TTATCTGATT TTTTATCGGA 3540

GAAAAGCCGA GCGAGAAGTA TGTTTCCCTG GGAAGTAAAG AAGAAAGACA AACAATGGAC 3600

GATAGyGTTC ATTGTTGTAT TAATCAATGA AAAAGmCGAG CAATCGACAA AGAAAATTAC 3660

GTTTACAGCT GAAGAAACAA AAGAACAAyT GGTCGTAATG GAACGACCGA CAGAAGAAGA 3720

TTTTGAACTT ACAAATTAAA ATTAAAATGG AGGAAATAAT GATGAAAAAA ATTCTTTTTG 3780

CTAGTTTATT TAGTGCCACA CTACTATTTG GGGGAAGTGA AATTTCTGCT TTTGCACAAG 3840

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CAGAAAAGCC AACAGATCCA ACACCGCCAA TTGAGCCACC TGTAGACCCT GTAGAGCCAC 3960

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TTGGGCTTCT CTCTTTTTTC TTGCCTATAT TTTTAGTCTT TGGAGGCTTA CTTTTTTTTC 4680

TTTTATTATT AACGAGTACG TCAGATACTT CAAAAAATGA TTGTATTCAG CCAAGTATAA 4740

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AAGATGCTTA CCTTTTATCA TGGAAAGCAG GTGGCTTTTT ACCGTCTGCT AGTATTTCTC 4860

AAACGATGGT AGAAAATGGG TTTAATTTTA CTAATCCATC GGGGACGTCA TTTTGGCAGG 4920

CrCACAATAT GGGCGGTGTT AAAACGTCAA AAAAAGAAGA TTTTCCTGTA ACTTTAGCAA 4980

CATTCGGCCA AGATTCTGTT GATATTTCTG GTACAAAGCC AGGGTCAAAC GTCGGTGATG 5040

GCACTGGTGG GGCATATACC TGGTTTAAAG ACTACAATGC TGGAATTGTT GGAAAAGCAG 5100

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CAGGTGATGG CGGAAATGGC GCAGGTTGGG CTAATTCTGC TCGTGCGAAA GGGTACACAG 5640

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CTGCACCGCC CTATGGGCAT GTGGCAGTTG TAGAGTATGT CAATTCTGAC GGCAGTATTC 5760

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AGTCGCTAAA AGAAAAGAAA AAGCAACTGT TTATGCGACA GAGCAAGGGC TATCCGGGGT 6240

ATTCCCAAGG GATkCAGATA AAGTTGTTCC TAGTGTTGTG ACCGTTTCTC AATTAGATAA 6300

GGCACCTGAA ATTTATCGAA CCACACAAAA rGATACAGGA AAAGAAAAAA CAGCATTGGT 6360

CCGGCTAGAA TATTCAGTTC GAATCGCAGG AAGCCAArCG CAACGTGGAA ATTTTATTTA 6420

CAAGGTAACT TTCAATGAAG AAAGCAAGAA ATTTACAACC ATTGAGAATT TAGGTGAGGA 6480

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ATAAGAGCTT TCTTGATTAT CTAATTGGTC GAGGAAACTT CTTGTATCAA AAGAAAAAAA 8820

GATATGAACA TGGGCTACTT GTCCAATTCC ATAAAGAAAA AGTCCAATAC AAAGTTAGAA 8880

AATAACAGTA AAGTGTTTAC AAAGAGATTG TGAGGGATGA AGGTGGATAA AAGAATTGAA 8940

GCTGTGACAA AATTTTTAGA GTCTTTAGGA ACTGTAGAAG ATTACACCGA GGATGTAGCT 9000

GTTAAGTATA GAAACTTGAT TCTGAAATCG TATGAATTAT ACGAGAATAA GTATAACGAT 9060

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CAAGCATTAG AAGAGAAAAT AAAAGAACTC GAATTTGTTT TGGACGGTAC AGACTACAAG 11160

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TTGTATCGTC CGCTAGTCGA CCAATTAACA TTGTTTAATC AGTGTTTAAT TGGCGCTAAG   11220
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GATTTAGAAA AAGAAATTGG TAACCGCTAT GGCATGCCTC TAGGTCGTGT CATAACTGCT   11340
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CCAAACTTGA CTAAAAAAGC CATAGAAGGC GCACAATATA CAAATGGGAA TACGCTAATC   11460
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TTTTTAGGAC AAAAAATACT TTATATTGAT CCTAAAAATG AAACCGTCCT TTTTTTCAAA   11580
CGAGCATTAG ATAAGTTCGG ACATATTCCA GAATTTAAAG CTTTGTATCA ACGCATTAAC   11640
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ACAGACAGTC ACACTGCAAG TGAyAAGAAG ACGCTrATTT TAGATTCTGT CAATGCGGTG   11820
ATGAAAGGTA AAGGrAAAAA ACACCTAACG AAAGTAATCG AGGTTATTCG CGAAAAAGAC   11880
CCTAAATTAG CmAATTTAAT CTCTGGCCAC AATGTTGGGT TAGGyAAAAT TCTTTTAGGG   11940
AACGATTACA GCGAACCTAT TCGCTTTGAA AATCAAATCA ATGTCTTAGG TACCCAGGGG   12000
CTTAAAATCC CTACACAAGC GGAAATAGAC AGCGGACGAT TAAACAATGA ACAAATCGCA   12060
GGCATGTCwA TTATGGAAGT TATTATGAAA ATGACAACGA TCTTCTCTAC AGATAAAACT   12120
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ACACAAGCGT TTATGGATTA TGATAAAGAA GATAAAAAAG AACTATTGTC TTATAAATTT   12300
GCGTTCCGGC CAAACCAAAA AGAAGCACAG AAAAAAGTTT TAGAATTTTT TGGTATGGAT   12360
ACGAACCCAG CAAATATTCA GTTAATTAAT GAACTAAAAT CAGGGACTTG TTTATTCCAA   12420
GACCATCGAG GGCGTAGCCA gCCTATTGCA ATTGATGTTT TATTCGATAG TTGGTTAATG   12480
GCCGTTTCGT CTACTAATAA AGAGGATGAA GCTACTCAAA TGGCGTTGGC AATGGAACAA   12540
GGATCATAAA AAAGGAGAAG TGAGCATGAA AAAAGTACTA CCTTTTATTG CCTTAGTCGG   12600
CTTGTTATTG TTGTCAGGTT GTGGAACAGA TATGAAAAAG ATATTGACTG CCGATGGTGG   12660
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AATAACCTTT GACmTTACTA GCAGrAACtC TTTCATTaTG GAAAAAGTrG AwTmCAArGw   12840
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AGACAATGCT TTTGAGTTAA TGACTAAAGA AAAAGAAAAG GATTCTGCTT TTGGGGTTAA   13140
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AGAAGCAATT ACTAACGCTT CTGCAGCAGT CAAAACATTT GTATGGGCTG GGGTAAAAGG 13200

ACTCGGAGAG TTTAATGCAG TTATGGTAAA AACACTATTT AGTATGGATA TTATAACTGC 13260

TATTAAGCAA CCGATTATGA ACCTAACGTC TAGCATAGCA ACTAATATGT TAGGAATTGC 13320

GGGAACGATT GGTATTGCCT TTGTCTTTGT TATTTTAGGT GTAAAATTTA TTGGACAACA 13380

ACGATACAAA CGGTTTTTTG GTATTTTTTT AATGACGATT CTTATTTTTA CGGGTCTTTC 13440

CGTCCTAAAA GATGCCAACA CGTCCAATTC TTTGTTTGAT ATGATGTTTA GTGTAGATAA 13500

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CGAAGAAAAT AATAAGTTAA TGGAAGAAGT TGTAAATTAC GAAAGTAAAG ACTTAAAAAA 13860

CCGTTCAATT ATGTATTATA ACAACTGGAC CAATACTTTT TATGGCTTGT TTTATCTGGT 13920

AGTTAACTTC ATTCAAACAG TGGTGTATTT CCTGTTAAGT TTCTTACGAT TAATTATTGC 13980

kGTCATTCAA TTGTTCCTAT TGCCGTTGTT ACCGTTATTG TTGTTCGCAG GACTCTTTTT 14040

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GGGAATGGTT GGTTTTGCGA CTATTTTCTT TGCAAGTTTC TTATCACTAG GGTTTCAATT 14160

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TAAAGCAGCT ATTAAAAAAC GTCAAGAAGA AGCAAGGAAA CATGGTAAAG CAGAAACTGG 14460

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GAAGCCAAGr CCTCAACATA AAGCGCCAAA TGCTATCGAA AAAGCACAAG AAGGATTAAG 14580

ACAAGCGCAC GAAAAAGGAC GTATGCAAGA ACAGAAATCT GAAGAACAAC TCAAACGGCA 14640

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TCAAACGCAT TCTACACCAC AACGTGTACA AyCCAAGGTA AATGAGCCAA TCACACGTAT 15120

GAATAGACAT AATACGCCAA TCATTAAGAA AGAAAAGAAA ACTAAACAAy CACCAGTTGT 15180

TCGCAGAGAA CGCAAGAAAC CTGGTACACA GAAGATAACA AACAAACCTA AAGGAGTGAG 15240

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TTCCCGCAAC GACAGGTTCA GGAAAGACAA CATTACTACA ATTAATCGTT CAACACGCCG 16020

TAAAATTCAA CCTCCCTGTC ATTCTCATTG ATGGGAAAGG CGCACGCGAT ACGCTAGAAA 16080

GTATGCGAGA GATTGCACGG TATTATGATA AAGAAGTACA TGCCTTCACA GACGATGGCG 16140

ACATGCGATA TAACCCAGTA GAACACGGAA ATGACGTGTC GATTCGAGAT AAGTTGGTGT 16200

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CAAAGAAAAA TGAAACGAAA GTCCCGATTA TTGATGAAGA AATGGACGAA GTAAGTGaAG 16500

CAACCACACC AACAAACGAC GAGGTAACGA GTGAAGATTT AGAACTAGAA GAAGGTGACA 16560

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TTTATTATTT GTTAAAACGA AATCTTTTTT ATTTGTCAAA AAAAGaAAAA ATAATGTTTG 16680

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ATGTGTCATT CAATGGATTA ATTTACAAAG AATATATCCG TACATTGGCG CAAATGTTAG 16920

TCGGTGATGT GAATTATTTT GCGTCCGAAA TGTATCGAAA AAATGTCAAA CGTGAAGTCA 16980

TTGTGATCTT TGACGAACCT GCTTCTTATT TAAATGAACA GTTTATTGAT ATGGTAAACA 17040

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TCCCCCTTAC GCCTGCGCCC CCTCACCAAA TCTTGATGGG GCTGTCGCCA AGACCAGAAA 17940

CCCAAAAGAG TGGTTCTGTT TGATAACTAG TGGACTATTG ATGATTGATT TAAAGTAACA 18000

ACCCCCTAAA TCCCCCAACA AAACTTGGGG GACTTAAGAT CCAAAAAAGA ACTTCTCCAC 18060

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TtCCGTTTTA GAAGTAAAGA AAATAAAGAA GTCAATTGGT CATTTGAAAT TGAGTTGACG 18840

ATGAAAACTA GGCGGCGATA TCGGGAGGGC ATTTTCCCAA AGTACATTGC AGAATTAAAA 18900

CGTCTGCCGT ATGCTCGACT AATTTATGTG ACACCTAGTC CGTTAATCGA AGAAGAACTA 18960

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TCCCATCTTA AATTTTAAGA GGGGAAGCTT ACAAGAAATG AGGAAACGTT ATGGACTTTC 20640

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TAGAAAAAGA CGGAAAAAAC GTTCAGTTTT ATGTTTTTAT CCTAATTATG AGGTCGCTCT 20820

TTATCCAGTC GAAACGTTAC TGGCTTACCT TGAAAAGTTA 20860

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3182 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

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TTTAACTcTT TTCCAGaATA AAGAACCTGA GTCTCTCCTA ATTCTATTCC CTCAAATTCT      60
TCATAAGGAT CGCTATATGC CCAACCGAAA AAATCCAAAA ACGGCGTTCC GTTCTTGACG     120
GGAGAGGTAT CATGCTTAAA ATGTTCAATA TTATGCGTTG CCCaATCGCT ATTACCtAAA     180
GCTAAAAGAG TTAGACAGTC TTGAACAGTA TCAAAATCTA TCTCCCCTGT TTCAAAAGCG     240
TATTTAATAT TCATATAAGG GTTCAAATAA TAAGCACGGT CCAGTAATTT TTCTCCTACG     300
TTTTCGACAT AAGCCTCTAC CATTTTAATT GCTACTTCCT TGGTTAACTC CTTACGAACA     360
GCCTTTTCTT CTTTGTAGGT TTGTTGTTCT TCTGATACAT CTAAATACTC ATCTACCTTC     420
AAAGGATTCG CTTGTTGACG AACAATAAGT GTTTCTGATG AAAATTCATT TAATATCGGT     480
AGCCCTGCTA TTTGTGAATA TGTTTTACTA GCTAAATCAG CTTTCATACC AATTTTATTT     540
ACGATATTTT GCCAAAGGCA ATCGTTTTCC TCTTTTGTAT AGCTTCTGTC TGTATCTATA     600
ACTAACCGAT ACCTTAGACC AAAATCTGAA ACATTATTTT TTATCGTAGG ATAGAGAATA     660
TAACTAATTC CTTTTAGGGA TTCAGCAATC TTTTTTATAA AATTTTTTAA ATCTCTATCC     720
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TTACCTATCA GTTCACCAGC GAGAAAATAA CTTGCTTTTC GCTTAATCGG TTCTATTGAT     840
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CTCaATTTTw AATCACATCC TCTATACACA TTCATTAAAC ATTTCAGCAA GTGCATTTAC    1020
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AGCCaATATT TTATCAGAAT TTTTCTGGCC ATTTTCATAG TCTATTnTCn CnCTCGGAAA    1140
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TATTGTATCT TTATCAAATT CTGGATACAT TACTCGCACT CTCCTTTATT AAATTTATAA    1260
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AtTTTCGTTT TCATTTTGAT TTTCCTCTCA TTCTTTGGTA AAATGAAAGA CAAAAGACGG    1440
CTATATTTAG CCTTTTTGGT GCCTTTAACA CGTTCACTTT GGTCGGTTAG TGTGTTAAGG    1500
CTTTTTCTTT TGCTCTCATT CATCATAATT GCTCCTTAAT TTGTCGCTAC TGGCATTTTA    1560
AGCGTTGTTT GATATAAAAC ACCTTGACCA TTCAAAATGC TCTTAATCGT GTCATAATCC    1620
ATTTTAAGAG TAAGCAATGT AGCTACTTGT TGCTCTCGTT TGTTCACTGC TTCGATCTCT    1680
TCTGACGTTA AAAAATCTAA TATCGTTGAT TTTTTACTTA CCTCTCGAGC TTCTCTTAAT    1740
TGCTTAGCAT TAAAACCTAA TGCTGTCTTA TAAACAAGGT CTGTATAATG CTTGTAGTAA    1800
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TGCGGGGAAA GCCCTAACTC CTTGATAACA TCCGTCATTG ACTTACGCAC ACTTTTTTCC 1860

TTTTGTCGTT CCATACGTCT AGCGTAGAGT CCGTTTTTCA TGTCATAGAA CTGTCGCACC 1920

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GCTTGTTCCT CGTTTAATTG ATAGAATTTA GCTTTTTGCC CACTCTCCAT TGCTCGGATT 2040

TCAAATCCGA CCTTGCCAAA CTCTTCTAGG TCTTTTTGAT ACTTTTTTAT TAGTTTAGAA 2100

ACACTTTCTC TTTTAATTTG TGAATACTTT GCAATAACCT CATCGGTCGT ATAAGGTTCT 2160

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TCACTAATGG AAAAATTCTT GTACTTTTTT GGTACCCATA TTAATTTGAG CATTGTTGCC 2460

TCCTCAAGTT AAATCTGTAG TAACGGACGA TTGACTATGT GCTATCTCGG aTTCTCTATT 2520

GGCGGGTGGA TwTTTATTAT TCATTTTCGA GAAGCCAAGA TCTTAgTTGA TGCTTACTCC 2580

AGCAGGTTTT ACGATCAGAT AAACGCCTTC CtGTkGGTAG TCCtTTCgCT ATCaATTCaT 2640

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ACACTTGTTT ACTGATTGCA TTCAATTGCT TTTTATCAAG CGTATGGCAC ACCTCAACAA 2820

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ATTCCCaAAA AAwGGGaAGT CAAGTTATTT CTCATTTTTG GGAATTAAAT TTGATTTCTG 3180

CC 3182

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

AnATAnnATA AATGTAATAA TTAACCACAT TATTCCgGTr AATTGAACGG CTAAATAAAT 60

ATTATAAmmm mCAAATCCTA AAGTGAAGAG AAAAAGTAAA AmATAACAGT TACTTCTTTT 120

AAAATGTGCT TTCCATGATT CAAATGCTCG TTTAACGGTG ATTGCTTGAT AATTCATGCC 180

CTCTTCCAAA ATGAAATCAG TCATCATTTG GAGTGCTGGA CCAACACCAA AAATAATCCC 240

TCCAGCTAAA CTAAATAAAA CAAACAGTAA ATTTAGTTTG ATTACTGTCC AGGAAAGGTA 300

AAACAACCGT TGAATCCCTG TACTTTCCAT CTTCCTCTTC CTTTCTATTA TGTAAAAGGC 360

TAAGCCAAAA GCGCTCAGCT AATGCCTCAG CCTCCTGTGA TTATTTTTGA GATTGGATAT 420

ATTCGTCTAA TTGTGTTTGC ATTTCTTTTT GAACTTTATC CCaGCCAGCT GtTTTTAGGT 480

CATcCATTAA TTTTGGGAAG TGTTTCTT 508

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CAGTCACGAA TTGATTTAAA TCCACATTTG TGGAATTAAC AAATTCCACG ACCATCAGCA 60

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TTGTTTTGAT TAATATCGAA GTTtCTGCCG CCGATmAmAC CAAGGATACG ACCAGTAGCG 240

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TCATCAAGCA AATAACCATA ATTTGCGACA GCGGTTTGCa TCGTGTTGTA AATATTCTGa 360

TCAATGGTTG ATTGGATTGT ATAGCCTTGC GACTGGATTT CGCGACGTGC TTGTTCTTCA 420

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GCACTTTTAC CAAAGAGTCC TTTGGCTGCT TCTTCCACGC CyGCAATATT TTCACCTTTG 840

TTATTACGAC CAAAAGGGGA GACATTTAGA TAAGTTGTCA CGATTTCGTC CTTAGAAAAG 900

TA 902

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

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TTAAGGCCTG TGTGCCATCA TTTTCAAACC CTTTATCTGC AAGgCTTTCA TATAATTCTG 120

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CTTTTTCTAA AGTTAATCCT GTCGCATTTG CATAAACGAG CATTTCAGTC AAACCGGTCA 360

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CCGTGtAGCA TAAACGTTTT ACCAAATGkT TTGGAAAATk GGtAAGACGG nGkCaTAACT 480

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ACCAGaAACT GGCGCATCCA ACGCATGAGC ACCCACTTCT GCTGCTTTTT TGGCAATCTT 600

TTCAGCCAAG GTCGGCGTAC TTGTGGTTAA ATCTACTACT ATTTTACCTG TAAGATCTGC 660

TTGAAAAATC CCTGTTTCAT TAAAATACAC GCCTTCAACA TCTGAAGGAA AGCCAACCAT 720

TGTAAAAATG ATATCACTCG CTTCCGCAAT TGCTTTTGGC GTATCATACC AAACTGCTCC 780

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TAATTCTTTT AAATCCTCTA GATAGGGACC ATTTCCAACT ATTACTAAAC GAGTTTGTGG 1500

TAATTTTTCA ATAACTTGTG GTAACCCTTG AATAATTGCT TGAATATTTT TTTCATAAGA 1560

AATTCGACTT AACGATAACA ACATAATCTG TTGCTCTTCA ATACCTAGTT GTTGACGCAT 1620

TCCAGCGATC ATTTCCTCAG TAATATCGGG ACGTAAAAAC TTATCAATTT CGATCCCTGT 1680

TGGAATAATT CTCATTGGTG CGGTTACTCC ATAATCCCGT AATTTTTCAA TTACACGTTC 1740

ACTGGGACAA ACAACACCTG TCGTATGATT TGTAAACACT CTTGAAAAGA ATTTAACATG 1800

TGATGGACGG ACAACTTTTC CTTTAGCAAT ATAATGTAAG TAATCTTCAT ACATCGTATG 1860

ATACGTATGG ATGACAGGAA TTTTCATTTT TTTCCCAACC ATTTTCCCTA AAATACCCGC 1920

ACCAAATTCA GTATGTGTAT GAATTAAATC TAATTCCAAT TCTTTGGCAA TTAAATAGGC 1980

GTACCACATG CCGCGAACCA CTACTCGGCG ATCTTTAAAA GATACGAATG GCACACTAGG 2040

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CATTCGTATG ACATCTTCTT CAAAATCAGT CGCGTTAGGA TCGGTTGTCG TAAAAATATA   2100
CACTTCATGG CCGTGCTTTT CTAATTCATC TTTTAAGGTC TTAATAGAAG TCGCTACCCC   2160
ACTCACTTGC GGGAAATACG TATCAGTAAA AAAACCAATT TTCACTCTCA TTACCTCCAT   2220
TTCATCTAAC AATAACTGCC TTCAATATTT GTTAAGATAA GACTGTTTCG TAGACTTCTT   2280
TTAACTCGTA ACCAATTTGC TTGATACTTC TTTGCTCTGC TACTTGATAG CCTGCTTCTC   2340
TAGTGCTAGG TATTTTCCCT TCTAATAAGC CTTCAATATA TTTTTTAAAT TCTTCAATAG   2400
AATGACCCAT ATAACAATTT TCATTAGCTA CTAGCCAGCC TTGATAAACT GGAATATCAC   2460
GCACTAAAAC TTGTTGCTGA CTAGCTAATG CTTCTAAGAC AACAATTCCT TCCGTTTCTT   2520
CACGCGAAGG GAAAAAGAAG AGATTCGCTG CCGCATAGGC CCCTTCGATG ACATCTCCTT   2580
TAATATAACC TGGGAAAATA ACATTTTCTG GATGATCTTC TTTAACTAAT TGTCGAATAT   2640
TTTTTGGGAT AGAATACATT GGTGTATCAC CAAACCAAAT AAATTGATAC TCTGGTAACT   2700
GTCGCGCAAC TTCAATAAAA TCAGTGATTC CTTTACGTTC AAAAAATAAT CCCACACAAA   2760
TAATTACTTT TTTCTCTTCA TCTATTTTAA AATATTCTCG GAATTTTTGT TCCTTTTCTT   2820
CTGAAGGATA AAAGCGTGAT AAATCAATAC CATTTGAGAT CGCCGAAATA GGCACTTTAA   2880
TGCCATATCC TTCTAGCAAT GTTTTAGAAT ACGGTGTTGG TGTAATTAAA TGATCCGCTT   2940
TGGAATACAA ACTGATAAGA TATTTTTTTA CTAATGGTGC CAGTTGATTA GACCCAATAA   3000
AGGAATTACG AAAATCTTCT TCTGTCGAAT GGGCATGATA AATAACTTTT TTTCCTAGTT   3060
TGCGTGCTTT TCTGACCATA CGATGGCTAT TTACGCCATA TGTATTAATA TGCAATATAT   3120
CATAGTCACT GCAATCAGCA TCTAATGTAT ATTCTATTCC AACTTCAGAG AGCGCTCGTT   3180
TCTGGTGATC TAATGCTCGA CCAATACCTG ATTTGGCTAA GATTTTCTCA CCTTCAAAAT   3240
ATAACAATAT TTTCAAACCC GCTCCTCCTT TTCTGCTTTA CTAACTATAA TAAACACATT   3300
ATACCATAGC TAAAATTTGA TGTATTCATT CTTCGGTAGG ATCCTTTTAA TCTTATAAAT   3360
GTTTTTAAAG TCCCTTCTTC AAGCTTATCA AAAAATAGTG AATAAAACAA AAAAAGCAAA   3420
AACCAAGTTG GTTTTTGCTT TTGCTCAACT CCGGCAGTAG GACTCGAACC TACGACATCA   3480
TGATTAACAG TCATGCGCTA CTACCAACTG AGCTATGCCG GAATAATCGC GTGGCGACGT   3540
CCTACTCTCA CAAAGGGAAA CCCTTCACTA CAATCGGCGC TAAGAAGCTT AACTTCTGTG   3600
TTCGGCATGG GAACAGGTGT ATCCTTCTCG CTATCGCCAC CACACTGGGT GTTGTTTCTT   3660
ATTGAGTTGA ATCTTCATTC ACTCAAAACT GGATTGAAGT TTGAATCAAA ATAACCAAGT   3720
TGCTTTTACT TATCCATTCT TTGGTTAAGT CCTCGACCGA TTAGTATTGG TCCGCTCCAA   3780
CTATCACTAG CCTTCCACTT CCAACCTATC TACCTGaTCA TCTCTCAGGG GTCTTACTTT   3840
CTTAAAaGAA ATrGGAAATC TCATCTTGAr GTGGGCTTCA CACTTAGATG CTTTCAgCGT   3900
TTAwCCCTTC CCTACAAAGC TACCCAGCAA TGCCCTTGGC AGAACAACTG GGTACACCAG   3960
CGGnAAGTCC ATCCCnGGTC CTCTCGTAC                                    3989
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(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

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CCTnCCTAAT ATATCTTCnA TCACtGTAAC TTTACTkGTA AtATCAGATA TTGaAAATTT        60

ATTTTCyTGt AAAGTTTTCA TTTTATTAGA TAGAGAAATC ATTTTATTTA ATATATTTTC       120

CATCTCATCA AAAATAGCAG TGTCAACTTT ACCTTTCATT AAGCTTCCTA ATTTCTCAAA       180

AATATTATCT TTTCCACCAA TAACTTCAAC TGCTTTATTG ATGTCATATA TATTATTTAC       240

AAGTTTTGCA CTATTTATAT CTTCTGAAGC ACTAGCTAGA CGTTTCAATC CATTTGACAC       300

TTCTATCAAA CCATCGATAA CTTGTACATA TGTCGATGCA GTAAAAGTAC CTATTATTCC       360

TTTGAATAAA GATGAAATTT TTCCAATACT GGATTTCGCC ATATAGCTTA AAcTTCTTCT       420

AAACTCTCAA GCTTATTTTT AACACTTGTA ATATCTTCAG GAACCTTTTT ATTCAATTGG       480

TTAATTGATT CAGAAACTAG CATTAATTCT CCTGCTAGTA GTGCTACAGC TGCCAAACCA       540

GCGATTGCTG CAGGGAATGT AGCAATACTT AAACCACCTA TTACTCCAAC TAAAAGACCC       600

ATTGCACCAA TTGCTATACC GATATTAGCA ACCTTTTTAG CTATTGTTGC AATATCTGAA       660

GGTACTTTTT CATTTAATTG TGATAGTGCT TCGCTTGCAA TCATTAATTC TAGTGATAGG       720

AGTGCTACAC TAGCTAATCC TGATATAGCC ATCATTGGAT TAGCAGATGA AAAAGCGCCT       780

GCAATAACAA CTAATCCTGC CATAGCCCCG ATTGCAATTG ATAAACTCCC TAGTTTCTTA       840

GCGACAATTC CAATATTGTT TGGTACTTTC TCATTGAGTT GGTTCATCGC TTCACTTGCA       900

ATCATTAAAT CTACTGAGaT TAATGCAATA CTTGCAATCC CTTTTAAATT ATCAGTAAAA       960

TTTAATTTAC TAGCTATAAA AGCCAGACCC CCAATTGCAC TGATAGCCAG ACTCATGCTC      1020

GCTGTTTTTT tAGCTAGCCC TGTAAAATCA TTyGGTATTT TTTCaTCTAG TTGTTTCATT      1080

GCTTCTGCGC CTTCTTCAAG CACTTTTATt GCTCCGAATA ATAACGCAAG GTTACCAGCA      1140

TTTTTTAAAA AACCAGTCCC AATAGATTTT AAACTCTCTA ATGGTTTTAC GATTTCTGAT      1200

GCTCCTCCAC CTTTACCGAA TTTAGGCAAT TTTATTTTAC CGAATACTCC AAAAACTTTG      1260

GATAATATAG AAAGCCCTTT GGCACTAATA GCTATAAACT TTAAAGCTAC CCCAAATTCA      1320

AATAATCGTG GAATAAATGC ACCTAGGCCT TTCAAAGTAT CTCCCTTACC TAAAAATTCA      1380

AATATAGGTT TCAATAGATT GAATAATCCA ACAGCATCAT CTTTTACACC CTTTATTCCT      1440

TTACCTAGTC CCTCAAAAAA TGAAGCATAA TCAATAGTGC TTAAAAATTT CACTACTTkG      1500

TCAAAAAAAC GAAATATATC ATCTGAATGT TCTTCTGCAA AAGCTCCTAT TTTTTTTAAA      1560

TTATCTTCGA AAGCAGCACC AATTTTTCCA AATACACCTG CAATTCCTCC CAGGCCTTTA      1620
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TCCTTCGCCA TCTTATCAAA TGTATCGATA ATCGAGGTCA CTCCACGTGT TATAGCTGAA 1680

TTCATAATAG ACATACCAGT TCGAACGCCA CCAACAGAAT TTCTAGCTTG TTCTTCAAAT 1740

GATTTGAATC CTTCTGCCCC GTTTTTATTC ATCTCCACAA TTCTATCCAT AAATTGATCC 1800

ATAGAGATAT TTCCATTTCT TAAAGCTTCT CCCAATTGAT CAGATGTTAA ACCAAAACTC 1860

TTCCCGATTT GATCCACTTG GGCAGGCATT GCTGTTAGTA GCGAGCGCCA TTCTATCATG 1920

TCTGGTTTAC CTTTAGAATA AGATTGAGAT ATTTGCTCAA GTGCGCTTGA TTGTATTTCT 1980

CGTGACATGC CACCCGCTAA AATTGCATTA TTTAATGCCA AGAATATATC CGCAGATTTC 2040

TGTACATCTT TATTATTTGC TGTAAACCTT TGTACTGAAG CAACAGCATC ATCTAAAGTT 2100

GTAGGCAAGC CATTTAGCCC TTTTACAAGT TTGCTTTTGG CGATATCGGC TTGGTCGGCT 2160

GAAATATTCA TATTTGACAT TACTTTTTCA AAGTTATTTA AAGTATCTAA TCTTGAAATA 2220

GAACCATCGA TAGAATTTGT AATCATACTA GTtGCCTTAT CAACAGCCTT TACAGCTAGT 2280

CCTACACCAA GCATTTGATT TAGTTTGGAT GTTAAAGGAT TGAATGCTCC TAATATTTTA 2340

TTGCTTGCAT TGTTAGCTAG CCCGCTCAAC TTATCTAGAT TTGATGAAAC ATTTATCTTG 2400

TAGGTCCGTT CACTCATACT TCGAAGACTA TTTTGTAATT TTCGACTCTC TTCTCCAGTT 2460

TCTCCTAGAC CACGACTATC AATTTGTAAC ATAGCCTTGC GATTATTCAA TCGACTAATC 2520

TCATTGTCTA GTTTACGAAG TTGTGCTTCT GAACCTTGCA ACTGAGTTGT TACTATTTGT 2580

AAATTTGCTT TCCTAGATTG TAGTTGTTTA ATTTGTkGAT TTAAGGTkGA TATTTTTtCT 2640

TTkGCAtCTT TAGTATTTAC ATCTGCCTTA ATGGTTGCTT TCTGTGCTTG CAATTTTTTT 2700

ATATCAACAT TAATATTTTT TATTTCTTCT TTTGCTTTTT TTAGTTTCGT AGTATTCCAC 2760

TCGATAGCAG GGCGTTGACC TTTTAGTTTA GCTATTCGTC GATCTAAACT ATCTAGTTCT 2820

TTTTCTATAT CTTTAATATT GTCCTTAATA CGAATGGAGA TATTTTCAAC GGCCAATTAT 2880

TCCACCTCCT CCAGCTCATC TTGCGATATA AATTGAACAA CAAATGGTTG TGGTTGCTTA 2940

GGTTTTGGTG CATTTTCTTG TGACGACTTC CAATCCATAA AGTTTTGATA ACTTTGCTCA 3000

TTAGCATAAT GGCCATATGC TACAATCAAT TCAGAAACGC CCCAACCACT CAATACATGG 3060

CTGGGACGTT GTCCTAAGAT TTTTGCTACA AAATGAGCCA TATACGAATA ATGATtAAAC 3120

TTAGCAAAAT ACGTTyCTgC GCTgTTGTAA TGAAACACCA TtGTTtAAAC TGtCACGCAC 3180

GATTATCCGA AAAAAGCATC TGCtTCTTTG AACACtTCTG GGtGATTTcT GTtAATGCAG 3240

TAAAnGTTCA ATCACTGAAA TGGAAGCaGk ATCGATTACT CTCAnCA 3287

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAAAATTAGG CCTTATCGGA CCATGTTTTT CTACATTCAT TGGTTGAAAT AGCATTAATT 60

TTAGTCGTGA kCGAATTGTC TTATCGTTTT ATCGAACATC CACTGACACG ATTGTCTTAT 120

AAGGATGTCT GGACTCAATT CACTGAGTTC TTACGGAAAC CGTGGGACCT TCGTGAAAAA 180

GGGACAATGG CCTTTATGAC AGTGATTAGC GTGATTGCAG TATTCGGTTT AATTGTGGCT 240

CCAGCAAACG CTAAAAGTGC GCAACAAGAG CAACTAGAAA AAAATATTGC GAAAAATCAG 300

CAAAAAAATTG AAGAACGTAA AAAAGAAGTC CAAGAAAGTG GCACGAAAAA TAGTAGCACG 360

TCCACAGAAA GTAGTACAAA ACCGAGTGAA AGCCAAGACG TTCTACCCAC ACAACTCACA 420

CCAGAGCAAG TAAAAAAAGC GCAGAATTTA GAAATCACAA CTATTGGTGA TTCTGTTATT 480

CTAGATGGTG CTAGCGGGTT ACAAGATATT TTCCCTAAAA TGATTATCGA TGGGGAAGTG 540

GGCCGTCAAT TGTATAGTAG CATTTCACTA ATTGGTGAAC TAGACAAAAA GAAAATGCTT 600

AAAAATACTG TTTTAGTGAG TTTAGGTACG AATGGTCCTT TTACAGAGGC ACAATTTGAT 660

GAATTTATGA AAGCGTTaGG TAATCGAAAA GTTTATTGGA TTAATGTTCG CGTCCCAACT 720

AGAAGATGGC AAAATCAAGT GAATAGTTTA CTTAGTCAAA TGGACAAAAA ATACGATAAC 780

TTAACGGTCA TTGACTGGTT TAATTATAGT AACGCCCATG ATGATTGGTT TTATGATGAC 840

CGAGTTCATC CAAATGTGGC AGGTGGCGAG cAATACACAC ACTTTATCGC GGAGAAAATT 900

TTACAGTAGC AAGAAACTTc CAGCTCAGAT GAAAGGGGCT GGgAAGTTTT TTGTTATAGG 960

GAAAAGCAAA TATAGGTAAT TTAATGATTT TCTTGGAAAA CCTAAGCTTT TTTTTTTAGA 1020

TATCnGGGTA TACnGGTTTT TTGGTTACCA GnTCCCCGnA AGGGATTTAG CCAGGTAATT 1080

GGCCGGTACC TTACCTAAAA GATG 1104

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GATTnCGTGA AGCGGTTGAC ATATGATTGC ATCTTCATTT ATAATAGATT CATGAAAGGT 60

TATTCATGTA AACGGAATAA TCGCTATTnT ATAGGGAGTG AAGGTGTTTA AATGCAAAAG 120

AGTTATAAAC TAGAAGGACT TGATTGTGCA AGTTGTGCAG ACAAAATTGA AAAATCTGTC 180

CAAAAAATTC ACGGAGTAGA AAAAGCGCGT GTGGACTTCA TGGCTGAAAA GATGACACTG 240

GAAGTTGAAT CAGGACATGA TTTAGAAGTC GAAAATGAAG CGCGTGCAGT GATTGGTAAG 300

TTAGAATCAG ATGTCAAAGT TATTTCTTTA AAAGATGTCA AAGAAGAAGA GGGACGTAAT 360

CCAAATAAGA ATCGCTTAAT TCGTATCATT ATTGCATTTG TTTTATTTTT TAGCACTTAT 420

TATCATTAAA CCAAGTnATA ATTGGGTTGC TTTGGCATCT TATTTAGTCG TTTATGTCTT 480

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AATTGGTGGC GACATTGTCA AACGAGCGGT AACGAATATT TTTCGTGGGG AAGTGTTTGA    540
TGAAAATTTC TTAATGTCTG TGGCAACGAT CGGGGCATTC TTTATTGGGG AATATCCCGA    600
AGCTGTGGCA GTAATGTgTT CTACCAAGTC GGcGAATGGT TCCAAArTGC TGCGGkTGAT    660
CAATCCAGAA AATCmATTGC CAAATTAATG GATATTCGTC CAGATTCAGC AAATCTTTTA    720
GTAAATGGAC AAATAAAAGC GGTCGCTCCA GATACAATTG AAATTGGGCA ACAAATATTA    780
GTGAAACCAG GTGAAAAAGT TCCATTAGAT GGTCAAATTA TTGATGGATC AAGTATGGTA    840
GATACCTCTG CGTTGACTGG TGAATCCGTT CCAAGAACGG TCAAAGTCGG CGATGAAAtC    900
TTAGgTGGTT TtATCAATAA AAATGGGgCC TtGACCATTA ATGTtACGAA AAAaTTtGGG    960
GATyCAaCAG TTaGCAAAAT TTTAGATTTA GTTGAAAATG CTAGCAGTAA AAAAGCCCCT   1020
GCAGAAAACT TTATTTCTAA ATTTGCTCGT TACTATACAC CAGTTGTCGT TGTTTwAGCy   1080
AtCCTAwTGG CAGTGaTTCC aCCatTTATT TTCCCTGATA CTTCTATTAA TGAATGGGTT   1140
TATCGAGCAT TAACGTTCTT GGTTATTTCT TGTCCATGTG CCTTAGTCAT TTCTGTTCCT   1200
TTAAGTTTCT TCGGTGGAAT TGGCGGAGCA GCAAACTAGG TGTTTTAATT AAAGGAAGTA   1260
ACTATTTAGA AATTTTAGCG AATACGGAAA cAATTGTTTT TGATAAAACT GGTACGCTAA   1320
CAAAAGGAAA TTTTGTGGTT CAAAACATAA CTAGTGTTGT CTTACCCGAA GAAGAGTTGT   1380
TGCGTTTAAC AGCAACAGCA GAACAATTAT CCACTCATCC AATTGCTATT TCTATTAAAG   1440
AAAGCTATGG CAAAGAAACT GTTCCAGCAA CAGCAATTGA AGAGGTTGCC GGACAcGGTA   1500
TCAAAGCCAC AATTGAAGGT AAAACAGTTT TAGTCGGTAA TGCGAAGTTA ATGAAACAAT   1560
TTGGTATCGA AGCACCAGAA GTGAAGGAAG CGGGAACTTT AAtTTTTGTC GCTATTGATA   1620
ATCAATTTGC AGGCTATTTA GTGATTGCGG ATCAATTGAA ACCAGACGCC ATTTCAGCAA   1680
TAAAAGAATT AAAGGCTGAA GGGGTCAAAC AAACTGTTAT GCTGACTGGA GACAATCAAC   1740
AAGTTGCAGA AGCTATTGCA AAAGAAGTTG GTGTTGACAA AGTTTATGCA GAACTTTTAC   1800
CAGATGGTAA AGTGGATCGT TTAGAAGAGT TGTTAAAAGC ATCTTCACCT AAAAAACAAG   1860
TTGCCTTTGT TGGTGATGGT ATGAATGATG CACCTGTTTT AGCCCGGGCT GATGTTGGGA   1920
TTGCCATGGG TGGTTTAGGA AGTGACGCGG CAATTGAAGC TGCTGATGTG GTGATTATGA   1980
ATGATGAACC AAGTCGTATC GCCTCTGCGA TTAAATTATC AAGAAAAACA TTGAGAATTG   2040
TTAAACAAAA CATTATCTTT GCGATTGCTG TTAAAATCAT TGTCTTGGCA CTAGGTGCAT   2100
TAGGCTTGGC TTCAATGCAA GCAGCAGTGT TTGCTGATGT TGGTGTAACT ATTATCGCTG   2160
TTTTAAATGC TATGCGTTGT TTACGTGTAG AAAAGATGAA AGATAATAAC TAAGCCTTAA   2220
AAAGTACAGC TGAGACGAAC GTTTTTAGCT GATTATCAGG TTTTGAGCGT GGGACAAAAA   2280
TCACTTTGAC TTTTTGTTCC ACGCTTTTTC TCCTACACAA TTTCTATTCG TTCTTAAATT   2340
GCCAGAGTTC TTGTAAAGAA ATCTTTAAAT TTTTCGCTTT GTGGCATATA ATAAGAAAGA   2400
ATTTGTACGA AAATTGCGCT TCGCTTTTTT TTCATGGTAC AATAAGCAAG AATGGATTGA   2460
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TTTACAGGAG GGAACCTCAA CATGGCATCA AATGAAAAAA CACGATATAA AGCAATCATT 2520

GCAGACCATA CGTATACAAT TATTGGCCAA GAGTCAAAAC AACATATGGA TTTAGTCACA 2580

AAAATTGTCA ACGAACAACT GGCGGAAATT AAACATCTTT CTCCGCAAAC TGATACGGAA 2640

CAAGCTTCTG TTTTATTAGC AATTAATGCA ATTTCAGATC AACTAAAAAA ACAAGAATAT 2700

GCTTTAAAAT TGGAAAAACA AGTAGCAGAT TTAAAACAGA AAACCATTCG TTTGGCTGAA 2760

TTAGAGAATC GTGTGCGCCG AATGGAAATT ATCGAAGAAG AAGCACGAGA TGTTTTGAAA 2820

AAGAATGGAC AAGAAGATGT AGAAATTCAT AATCATGTGG AAGCCCAACA AATTTTGAAT 2880

GAAAATCGAA AACAGCAGAT TCAAAATAAA GGTGTTTCGG AGTAGTTCCT GAAAGGATGA 2940

CAAGATGTTA ACAATACTTA TTTTATTACT TTTAGCCTTT GGATTTTATA CAGGAGCTAA 3000

ACGAGGCTTG ATTTTACAAG TGCTCTATTC GGTAGGTTAC TTAATTTCAT ATTTTGTTGC 3060

TCGTACCTAT TACAAAGAGG TCGCTTCTCA TTTAGAATTG TATATTCCAT ATCCATCGGT 3120

TACGCCAACG TCAAAGCTTG TCTTTTTTAA TCAAGAGATT TCTTTAGACT TGGACAAAGC 3180

CTTTTATTCA GCGGTTGCGT TTCTATTATT GCTGTTTGCa GGCTGGTTGG TCGTTCGTTT 3240

TTTAGCTATC TTTTTACATG GATTAACATT TATTCCAGTT TTGAAACAGG TAAATGGACT 3300

ATTAGGTGGC GTATTAAGTG TTCTTGTGTT ATACGTGGGT CTTTTTCTAG TGTTAGCTAC 3360

GGCGTCAATG ATTCCGTCAG ATATTGTCCA AAATCAGTTT CGGTCAAGTG GCTTGGCACG 3420

AGGCATTGTA AAAAATACCC CAATTCTAAC AAAACAAGCA TATGAATTAT GGGTTGAACC 3480

AATTACGAAA TAAAGCTGAA TGGGACTGAG ATAGAGATAA GAAGTAAGTG AGCAAAGCGA 3540

AACTTCTTAT GTTATGTCTC AGTCTTTTCA ACAAATGAAA AAGTTAGAAA AGTAGGTGGA 3600

AAAATGAATC AGCGTATTCT ATCAACATTA GGGTTTGATA AAGTAAAACA ACAGTTGTTG 3660

CAATTTATTG TGACAGCTCA GGGGACAAAC GAAGTTTCGG AATTATTACC AATTGCTGAT 3720

GAAAATAAAA TTCAATCATG GCTAAATGAA ACACAGGATG GTTTAAAAGT TCAACGATTA 3780

CGTGGTGGAA TCCCCATTCC TAAATTAGAA AATATCCAAC CACACATGAA ACGGATTGAA 3840

ATTGGTGCGG ATTTAAATGG CATAGAATTA GCACAAGTAG GCCGTGTCTT GTCGACTACT 3900

TCAGAACTGA CTCGTTTTTT TGATGAGTTA AGTGAAAATG AAGTTGATTT TGAACGTTTA 3960

TATATGTGGC GAGAGCAACT AGAAGTTTTG CCTGAATTAA ATCGCCAACT CAAACAAGCC 4020

ATTGATGATG ATGGCTACGT CACAGATGAA GCTTCGCCAG CCTTAAAGGC AATTCGGCAA 4080

AATATTCGTC GTAGTGAGCA GACCATTCGA GAAGAACTAG ATAGTATTAT TCGTGGGAAA 4140

AACGCACGTT ATCTGAGTGA TGCCCTTGTT ACTATGCGAA ATGAACGCTA CGTAATTCCA 4200

GTCAAACAAG AATATAAAAA TATTTTTGGT GGCGTGGTTC ACGACCAAAG TGCTTCAGGA 4260

CAAACCTTAT TTATTGAACC TAAACAAATT TTAGAAATGA ATAATCGTTT GCGACAACAA 4320

CAAATTGCCG AAAGAAATGA GATTACTCGC ATCTTGGCAG AACTGTCGGC TGAGTTGGTT 4380

CCTTATCGCC GAGAAATTAC GCATAATGCT TATGTCATTG GTAAACTTGA TTTTATTAAT 4440

GCTAAGGCGC GACTAGGAAA AGAACTAAAA GCAGTTGTTc CAGAAATTAG TCmAGCAAAT 4500

CmTGTAGTTT TTAAACAAGC CCGGCACCCA CTATTAAaTC CAGAAAAaGC TGTAGCCaAT 4560

GACaTTGTGA TTGGAGAAGA ATATCAAGcA ATTGTGATTA CAGGGCCTAA TACCGGCGGG 4620

AAAACCATTA CTCTGAAAAC GTTAGGTCTT TTACAATTAA TGGGTCAAGC TGGATTwCCT 4680

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GATGAACAAT CGATTGAACA AAGTTTAAGT ACTTTCTCTT CACATATGAC GaATATCGTG 4800

TCTGTCTTAA AGAAAGTCGA TCATCAAAGT TTAGTACTAT TTGATGAATT AGGTGCTGGG 4860

ACAGATCCGC AAGAAGGGGC CGCTTTAGCG ATTGCCATTT TAGATTCATT GGGCGCTAAA 4920

GGAGCCTATG TGATGGCAAC AACCCATTAT CCTGAATTAA AAGTGTATGG CTATAATCGA 4980

GCTGGAACAA TCAATGCCAG TATGGAATTT GATGTAGATA CTTTGAGTCC AACCTATCGT 5040

TTATTAATTG GCGTGCCTGG CCGAAGTAAT GCTTTTGAAA TTTCGAAACG TCTTGGATTA 5100

GACAACAGTA TTATTGAGGC TGCAAAAACAA ATAATGGACG GTGAAAGTCA AGATTTAAAC 5160

GAAATGATTG AAGACTTGGA AAACCGTCGC AAAATGGCCG AAACTGAATA TTTAGAAGCT 5220

CGCCACTATG TCGATGAATC GGCCGCTTTG CATAAGGwAC TGAAAGAAGC CTA 5273

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GGTTTAAGGC TTCCACTTTC CCAATGTTGC TTGTAGGTTT GCTTTAAGGC TCGATTTCTG 60

CTGATGTTTG TTGCTCTTTG AGTTGTTTAA ATGTGAAGAT TTCTCGGTTG AATAGGTTGA 120

rGTCTTGATG GGTTAGGTTC ATTTTATTCC CTCTTTTTAG TATCTTCTAG TTACTCTTAA 180

TAATTTTATT TTTCAATAGC CATTGTAAAA ATAACACAAG GACTACAATT GGCCAAAGCG 240

TGATTGGGAA AAAGAGCCCT ACAAAAATGC CTGGTACAAG AATCGTCCCT AAAATCTGTG 300

TTGTTAAACT CGTAGCAAAA ATTGCGACAA CAAAAAGCGA GTCAATTGTT GGGAAAAATT 360

GCGCGACCGC AAACCCGATT AAAATAGCTG AAAAAACGAC GGGAAAAATA TCGCCACCTA 420

TCCAACCTGT CTGTAAACAA ACTTGTAAAA ATACTAGTTT CATTATCGCA GCGATTACCA 480

AGATATACCA GGCTTGTTGA CTACCAAAAC TAGGAACTAA ATGCATAAAA GATTGTCCTG 540

AAAATAGTAA TCTTGGCATT AAAATAACAA AGAGAAAAAT ACAGGCTGCA CCAAAGGTTA 600

CCAGTATGCT TTGCTTTTCT TCAAAAGGTT GGCATAGTTT AGCCAGAGCA GCTTGCAACC 660

ATTGATAGGC GTTACCAATC ACAAAAGCAG TTAATAAAGC GGGTAAAATC AGCCATAACG 720

AAGCCATTTC AATTTTTCCA GTTCCTAAcT TCGTAATAAA CGATGGGTGT CCCACCAATT 780

TCATTAAAAA GGTAAACACC ACCAACCCGT TCACAATAAA TAACCCGTTC ATCACTTGTT 840

TCAGTTTCTT TTTATCTACA GGAGCGAGCA TCGTATCGTA GCGCTGAACA AACTGTTGCG 900

GATGTAGCAA GCGCTGGATT TTTGTCCAAA ATACTTGCTG TTCTTGCTCG TCATAATGAA 960

AATAAAGGTA CCGTAACTTA TCAGATTGCC AGACTGACAA CGAAATAATC GCTCCCAGCA 1020

ATGCGGCTTC AGGACCGACA CCAGCCCCGA AAATTAAAAT TACCAAGGCG GCCAATAAAT 1080

TTCTAAACAC ACCTGAATAA TCGACCGATT GTTTCGCCTT CAATTCTGTC AGAGCCTCAT 1140

GCGCCGTTTG TGGTATTTGC CCGAAGCGTT TCTTCAGATA ACTCAATACC AACGCTCCTA 1200

GCACACACAA GACAAAATAA TAGAGAATTG GCCATTTCAT TTGCGCTGGC AACACCTCCC 1260

AGAGCAGAGT CGTTAGCTCT CCTTCAATGA TTAAAAATGC TCCTGAAATT CCCGCGATGa 1320

TACTACTTAA AAATAACCCA CTGACGATaA TTGtCCACAT TTTTCTGTTA CGCATACTTC 1380

CTCCAAATGA TAGTTGTTTC TTTtATAGTA GCAGATAGTT AGTGGnTTGT GTTTGAAGAT 1440

TTtGGGAAGG ATTaTTTTTT TGAAAAATTG AGGTTATGAA AAGATTCCAT TTTTTATTGA 1500

TCAAATTATC CTTCTTGTAT AATCGTTTCT TTTAGCTATA TATATTCCAT TAAATTAAAA 1560

ACCGCCACTT ATATTGCTTC TTAAGTTCCC ACAAACAACG CCACTTCCAG CGCCAACAAG 1620

TCCACTTCCT TATCAAAGTC CAACAGCACT AGCTGTTCAA TTTTCTCCAA TCGCTGTAAT 1680

AAAGTATTAC GATGAATAAA GAGTTTTTTG GCTGTTTGAG ACAAGTTTCG TTTTGATTGA 1740

AAATAGACAT TCAGTGTATG GACAAAGTCG GTATGTTGCT GTTGATCACT TTTCTGCAAT 1800

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TCAGGTGGAT TTTCAACTAA TAAGACAAAG GAACTGTCAA TTTCAATACA AACAATTTTT 2160

TGTTTGTCCC CTAAAATAAC TTGGTTTAAC TGGTTACCTA AAATAGACAT TCTTTCTTGC 2220

CTTTGGCGTT CATTTAAGGT TAATGAAATT AGCAAAATCG CATAGGGCTT ATCTATTGCC 2280

AAGCGATAAT ATTGTTGAAA TTGTTGGAAA ACAGCTTGGT CCCTCTTTTC ATGCGCAAAC 2340

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TCCTGCAGCA AATGAAAACT GCTACTTCCC GTTTCTAAGA TTTGGTAAAT TTTATTATGC 2820

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CACGCTCCTT TA 13932

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

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CAAGTCAACT AGCAAATTAA AAAGCTTTTT TGGTAGCCAA GCAGCTTATA TGGCTCGATA 300

TGCACCAATT TCTGTAATGA TTATTCGCTA ACAAAATTGA AACaGTTAAA AAAGCCGCCA 360

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GAATTGGTAA TCCGACGTCA TTCGCTAATT GGATCATCTC TTGTGGAACT TCATTGAAAT 1800

AACGTTGGAC TTTAAAGCCT AGAGCAGCGC AGTTCATATT TGCTAGTTCT TGAATAAGAC 1860

GTTTTTGCAA GCAAGGCTGA TCTTTGAAAA TATAGCCGGT AGTTAATAAA ATTTCTCCTG 1920

GCGTTAACCA GTCAAAAGCA TCAGGATTTT CTAAAATATT TGCTTGTAGA ATTGGCGCAT 1980

CTAAATTGGT CTCGTGCGTC AATAAGGTTA AACCAGGTAG TTCTTCTGCA TGGAGTAGAT 2040

CATTGACCGT CATCATTAGC AAGGCCTCCT TTTGTATGAA TTATCTAAAA ATTAAGTGTA 2100

TTTATTGTAA GATGTTACAA AACTATTTTA GGGAAAATAA GGTATCCTTA TACTAATAGA 2160

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GCTTACAACC TATAGAAACG CATCGTTTAA AGATATAGCA ATAGTATACT TAATTTTTAA 2280

TGCTTTTACT ATTGTTTCAG CTACTTTAAA TTTCTCAAGT ATTTCTATAA TCTGTAAGTT 2340

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TTAGAAGGCG CAGATGTGAA TACTCTTGGG GTTAAGGCGC TAGATGATAA AACGTTAGAA 2940

ATAACTTTAG AACGGCCCAC CCCTTATTTG AAATCATTAC TTTCGTTTCC TGTTTTGTTT 3000

CCACAAAATG AAAAATATAT CAAAGAACAA GGGGATAAAT ATGCTACTGA TGCAGAACAT 3060

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TGGGCTTATG TTAACTAATT GAATGAAGGT AGGAAGGGGT TTGTCATGCT TTTAGAAAAC 4140

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AGCTATGATA TTCGAATTGA AAACGAGGTC TGTACTGCGG TCGCACCGCA GTTAAGGCCT 4260

TTAGAGAACG AAACAGTTAT CGATGTGAAT CAGCAACTCG TTTTACCTGC GCTAAGAGAA 4320

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ACGAAAGGAA TTTTAACACG TATTGAAGAA GAAACTTGGC TGTTACCTGA ACAATTACCA    4440
ACTAGTTTAG AACGTGCTTG CCAAGTTATT GAGCAGTATA TTCAACAAGG CCATTATCAT    4500
ATTCGCAGTC ATTGTAATGT AGATCCATCT ATTGGAACGA AACATATTGA AATTACTAAA    4560
GAAGCATTTA GTCGATATGA ACAATACATT ACTCATGAAA TTGTGGCTTT TCCTCAACAC    4620
GGATTACTCC GCTCACAAGT CGAACCTTTG ATGCGCGAAg CnTTACGCAT GGGGGCAACT    4680
CATGTCGGCG GCGTTGATCC AGCCCTTGTG GATCGTCATG TGGATCATTC AATCGCAAAA    4740
ATATTTGAAT TAGCTACCAC ATTTAATAAA AAAATTGATG TTCATTTACA CGCCCGTGAT    4800
ACTTTGGGAC TTTATGAATT TAATAAATTT GTTGATTATA CAGAACAAGC AAAGATGTTT    4860
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GACATTGCGC AAAAATTCAT CGAAACAGGT ATTGATTTGA CTTCGACTGT ACCAATTGGA    4980
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ACAGCCGCTC AAAGATTTAA AATTAGCGAT GAGTATCGCT TGAATCGTTT ATGGGGCTTA    5160
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GATTCTGCAG ATTTCCTACT ATTTAATGCT GAGAGCACTG CTCACGTGAT TGCACGCCAA    5280
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GCAAAATCCA AGCGATTATT CCGCAAAATC AAGTCACTGA AAAGCAACAA GGCACTGATT    5520
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ACCTTTCATT AGGCTGGCGT GCTAGCCAAC CTGTTAAAAA TTTAAAAGAG CGTTTAGCAG    5640
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ATGTAGAACT AGAAAACTTC TGGGGCGTCA AAAGAGCCTT AGAAAAATAT GCGCATGTGA    5820
TTGATTATGA TATTGTTGTC TTTCCACAGC ATGGATTATT AAAAAATCCC CAAACGGTTT    5880
TACTCATGAG AGAAGCTCTA AAAAATGGTG GAACAATGGT TGGTGGTTTA GATCCTGCAG    5940
GCATTGATTA TGCAATTGAA GAATCTTTAG AAACTATTTT CGATCTGGCA GAAGAATTTC    6000
AAGTAGGAAT CGATATCCAC TTGCATGATA CGGGGGAAGT GGGCGTTTAT ACAATTGATA    6060
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ATGTGTTACG CCAAGCTGGT GTATCGGTTC ATTTAGGTAG TGATGGCTTT TTTGACTCTT    6300
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GAAAGATTAC AGAAGAGCAA CTTACTCAAG CTTACGTCCA TGGCTGTGGC AAAGTAGCAC 6420

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GCTCCTTTAG GCTTTTTCTC TATTGTATCA AATCAATACA ATAAGTCGAG GAATATGTAA 8520

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TTATTTGTAA CTCATGCGCA TCAATGGGGA TTGTAGGATT TCCAGTTAAA TTAAAGTAGA 9360

CATGGATTGG TTGGATTAAA AAGTGTTTGT TCATCTGTAG TTGCCTGGAT ACTCAATTTG 9420

CCATTCATTT TCTTCAGTCA ATGTATACGT GACTGAAACA GTGAGATTCC AGGAAAACCA 9480

TTTTCACCAG CAGGACTCTC TAGCCAAAA 9509

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CCATTCCTAA AAAAAATTCA AAATCTTTCA GAGAAGCTGT TAAAGGAATT TTTAAGTTCA 60

CAGATATTAA CTTAGCGCGT GAGGCTAAAA ATCGATTGAT TCATGATTAT ATCGATCAAC 120

CAAAATATTC AAAAGcTTGC GCATCATTGG ATGATGGATT CGAAGACGCC TTTCAATATA 180

CCGTACAAGG AAATTCCCAC AATCGACTAA AGAGTACCAA TCTAATTGAA CGACTGAATC 240

AAGAAGTACG CAGAAGAGAA AAGATTATTC GCATCTTCCC CAATCAAACA TCAGCCAATC 300

GCTTAATTGG AGCCGTTCTT ATGGACCTAC ATGATGAATG GATTTATTCT TCAAGAAAAT 360

ACATCAATTT TGATAAGTAG AAATGGTAAA AACATTGTAT AGCATTTTAC ACAGGAGTCT 420

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ACAGTGCTCC TTCCAGTCCA AACACAGTTA AAAGAACACT ATCCGCGAAC GGTTTCCCTC    600
GTGAAAAACT TAGTCAGTCC GCTGCCAGAA GAATACCGTT TCTTGACAGA GGTACTCTTA    660
TCTGTATTAC TCAGCGGAGA AATTTCTGAA ACGATTCCTT ACCAAGCGCT CCTCGTGGCG    720
CATGGTGAAT CGACTGCCAC AAGTATTCAA GCCGTTGCCA ACAAATTATG TGGTACCTAT    780
ATTTTCGATG CGATTAACAT GCCCTTAACC TCCTCCGTCC GAGATATCGT CGCCGAAGTT    840
AAAGAGTGGC TTTCTCAGCG GGACACATCA CAAGGCGTCA TTATGCTCGT CGATATGGGT    900
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AATAACCTGA CCACTGCCTA TGCGTTGGAA ATTGGTCATC AATTAATGAA CGAACAACTT   1020
TTCTATGGTA TTGCTAAAAC CGCTGAAAAA AAATTTAAAA CCGATGTACA GTACTTTGAA   1080
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GTTTCTAAGG TAAAGTCTAG TTTAACGACG CTTTTTTTCT TACCCTCTTT GTCTTGTTTT   1920
TCGACTTGTT GGATAGTTyC TTGAAGAGGG GCTACTtCGC CTAGATAATA GAAATCTGTT   1980
TCGTTCTCTT TTTGATTATA TTTCCGTTTC ACAAATAAAT GAAATTTATA TTCCCCAGGA   2040
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AATGTTCGTT CATCAATAAA TTCATCCTCA TAAGCAATAC GTGCAGCTTT AAAATCTTTG   2160
CCTTTATCCA AAGTTACAAA AATAGCAAAA TGATTATTAC TGTTTGTATA GCCACCAATA   2220
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TTTTTGTATA AATTTAACGG TTGGGATAAA TCATACTCCA TAGATTTGTT AATCCCTGTA   2340
TGGATTACAT CTAACATCAA ATTGATGAAA TAAGAATTCT TTTTAAACTC TCTGAATTTT   2400
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ACCCATTCTA GGGTTAGCGA CTGTGCCTCA TGCCATTCTT GAATGAGATG CTTTTGAATA   4200
GAAGAAACCA TCTCGCCATT CTCTCTTGAA GTTAATCTAA CATTCCACTC ATAGTTAAGT   4260
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TCAAACAAAT ATCCTTTTGA ATGAAAACCT TCTTTTTTAG AAACTCGTAC TTCTACATTT   4380
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TTTAACCCTC TAAtCTAATT GATTTTGTTA GTTTwATTAT ATTTAGGATC GCATAAATAA 5160

GCTAGGGTTG CAATATwAGt GGCGkAAATT TCATTTATTA TATTTGTTTT TTGATTTACT 5220

ATACTTTAAT TATTTAATAA CTCTTCA 5247

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

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GTACCCcTTT GGaAATmAtT TArGTACcAT TATTTAGCAC CTTtCCcTGa CTTAGAAGAA 120

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TCCGATCCTT ATACAGGACA ACCACTGGGA GAATTGTACA CTGTGTTTTC AAGTCAAGAA 300

TTGCTAGGCA ACCAAGCAGA CTTATTGAAA AAATCAGGTA TTAATGCGTT TATCTATGAT 360

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CAAGTTCAGG AAGAGTTGAA TGATATTGcT TCCGCAATTA ATTTTATGGT AGACAGTTTA 780

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AATTATTTTG TGCATGGTAT TGACTATCAA CGACAAGACA ATGCTATCAA GGTCCACGCC 1200

TACCGAGAAG GCGAAAAAAT TATTGTGGCT GTTGTGGATA ATgGAAAAGG AATCACCGCC 1260

AATCGGTTAG AGGAAATTCG CGAACGTTTA AATCAAACAG AAATAGACAC GGAACAATCC 1320

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ACCATTGAAG GGAAAGAAGG AGAAGGGACG ACAATTCGTC TTTCGTTTGT AGCATAAGGG 1440

GTGAAAAGAT GTATCGAGTG ATGTTTGTTG ATGATGAATA TATGATTTTA GAAGGCTTAA 1500

AATGGATTAT TCCTTGGCAA GAGTTAGGCT TTGAAATTGT TAAAACAGCG CGTAGTGCGC 1560

AAGAAGCATT GGCTTTTTTa GgAaaCAGAA TCCATTGATG TTTTATTaAC AGATATTACG 1620

ATGCCAGAAA TgAGCGGGAT CgAaTTAaTg AGCAgCA 1657

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GCTAGACTCG GAGTCGCCTC CAACATCATA ACACTCTAAA AGAAACATCT ATAAAGTGAT 60

CGGTTTATTA ATTATTTAAC AAATTCGATA ACTACCATTG GTGCTGCATC GCCGCGTCTT 120

GGTTCTGTCT TCAAGATACG AGTGTAACCA CCTTGGCGTT CCGCGAAACG AGGTCCTAAA 180

TCGTTAAATA GCTTTTGTAA AGCTGATTCA ACAACGATAG ACTCATCTTC TTCACGAACA 240

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AATGCCTGCA CGTTTTAAAC AGTTATATGA ACGAACTGAT AAATCAAGTT CTTCAATCGT 720

CATTTCTAGC ATTTTCTCTT TTTGAGTTTC TTCTTTTTCC ACCATGATTT CAGCGTTTTT 780

CGCTTCGTCA GTAAGGTTTA CAAAGATATC TAAATGCTCA GTCATGATTT TCGCAGCTAA 840

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CGACTTTAAA CATTGCATTC GGCAAAGTTT CGACGACTGT ACCTTCGACT TCAATCATAT 2700

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GTTGCTTGAT TTAATTTCTT ACGCCCAACT TCCCCTTGTT TTGACCATTC TACAAATCTA    4680
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TCGTTTATTT TTAAATACAC GGTTAGGCGC TACTGGACCC ATTGACCCAG GACGACGGTG    13560
ATAACGAGAA CCATGAGACA TAGGTCCGCG GCTTTGGCCG TGACGTTTGA TTGCCCCTTG    13620
GAATCCTTTA CCTTTCGTAG TACCTGTAAC ATCAACAACG TCTCCTGCTT GGAAAACATC    13680
TACTTTGATT TCTTTACCTA CTTCATATTC TCCtAGCTCA ACATTCTTGA ATTCTTTAAT    13740
GAAGCGCTTA GGAGCCGTGT TTGCTTTTGC AACATGACCT yTCGCAGGTT TGTyTGATAA    13800
AACTTCACGT TTGTCTTGGT AACCAACTTG GATAGCTTCG TATCCGTCAG TTTCAACAGT    13860
TTTTaCTTGt AAAACTACGT TTGGCGTAGC TTCaACTACT GTTACTGGAA TTAATTCACC    13920
AGACTCAGTA AAGATTTGTG TCATTCCCAC TTTTTTCCCT AAGATTCCTT TGGTCATGAG    13980
TACACCTCCA TCTTAATTTT ATAGTTTGAT TTCAATATTA ACACCAGACG GTAAGTCAAG    14040
CTTCATTAGA GCGTCAACTG TTTTTGGTGT TGGGTTCACA ATGTCAATTA GACGTTTGTG    14100
AGTACGCATT TCGAATTGTT CGCGAGAATC TTTGTATTTA TGAGTCGCAC GAATAACTGT    14160
GTAAAGTGAG CGTTCTGTTG GTAATGGAAT CGGACCTGAT ACGTCAGCTC CAGTTCTTTT    14220
TGCTGTTTCC ACAATTTTAT CCGCTGATTG ATCTAAAATA CGGTGTTCAT ACGCTTTTAA    14280
ACGGATACGA ATTTTTTGTT TTGCCATCTT GTTCCCTCCT TCGCCTATTT TAAAAGTAGA    14340
CATAGCTCCA CGAAAATTTA TCCGGCATGC TCGTTCATGG CAAAGCGTCC GAGCGTGTCG    14400
CAACCTCTCG CTTCACAGCC GGCAAATCAA ATCGTTGATC TACCAAnGCT TTTTACACTC    14460
CTGTAAACAG CACCTTTTTG ATTATACTAT GAAAGGATAG TGTTAGCAAG GATTTTCTGC    14520
GTTTTTTGAA AGAATTTGnC nnGTTTAGAA AAGCATT                             14557
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(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

CCCCCCGGAG TGTAAAAGTA ACTATGATGC ATACTTTGGA TAAAATTcTT CCAAAATAAA 60

mCCGTkGGCC cATkGAGACA AAGCGCTCcA AGAAACTGGC TTTATTGGCT AGATTTATCG 120

AACCATGAAC GACATAAaCT ACTTTTTAAc TGCTGTTTGT GCGGTAGAAC ATCCAGATAT 180

TGCCAGCGGC CTAATAATTC TTCTTCAGCT TCTAATCCTT GACGATCCGT TTGAATTTGT 240

TTCAAAGATT CTTGAATATT CTTTAATTCC GTCAAATAGC TTTGTAATGT TTCTTCATCA 300

AAGGTTTGTy CCAACTCTTC TAAGGTATAG ACTTTTCTTT TTATCTTTAA CCCTTTTCCT 360

GAAGAGCGTG TCAAAAATAA AAGAAGCTCT TGCAATTGTT GTAGCATCGT TTCATATTTA 420

CGTAGCTGTT CAGTTGACTG TTCTGCTTGT AAAAAAGAAT ATTGACTCTT TAAGGCTTGT 480

TCTTCTTCAG GCGAATGAAA AATCCGTTTT ACTTCGACAA TTTGCAAGCC TTGAATGGCT 540

TGTAGAATTG CTGCTTCTTT TTCGGCAGCG GCAATTATTG TCATTTTTTC CATTTTACTA 600

ACTGCCATAA ACGTCTTTCA CCCTCTCAAT AATTGAATCA ATGACTTGTT CTTTGTTCGC 660

TTCATAACGT TCGTGAAGCG CTTGTTCAGT GCGCTTTGTT TCATCTAAAA GTTGTTCTTT 720

TTCAAGTTGT AACATCTTTT CTTGCGTTGC TAGTGAATCC GTCAGCACTT TTTCAACAGC 780

TTCTTCACTC TCTTGACGTA GTTCAGCTAA ACGTTCTTGC TTCTGTTCTT CATATAAACG 840

ACAATTCATC TTAGCTTGTT GCCGATGCTC TTCCACCGCA TCTTCCGCTG CCTTGATTTG 900

CTCTAGTACT TCTTGTACCA TTGTCTCCAC CTCCTTAGTT TTTACACCTT TAGCATATAA 960

GAAAAAGGAC TAGCGAAATA GAGATACGCT CAGCCCTTTT GTTTTAGGTA TGCAAAAAGG 1020

CGCAAACTCA AAAATTGTTC TTCTCACCCC TTGAAGAACT GAATCCTTGA AGCTTTCGCC 1080

CAACCATTCT TTATTCAATA CTCTACCATC TTAGCAAAGT TTTTCGCAAA ATTCAATACT 1140

TACCCAAATG AATTAAAATA ACAAATTTTC ACTTTTATAA TAGGTAATAA AAAGGCATTA 1200

TTTTTTCGCT TTATAATTAT TGATCTTGAA TTTTTTTCAC ATAGATGTGC TATACTTACG 1260

TAAACAATTA AATTTATTTr GAGGGATCTC TGATGAATAT ACGATATATT TCAATCTCTG 1320

GTAATACACG CTCATTTGTT CAACGTTTAA CAACTTATTC TGAAGAGCAA CATCAGCACA 1380

ACGAAAAAAA TCCTACGATT ACTTTCAAAG AAATTTCGGA AAATTCTCCG TTAGAAGTAG 1440

AAACAGAACC ATTTTTTACC TTTGTGCCTA CCTATTTAGA TGGTGGCGAT GGCATCAACA 1500

ATGGCAATAC CGAAATTTTA ACAGAAGTCA TGCGAGAATA TCTTGCTTTT GAAAATAATT 1560

ATCGTTATTG CTCTGGCGTG GTGGGCAGCG GCAATAAAAA CTTTAACCAC CAATACTGCC 1620

TGACAGCTAA ACAGTATGCG GAACAATTTA ACTTCCCCTT CTTAGCTGAT TATGAATTAA 1680

GAGGTACCCA AGCGGATATT GAACGAATTT ATGCTATTTT AAAGGAAAAC CAATAAGCAA 1740

GTTTCATTAC TAAAAAGCTC ACCTATGATA GACTACATTT TGAGGTGAAG AAAAATGAGA 1800

AATACATGGT TAGCAGAACA ACTTCAGTCA ATCAGTGAAG AACCCAATTC TTTTATTATC 1860

GAGGAAACCA TCaAATATAT TGAACAATTA GAAGATGATA ATGAAAGTCT TCAAGTTGCA 1920

TTGGAAGGGA CTATTTGGGA GTCCTAAAAA TGGGACGACC ATTGGGAAAA TATTTAACnG 1980

A 1981

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1652 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

TCATAGGGCC TATTTTTTGT CAAGGAATCT TCTTATCTTT TTTGTTTAAT CTATCAAATT 60

AAAATATTTT ATTTTTTAAT ATAAAATTAT TTCAATAATT ATTGAACATT TCAAATTGAA 120

TTGATTTTTT CAGACGTAAC TTTAGGcTTG AGCCAGAATT TTTTGCGCTT CATCTATTGT 180

TCGACAATCA CTGAGCCGCT GAATGTTTTC GAGATCTGAA CAGAAAAAAG CTAATTCTTG 240

AAGCATGCTT AGTTGCCGTT GACTTTTTAA AGCAACGACA AATAACAAAG TAGCTATTTT 300

TCGATCTGCT TCCGTACCAA AGTTGACCCC ATCAGGCACT TGAATAAAGC AAATCCCTTC 360

TTTTAAAACT TGTTCATCTT GTCCTTCCGC ATGAGGTAAT GCCACGAAGT TACCGATATA 420

CACACTGACT TTTTGTTGAC GTTGATACAT TGCTTTGACA TAGTCAGGCG TGACCAACTG 480

ATTTTTTAGC AGTAATTCAC CAGAAGCTGC AAGTGCTTCC TCCCAACTAG CATACGATTG 540

ATTCAACATT ATTTGCTCCG CTGTAATTTC AAACATCTCT CAACACCTAG CCTTTCATTT 600

CTTCAATTAA TAATGACGAA AGCAACTGAT AAACAATGGC TtCATTTCCT GAATGAAAAA 660

TTTCTGTATT TAAATCATTC ATAATAATCG CACCACTGAT TTTTCCTAAA ATTTTCCCGA 720

TTGTTTCATC AATCGGTATC GGCGCTAGCA TGAGTAACAT ACGTTGTAAC TGCATCGGCT 780

TTTTATCCAT ACCTTCAATC ATAAGTGGCT GGGCCAGATT AAAAATACAA AAAACAGGCT 840

GTGTCACTGC TGTACTTGAG GTATGGAATA AGGCCATTTC CGTCTGAGGA ATCCCAATAG 900

GCGCTTGCTC GTAACGTTTC ATCAATTGCT GACAGACGAT TGCACTATCG GTGATTAAAT 960

CTGCGGAAAG TTGCGCGAGA GCTTGTTGAA CGGTTTCTGC TAAATCCGCT TGATTATTTA 1020

AATCTGCTAT GAAAAATGTT TCTAATAGTT TACTAATTTC TTCCATGAAA GCGACCACCG 1080

TTTCGTAGCT TTCTTCGCCA CCTATTTTTT TCACAGGCGC TTTCCTAAGC GAGCGTTTTT 1140

CGTGACTAAT CCGCTTAAAC TCTTCTTTCA ATTGGcGGAT TTCATCGTCT AAAAGTAACG 1200

GTGAGATCAA TTTATATTTA CCATTGtATC CtGGTAATAA CGArTGgAAA TCACTAAGTC 1260

ATAGTTTTCC TCAACATTCA CCTTACCTAA ATCCGCAATC CGAAAAAAAT GAATCTGGTT 1320

GATAAAAGGA AAGTAGCGCC GTAATCGCAT TTCCAGCATA CTTGTCGAAG CCAAACCGCT 1380

AGGAGAAAAA CCAGCAATAT CAACTTCCAT AATTTTGGGA CTCCGTTCTA AAGAATTGGC 1440

AAAATGAAGC ACCATGTAGG CAATTTCCTC TTCCGATAGA TTCTTTTGCG GAAAAATTTG 1500

CGGCAACGCT TGGCGTAAAG CgCAGCTATT TCTTGATATT GATTCATGAT CCGTTCTAAA 1560

ATGGGATTCG TTAAATCTnC TTCTTGTAAA ACCGCCCGAG AAAAAACACC TGATAAATGC 1620

GTCAACAACA TTnTATACAA ATnGGTATCT TC 1652

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

GTGATTCGAG nCGGTGCAAA nTGGnCCGAT GGTACCGnTA TTACTGCTGA TGATTTTGTA 60

ACGGCATGGC AAAGAGTGGT AGATCCCaAA ACTGCTTCTC CTAGCGTTGA GCTTTTCTCT 120

GCTATAAAAA ATGCTAAAGA AATTGCTTCA GGAAAACAAT CGAAAGAAAC GTTGGCAGTA 180

AAAAGTAATG GCAATAAAAC GATAGAAATT GAGTTAGAAA AACCCACACC ATATTTTACA 240

GATTTATTAG CATTAACAGC GTACTATCCT GTACAACAAA AAGCGATTAA AGAGTATGGG 300

AAAGACTATG GCACTTCACA AAAATCAATT GTAACAAATG GGGCATTTAA CTTAACAAGT 360

TTAGAGGGAG TGGGAACTTC TGATAAGTGG ACGATTTCTA AAAATAAGGA GTACTGGGAT 420

CAAAAAGAGG TTTCAATGGA GAAAATTAAC TTCCAGGTAG TTAAGGAAAT TAACACAGGG 480

ATTAATCTTT ATAATGATGG CCAGTTAGAC GATACCCCAG TTACAGGGGA ATATGCTAAA 540

CAGTACAAAG ATAACAAAGA ATTTTCCACT ACTTTAATGG CTAATACCAT GTATTTAGAG 600

TTGAATCAAC GGGAAAAAAA TTCTATTCTA CAAAATAAAA ACGTTAGAAA AGCCATTAGT 660

TATGCAATAG ACAGAAGTAA TTATGCTAAA AACATTTTAG ATAATGGTTC TATTTCTGCT 720

GTTGGTGTTG TTGCTAAAGA CGTTGCTTTT GATCCTAGTA CAAAAAAAGA TTTTGCTAAC 780

AAAATGTTGG TGCATTTTGA TACAGAAAAA GCGCAATCCT ATTGGAATAA AGCGAAAAAA 840

GAATTAAATA TTAAAGAACA AGTAACTTTA AACATTTTAA CCAATGAAGA AGAAACAACC 900

AAAAAAGCAG CTGAATACAT TCAAGGACAA TTAGAAGAAA ATCTAAAAGG TTTaAAAATT 960

ACGATAACAC CAGTTCCTGc AAaTGTACAA aTAGAGCGAG TTATGAAaCA TGATTTTACT 1020

ATTAGTcTAA GTGGCTGGCA GGCAGATTAT CCTGACCCTA TGAGTTTTTT AGGtAmCTTT 1080

GrAAGTwACA GkGTGTTGAa TTTTGGAGGT tATAGCmATA CTAAaTATGA TGAATACTTA 1140

AAAGATACCT CAGATAAGCG TTGGAAATCT CTAAAAAAAG CAGAAGAATT ACTTCTTGAG 1200

GATGCAGGAG TAGTTCCATT TTTACAAGTA GGTAATTCTA AATTATTAAA GTCAACGATG 1260

GAGAAATATA GAAACGCATT CGATAGGTGC AAAATATGAT TACmAAAAGA TGAAAAGACT 1320

AGAGTAGTTA CTCTAGTCTT TTGGTTATTT TCTTTTCGTT TAGtTTTaTA wGaTTAtTTT 1380

CyTTAGtAAG tAAAGtAwCy GGtTTACyCa TAGaACCaTT ATTTTTTTTT GAGATCATTA 1440

GATAAATGtT AwCtTTCaTt AATTTTGcTA GCTCGACcAT TTcTAAGTCy CCcTAATAGA 1500

TCGACATATT TAATgAGTTA TTTAAAGAAT CCaTGTTGTT TGTTAAAAAG TAACCAACTA 1560

AATTATAAGT TATTAAATAA TTTAGTTTAT ACTTATATGA CGGGAATTTT TGCAATAAAT 1620

CATTGTAGAT ATTCAGAACT TCTGTACAAC TTTCAAAATC TCGGTTTTGA ACGAGTTTAG 1680

TAGTAATGTT TTCAAGTAAA TAGTATGCTG CTTCACTAGT AACTGTTGGA GCGTTTGAAT 1740

CT 1742

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TAGTATTTCC TGTAACATTA TTTAGAAATA AATTTATTTC TAAATTAGGC AAGCTTTTTT 60

AATACAACAT GATTAACAGT AATAATCACT TTCTTTTTGC GATATATTAT CATTAAAAGG 120

ATATAGATAA TTTAAAAAAT ACCCCCCATT GTCGTTCAAG AATTTTGGAG TTTCCTAGCC 180

ATTAGTTTTC TTATATTCAA TTATTTTTCA TTGTCCTATA TGAAATTTTG CAACTATTCT 240

AAGGCTATGA AAAAAACTAA CCATCCTTAA AGAATTTATA TCGGCATTAG TAATTCTAAT 300

ATTTATTTCT TAGAGCAAAA CCACTAATTG TTAGTTAAAC TCTTTTTTTA TTATACAATG 360

CTTTTACTGA TAAAAGTTCT ATCCTCATTT TAATAAAAGA TTATTTAAGT TTCTATCTAA 420

TGAATTTTAC GGATTTGCTA ACGTATTATT AATTGAGTAA CCTTTTTCAA AATTGTCCCT 480

AATGCTGTGA AACCAATACT AATTTCAACA CAAATAACTA AAACTTTAAT TATCTTCtTT 540

TTCATTAGCT TTTATCTCGr AAACAAAAAT TATAAAACGT TTTTTAACTT ACCCTAACTA 600

TTCTTATTnT CTAAATGTTA CAGAATAGTT ACGGTArGTk AAATATAGTA CTTTCTTTCT 660

ATTTCATTGC CTGTACGCTC TTTTTTATCT ATATATTATC CATCAAATAC ACATTCATAC 720

TATCTATCAT AATTTTTATA TTCTATTCgT TGTACAATAG TTATAAGAAA TATATTCAAA 780

CAAAACGCCT TTTCTTACTT AACTATTTTA ATTTTCTAGA AAGCATAATC TTTTGTACTA 840

TCTATTTACC TTAAATAATG CAATTCTATT TATCATGGAG ACAAAAATTT AAAATATTAC 900

TTTATGCTTT TTGACTAACA CTATTATATT AAATTGAtAA CGTTTACTCT TGTAATTGAT 960

AACAAATCTC TTTAGTAGTA GAATAAACTT TACTATATAC TTGAAAGAAT TTATTATATA 1020

ACAACACATT TTTTTCAATT GGTTGATATA CTTTTTTATA TTTCACAAAC ATTTTAATAC 1080

AACTATCAAT GTTTGCACAC ATACCACAAC CAATAACTGC TAATATTGCA GCTCCCAAGC 1140

TAGGACCCTG TTCCGTTTCC AATGTAGTGA TAGGAAGGCC AAAAATATCA GCCTGTATCT 1200

GAAGCCATTG TTGATTTTTC GTTCCTCCAC CTACAGAAAT AATTTTTTTT ATTTTCAAAT 1260

TTTTTCTTTG TTCCATGATT ACTTTAGATT CTTTTAATGA AAAAGTTATT CCTTCAATAA 1320

CTGATCGTGT AAAATGTTTT AGACTATGTC GACTATCGAT ACCAATAAAA CTCCCCCGAA 1380

TTTGACTATC TTGATACGGA GTTCTTTCTC CTCTTATATA GGGAGTAAAA ATCAAGCCCT 1440

CACTTCCTAC TATTACTTCA TCAATATTCG CTAACAAATC AGAAAATTCT ACATCTTTAG 1500

CAAATGTATC TCTAAACCAT TTTAAAGAAT TACCTGCTGC CAACGTTACT CCCATGGAGT 1560

AwTArGAATT AGGCAGAGCT GAATTAAATA AGTGGAGATT ACCTTGATAT TCGTTCTCAG 1620

CATCGTCTTC CATTGACAAA AAGACGCCAC TAGTACCAAT TGACAGCATT GCTACTTCAG 1680

AATTAACTAt CCCAGCTCCA ATAGsCGCAC mAGCATTATC AaGCTCCACC TGGCAAAAAT 1740

TCCACTTTGG TTCCAAGnCC AAACCTATTA ATCCACGGAC CTTCTCCATA TnACCACTTT 1800

AGCTGAAGnC CCAAATAAGG TTGGCAAAAC CCCCTAGGAA ATTAACTTTC AGGAATGTCT 1860

GG 1862

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

TTATTTGATT TTACCGATGG TnAnTCTTCC CACATTTACT TGGCGGTGGG AATCAAATtG 60

TTTTAGCTTT AGGCAATCAA CCGACTACGA TTTGGGCTTT AGTCGGCTTA CTGGTTTTAC 120

GTTTTGTTTT TTCAATGGTT TCTTACGGTT CGAATCTCCC TGGTGGTATT TTCTTGCCTA 180

TTCTAACTTT AGGTGCCATT ATCGGAACAT TGTATGGCAG TCTACTTGTC CAATACGTAG 240

GGATGGATCC AATTTTTGTG AAAAACTTTT TAATTTTTGC CATGGCTGGT TATTTTACTG 300

CGATTGGTAA AGCACCGTTA ACAGCGATTA TTTTAGTAAC AGAAATGGTC GGCAATTTTT 360

CTCATTTAAT GTCTTTAGGG GtTGTCGCTT TAGTTAGTTA TATTACCATC GATAGTCTTG 420

GCGGCAAGCC AATTTnATGA AAGCTTATTA GAACGTTTGG TTCCTTCTAA AGTAAGTAAT 480

ATTCGTGGCC ACAAAACGAT TaTCGAATTA CCTATCACTG CAGAAAGTTC CTTAGATGAT 540

ACGATGGTAC GTGaTTTTGT CTGGCCTAAA CAAATGTTGC ycACTTCCAT TCGGCGTGGC 600

GAATCGGAAA TTTTAACACA TGGTGATACT GTTATGCATG TTGGCGATGT GCTCATTATT 660

TTGACCGATG AAAAACTCGC TTACCAAGTC aAAAAAGAGA TTTATCAAAA AACTTTACCG 720

AATGATTTAG TGAATTAAAG AAAGCtGCTG AACCTGAGTT CAGCAGCTTT CTTTTTTTCT 780

TATGACTGTT TTTTAATTTT TTTGAATGTT TTTGACCGTT TTAGATTGAT TAGCGTTTTC 840

ATTTGTGCTa TTATATCCaT GAAATGAGGG ATGAAAATGC TTACGGAAGA ACGACATCAA 900

AAAATTTTAC AATTGTTAGA TCAAAAATCA GTCGTCAAAT CGCAAGAACT TGCTAGCTTG 960

TTCAATGCTT CAGAATCCAC AATCCGCCGC GATTTACAAG AATTAGAAGA CGCCAATTTG 1020

TTAGAACGCA TTCACGGCGG CGCTAAGCGT AtTCTTAATT TAGGCTTTGA ACAAAACATG 1080

ACGGAAAAAT CAATCAAAAA CACGCACGAA AAGCAAAAGA TTGCTTCTTT AGCCGTTAGT 1140

TGTGTACAAG ATGGCGATAT GATCTATTTA GATGCTGGTT CAACCACGTT AGAAATGATC 1200

CCTTTTTTAG TTGGGAAACA AATCCATGTA GTGACGAATT CCGTGCATCA CGCTGCAAAA 1260

CTTAGCGATA TGGAAATTCC CACTATTATG CTTGGTGGTA CTTTGAAGCT CTCCACTAAA 1320

GCAATCATTG GTGCCACTAG TATGGAACAG CTACAACATT TTCGTTTTAA CAAAGCTTTT 1380

TTAGGAACTA ACGGCGCACA TTTAGAGTTT GGTTTAACGA CGCCTGATCC CGAAGAAGCA 1440

GCGCTAAAAG CCTTGGCTAT TCATCAAGCA GAAACAGCCT ATGTTTTACT GGATCATACA 1500

AAATTTAATG AAGTAACGTT TACCAAAGTG GAAGAATTAG AGTCAGTTAC TTTACTAACT 1560

GACTACTGCC CTGCTGAATC GCTTCAAGGA TTCCAGCAAA AAACTATTTT AATGGAGGCA 1620

AACAAATGAT TTACACAGTG ACTTTAAACC CTTCTATCGA CTTTATCGTT CATGTCGATC 1680

ATCTACAAAT TGGTGATTTA AATCGGATGA CGAATGATTT TAAATTACCT GGCGGCAAAG 1740

GAATCAACGT TTCACGTATT TTAAAACGTA TGGAGACAGA ATCCACTGCC TTAGGTTTTT 1800

TAGGTGGTTT TACAGGCTCA TTCATTGCTG ATTGGTTGAA AAAAGAAGAA ATCCAAACGA 1860

ATTTCACTCC CGTGTCTGCT GATACACGAA TCAACATTAA ATTGAAATCA GATACTGAAA 1920

CAGAAATTAA CGGCTTAGGA CCTGCTCTAA CAAACGAAGA AATTCAAGAA CTAAAACAAG 1980

CAGTTAGTCG TGTTCAGGCT GGTGATATTG TTGTTCTTTC AGGAAGTACA CCTGCTTCTC 2040

TACGCAAAGG ATTTTACGAA GAATTAATCC AAATTGTGAA GGAAAAAGGC GCAGAATTTG 2100

TTATTGATAC GACAGGTGAA GATTTAATGA ACGCTTTGTC ACAAAAGCCT TTATTGGTCA 2160

AGCCAAATAA TCATGAGTTG GCAGAATTAT ATCATACAAC CTTTACAAGT ATTGAAGATA 2220

TTTTACCTTA TGGACATCGG TTACTAGAAG AAGGAGCACA ACACGTAATT ATCTCAATGG 2280

CTGGTGATGG TGCATTACTT TTCACAACAG AAGGTGTTTA TCGTTCCAAC GTTTTAAAAC 2340

GTCCACTGAA AAATTCTGTC GGCGCTGGCG ACTCAATGAT TGCTGGTTTT ATTGGCAACT 2400

TTTCAAAAAC ACAAGATCCT TTAGAGGCTT TCAAATGGGG TGTCGCTTGC GGTAGCGCGA 2460

CCGCATTTTC TGATGATTTA GCCTCAGAAG ATTTTATCCA AGAACTTATT CACGAAGTAA 2520

CAATTGAAAA AATTTCAGAA TAAATCCACT AAGGGAGGAA AATAGAGTGA ACATTAATGA 2580

TTTATTAATA AAAGATGTCA TGATTATGGA TTTACAAGCT ACTGATAAAA AAGGCGCGAT 2640

TGATGAAATG GTCCAAAAAT TATACGATGG TGGCCGCATC TCTGACATTG ACACTTACAA 2700

AGAAGGAATT TTAAAACGCG AAGCACAAAC ATCGACTGGT TTAGGCGACG GCATCGCTAT 2760

GCCTCACGCA AAAAATAGTG CCGTAAAAGA ACCGACAGTT CTTTTTGCTA AAAGTAAAAA 2820

AGGTGTTGAT TATGAAGCAC TAGATGGACA ACCTACTTAT CTATTCTTCA TGATTGCTGC 2880

TCCAGAAGGC GCCAATGATA CACATCTCCA AGCGCTTGCG GCCCTTTCTC GATTACTTAT 2940

CGATCCAGAA TTTGTTGGCA AATTGAAAGA AGCGGAAACT CCAGAAGCTG TACAAGCACT 3000

TTTCCAAGCA GCGGAAGATC AAAAAGAAGC GGAAGAAAAA GCAGAACAAG AACAAACAAC 3060

GCCAGCACCA GAAAGCAATC GTAAATATAT TATTGCTGTG ACTGCTTGTC CTACAGGAAT 3120

TGCTCATACT TACATGGCCG AAGATGCGCT GAAGAAAAAA GCAAAAGAAA TGGGCGTAGA 3180

CATTAAAGTA GAAACAAACG GTTCAGAAGG AATTAAAAAT CGTTTAACTG CTGAAGATAT 3240

TGCTCGTGCT GATGGCGTGA TTGTCGCAGC CGATAAAAAA GTAGAAATGA ATCGATTTGA 3300

TGGTAAAAAA TTAGTCAATC GTCCCGTCAG TGATGGAATT CGTAAAACCG AAGAACTAAT 3360

TAACTTAGCC ATTAGTGGTG AAGCTCCTAC TTTCCATGGC AGTGACTCGG CTGCAAGCGA 3420

CCAAGAGGAT TCAGCGGAAG GTTCAATCGG TTCTCGTATC TATAAAGATT TAATGAATGG 3480

TGTTTCTCAT ATGTTACCTT TCGTTATTGG TGGCGGAATT GCCATTGCTC TTTCCTTTAT 3540

GATTGATCAA TTTATCGGGG TTCCTCAAGA TCAATTAGCC AATTTAGGGA ATTACAATGA 3600

CGTAGCTAGC TGGTTTAACC AAATTGGTGG CGCAGCATTT GGCTTTATGT TACCTGTCTT 3660

AGCTGGTTTT ATTGCTTCTA GTATCGGGGA TCGTCCAGGC TTAGTTGCTG GTTTCGCGGC 3720

TGGTGCATTA GCAAACGCCG GAGGAGCTGG GTTCCTTGGG GCCCTAATCG GTGGTTTCTT 3780

AGCTGGTTAT GTAGTGGTTC TTTTACGTAA AGTTTTCAAA GGCTTGCCAA AATCATTAGA 3840

TGGAATTAAA ACCATTTTAT TCTATCCAGT TTTTGGTTTG ATTATTACAG GCTTATTAAT 3900

GTTAGTCATT AACATCCCAA TGAAAGCAAT TAATGATGCG TTAAATCATT TCCTACTTGG 3960

CTTAGATGGC ACAAATGCTG CTTTACTTGG TGCCTTATTA GCTGGTATGA TGGCCATCGA 4020

CTTAGGTGGA CCAGTTAACA AAGCTGCTTA TGTTTTCGGT AcAGcTACGC TAGCAAGTAC 4080

TGTTGCAGAA GGTGGCAGCG TGGTCATGGC TTCTGTAATG GCTGGCGGAA TGGTTCCTCC 4140

ATTAGCAATT TTCGTAGCAA CTCGTTTATT TAAAAATAAA TTTACAAAAG ATCAACAAGA 4200

TGCCGGCTTA ACCAATATTG TAATGGGACT TTCTTTTGTC ACTGAAGGGG CAATTCCTTT 4260

TGCAGCAGCT GaCCCATTaC GTGTGATTCC AAGTTTCGTG GTAGGTTCTG CCTTTACTGG 4320

TGCGTTGGTT GGTGCGTTTG GTATCAAATT ATTGGCACCA CATGGAGGAA TCTTCGTCGT 4380

CTTCCTATTA AGTAATCCAT TACTATATCT ATTGTTCATC TTAATTGGGG CGATTATTTC 4440

AGGAATTGTC TACGGACTTT TGAAAAAACC TGTCGAAGTA CCTGCTTAAA AAAAGCAAAA 4500

AAGCGATTCA ACCATGGTTG AATCGCTTTT TTATTATTTT CTCTTTATCG CATAATTTTC 4560

TAAATACTCA GGATTTCCTT TGCTTCTGAT ATACGTGTAC ACGCCCATCA CAAAGGCCCC 4620

AAGGGTATTG GTAAATAAAT CCCCCATCGT ATCCATTAAA GCAGCACGCC CAATAAATGG 4680

TTGGCCGTTG GACATATTAT AGCGTTGTAA GTTCATGTTC CCTAATGAAT CGCAGATAAA 4740

TTCCCAGAAT TCCCAGAAGA CGCCACAAAG CCCTGCAAAT GCAAACCCAA ATAATAAAAA 4800

TAACCACGGG GAAACATCGG CGTAcTTCGT TTTCTTCAAT AGGAAACCAG CAATACCATA 4860

ACCCACAGCA GTTAACAGCA TCGGACTAAC AAAGTGTAAA ATTTTATCCC AGAACGAAAT 4920

GATTGAGATC ATATGCAACG AGGTTCCTAG GAATACTGAA ATAAATAAGA AAAACCAGTA 4980

AAAATAAACG ATAGTCGGTG GCATAATAAT TTTTAAAAAT TTATTGACAA GATCCGGTAA 5040

AAAGATTAGA CCAATTCCAA GTAAACATTC GATAACAAAC GTCACACCTT GTTTTGTTGA 5100

ATACTTAGCC GTAAAAAATT CCCAGAGATT GTACGTCAAG CATAAGATGC CAAACACCAC 5160

TAATCCATAT TTAATTTTCG AATAATTTTT ATCCaTTTTG ACACACCTTT CAAAAGTTAT 5220

TTTATATGAA AAAAACTGTA GATGAAAGAC ACCTTCCATC TACAGTTTTA GAAAACTCTA 5280

TCGAATGAAG AGCTTATTAA AAATGTTTAT TTTTCAACAG CTGTTTCAGT AATTGTTTCA 5340

ACAGCACGTT TCATACGAAT ATCGTGTTCT AACATGTCGT TGTTTAATAC TTTACGTACT 5400

TGCGCTTCAG GCATGTTGTA TTGTTCTGCT AAATCTTTCA CTTCAGCATC GATGTCTTCT 5460

TGTGTTACTT CGATGTTTTC AGCTTTGGCA ACTGCTTCAA TCACTAAGTT TGTTTTTGTG 5520

CGTGTTTCTG ctTCGCCTTC AAATTGTTTG TGTAAATCTT CTTCTGTAGA ACCAGTTAAT 5580

TGGTAGTACA TTTCAGGAGA AATTCCTTGG CGTTGCATGT TGTTTAAGAA TTCATCCATT 5640

GAACGGTGAA CTTCGTCGTG AACCATTACG TGTGGTAATT CAACGATTTC AGCATTTTCA 5700

ACAGCTAAAC GAATTGCTTC TTCGTCTTTT GCTTCTTCAG CTGCTGCTTC TTTTGCTTCT 5760

GTCAATTCTT TACGGAATTT TTCTTTTAAT TCGTCTAATG ATTCTACTGA ATCGTCAACG 5820

TCTTTTGCAA ATTCATCATC CAATTCTGGT AATTCTTTTG CTTTTACTTC ATGAACAGTT 5880

ACTTTGAAGA CTGCTTCTTT ACCAGCTAAA TCTTCTGCTT GGTAATCTTC AGGGAAAGTA 5940

ACGTTTACTT CTACTTCTTC GCCAGCTTTT TTGCCAACTA ATTGGTCTTC AAAGCCTGGA 6000

ATAAATGAAT TAGAACCTAG TTCTAATGAG TAATTTTCGC CTTTGCCGCC TTCAAATGCT 6060

TCGTCGCCTA AGAAGCCTTC AAAGTCGATA ACTACAGTAT CGCCATTTTC AGCAGCGGCA 6120

TCTTCTTTGA TTACTAATTC AGCTTGAGAT TCTTGTTCGC GTTTCAAACG TGCTTCCACG 6180

TCTTCATCTG TTACTTCACG GTCTTGTTTA GACACTGTTA AGTTTTTGTA TTCGCCTAAT 6240

TTTACTTCAG GTTTTACAGT TACTTCAGCA GTGATAACCC AGTCTTCCCC TTTATTCATG 6300

CTTTCAACAT CAATTTTTGG TTGTGCTACT GGTTCAATTC CTGCtTCTAA TACAGCCGCT 6360

TCATATGCTT CTGGTAAAAC AGCGTTTAAC GCATCTTCGT ATAACGCTTC TTCTCCATAC 6420

ATACGGTTAA AAACAGTACG TGATACTTTT CCTTTACGGA AACCAGGTAC GTTTAAGTTT 6480

TkTTTCACTT TATTGAACGC TtGCGTTAAT CCTTTTTCGA TTACTGCTtG TTCGATTGAA 6540

AAAGTTAATA CACCATCATT AGTGCCTTTT TTTTCCCATT TCGCAGACAT TTGTTTCCCT 6600

CCGAATAACA TTTAATTTaT ACaTCAAACT TwATwakGCA TACCTTAAAA TAGACACTAT 6660

CCCTGGnAAA TGTA 6674

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

TAGCATTnAT GATTGTCTTT AACTACATTC CAATTTATGG AATTATCATT GCTTTTAAAA 60

ATTATACGAT TGTTGACACG GTTTCTTCTG CACCATGGGT TGGACTTGAA AATTTTCGAA 120

TCATTATGGA AGATAGTTTT TTTTGGGAAG CAGTTCGTAA TACCTTAGCG ATTAGTTTAA 180

TGAAACTTTT TTTAGGATTC GCTATTCCGA TTATCTTAGC GGTAATGATT TTTGAAATGA 240

GAGATGGACA TTTAAAAAAA GTGATTCAGA CAATTTCTTA TATTCCGCAC TTTTTTTCTT 300

GGATCGTTTT AGGCGGGATG TTGATTTCGT GGCTTTCAAC AAATGGCTTT ATCAACCAAG 360

TCATGATGTC GTTAGGCTTA ATGAATCAGG GCGTCAATCA TTTGTTAGAT CCTGATAAGT 420

ATTGGTGGAT TGCTGTTCTT TCTGATTTGT GGAAAGAAGT AGGTTGGGGC ACGATTCTCT 480

ATCTTGCTGG TATGTCTCGC ATTGATCCAA CGTTTTATGA AGCCGCGAGA ATTGaTGGTG 540

CTTCAAAATT AACACAAATC CGAACGATTA CTTTGCCCTT ATTAGCGCCG ATTATTTCGT 600

TGAACTTAAT TCTAAATGTT AGCGGTTTAT TGGGATCGAA CTTAGATCAA ACGTTGGTTT 660

TAATGAATGC TCAAAACCAA AACAAATCAG AAGTAATTAA TTCATTTGTT TATCGTATGG 720

GGynAACGCA AGGGGACTTT TCTTATGCGA CGGCAGTTGG TTTAGGGATT TCTGTTATTT 780

CAATTGTTTT ATTAGTCATT ACAGATCGCA TTACTAGAAA AATGAACAAT GGTCGGTCGG 840

TTATTTTATA AAGGAGGCAA CAGCTGTGAT TAAAAGAAAA TCAAAAGAAA ACAAATGGTT 900

TTACTTTTTC AATACGTTAA TTCTTGTGTT GTTTTCTTTA TTAATTATCG TGCCAATTTG 960

GAATATTTTA GTTTCCTCAG TTTCGTCAAG TTCGGGTTTA GCCGGTAAAG GCTTGGTTTT 1020

ATGGCCGAAA GGATTTACGC TAGAAAATTA TCGGAAAGTT TTTTCGGATA GTAGCATTCC 1080

GCGAGCGTTT TTGATTTCTG TTTTAAAAAC AGTTATTGGT GCGTCGACGC ATACACTGTT 1140

CTGTGCGATT GTCGCCTATG GACTTAGTAA ATCTAGACTA GTCGGGCGTA ACATTTATAC 1200

AACGATGGGT GTCATTACAA TGTACTTTGG TGGGGGCATG ATTCCCACGT ATCTTTTGAT 1260

TAAGTCATTA GGACTCTTAG ATACCTTCTG GGTATATATC ATTCCAGCTT TATTTAGCTA 1320

TTATGATGTA GTTATCTTAA TGAACTTTTT CCGAGAAATT CCACCATCTT TAGAAGAATC 1380

CGCCAAAATA GACGGCGCCA GTGAGTTTCA AATTTTTTAT AAAATCTTTT TACCTTTAAC 1440

AAAACCGGCA TTAGCCACCA TCATTTTATT TAATGGGGTT GGTCAATGGA ATGACTTTAT 1500

GACCACAAAA TTATATATTA CCAAAGAaTA TCTGTATCCA TTGCAGATGA AAATTtATGA 1560

AATTATTGTt CaATCAmACT TGAGTaCCAT GACAGAGAgC GGCAGTACAG ATATGGTGGT 1620

GCAGGCAACG 1630

(2) INFORMATION FOR SEQ ID NO: 374:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

TCATCCATAA TTCCTTTTTC CGCTGGTTCT TTTCCTAATG CAAAACCAGG TAACCCATCC 60

GCGACCACGT TAACAAACAA CAGTTGAACT GCAGTAAATG GCGCACCCCA ACCAAGTAAC 120

ATGGCAATTA AAACAATAAA AATCTCAGAA ATATTACAGC TTAATAAGAA GTTAATGGCT 180

TTACGAATAT TTCGGTACAC GGCACGTCCT TGCGCCACTG CATCAACAAT AGTTGCAAAG 240

TTATCGTCCG TCAAAATCAT ATCTGAAGCA CCTTGGGCCA CATCTGTTCC AGTAATCCCC 300

ATTGCGCAAC CGACATCACT AGCTTTCAAG GCTGGCGCAT CATtcACGCC ATCTCCGGTC 360

ATTGCTACAA CAGCGCcAGA ACGTTGCCAT GATTGAACAA TTCGAATTTT ATCTTCAGGG 420

GTTACACGTG CATAAACGGA TAAATCTTTA ACACGTTTAT CTAATTCTTC ATCACTCATT 480

TTTTTCAGTT CTGAACCAGA TAAGGCTTCA CTTTTATCTT TTAAAATTCC TAATTCTTTA 540

GCAATTGCAC TGGCTGTTAC CACGTGATCA CCAGTAATCA TGACTGTTTT AATTCCAGCT 600

TTTTTCGCAC GAGCAATGGC GCCCTTACTT TCTGGACGTG GTGGATCAAT CATGCCAATT 660

AAGCCTAACA AGCGAAGATT TTTTTCTAAA GCCTCTGATG TAATTTCCTT GGGtGGTTCA 720

TCATATACGG CATAACCGAC AGCAATAACT CGTAACGCTC GTTTTCCGAA ACGATCATTA 780

ACAATAGCCG CTTGATCGAC ATCTCCGAAA CCAAAACGAG GTAGTAACAC ATCAAAGGCT 840

CCTTTAGTAA TTGrGrTGTA CTTTTTCCCC CATTGATGGA CCGTA 885

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7664 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GCGTGATTAT CTATACGTTG GTTCAATGTT ATTCGGTTTG TTTTTCGGTG CTGGAAATTT 60

AATTTTCCCT GTACATATGG GACAAGAAGC GGGGGCTTCC GTCTTTTTAG CAAACTTGGG 120

CTTCTTAGCC ACTGGAATTG GCTTACCTTT TCTTGGTGTC ATTGCTATGG GTGTTTCTAA 180

AAGTTCAGGT GTTTTTGACT TAGCTTCTCG GATTAATCGT CGTTATGCTC TTATTTTTAC 240

CTTACTATTA TATTTAACGA TTGGTCCTTT CTTTGCTTTA CCAAGGTTAG CAACTACTTC 300

TTTTGAGATT GGTCTTGCAC CATTTGTTCC GAAAGACTTG CAATGGCTGG TTCTTGCTGG 360

TTTTTCCGCA TTATTTTTCT TAGCTGTTTG GCTCTTCTCT AGAAAGCCAA GTAAAATCTT 420

AGATTATGTG GGTAAATTTT TAAATCCGTT ATTTTTAGCA TTGCTAGGAA TTTTGATTGT 480

TTTAGCCTTT GTAAAACCAT TAGGTCATGT GGCCAGTGCC GCTGTTGGTG AAAATTATAT 540

TTCAAGTCCT TTCTTTAAAG GATTTACAGA AGGTTATAAT ACGCTGGATG CTTTAGCTTC 600

ATTAGCTTTT GGGATTGTTG TCGTTTCCAC TTTACGAAAT ATGGGCGTCG AAAAACCAGG 660

AGATATCGCT AAAGGAATGA TTAAATCAGG TGCTTTCAGT GTTGTATTGA TGGGGATTAT 720

CTATACCTTA CTTGCTTATA TGGGAACAAT GAGTATCGGG GCTTTTCCAA TCAGTGAAAA 780

CGGCGGGATT GCCTTAGCCC AAATTGCCAA TTACTATTTA GGCCTACCAG GGAGTATTTT 840

ACTGGCTTTT ATCGTAGTTC TTGCTTGTTT AAAAACCGGT ATCGGCTTAA GCACAGCCTT 900

TTCTGAGACT TTTGAAGAAA TGTTTCCGAA AGTTTCCTAT CAAAAATTCT TGGCAATTGT 960

TGTTATTTTA CCAGCTATTT TTGCAAaTGT CGGCTTAACC AACATCATTC AATTTGCCGT 1020

TCCAGTCTTG ATGTTCCTTT ATCCATTGGC GATTACTTTA ATGCTTTTGG TAATCATCAG 1080

TCCTATTTTC AAACATCGAC GGGAAGTCTA TCAAGCAACG ACCTATATCA CATTGATTGC 1140

TGCTGTTTTA GATGCATTAA ATAGCGCGCC TGCCTTTATC AAAGATACGG CGTTTGTAAC 1200

AACGCTTTTA GAAAAAGCCG GCCAATACTT ACCATTGTTC ACTATTGGTA TGGGCTGGGT 1260

CGTTCCAGCA ACGGTTGCTT TTCTAATTAG TTGGGTTTGG GTCATGATTT CTAAAAAAGA 1320

TCCTATTCTT GATTAATTCT TACCAAAACG ACACTAGAAA AAATGCGGAA GCGCATCTTT 1380

TCTAGTGTCG TTTTTATGTA TATTCGTTGT ACCAAACTCT TGACTATGGT AAATTGAAGT 1440

TACCAACAAG TACTGGAGGA AATTGCCCAT GTTAGTTACA ACAACCGAGA GAATTAGCGG 1500

TCAAGAATAT GAAATTATTG GAGAAGTTTT CGGGTTAACC ACACGTTCTA AAAATATGTT 1560

TAAAGATTTA GGTGCTGGAC TAAAAAGCGT AGTTGGCGGT GAAATCAAAG GTTACACTGA 1620

TATGCAACGA GAAGCACGCG ACCAAGCAAT CGAACGTTTA AAAGCAGAAG CCTCTAAATT 1680

AGGTGCAGAT GCCGTTGTGA TGATGCGTTT TGATTCTGGC ACAATTGGCA CAGACATGCA 1740

ATCTGTCGTG GCTTACGGAA CAGCTGTTAA ATACATCTAA ATTTTGCAAC TAAAAAGACG 1800

CAGACCTTTT CTTGTAAGGT CTACGTCTTT TTAGTTTTCA TATTTCACTT CTGCTAAATA 1860

CAATCCTTCT GGATGAGCAG TCGGACCTGC TAAATTTCGA TCTTTGGCTG CGATAATTGC 1920

TGGAATCGCG GTTGGTTCCA GCCGCCCATT GCCGATTTTC AATAGCGTAC CAACTAAAAT 1980

CCGAATCATT TTGTACAAGA AACCATCGCC CCGAAAAGTG AATGTTAATT CATCCCCCGT 2040

TTCATTGACA TGAACACTGG CTTCATGAAT GGTTCGGACT TTATCTTCTA CCGAACTTCC 2100

TGAGGCACAG AAAGAGGTAA AATCATGGGT GCCTAATAAA TCAGGCAAAG CTTGTTGGAT 2160

TTTTTCGAGA TCAATGGGAT ACGGAAAATA ACTAGCATAA AAACGTCGAA ATGGACTTCG 2220

CGGTTTGCCA ATATCCACTT TAAATTGATA GGTTTTTTCG ATCACATGAT AACGTGCATG 2280

AAAGTCTTCT GAAACACGTT CCCACGTGCG CACAGCAATG TCTTCGGGTG TTTGTGTATC 2340

TAACGCAAAG CGCATTTTTT CCAACGGACG TTCCTGCGGA TAATCAAAGT GAATCACTTG 2400

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GCCCaTTGCA TGAACACCTG CATCTGTTCG TCCTGAACCA AAAACCGTCA CGGAGCGTCC      2460
ATTATTCATG CGTGCTAACG TTTTTTCTAT TTCTTCTTGA ACGGTACGCT CATTAGGTTG      2520
CTTTTGAAAG CCATGAAAAT GAGTGCCATC ATAGGCAATG ATTGCTTTAT AGCGGGGCAT      2580
AATTTTTCTT CACCTTTTCT AAGTTCTTAA TACAAATAAG CCAATGGTTA ACAAGACAAA      2640
GCCAAACATT ACTATTGTAT CTCGTAGGTG CCAATGAAGA ATGCGGTATT TTGTCCGTCC      2700
TTCACCACCT TGATAACCTC TTGCTTCCAT GGCAGTCGCT AAGTCTTCCG CACGATTAAA      2760
ACTACTTACG AAAAGCGGAA TCAAAAGTGG AACAATAGCT TTCATTTTTT GAAGTAAGTT      2820
TCCTTCACCA AAATCAACAC CACGGGCACG TTGAGCATTC ATAATCTTTT CCGTTTCATC      2880
CATTAATGTT GGGACAAAAC GTAAGGCAAT TGATAACATC AATGAAACTT CATGAACTGG      2940
AAATTTCACT ACATGAAGTG GGCGTAGCAA ATATTCAATC GCATCTGATA ACTCTAATGG      3000
TGCCGTCGTT AAAGTTAATA ACGTTGACAT GAAAATAATT AAAACAAAAC GACAGAAAAT      3060
AAATAGCCCA TTCGTCACAC CAAACTGGGT TATGGAAATA ATTCCCCACT GAAAGTACAC      3120
TTCCCCCCCT TGTGTAAACA AGGTTTGAAG AGCCaCAGTA AACAGAATTA GCCaTAATAA      3180
TGGCCGAACA CCGCGGATAA AGAAGCGGGC GCTGATTTTT GATAATGAAA TAGCAAAAGC      3240
AGTAAAGGCT GCTATTAAAA CATAACTCTG CCAATTATTT GCTAAAAAGA TAATTCCAAT      3300
AAAATAAAAA CTAGCTAATA ATTTTGCACG CGGATCTAAA CGATGGATAA AAGAATCGCC      3360
TGGAATATAA CGCCCAAAAA TCAATTTATT CATCATTTTG CCTCACCTGC TTCCTGCATT      3420
TTTTTCAGAA GCTGATCGGC TAATTGATCG GCCGTTAATG GTAATTGCTC AAAAGAAAAG      3480
CCTTTTGCCA CTAATTTTTC AGCAAATTCG GCTGCAGTTG GCACGCCTAA TTGTTTTTCT      3540
TTCAGCCATT GTGTCTCTTG AAACACTTCT TGTGGTGCTC CCGCTCGGAC GATTTGTCCT      3600
TTTTCTAAAA CAATCACGTG ATCTGCGTAA TTAGCCACGT CATCCATCAA ATGTGTCACT      3660
AAAACGATGG TCATATTATG TTCCTTATGC AGACGACTAA ACATCTCCAT CATTTCTTTA      3720
CGACCCTTAG GATCCAAACC AGCAGTCGGT TCGTCTAATA CTAAGACTTC TGGTTCCATC      3780
GCTAGCACAC CAGCAATTGC GACACGGCGC ATTTGACCAC CTGATAACTC AAACGGAGAA      3840
TGTTGTAAGT ATTTTTCATC TAAGCCGACT AAATCAAGCA TTTTCTTAGC TAATTTTTTC      3900
GCTTCTTCGT CTGAAACACC AAAGTTTTTC GGTCCGAAAG CGATGTCTCG CTCCACTGTT      3960
TCTTCAAACA ATTGTGCTTC TGGAAATTGA AAAACGATCC CAACTTTTTT ACGAATTGGT      4020
TTTAAATTCT TATTATCAGT TTCTGGCGTA ATTACACGCT CTCCAATTGT CACTTGGCCT      4080
TTAGTTGGTT TCACCAAAGC ATTTAAATGT TGTAATAGCG TTGATTTGCC ACTGCCAGTA      4140
TGTCCGACAA TCGCTGTATA AGAGCCGTCT TGAATCGTTA AATTAATATC GAATAATGCC      4200
CGTTGCTCAA AAGGAGTATT GGGTTGGTAA GTAAAATCTA CTTGTTTAAA ACGGATGTCC      4260
ATAACCAATC CACCATCCCT TCTTCTGTTA AATAATTCGT TGGCACAACA ACGCCACGCT      4320
CTTTCAAAGC TACTTTTAAT TTTTCAGGAA ACGGTAAATC CAAGCCCATT TCAACAAGCG      4380
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CTTCTCCTGC AGAAAAAATC TTTTCTGGTG TTCCTTCGTT TGTCAATTGT CCTTGGCGCA 4440

TCACTAAAAT ACGATTCGCA TTAGCCGCTT CATCAATATC GTGGGTAATA GAAATAACTG 4500

TTAAATTACT TTCTTCTTTA ATCTTTTGAA TGGTAGCAAT TACTTCTGCA CGACCTTCTG 4560

GATCTAACAT ACTTGTCGCT TCGTCTAAAA TAATAATATC TGGTCGCAAA GCAACCACAC 4620

CAGCGATAGC TACTCGTTGT TTTTGGCCGC CAGATAGCCG AGCAGGTTCT CGCTTGGCAA 4680

AATCTAACAT ACGAACCCGT TCTAATGCAT CGTGAACACG TTCGACCATT TCATCACGCG 4740

GAATACCTTG ATTTTCTAAA CCAAAAGCCA CATCGTCTTC GACTGTTGAA CCGACAAATT 4800

GGTTATCTGG ATTCTGAAAA ACCATTCCTA CCATACGCCG GATATCCCAG ACGTTTGCTT 4860

CATTTAATTC TTTGCCGCCA ACTTTGATAG TCCCAGCAGC TGGCAGTAAC AGCCCATTGA 4920

TCGTTTTGGC TAACGTTGAT TTACCAGAAC CATTATGGCC AATAATAGCG ACCCATTCGC 4980

CTTGTTGAAT GGAAAAAGAC ACATCTTTTA AAGCGGGAGA AGCATCTTCT GGTTGATAAT 5040

TAAATTGGAT ATTATTTAGT TCAATGATTG GTTGCATCGC ATACTCCCTC AATCTATTTA 5100

TTCTTTCTAA CACTACCAAA AAAGTAGCGT TTTTTCAATC ATCTGTTCTG ATTCTTCACA 5160

CTATTTTTTA TTATACCAAA AGAACGGTCA TTATGGGAGC TCTTATCTGT CTTGACAGGT 5220

CTATTTTTCA TAAAAATAAC TTCTTGTTCT CATAAAACAA GAAGTTACTG ATTTTCTTTT 5280

AAAAATGTGT CTTCAAATAT TCAAACGCAT ATTGGGCATA TAACTCAGCA CCCATTGCCA 5340

TCGCATCTTC ATCAATATTA AAACGACCAT GGTGATGTGC CCACTCCGTA TCTTTCTCTG 5400

GATTACCACT TCCCACTAAG GCAAAACAAC CAGAAGCATG TTCAGTATAA TAACTGAAGT 5460

CTTCGCCACC AGTTGTCGGC TCTTCTTGTC TTAAGGCCGC TTCACCAAAA TTTTCCTTAA 5520

TTAGTGTTTG GGCAAACAAG GCATCCTGCT CATCATTAAT CACTGGCAAC GTCCCATATT 5580

GATAATCTAA CGAAGCCGTC CCACCGTAAA TAGCGGCTGT TTGTTCCGCA TAGCGTTGTA 5640

GCGCCTGTTC TACTCGATTA CGCGTTGCTA CACTAAAGCA ACGAACCGTT CCTTCCAAAC 5700

GTGCATTCTC AGCAATCACA TTAAAACGGG TCCCCACATC CATCCGTCCA ATCGTGACAA 5760

CTACTGGATC TAAAGGATCT GTCTCCCGAG AAACAATCGT TTGCAGATTC ATCACGAAAG 5820

AAGAAGCTAT GACTGCCGCA TCAATACAAG CGTTTGGCAT GGCACCATGG CCACCACGGC 5880

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CGGTTCCTAC AGGCATTTGT GACCAGATAT GTAAGCCAAA TACATCATCA ACACCGGTCA 6000

TTGCGCCTTG CGCAACCATT GCTTTAGCAC CTTGCGCATT TTCTTCAGAT GGTTGAAAAA 6060

TTAACCTTAC TGTTCCCTGA AGTTCTTCCT GGATTTCTTT TAATACTTTA GCCACTGTTA 6120

CTAACATCGC GGTATGGGAA TCATGCCCAC ATGCATGCAT CTTGCCAGCT TCTAAAGATT 6180

TATAAGCTAA ATCTTCATTT AATTCCTGTA CAGGTAAGGC ATCCATATCC GCCCGCAGCG 6240

CAACCACTCG GCCTGGTTTG CCGCCCACAA TTTCAGCAAT TAAACCCGTC GGTTCTGTTT 6300

TGCGATAAGT AATTCCTAAT TGATCAAGAA CTGCCGCGAC TTTTTCTGTC GTTCGAAATT 6360

CTTCAAATTG TAATTCTGGA TGTTGGTGTA AATCCCGTCG AAAAGCAATC ATTTCTTGTG 6420

CATGCTGCTT GACTAGTGCT TTGATTTTTT TCATACTTAC GCCCCGTTTC TACAAACTTA 6480

ATAAAATACT TGAAAAAATA CCCGCTAAAA TAACCGAAAC AATGGTGACT GTTACGAAAC 6540

CTGCCACTAA CATCGGTGGC ATTAAATGGC TCGTTAAAGC CGCCTGTTCT TGTTCATCTT 6600

CTGTCAATGA TTGAATCACT TCATTAGTAA TAATATAATC GGCTGGAAAG CCATATAAAG 6660

CTGTCAACGA AACAGCGAAT GCCATCTCTT TACTCACACC TAATACACGA CCAACAATTG 6720

CTGAAAAGAT GTACATCCCG ATAACACCAA TCACAATAAT CCCAATCATT GGTAAAAATA 6780

AATCCATCAA CATTTCAGGT GTGGCTTGTT TTAAGCCATC AAAGACAAAA AGCATTAACC 6840

CTAAAATCGC AAAACCAAAG CTATTTGCTT TCTGCAATGG TTGCTTTTCT AAAAAGCCTA 6900

AAGACGTTGC AATCACGCCA AAACATAAAC ACAGCACAAA AGGACTAATC GTCACAAACG 6960

GTGCCGTCCA CACAGAAACA TAATAAGCAA GTGTGGCAAC TAAGGCTAAA CGTAAAATTC 7020

GTGAATAATC TGTATGATAT CGTTTGGGTA CTTTTTCAAA TAGTTTAGGC ACATCTGGTT 7080

CTGCTCCTGT TTCTTGCCCC TCTTGTTCAT GAACCGGCTG CCATGTCCCT GCTCGATATT 7140

CTTGAAGCTT CCGCTTTCCT TCTTTTTTTA GAACAATTGA AGTTAAGGGA TAACCAGCAA 7200

ACCCTTGAAT GACATAAATT AAAATTGCCA AAACCGAAAG TGAGGCTAAA CCAGCTGATT 7260

GAGCCGCTTC TGACATTACT AATGAAGAAA CTAAACCTCC TACTAACGGC GGGATTGCAA 7320

CTAAAACTGT TTTTAAGTCA AAAACAAAAG TCCCCACAGC TAACAACAAG GCAATAATGC 7380

CCAGAATACC TGACAAAGCA ATCACAATCG TTTTCCATTG ATTAACCAAT TCTTTAACAG 7440

AGAGCAGAGT GCCCATATTA GTAATCAACA GATACATTAA TAAAGTGGCA ACCACTGTAG 7500

GAATCCCTGC CACTTCCACA ATATTTTGTG GAAAAATAGT CCAATAACCA AGAATAAATA 7560

AAACACCACA AACAAAAACG GATGGAATCC AAGCTTTTGT TTTGATAGAA ACTACATCAC 7620

CAATGTATAA AATAACCATC AGCAACGAAA AAGCAAACAT TTGC 7664

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AAAAAAATTT TCAAAAGTCA AAAATGAAGG GGATTTTCAA GATGGAACAA TCATTAATTG 60

TGAGAGGGAC ACCACAAGAG TATCTTTGCG AAATTGGTTC GTGGGAATTA TTAGAAGGAC 120

AACTATTATG CAGAAATATT CATCGTGTAT TCATTTTACA CGGGACTGAG TCATGGCAAG 180

CGGCAAAACC GTATTTTCCG ACGTTTCAAA AAGTAACAGC TGTTTTTGAA AACTATGGAG 240

GTGTTTGTAC AGATCAACGT GTGCAAGAGT TAGAAGCGCA AGTGCTGGAC AATCATTTAG 300

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AGGCCATCGT CGCTGTTGGT GGAGGAAAAG TGGCCGACTT GGGCAAAGCC TTAGCACACA     360
AAATGGCGTT ACCGGTAATT ATTTTGCCCA CTTTAGCAGC TACTTGTGCA CCGTGCACGC     420
CATTGAGTGT AATGTATCGA GAAGATGGAG CAATGGAACG ATATGACGTT TTTCCGCAAG     480
CAAACGCTTT GGTGTTGGTA GAACCAAGAG TGTTATTACA TTCGCCTCGG TCCTTAATGG     540
TGGCAGGTAT TGGGGATACA TTAGCTAAAT GGTACGAAGC AGATGCGATT ATTTCGCAGT     600
TAGATGTCCA AGTGTTACCT ATTCAAGTTT CTCATTTTGC CGCGGAAAAA TGCCGCGATA     660
TTTTGTTAAA TGAAAGTATC AATGCTTTAA AAGCGATGGA AGAGCAACAA TTAAATCAAT     720
CGTTTATTGA TGTCATCGAA ACAAATTTAA TTATTGGTGG AATGGTGGGT GGCTTTGGCG     780
ATGATTATGG TCGGACAGCA GGTGCsCATT CCATTCATGA TGCACTAACT TTGCTGCCAG     840
CTAGCCATCG ACAATTGCAT GGAAACAAAG TGGCGTATGG TGTGTTTGTT CAATTAGCCA     900
TTGAAGAAAA ATGGCAAGAA ATCGCTGAAT TGATTCCTTT CTATCACCAA CTAGGTTTGC     960
CTATTTCTTT AAAAGAAATG GACATGGACT TAACTGAAGC CGAGTATCAA GAAGTAGCAG    1020
AmCGTGCTTG TATAGAAGGC GAAACGATTC ATTATnTGAA ACAAAAAATT cCCtGAAATT    1080
GTGAAAcAGC GtGCAaGrTT TrGAAAAaTA TaCAGCGACA AAATAaGTGC CAAaCAGCAA    1140
CTAGTTCATT TGAATTATTT GAATTAGTTG CTGTTTTTTA AGGATCCTTT TTTGAAAAAA    1200
GAAACCTTGA GAAATCCTTG CAAATTCAAT AAAAAAAAAG TATGATGATG GGAGGACAAA    1260
TTATAGTAGA AAGTAGGGAA ATGAATGACG GAACCAGCCA TTCGTTATCG TTTAATCAAA    1320
AAAGATAAAC ACACAGGTGC GCGTTTAGGT GAATTAATTA CTCCTCACGG CACATTTCCA    1380
ACACCAATGT TTATGCCGGT AGGTACACTT GCGACAGTTA AAACAATGTC ACCAGAAGAA    1440
TTAAAAGAAA TGGGTGCCGG TGTTATTTTA AGTAATACTT ACCATTTATG GTTACGCCCA    1500
GGTGAAGATT TAGTCGAAGA AGCAGGCGGT TTACACAAAT TTATGAACTG GGATCAACCT    1560
ATTTTAACTG ATTCAGGTGG CTTCCAAGTC TTCTCATTAA GTGATATGCG GAAAATCGAA    1620
GAAGAAGGTG TGCATTTTAG AAATCATTTA AATGGTTCaA AAATGTTCCT TTCTCCAGAA    1680
AAAGCGATCA ATATTCAAAA TAAATTAGGA TCAGATATTA TGATGAGCTT TGATGAATGT    1740
CCACCATTTG ATGAAAGCTA TGAGTATGTC AAACGTTCGA TTGAACGGAC TTCTCGTTGG    1800
GCTGAGCGTG GCTTAAAAGC CCATGCGAAT CCTGATAGAC AGGGATTATT CGGTATTGTT    1860
CAAGGTGCGG GATTTGAAGA TTTACGTCGT CAAAGTGCTA AAGATTTAGT GAGTATGGAT    1920
TTTCCTGGCT ATTCGATTGG TGGCTTATCT GTTGGTGAGT CTAAGGAAGA AATGAACCGA    1980
GTCTTAGACT TTACGACACC GTTAATTCCT GAAAATAAAC CACGTTACTT AATGGGTGTG    2040
GGTGCCCCTG ATTCATTAAT TGATGGAGTG ATTCGTGGGA TTGACATGTT TGATTGTGTG    2100
CTACCAACAC GTATTGCGCG CAATGGTACT TGTATGACTT CACAAGGTCG CTTGGTTGTT    2160
AAAAATGCCC AATATGCAAG AGaTTTnCGT CCGCTTGATG AAAAATGTGA TTGTwAkGTT    2220
TGTCGTAATT ATACGCGGGC CTATATTCGT CATTTGATTA AATGTGATGA AACATTCGGA    2280
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ATCCGTTTAA CATCGTATCA TAATTTATAC TTCTTGTTAG ACTTAATGAA AAATGTCCGT 2340

CAAG 2344

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TAAGTTTTGT TTCAAATTCT TCTACATATT CTCGATACAT AAAAACACAT CTTGAAATAC 60

TCGGTCTAAG TTCCTTAACC CTCTCTTCCA ATTTTGTACA TTCTCTTTTT ACATAAGAAA 120

CAGTTAATTC GTTACTGTCT TCAAGTTCTT TTACACTCAA TTGAAGTTTA TGAATAGAAC 180

TCATCACATG AATCATTTTC TCAATAGTGG CATCCATAAG TTTTATATTT TTTTTGATTA 240

ATTCTTTATC CATTCTATCA ATCCACCTTT CTAAAACGGG TACATTTCTT CTAATTCGAA 300

CTCTCGTTCC ATATAGGACC GAACACTTTT ATTATCTCTA TTGGTAAACA ACAAGTCTTT 360

TGcATCaACa CTCaCCATTT CaATAATCTC TTCaTGCTTT TCTTTTnAAT TCTGCTAAAT 420

CAATGCGTTC CATCAATTCA TTTGTTCCTA ACAGATTATC AATCTCTTTA ATCATCTTTA 480

ATGAAGGGGC TAAATAATTT GATAGCCATC GAAGCGTCTT TTCAATAGAC GGTTTTTCAC 540

CTTGCACAGA CAATTTTAAG CCTTCCAATT TATCAACAAC ATCATGCCAA GATTTACAAT 600

AAACTTTCAT ATCATCTTCA ATGTCATAGA CAGTCAAAGA TTGATTAATA ATTTCTTTCA 660

CTAACCAATC TAGCGACTCA CCGCTTGATA GAAAATATTC TACAAACAAA AACGCCTTTT 720

CATCAGAAAG GCGAATTTCG TATCGATTTT TAATTTCATG TTTTTCTCTT GCTTCTTCAA 780

CACTCATACT TTCTTTTCTT GCTAACTCGT AATCTTTTTG GTAAAAGTTA AAATACAGTG 840

GCGATTGACG ACTACCAAAA TAAAGGGATA AACCTTTATT CACCATTTTT TTATTTTCGT 900

AAACAAATCC ACCGCTAAAA TCAAAATTTT TAAATGTGGT GTCAACAAGC CCCTGCTCCA 960

TTTTTTCTTT TAAAACATAC AAATCAAAAT TTTCTTGCCC CTTCACAATC AATTCATCAA 1020

GAGCAATATC AATTCGAGTG ATTTTTGTAT CTACTAAAAT GCCTTGACCG AAAATATCGT 1080

CATCATAAAG AGAGCGAAAA AATTCTGTCC aCGATCGGTk GTTATCTTCC TCAAAGATTT 1140

CTTCTAATTG ACGACAGCCT tCGCCAGACA AGTCCaACAT AATTCCCATA TTGACATTTT 1200

CCGGATTCCG AAAAATCCGA ATAGAGCTAT ATGAAAATGT TTCCGTGTAA TGATAAAACC 1260

CTCTAGATTC ATGAGTAAAC CAGTTCATAT CCATGTGCAA CAACTTTTCA AyAACTGTCC 1320

GAACATCTAA TGTTTTAAAT CGTATTCTTA AAAAGTCAAT TTTTGCTTCT ACCGAAGCGT 1380

GCCCACCATC TAAGTTCAAC ACATTAATAA TCTTTTGTTC TAACTCTTTA GAAATAACAC 1440

GTTTTCCAGA TTCTATTTTT GAAATTAACG AACGCTCrAT TCCTAATTTA CTTGCCAATT 1500

CTTGCTGTTT TAATTTTAGy TCTTTTCTAT ATCGCTTTAA ATCAACACCT CTCACTGCTT 1560

TAAACCTACT TCCAAAAAAt GTGACAACTT TAGTCGAAAA ATGTGACAAA ATCATAATCG 1620

CTCAATCCCT TGTAGGACAT AGCTTTTAAG CAACTTTTTT ATACGGTATA TTAAATTCTA 1680

CCCCCATGTT ATAAATAGGG GGTTTTtGAC GTAAGGTGGG CATTCGCCCA CCTTACGTCT 1740

GTTCATTTTA AAAGGATTTT CCGTTGCTAA AAGTATACGT GGGCTTTCGC TCTGCTTCGC 1800

CCACGTATAC TTATTACTAG CAACAATCCT TCAAATAAAC AGCCGTTATT CAGCTGTTCC 1860

TCGTTCTAAT GCACCAATTC TCTCTTTTAA GCTTGCATTC TCCGCAAGAA TAGATTGAGA 1920

CACCTTTAAA AGTTGCCTCA TATCTCTTTT CAAATCCTCA ATTTCTTGTT TATTAATATG 1980

TGTAGCTTTA TTCTCATCAG ACATAAATAC TTCATTTATT GCCTCATTAA GCGGAACATT 2040

ATTTTCACGC AAACGTAGCA ACTCTTGAAA ATTTTCTATA TCTTTAATAG AAAAAACCTT 2100

ATAGCTATAA CTATGACCTG CACTATTCTT TGCATATCGG CGTTCAAAAC GTGTATCAGT 2160

CATTTTTTCA ATCCTATTTG CCCAATTTTT CAGTGTTTTC AAAGCAATAG CATTGTCTAG 2220

CTCTAAAATT ACTTGATCAA ATGAATACAT TTTCCACACC TACTTATTAA ACATTTCTTT 2280

CCAAGCAGAa tCCATATGCT CCTTAAATCT TGTTTCTAAA TACTTATCAA CTTCTTGTGA 2340

TGTTGAAAAT TTCTTTTCCT CAATTGGTCT ATCTTCCTCG TAAACAGCTT CTGCATCTAA 2400

AACAGAAATT ACTAATAATT TATA 2424

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

GACGCTCTTT TACCAATCAA AGAGTAAGGC ATAGCCTAAA GAAAGCAGCT CTCGACCAAA 60

ATTTTTGATA TCTTTTGGAA AAGAAGAAGC CGCAGTGATG CCTGAAACAT TTGAGATGCC 120

TGCTCGCTTG GcTAAAAGTT GCGAGCGGTA CATGTGAAAG TCACTAGTAA CAATCACTAG 180

CCGTTTAAAA GAAAGGAGTT TTTGTGAATT GACAATATTT TCTTTGGTGC GTGTGGCACG 240

ATTTTCTAAG AGAATCTGTT TTTCTGGAAC ACCTTTATTT AGCAAGTATT GTTTCATAAC 300

CGCGGCTTCC GTAGCCGGCT CATCTGCTCC TTGCCCTCCG CTAACAATAA CGGGTGTCTC 360

GGGGTGTTGT TTAATATAGG GGATAGCCAC ATCTAACCGA GCTTGCAAAA CACGGCTGGG 420

CAGTGCGGTT TCTTTAGACG TCCCTAAAAC ACGGGCCCCT AAAATTAAAA TAGCATCTGG 480

TTTATCGGTG GGTTGCGTAT TTTTGCCAGT AAAAATAAGT AGACCTAAAA TCAAAAGAAT 540

ACAAAAGCCA AAACTGACAA TGGATAAACT TGTTATTTTT AACCAATGCA TGAAACATCC 600

CTCCTTGTAA TGTTAGTGTA TACGAAGTAC CATAGAAAAA GCGATAGAAA ACAAAAGACT 660

TATAAAAAAA TCTATGTTTT AATAGAAACT TTTGAAGAGA GGGAGCGAAT GCATGCGTAC 720

AGAAGAAGAA ATGTTTCAAC TTATTATGGA TGTAGCAAAA CAAGAAGAAC ACATTCGAGC 780

TGTGGGAATG GTGGGGTCTC GCACGAATGT GAAAGCGCCA AAAGATAGTT TTCAAGATTT 840

CGACATTGTT TATATTGTAG AACCATGTGC TGAGTTTTTT GAAACAGCAA CGTGGATAGC 900

AAAATTTGGA CAACCATTAA TTATGCAACG TCCCAAGGAA ATGACCTTAT TTCCCACAGA 960

ACCGAAGACG CGGGAAACAT TTTTAATGTT ATTTGAAGAT GGCCAACGTA TCGATTTAAC 1020

GTTGTGTCCT CTCGCAGAAA AAGATAATTG GCATGAAGGC GATTCTTTAG CAATTATCTT 1080

GTTAGACAAA GATGAAAATT TGCCGCCTTT ACCTGTAGCA TCTGATAAAA ATTATACAGT 1140

AACAGTTCCG GATCAGCAGC AATTTAACGA TTGTTGCAAT GAATTTTGGT GGGTTAGTAC 1200

GTATGTAGTT AAGGGGCTTT GTCGGAATGA ACTATTTTAC GCTGTCACAC ATCTCTATGA 1260

ATATTGTCAG CAGGAACTGT TGCGCTTGCT TTCTTGGCAA GCGGCTTGGC AGGAACCGGA 1320

GCCAATTTCT GTTGGGAAAC AATTTAAGTA TCTGAAAAAT TATGTCACTC CTGACACGAT 1380

GGATCAATTA GCATCGTTGc TGGaTTTTTC ctAGTaAAGg AgCcTkGTTG GaACaGCtTA 1440

ATwAAgrCcC CAAGCCTTTT TTGGACGT 1468

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13085 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTTTAGGnC ATmCGTAAAC ATCTTCTCCT CCTTTATTCG TTCATTTTTT TATAGATAAC 60

GTAnGGGAmA AnGGATACGA AgCTTACTCA CTTTCGTATC AAAAAAgCAw TCTTCACTCA 120

AGTGCTACAC GCTTTTTTGG TTTTAAAaTG ACATTTAAAA GGACTGCTAC CAAAGTGGTT 180

AAGATAACTT CCGAATTACC GAAAATCGTT GTTACCCAAG TTGGAAAACC AGCTAAGCTT 240

CCAGTAGACA ATGTGACACC AATTCCAAAT GCTAGAGCTG TTCCGACAAC CCCAGTATTT 300

CGAGGAGTCA TTTCCTGCGA AGCAATCATC CGAATACCTG TCATAGAAAT AGAAGCAAAA 360

ACTGAAATCG TTGCGCCACC AATTACCGCG TAAGGAATCG TAGTTAATAA TGCAGCTACT 420

TTCGGAACAA AACCAGCAAT TAATAATATA ACTGAAGCGA AAACCAGAAC ATATTTATTA 480

ATCACTTTTG TTACCGTAAC CAGACCAACA TTTTGTCCAA AAGTTGCCAC TGGGATTGAT 540

CCAAATAAAC TGCCAATAAA GTTAGTGAAA CCACTCCCCA TAATTCCGCC AGATAATTCT 600

TCATCCGTTG CATCCCGATC CATTGCCCCA ACCGTTGTTG CTGTAAATTG ACCGATGGCT 660

TGAACAGCAT CAACAATAAA CATCACCACA AGCGTAAAGA TTGGTACCAA TTGAAAATCC 720

AGTCCAAAGT GAAACGnGGT AATTACCTGA ACGATTTTAG CATTTTGAAC TGGCTCAAAA 780

CTAACCATCC CTAAAGCTAA AGAAATCAAA TAGCCAATAA CCATTCCGTT TAAAATTGCG 840

GATAACTTCA AAAATCCTTT TGCAAAATAA TTGAAGTAAA AGACAATCGC AAAGGTTAAT 900

AATGCAACTA ACCAATTCCG GGCTGAACCA AAATCAGCAC TACCAGCTCC TCCTGCCATA 960

TACTTAATCG CAACAGGAAA CAAGGATAGT CCAATGCTTA AAATAACCGT TCCTGTTACT 1020

AAAGGCGGAA ACAACACACG GATTTTTTTA ATGaACAAAC CAACAATAAT AACAAGAATA 1080

CTGCCAACTA ATTGGGAACC AAAAATTGCT GCAATCCCAA AATCAGCTCC GATGGCCATC 1140

AAAATCGGTA CATACGCAAA ACTTGCCCCC ATCaTAACTG GTAACCGTGA ACCCACTTTT 1200

CCAAAAATAG GGAAAAGTTG AATTAACGTT GCAACTGCTG AAAAAATCAA TGATGTTTGA 1260

ATCAAAATAG TCGTATCACT AGGACTTAAT TGGCAAACTT TGGCAATCAT GATTCCCGGT 1320

GTGACAATCC CTACTACTGC TGCGACAACG TGTTGCAATC CCATCGGAAT TGCTTCAGAA 1380

ATTGATAGTT TCGCATCATA TTCAAATAAT GCTTGCTCTT TTTTTTCATT CATAGGATCG 1440

TTTCCTTCTT CTTTTTATTC TAAAAGGATT GTTCCCCTTA ATCAATAAAG AATGCAATCC 1500

TTTTTCCCTC AGAAACATCT TAAAAATTAT CCTTTGACAG CAACTGCTTC AATTTCAAAT 1560

AAACCATCTT TTGGCAACTT GGCTACTTCT ACACAAGAAC GTGCAGGCAA AACTTCTGAA 1620

AAGTAATTCC CATAGATTTC GTTAATTTTG CTAAAATCAG ACATATGTTG TAAAAACACC 1680

GTTGTTTTCA CAACATTATC ATAGGTCATC TCGACCTCTT TTAAAATCGA ACCTAAATTG 1740

ATAAAAGCTT GTTTTGCTTG TTCTTCCACT GTAGTCTTCA TTTCGCCCGA TTGCGGATCT 1800

AATCCTAGTT GTCCAGAAAT GTACAACGTA TTTCCCGCTA AGACAGAATG TGAATAAGGT 1860

CCTACAGTAG CTGGTGCCTG TGCAGAATTA ATCATTTTGT TTGTCATCGT TTTCCTCCAT 1920

TCTATGATTC TTTATTTTCA ATTAAAGTCC CTGTTTTTCC AGATAATCCT TCTTTGGCTT 1980

TTTCTAATAA CGTAATCAAT GTTTTTCGAC CTGGCTTAGA TTCAGCAAAC TTAATCGCTG 2040

CTTCAACTTT TGGTAACATT GAACCTGGAG CAAACTGACC TTCTTGCGCA TATTGTTTCA 2100

TTTTTTCTGT TGAAACATTC CCTAAGGCTT CTTGATTTTC TTTACCAAAA TTAATACAAA 2160

CTTTTTCAAC TGCTGTTAAA ATCACGAGCA GATCAGCATC CACTTGTTCA GCCAGTCGTT 2220

CACTACAAAA ATCTTTGTCG ATGACTGCAT TGACACCTTT TAGTCGGTTC CCTTCTTGAA 2280

TGACTGGGAT GCCACCACCG CCGCCAGCAA TGACTGTTTG GCCAGCATCA ACCAATGTTT 2340

GAATCGTGAG AAGTTCGACA ATATTTTTTG GTTTAGGAGA AGCGACGACT TGGCGATAAC 2400

CACGGCCAGC ATCTTCCATC ACTTGTATAT TTTTTTCTTT GACTAATTGT TCTGCTTCTT 2460

CTTTTGTCAT GAAGCGACCA ATTGGTTTCG TTGGTTTTTT GAACGCCGGA TCATTTTCAT 2520

CCACGACCAC TTGAGTGACT ACGGTGGTGA CGGCTTTACT TATATTTCGT TGACGCAACT 2580

CTTCTTGTAG CGCATTCTCT AAATCATAGC CAATGTAACT TTGACTCATG gCTACGCACA 2640

TGGATAACGG AACAACTGGA TATTGTGGAT TATTAAAGGA AAATTCTTCC ATAGCTAATT 2700

GAATCATCCC CACTTGAGGA CCATTGCCAT GAGATAAAAT AACTTCATAT CCTGCTTCAA 2760

TCAAATCTGC AATCGCTTTG GAGGTCTGTT TTACGGCAGT CATCTGCTCC GTCAAATTAT 2820

TTCCTAAAGC ATTGCCACCT AAAGCTACTA CGACGCGTTT GCCCATTGCT TCACCTCATT 2880

TTCTGTTTTA TAAAAAGGAC GATGCTTTTT CTTTTTCACA ACGAGTTTTC GTATTAACTG 2940

TCTGTTGTCG TTGCATGAAG TCAACGCACA TGACTAAGCG TTCTTGACTC GAGACAATCA 3000

CACATTCATG AATAGACTTG GGAAGGTCTT ATTTGTTCAT GTTGAAGAGG CAACTTCTAA 3060

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TTGGTGTCGC TTTATCCGCT AATTCTGTTA AGGTTTTTTG CGGATTTTTT ACTTTACTTA 3180

AGAAAATCAT AGCCGCAATA ACATACGGTT TGTAGCTAGC TTCTTTGTAA AGTTCGACCC 3240

GATAACGATC GAAAACAGAA GCTTCCACTT CGCCTTCTTC ACAACTAACG CCAGTAATAT 3300

CAGCTGGTAG ACAATGCATA TACAAAGCTT TGCCGTCTTT TGTTGTTTTC ATCAATTCTT 3360

CTGTACATTC CCAATCTTTG TGCTTTTTAT TTTGAGAAAG TAATTCTTGT TCTAATTGAT 3420

CAATTCCTGC TTGGTCACCA TTGCCATATA ATTCAGTTCG CTTTTCCATT GCCGCAAAAG 3480

GTGCCCAGCT TTTCGGATAA ACAACATCCG CATCTTTGAA TGCTTCTGCC ATACTATTCG 3540

TTTTAGTAAA GTTTCCACCA AATTCTGCCG CATTTTTCTT CGCAACTTCT TCTACTTCTG 3600

GCATAATTTC ATAACCTTCT GGATGTGCTA AGACGACATC CATTCCTAAA CGGGTCATTA 3660

GACCAACAAT TCCTTGAGGA ACAGATAATG GTTTTCCATA AGATGGTGAA TACGCCCAAG 3720

TCATGGCAAC TTTTTTCCCT TTCAGGTTTT CAATGCCACC AAATTCATGA ATTAAATGCA 3780

ACGCATCCGC CATTGCTTGC GTCGGATGGT CAATATCACA TTGTAAATTC ACTAACGTTG 3840

GGCGCTGTTC CAATACCCCA TCTTTATATC CTTCTTGGAC AGATTCTGAT ACTTCGTGCA 3900

TGTAAGCATT GCCTTTACCA ATGTACATGT CATCACGAAT ACCAATGATA TCAGCCATAA 3960

AAGAAATCAT GTTTGCTGTC TCACGAACAG TTTCTCCGTG AGAAATTTGA CTTTTTCCTT 4020

CGTCTAAATC TTGAACTTCT AAGCCCAAAA GATTACACGC TGAAGCGAAA CTAAAACGTG 4080

TTCTTGTAGA GTTGTCGCGG AATAAAGAAA TCCCCAAGCC ACTATCAAAG ATTTTAGTTG 4140

AAATATTATT TTCTCTTAAA TAGCGTAATG TATCGGCAAC TGTGAAAACA GCTTCTAATT 4200

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ATTTATCTAA TTTCTCAATA TATTCTTTAA ACGTTTCCAT TCCATCTGCT CCTTTTTTCT 4320

TGTCTAATAA TCCTTTACTT AACCACAATA GACCGTTGGT AATGCCGCAT AAACGGCTGC 4380

ACAACGAACC AAATCATCTT TCCAAGTTTT TTCATTTGGT GCATGTGCTT GTGCTTCGGC 4440

CCCTGGCCCG AAACCAATAC AAGGAATACC ATTACGTCCC ATAATTGAAA CGCCATTTGT 4500

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ATAAGAAGGA CGATCATAGT TGTACATTGA AACCGTCACA TCATCTCCAT ATTTTTTAAC 4740

AGCTGGTAAA TTGCGAATTT CTTCTAAACA ACTTTCCCAA GTTTCTCCAG CAGTCATTCG 4800

ACGGTCTAGT GAAACGGTAC AGCCATCCGC AACAGCACAC CGACTTGGTG AAGAATGGAA 4860

AATTTGCGAA ACAGTCACCG TACCACGTCC TAAGAAACGG GCTTCTTGCC ACTCTGGATT 4920

GTACTTAGGA TCTAACATAC GAACTAAACC ACGAATCGCT GTGCTTTCTG TATCTCCATT 4980

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GCCTCGTTGA CCACGATAAA TCCCACCATC TGTTGGCTCT GTTGAAACAA CAAATTCTGG 5160

ACGGATACCG TCTTCTTTGA TAATGTACTG CCAACATAAG CCGTCACAGT CTTCTTCTTG 5220

GACAGTAACT GTTACTAAAG CAGTGTATTT TTCTGATAAT AGACCTAAAT CTTTCATGAT 5280

TTTAGCGCCA TAAATAGCCG AAACAATCCC GCCCTCTTGG TCAGACGTAC CGCGACCACC 5340

GATCTCAGTT TCTGTTTCAT AGCCATCGTA AGGATCAAAT TTCCAGTTAC TCATTTCACC 5400

AATTCCGACA GTATCCATGT GCCCATCAAA AGCAATTAAT TTTTCACCAG ACCCCATATA 5460

ACCAAGTAAA TTTCCTTGAG GATCAATGTC AATTTTATCG AAACCTAATT TTTCCATTTC 5520

GGCTTTTGCT CGCGCAATTT TGTTGCCTTC TTCTGCACTT TCTCCTGGAA TTTTGACAAG 5580

GTCTCTTAAA AATTTGACCA TATCTTCTCT GTAACCTTCT GCTGCTGCAT TTACTGCATT 5640

AAAATCCATT CCTTTTACCT CCATAAAATT TTTTTATAAT TGTCTGGATC AGTGTcCCCT 5700

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TCAACTACGA CCATAATCGG TGGGTTTTCT GGAAAAGCAT TAGCAAAATA ACCAATCACT 6120

GCACCAGCTA AACTGCCGAC ACCAGCTTGA ACAAAAACAT GACTAGGTCG TTCAGAGCCA 6180

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GTCGGAATTT TTTCATATCC GTCCCAAGCG GTGTCTTGAA CCATGACACC GTTTTCAGTT 6300

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ACGGTTGCGC CTTCTTTTTC AATATTTTCT TTTCTCGTCT GTGTTGAACC cTTCGGCATG 6420

AGTACAACTG ATTTTTGGCC TAATTTATTC GCAGCCCAAG CGACTCCTCG TCCATGGTTA 6480

CCATCAGTTG CTGTAAAAAA CGTAGCTTGT CCAAAAGCTG ATCGTAATTG ATCAGAAGTT 6540

AATTCATCAT ATGTTAGTTC CGAAACATCT TTCTTTAATT TTTCGGCAAT ATAGTTAGCC 6600

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TTAACAAAGA AATCATTTAA CCCCAGATAC GCGGCCATAT GATTCAATTC TGCTAATGGT 6720

GTTTCTGAAT ACTGTGGAAA ACTTTTGTGA AAAGCCAAAG CTTTCTCAAT TTTTTCTTTA 6780

GACATCAGAG GTAAGTACTT ATCCTCCGTC TTCGGCATTT CATTTGCTGT CCATTTAATT 6840
TTTTCCAAAA ATACTTCTCC TCCTTCTATT TTTAAGTTGC TTTACGAAAA ACAAATTTTC 6900
CTTGATTTGC CAAGATGACT TGCCCAGCTT CAGCAACTTT TTGACCTCTT AAATAAACCA 6960
TTCGAGCCTG TCCTTGTGTT TCAAATCCTT CATACGGCGT ATAATCGACA TTTTGTAACt 7020
GCGTTCTCGC AGCAATCACG CCGGTTGTTC TGGGATCCCA AACAACTAAA TCGGCATCAC 7080
TGCCTTCTTG CACCACACCT TTTTGTGGAT ACATCGAGAA TTGTTTAGCA ATATTTTCAG 7140
AAAGCAGAGC AACCATTTTT TCCAAGGTGA TTCGGCCCTT CGCCACACCT TCCGTGTAAA 7200
TTAATTCTGG TCTCGTTTCA ACACCTGGCA TCCCATTGGG AATTTTACTA AAATCATCTT 7260
TGCCAACTGT TTTTTGTCCG TAAAAATTAA AACTGCAGTG ATCTGTCGAT ATTGTATTGA 7320
TTGCCCCCTC TTTAATCCCT TGCCACAAAG CCCGTTGATC CTCTCGTTTG CGTAGTGGCG 7380
GTGAGCAGAC ATATTTTGCT GCTTCAAAAT TAGGCGCATC ATACAAGTGA TCATCTAGTA 7440
AAAGATATTG AGGGCAAGTT TCTACATAGA CTGATTGTCC TCTTTGACGA GCCCGTTCCA 7500
CCGCTTCTAA TGATCGTTTT GTGCTTAAAT GCACAATATT AACCGGCAAA TCAGCCATTT 7560
CCGCTATCAT CAAATATCTT GCTACCGCTT CTGCTTCAAC AGCCGCCGGT CTTGATAACG 7620
GATGATAGTG CGGGGTTAGC TTTCCTTGAG AAACATATGA TTGGaTTAAT TCATCTACTA 7680
AATCACCATT TTCACAATGA ACGCCTAACA TTCCATTAAC TTTTTTTATT TCCTTCATCG 7740
CTTCAAAAAT TTCCGCATCT GTGGTCCGCA AATTATCATA AGCCATATAC ATTTTGAAGG 7800
AAGTAATACC TGCAGCAATC ATTTCCTGAA TTTCAGCAGC TATCGTTGGT TTCCATTCAA 7860
TCATGGACAT ATGGTAAGTA TAATCACATG AACTCTTGCC TTCAGCCAAT TGATTCCAAG 7920
TAGCTAAACA GTCTTTCAAT GAGCCGCCTT TATTAGGTGT AGCCATATCA ATAACCGTAG 7980
TCGTACCTTT GGCCACCGCC GCTTGGCTTC CAGTGGTAAA GTTATCCGCC GTACTTAACG 8040
AACCTTTGCC ATTATTTAAT TCCAGATGCG TATGCGCATC AATaAAGCCT GGTAATACAT 8100
AACACCCCGT AACATCCTCA ATCTGAGAAT TTTCTACTGG TAAATTTGCC CCCATCTCTA 8160
CAATTTGCTC GCCGTCAATT CGAATATCCA ATTGACGACG ATTATATGCA GATACGACGG 8220
TTCCACCTTT GAGCAGAATA GACATTTATT TATCCCCCAG TCGTAAATTT CCTTTTATGC 8280
TTGCATACAA TAAGCATATT CTTCAATCAT AGTTACCATT AATGCAATTA AATCTTCTGG 8340
TACATCTAAT CCTTGATCTG TTAATTGAAT TGTTGACACC GTTCCCCATA GACGCAGTAA 8400
ACAAATTTTA TCCACAGGAT TTTGAACATA GAAACCTGAA TTAGTACTGT CATAAAAATC 8460
AGCTTCACTG TTAAATAAGG TAAATTTGTC TTTGTAAGGG GCACTTGCAT AAGGGCAAAA 8520
TGTTTCACAG TTGCCACATT CGTTACACAT CCGATCAACA TGGACAATTT GTGGTTTTCC 8580
TTCGACATAC ACAACAATAT TTGCTCGGTT TGGACAGACA TCCATACAAG ATTCACAAAT 8640
TGTGGAGCAT TCTAAGCAAC GACTAGCTTG ACTACAAGAC ATCTCGTCTG TCACAAGGAT 8700
ACCCCGTTTG TTTCTAACAA ATGCGACATC ACTATTTAAA TTATCTTTTT CATAGTGATG 8760

ATTGTGGACA AGACAAATAT TATTGGCCGC TTTGGTTGCA TCAGCGATTG CTTCAACAAT 8820

TGTGGCTGGT CCTAAATTAG CGTCACCAAT GACATAGACA CCTGGTATAT TTGTTTCCAA 8880

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AAATTCTGTA TCTACTTTTT CACCAACAGC GGCAATCACT GTATCAGCAG GAATATCAAT 9000

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AACACCATCT TCTAAAGCTA AATAAAGTTC TTCTTCATCT GCTGGCATAT TGCGTTTATT 9180

CCGACGATAA ACCACTGAGA CTTTTTTAAC ACCAGGTAAT GTTGTGGCTG CACGAGCACA 9240

GTCCATGGCT GTATTTCCGC CACCAACGAC GACAATTTGT TCTCCGTAAG GATTAATCGT 9300

TGGATTTTCT CGATTTGCTT TTAAAAATTC TAACGAGTTC AATGCTCGAC CAGATTCTAA 9360

ACGAAGGACC CCATGTTTCC ATGCACCAAT GGCATAAATA ACATTCGTAT AGCCTTGGTT 9420

TTTCAATTCC GCCAATGATG GCGCCTCTTG TCCTGTACGG AATTCGGCTC CCATAAATTC 9480

CGCTAACTGA ACGTCTTTTT GAACAGATTC CATAGAAATT CGAAATTCTG GTACAATCTG 9540

GCTACAAACG CCCCCAATTG TCTCGGATTT TTCAAACACA GTAACAGGCA TGCCTTCACG 9600

TGCTAATAAA TACCCAGCAG AGATCCCTGC AGGGCCTCCA CCCACAACAG CTGTTTTAGG 9660

TGCATTTTCT TTTGGCTGTG GCTTTTCTAG TGTCGTCAAT AATTCATCAT AAGCATGTTC 9720

AGCTGCTTCT AACTTCACTT CCCGAATATG AATAGATTCT TCATAAAATT GACGTGTACA 9780

TTTAGTCATA CAAGGATGTG CACAAATGGT TCCAGTAATA AAAGGCAACG GATTCTTATC 9840

GACAATTACT TGCAAGGCCT TTAAATAATT ACCTTCACTG ACATAACGAA GGTAAGCAGG 9900

AATATCCTGA TTGATTGGAC AACCACCGTC ACTTCGACAA GGAGCAATAT AACAATCTGT 9960

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CGCTTGTGTT TTAGCTTTCT CAACAACTTG AGCTAATTTA TCCAAGTTGA CATGGACCAT 10080

CTGAGGATAT TCTGCTGCGC TTAATACATT AGCAACTTGA TTCATTCGTT GATAGCCACC 10140

AGGTTTCAAC AGAGTCGTTG CCATAGTGAT TGGCCAAATC CCAGCATCGA ATATTTCTTT 10200

ACTATTGAAA ATATCTGCAC CGCCAGAATA AGAAATTTGT AGTTTCCCAT CAAATGCTTC 10260

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TTCATCACCA GGTAATTCAT TTGCTGCAAT CGTTACCGGG AAAGTGTTCG TAATTTTAAC 10380

TCCGAAGCTT AGATTTTTAC TATTAGCTAA TAATTGCAGA CGTTGTAACA TCGGTACTGC 10440

TTCTTCAAAT TGTAAATCTT CTTTAAAATG GTGATCGTCA AAAACCATAT AATCAAACCC 10500

TAGCTCATCC ATCGTTTGAC GCGCATATTC ATAACCTAAC ATGGTTGGAT TACATTTAAT 10560

AAAGGAATGG AGCCCTTTTT CACTTAATAA ATAGGCCGCA ATTCGTTCAA TTTCGTCTGA 10620

TGGACAACCG TGTAAAGTCG ACAGCGTAAT AGAATGACAG ACTTTAGGAC TAATTGCTTC 10680

GATATATAAG TCATCTACTT TTTTAAAATA AGATAGATAT TTTTTGGCAG CTGCTTGGCA 10740

TTCCGCCCAA ATCGGCGTTC CTTCTGCGTT CTGCATTTCG TTAATATAAC GATCAATTTT 10800

TGGTGATTGA ATCCCTGCCA AATCATAGCC AACACTCATA TTAAAAATGA AACCATTCGG 10860

GTCACCTAGC TCGAACTCTT TACTAAGTAA CTTCAAAACG AACCATGCTT TGACGTATTC 10920

ATCATAAGCT TGGGGAACGC GCAATTCTGT GGACCACTCA ACGTTGTAAC ATTCATCTGC 10980

TGCTGCGATA CATGGTTTAC TCACAGGTAA ATCTTCTCCA TCCAGTATCT GGACTGTCTT 11040

AACTTCAAAA AAACGAGAAC CTGTTAAATA GGCCGCAATA ATATTTTGTG CTAATTGTGT 11100

ATGAGGACCT GCTGCTGGAC CACAAGGGGT TTCCATTTTT TCTCCAAATA ACGAAATCGT 11160

TTTTGTAGGA TCCGCATGAT AAAATTTACG AATGCCAAAA ATTGTGCCAT CTTGTTGATA 11220

CTCACTAAAA ATCCAATTTA ATAAAGCCTC AATTGAGATG GGATGCATAA TATCACTCAT 11280

TAACGTCACT CCTTTTATTT ATAATGAAAG CTATTGATTT ACTCGTTTCC AGAAAGATTG 11340

TGCTTGCGTT TGCGCATCAT GCCAAACTTT CTCTTCATCA ATTCCTTGAA CTTCACGATT 11400

ACGCATCCGA ATTTCTCCAT TAATCACCGT GTCAGTGACC ATCCCACCAT TCATGCCGAA 11460

TAAAATGTGC ATGTTATAAT TCTCTTTTGT CATTGGTGTC GGGCCATGAT AATCAACAAT 11520

AATGACGTCT GCTGCTGCAT TAGGTTCTAA AACGCCTAGC TTTGTTTTAA AATAGCGATT 11580

AGCCATTTGC GGATTATTAT CAAACAGCAT TGTGGGAATT TCTGCCCAAG CCGCATTTGG 11640

ATCAGCTAAA TGATGTTTGT GGATAACATT TCCTACCTTA TAGGATTCCG TCACATCATT 11700

CGTATAACCA TCTGTGCCAA GACCCATCAA AtACCATACT CATTAAACAT GCGCATCGCA 11760

GGTGGGCAAC CGACCGCATT CCCCATATTC GACTCTGGAT TCGTGACCAC CATTGTGTCT 11820

GTATCTCTTA GTAATTCCAT CTCATGAGGT CCAATATGGA TGCAATGGCC TGCCATTGTC 11880

TGTTTTCCTA AAATCCCTAA ATCAAATAAT CGGTTCACAA TCGGCTTCCC ATATTTTTTC 11940

AAAGAATCAT GAACATCGGC TAAATCCTCT GCAATATGAA TATGATAACC AATCCCATCT 12000

GGCGTATTGG CTGCACATAA TTCTAAAGAA GCATCTGATA AAGTAAATGC TGCATGCATC 12060

CCCATCATCG CTTTTTGCAT ATCATCATTT CTTAAGGAAC TGGCTTTAAT AAAGGCGGCA 12120

TTTTCTTGAA CTGCTTCCCG CATTTTCTGC TCACCATCGC GATCAGAAAC TTCATAACAA 12180

AGGCAGGTCC GAATCCCTAA CTCGTCCGCT GCATTAGATA ATTGGGTTAA ACTCCCTGTA 12240

ATTTCTCCGT AACTAGCATG ATGATCAAAG ACAGTTGTAA CGCCGTTGCG AATACTATCT 12300

AAATAAGCAA CCTTACCACT TTGATAAGTG TCTTCTAATG TCAAGGCACG ATCAATTCGC 12360

CACCATTGAT CTACCAAAAT ATCCATGAAA TTTTTAGGAT GATAATTCGT TAAACTTAAC 12420

CCACGTGCAA AGGTACTATA AATATGATTG TGCATGTTAA TAAAGCCTGG CATAATCACT 12480

CCACCTTTAG CATCAATAAA TGTCGCTTCT GGATAAGCTT GTTTTAATTC TTCTGTTGTT 12540

CCGACTTGTT TCACAACTTG ACCATCAATC GCCACACACC CATTTTCAAA AAAATGATTC 12600

TGCGCATCCC GAGTGATTAA ACGCCCATTT CCAATTAATA ACATGTATTC TTCTCCTATT 12660

TTCCAACCTA TTCCCCACGT TTAGCAAACG CTTACAAATC AATCGCTCAA TCATTCACGA 12720

ATATAGCTTG TCTAGCTTTT CTAATCTATA TTTCCTACGA AAAGCATTTG AAGCGCTTGC 12780

ATTTTTTTAC TAACGAACTC ATTAACTTGA TTAAAGTATA TCACCTTACC TTAAAAAAAA 12840

CAATGCTACC TAAAAAATAT TTTTTAGAAT TTTGACAGCC GTTATCTTGT ATTATTATTT 12900

TTATCATGCT ATCATTATTT TTCAGAACAG GTAGTACGCG ACATTAAAGG ATTTAGCCCT 12960

GCCTATTCCA TTTAAAAATA TTATGTTAAA TTTGACACAA TCTTATAAAA ACTGTTTGTG 13020

CCAGGCACAT TAGAAAGGAG CTTATTTATG TTAACCGACG AAAAACTTAC TTTTTTAACA 13080

CAAAT 13085

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TTTTGGTATG AAACAGAAAA AGTGGTTAAT CGGACTTGTT GCACTGGGCT TGGTTTTAGC 60

aGCATGTGGA AGTGGCGGTT CGAAAACGAC CTCAAACGAA CCAGCTACAC AGAAAATTAA 120

CGTCGCATCT GGTGGTGAAC TCTCGACATT AGACAGCGCT CATTATACAG ATGTCTATAG 180

TTCCGATATG ATTGGTCAAG TAGTTGAAGG CTTGTATCGA CAAGATAAAA ACGGAGATCC 240

TGAGCTAGCT ATGGCGAAAG CAGAGCCACA AGTTAGTGAA GACGGGTTAG TCTATACATT 300

CAAGTTACGA GAAGCAAAAT GGACAAACGG GGATCCAGTT AAAGCAGGGG ATTTTGTAGT 360

TGCGTTTAGA AACGTGGTCG ATCCAGCATA CGGTTCAAGT AGCAGTAATC AAATGGATAT 420

TTTTAAAAAT GGGCGTGCGG TGCGGGAAGG ACAAGCCACG ATGGAAGAAT TTGGTGTCAA 480

AGCAATCGAT GACCAGACAC TAGAACTAAC ATTGGaAAAT CCAATTCCTT ATTTAGCCCA 540

AGTCTTGGTT GGGACACCTT TTATGCCTAA AAATGAAGCC TTTGCCAAAG AAAAaGGTAC 600

TGCCTATGGG ACTTCTGCAG ATAATTTTGT TGGCAATGGG CCGTTTGTAA TTTCAGGTTG 660

GGATGGCAAT TCCGAAACTT GGaAATTGAA GAAGAATGAT CaTTATTGGG ATAAAgAACA 720

CGTAAAATTG AATGAAATTg ATGtTCaAGT AGtGaAAgAA ATTGGCACAG GAGCCAATCT 780

TTTTGATAAT GGCGACTTAG ATTACACTGT TTTAGCAGAT ACTTATGCAC TTCAGTATAA 840

AGAGTCAAAA CAAGCGCATT TTGTACCTAA AGCCATGGTG GGTTATTTAA GCCCCAATCA 900

TCGCCGTGAA ATTACCGGCA ACGAACATGT TCGAAAAGCT TTTTTACAAG CGATTGACAA 960

AGAAACTTTT GCAAAAGAAA TTTTAGGAGA tGGCTCGACA GCTTTAAATG GkTTTGTACC 1020

AGCTAATTTT GCaAAAATCC AGATACAGGT GAAGATTTCC GCAAAGAAAA TGGTGATTTA 1080

TTGCCATATA ATATTAAAGA AGCCCAAGCT AACTGGAACA A 1121

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

nTCATTGAAT GCnCGGAACA ACGGAAGTAT GGATGGCGAC CCACCAGCGG CGATGCGTTA 60

TACAGAAGCT CGTTTATCAC AGTTAAGTGG TGAGTTGTTA AAAGATATCG ACAAAAATAC 120

CGTCGATTTC GTCTGGAATT TTGACGATAC AGAAAAAGAA CCCACTGTTT TACCAGCCAA 180

ATATCCTAAT TTATTGGTAA ACGGCTCAAC GGGGATTTCA GCAGGCTATG CAACAGAAAT 240

TCCTACGCAT AATTTAGCGG AAATCATTGA TGGAACTGTG TATTTAATTG ATCATCCTAA 300

TGCAAGTTTA GAGAAATTAA TGGAATACAT TCCAGGACCA GATTTCCCAA CAGGTGGGAT 360

TCTACAAGGA AAAGCAGAAA TTAAAAAAGC CTACGAAACC GGCCGTGGTA AAGTAATTTT 420

ACGTGCGAAG ACAAAGATTG AGCCTTTAAA AGGCGGCAAA CAACAAATTG TCATTTCTGA 480

AATTCCTTAT GAAGTCAACA AAGCAACGCT AGTGAAGAAG ATGGATGAAA TCCGTTTAAA 540

TAAAAAAGTA GACGGCATTG CCGAAGTTCG TGACGAAAGT GACAGAACTG GCTTGCAAAT 600

TGTTGTTGAA CTAAAAAAAG ATGTCAATGC AGAAGGTATT TTAAATTATC TATTTAAAAA 660

CACTGAATTG CAAATCAATT ACAACTTTAA CATGGTAGCC ATCGACAACA TGACCCCGCA 720

ACAAGTGGGC CTAAAACGGA TTTTAGAAAG TTACATTACG CATCGCAAAT CAGTTATCAT 780

TAACCGTTGT CAATTTGAGT TGGACAAAGC TCGCAAACGT GAGCACATTG TTGCTGGTTT 840

AATTAAAGCA TTGTCTATCT TAGATAAAGT GATTGCAACA ATCCGTGGCA GTAAAGATAA 900

AAAAgATGCG AAGAAGAACT TAGTATCCGA CTATGCGTTT ACTGAAGAAC AAGCTGAAGC 960

AATCGTTACT TTACAGCTAT ACCGTTTAAC CAATACGGAT ATTACTGATT TACAAGAAGA 1020

AGCGAAAACT TTAGAACAAC AAATTGCTGA GTTATTGAAC ATTTTAAACA ATGAAAAAGA 1080

ACTATTCTCA GTCATGAAAA AAGAActTCG CGAAGTTAAA AAGCAATATG GCAATCCGCG 1140

CTTAACTCAA ATTGAAGAGG AAATCCAAGA AATCAAGATT GAAACAGCCG TGTTAGTTGC 1200

GCAGGAAGAC GTGGTCGTAA ACnTGACGCA CGAAGGCTAT ATCAAGCGGA GTAGTATTCG 1260

TTCTTATACA GCATCAAA 1278

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ACTTTTTGCT TAAATTTCGT GATGTTTTGC ACTGACTATT CTTCCTCTTT TTGGTAACGA 60

TAAATGATTC GTCCATTTAA CCCCGCTTCT CCAACAATTT CCGCGCGGTC AGGTAAAGAA 120

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ATCCAAGCAT CACGAAATTG GAAAAATTCA TTTTGCTCCA CGATTAATTC AGAGATTTCT     180
CCAGCTTTTA ATGAAGCAAT TTTTTCTACA AAAGGATTTT CAGCCATTGA TTTCACCACT     240
CTTTCTCTTA AATATCAACT CTTATAGTTT ACTTGAAAAT GGCGCAATTG TCTGTAAAAA     300
AATCGAATCT TTGCCTTTTT TTAAACAAAG TCTTTTACTT GATTCTCTTA CAAAAAATGC     360
TATAATAACC TCAAAGGTCA AAAATGGTCA AGTGGTTTTA TAGACAGAAT TTATTCCTGC     420
TATCTAGTAC TTGGCTGGTT TGAGGAAAAA TGGTCTGTTT ATTAGAAATA ATAGAGCAAA     480
CAACTATTTT TCTGGCCTCA GTTATTTTGA AAGGATGTGT TTCATTCAAT GATTTGTCAA     540
AATTGTCAAC AAAATGAAGC AACAATTCAT TTATATGCAA ATGTGAATGG TCAAAGAAAA     600
CAACTGGACT ATTGCCAAAG CTGCTATCAA AAATTAAAAA ATCAAGCAAA TAATTCCCCT     660
CAAAATATGG GACAAGACCC TTTTGGCTTT GGGAGTTTAG ACGATTTATA TCGTTCTCTT     720
TCTCGCCAAA TGCAACAAGG TAATCCTTAT GAACAACAAA CACCACCCAC TCAATTTGGT     780
GATGGTGGTA ATGGAGGTCA ACCCCCTCGC GGAGGCGCTG GCGCTGGTCA AGGTTTACTA     840
GGCGAGTATG GGATTAACAT CACCGAAGCG GCACGCCAAG GAGATATCGA TCCTGTGGTA     900
GGACGTGACC AAGAAATTAA GCGTGTCATT GAAATCTTAA ATCGCCGTAC AAAAAACAAC     960
CCCGTTTTAA TCGGTGAACC AGGTGTTGGT AAAACAGCCG TTGTCGAAGG TTTAGCCCAA    1020
AAAATTGTCG ATGGCGATGT GCCCCAAAAA TTATTGGACA AAGAAGTCAT TCGTTTAGAT    1080
GTGGTTTCAC TTGTTCAAGG AACTGGTATT CGCGGACAAT TTGAAGAACG GATGCAAAAA    1140
TTGATTGAAG AAATCACTGA AGCTGAAAAT GTCATTTTAT TTATTGATGA AGTCCATGAA    1200
ATTGTGGGTG CTGGTGCTGC TGGTGATGGC AATATGGATG CTGGCAATAT TyTAAAACCA    1260
GCCTTAGCAC GTGGTGAATT ACAATTAGTC GGTGCCACAA CTTTAAATGA GTACCGTATT    1320
ATTGAAAAAG ATGCTGCCtT AGAACGTCGG ATGCAACCAG TCCAAGTAGA TGAGCCAACC    1380
GTTGCCGAAA CCATAACGAT TTTACATGGT TTGCAAAAAC GTTATGAAGA TTATCATCAT    1440
GTTAAATATA CAGATGAAGC GATTAACGCA GCAGCAAACT TATCCAATCG TTACATTCAA    1500
GATCGCTTTT TACCAGATAA AGCGATTGAC TTGTTAGATG AATCTGGTTC AAAAATGAAT    1560
CTAACTATCC AACTCGTCGA TcCAAAAACA ATTGATAAAA AATTAGCAGA AGCGGAACAA    1620
CAAAAACAAC aAGCTTCCGC AGAAGAAGAT TTTGAAAAAG CGGCTTATTA TCGTGATCAA    1680
ATCAATAAAT TACAAGCAAT GAAAGAAAAA CAAATCAGCG ATGAAGAAAC ACCAGTCATC    1740
ACTGAAAAAG ATATTGAAGC CATTGTGGAA CAAAAAACTG GCATTCCTGT CGGTGACTTA    1800
AAAGAAAAAG AACAAACCCA ATTGAAAAAT TTAGCTGTTG ACTTAAAAGC TCATGTTGTC    1860
GGACAAGATG ATGCCGTCGA TAAAGTAGCT AAAGCGATTC GTCGCAATCG TGTAGGCCTA    1920
GGCAAACAAA ACCGCCCAAT TGGTTCCTTC TTATTTGTTG GGCCAACAGG CGTTGGTAAA    1980
ACAGAATTAG CAAAACAATT AGCTTTTGAG CTATTCGGTT CAGAAGATTC GATGGTTCGT    2040
TTTGATATGA GTGAGTATAT GGAAAAACAC AGTGTTTCTA AACTGATTGG TTCTCCTCCA    2100
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GGCTATGTTG GTTATGACGA AGCTGGACAA CTCACAGAAA AAGTCCGTCG TAATCCTTAT 2160

AGTTTAATTT TATTGGATGA AATTGAAAAA GCGCATCCTG ATGTTTTACA CATGTTTTTA 2220

CAAATTCTCG ACGATGGTCG TTTAACAGAT GCACAAGGTC GTACAGTCAG CTTTAAAGAC 2280

ACCATCATTA TCATGACAAG TAATGCTGGA ACAGGAGCTG TGGAAGCCAA CGTTGGCTTC 2340

GGTGCTGCCC GTGAAGGTGT GACTAAATCT GTTTTAGGTC AATTGAACAA CTTCTTCACC 2400

CCCGAATTCC TTAACCGTTT CGATGGTATT ATCGAATTCA AAGCATTAAG CAAAGAAAAC 2460

CTGATGAACA TTGTCAGCTT GATGTTAGAA GAAGTAAATG GCTTATTAGC TAAACAAAAA 2520

TTACACATTG AGGTTCCAAC AGAAGTCAAA GAGAAACTCG TTGATTTAGG TTATGATCCT 2580

GCAATGGGCG CTCGTCCTTT ACGTCGAACA ATTCAAGAAC AAATTGAAGA CGGCATTGCT 2640

GAATACTATC TAGATCATCC TGAAAATCAT CAATTAGTCG CAGCGTTAGA TAACGAAGGT 2700

AAAATTATCG TAACTGGCGC ACAAGAAGTG ACTAAAACAG AAACTTCAAC ATCTGACCAA 2760

GCAGAATAAT CAAAAATCCA CACGCATTAA TAACAATGCG TGCGGATTTT TTTATGCTTT 2820

TCACTTTTTA TTTTCATCAA AAAAACTATA ATAGAAGAAA GATATTCGTA TACTTGTTCC 2880

TCATAGAAAA AATTCAATCT GGAACTCCTG TACATAATTG GAAACGCTCT TTTGCAGCAC 2940

ACAACTATAA TGAGGTGATA AAATGAAATT AGTGAATGTG ACCAATAGCT ACAAACAATT 3000

AGTAAATAAA CAATTGGAAA ACACGGATGC TTACTTTGTA AAAGTCTACT CAGCAGGAAA 3060

TACGACCGCT GTCTATTCAG AAGCAGCTCA CCATGTGGAA GTTCTGATTA TGAATAAAAA 3120

TCGTCGCATT CGTCCGACAG AAGTAAAAGA AATTTTAGCA AAACTGTTAA AACGATTACC 3180

TAAAGAGGCT TATGACCCAG ATGAAATTTC TATCATTGAG TTAAACCATG TGACCGAAGT 3240

GTCTGTTCCA TTAAAAGTTT CCCTCATGGA AAACTAAAAA AAACTGCCGA AGTTTCCCCA 3300

CTTCGGCAGT TTTTTTAATT TATTGTGACG TTATTTTTTT TACAAGACTT TGATAATTTT 3360

CCGACCAGGC TTCCTCATTT GTCGGACTGA CTAATTTATT TTCCTCGATT GCTTTTTTTC 3420

TTAAGTCATC CACTTCTTTT TTGAAATTTT CCCCCGATTT TTGAGCATAA TCTTTAGAAA 3480

AATATTTTGA TTGGCGAGAA TAAGCCTTCA GTTTCGCATC TTTAATCTCT TCTTCTGTAT 3540

CTGCAAAATA TTCATCATAA CGAAGATCGG TTATTTTCCC TGAATCTTTT AACGTAATAA 3600

CAGTTAAACG TCCAGAAAGC CCCTCCTCAA AATCTTCTGT TAGACTTGTA TAATGTTCTT 3660

TTGAAGGTTC TTTGATTTCC TTGGCTAAAG CCCTAGCAGC AGGAAGATAG CCATTATTAG 3720

CGCTATTGGA TTGACCTTTG GCTGTCTGGA AGGCGCCATC TAGGCGATTT TCAGCAACCA 3780

TTTGATTTTC TAGAAAAGTC ATCGTATTAA CAACGGTCAC TAACGATTGA TCAGTTCGGG 3840

CGTTGTTCGC TTGAAAATTT GCATAGCCGG ATAAACGTTT tGTCACTCCT GCCCATTCTT 3900

CAGAATAATA GTTTTTAGGT CCACGTTCAT CAAATTCCAC TAACTGAATT TGTTGATCCT 3960

TAACAACGAC ATCAATTAAA GCCGTATAGC CGCCATCAAA CACGACTTCA TGATGATAAT 4020

AATCCCCTTG AACTTCCCCG ATTTCTGGAC GACCTGACCA ATACATCTTT TGAGCTTTTT 4080

CTTCTGGACT AATTCCTGAT TGTCCATTAT TAGCTTCTAC TGTAGCGCCA GAAACAGCAT 4140

CAACTTCAAA GGTATGTCCA TTACGCTCAT AACTCACTTT GGCA 4184

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

AAAAACACGT GTGTCTGTTC CATaATAGAC ACGTGTAGGA TCTGCGCCAG GAACATATAA 60

AACGGCCATC AGCGTCACCG AAATTAAAGC GCCGATTAAA ACTAAGCTGA AAATTCGACC 120

GCGCTTACGA ACAAAGCGTT CCAGAAGAAT AAAAAGTAAT GGCCAAATTA AATAATTTTG 180

CGCTTCAACT GCCAATGACC AAATATGTAC AAATGGCGAT TGTGTCGCAA ATCCATCAAA 240

ATAAGAAAAC CCTTTAAAAA TTTGCCACCA GTTGTTGTAA TAAAAAATAC TACTAGCGAC 300

AACGCTGCGA ATATTGTTTA ATAAATCCTG CTGAAAGAGT GTAATATAAC TAACTGCACT 360

TAAAAGCATC ACAATTAATG CTGGATACAG CCGTTTCATC CTTCGCACAT AAAATCCTTT 420

TAAATCAATG GTCTGATTTT CTGCCCATTC TTGCCGCAAC AAGTCGTTAA TAAGATAACC 480

TGAAACAACA AAGAAAATCG GAACACCTAA GTAGCCACCT CGCATGACTT GGGGAAAAAG 540

GTGATACAAA ATCACGCCAA TTACAGCGAT CGTCCGAATG CCATCAAAAC CTGTAATATA 600

GCGTTTTTTC TTGCTATTTG CTGtCTGATT CATTTGtGCT TTCCAACTTT TCTATAAAAT 660

TAwTCtTTkC CyTTAtTTAA AGaAGCAAGT AACTTTaATA TACGtTTTTT CCtAGGAAAT 720

GGCAAGCAAA CTTTGCCTCC TTTAGGCTTT TTTTACAATT CAAAAAACCA GCATTTTTTA 780

AATCACAAAA AAACAACCAA AGCTTATGAA AATCACTCAT AAGCTTTGGT TGTTTACTCA 840

TATCGTTTTC GTTTaGakGA rGATGGaATC CCTAGGGCTy CACGaTwTTT TGcTACCsTT 900

cGCCGGGaTA TTTCCakGCC kGAATCTTTw AATCGCTCGA cTrATTTTGg ATCcAGATAA 960

CGGTTTACTT TTTACTTCTT GATCAATTAA TTTTTGTAGT TGCTTTTTAA CCATCGTTGT 1020

TGAGACATCC TCGCCATCTT CTTCTGATGA AAGAATACTT GTTGAGAAGA ATGAGCGCAA 1080

TTCAAAGACG CCAAACGTGG TTTCTAGATA TTTTCCATTG ACCGCACGAC TAACTGTCGA 1140

TTCATGAATA GACAAAGCAT CCGCAATTTC TTTTAAAGTC ATTGGTTTTA ATGGCCGATC 1200

TGCTTCTAAA AAGAAGGCTT CTTGACGACG CACAATTTCT TGCCCTACAC GTAAAATTGT 1260

ATCCCCCCGC TGATTCACTG CGCGCTCTAA CCATTCAAAT TCGTTTTTCT TATCCTTAAT 1320

ATATTCTTGG ACTTCTTTGT CGTCAGTCTC TTGCATTCGT TTGAAATAAT TTTCTTGAAA 1380

ATTTAATGTC GGTCGACCAG CTTTGTTGGA AATCACCACT ATTCGATCTT CCTTGATTCG 1440

GACAGTTAAA TCTGGTCGAA TATACAATTC CTCGGTCGCA TCAAAAATAT TCCCTGGCGC 1500

TGGCGATAAC GTTTGTATAT AATCAAAAAT CAATTGAATT TCTGCTAATT CAATCCCGAA 1560

TTTTTTAGCT AACGGGCCCC ATTTACGACT CACTAAGGCA TCAAATTCTT CCTCCAATAA 1620

AATATACGCT AAATTAGGCG CGGTATCGTC TCGTTCTGTT TGTAGCATCA AACATTCTTG 1680

TAAATTGCGT GCCCCCACAC CTGCTGGATC TAGCTGTTGT AACAAAGTTA ATGCATCTAG 1740

CATTTGAATG GCGCTTGCTT CGGTTTTCAC TGCCGCTTCT TCTAACGAAA TCGTTAAATA 1800

ACCATTCACG TCTATATATT CTACTAAAAA CAATACCAAT GTTCGCAAGT ATGTATCGCG 1860

GTAATTCAAA TGAATTTGAT CAATTAAAGA CTCAAATAAT GATAAATGAT AGTCTGGAAT 1920

TTGATTCATA TAATTATTTT CTTCGTCTTG ATTGGTGTAA GAACGACTAG TTATCGGAAA 1980

ATCTGTGGTG TACTGCGTGT CTACTTGTAA ATCAATCAAT GGATTCTCTA GTGCTTTCGC 2040

TTCAACAAAG GCAGCGAGTT CTTCCGTATT AAATTGTAAA ATTTGAATGG ATTGTTGAAG 2100

CTGTTGAGTC ATGGCCAACT TCTGGACTTG TTTTTGTTGT TGGGACATTC GTTGCTCAAA 2160

TTTCATTATT TTCGTCCTCC CTCTTGTAAT TTTTGTCAAT ATCAGCTAAA CTAGTATTCG 2220

TGCCGCGCCC TTAGTGTAGT GGATATCACG TAAGATTCCG GTTCTTGAGA CGGGGGTTCG 2280

ATTCCCTCAG GGCGCGTTAT TTAAATATGT TGATTTATCA ACGTTTCTGG ACACTCTTTA 2340

TTCATCTAAA GAGTGTTTTT TTCTTGTTTA GGAATGATTT TTCTATCCGT ATTTTTTTCA 2400

AATGTTGCTT GTGGCAAGCT CAATCGCACT TAACGCGACA ACATTTGTTC TGCTTCAGCT 2460

ACAAATCCAA TAAGGTTAAA ATTCCTCCGT TCCTATTGTA ACGCATAACG TTTCCTTTTT 2520

CTATCTGCTA AACAAAGTAT TACGACAAGC AAACACCTGC TTCTCTCTTA AAGTTCCCTT 2580

TCTGATTATA TAGTAAATTG CTTTTAATTT GTTAATTATT TTACCTAAAA CTTAATACCC 2640

TAATTAAATA AAGAACCTGG GGCAAAAATC ACTTTGGATT TTTGTCCCAG GCTTAAAACC 2700

TGATAATTGG CGGGAACAGA ACCGTTCAGC TCCGACCTCT AAAATACTTA ATTAGAAATA 2760

TACTACCAGC AATCACACCA ATTATGATTA CTAGCCAAAA TAATCCACTT ACAAGTAACA 2820

GCTCAGTTAA GGTCGTCTTC AGATTCTCCT CCTTTAAATG GCCTCTGCTT TGTTTTGCTA 2880

TGTAATTAAT GGCGAGATCA GACAACAGCT ATCAAAAAAA CGGACCAACA CGTGGTCCGT 2940

TTTCATTCAT TATTAAGCTT TTACGATGTT CGTTGCTTGT AAGCCGCGTG GACCTTCTTC 3000

AGTATCAAAA GTTACTGCTT GGCCTTCGTC TAAAGTTTTA AATCCATCTG ATTGAATAGC 3060

TGAAAAATGT GCAAATACAT CATTGCCATC TTCACCTGTA ATAAATCCAA AACCTTTGTC 3120

TGCGTTAAAC CATTTTACTG TACCGTTGTT CATATATATT TCCTCCTAGT GCATAAAAAT 3180

ATGCAAGTTA TTGCAAAAAA TGTTGAGTGG CAAAAGGAGA AGTATAGTTT TTAAATATAT 3240

AACTCAAATT ACTTATCAAA ATTGATTACT TAATTACTAT AACATATTTA TTAGGAATAA 3300

ACAATGCCCA CGACTCTTCC TTGGACTTTC TAAAATAATC AAAGATGCGC TTGACAAAGC 3360

CCTAGCAAAA AACACTCCTA TTCTCTCTAT TTCCAGTTAG TTTTGTTTAA CTTTAAATAA 3420

TCACTACGCG CCAAATAATC AAATAGCGGA GcTAATCCTG GTGAAAAATT TACTTCCTCA 3480

AACCGCTTAA TAAATTGTAC GCCTTTAATT TTATTTGGTT CGTTCAGGGT CACTTTTCCT 3540

TGGGCTTGTT TGGCAAAATA AAAATGTCCT TGCCAAACGA TTGAATCAAA AACAAGTGGT 3600

CCAGTAAAAA TTTCTTCAAG TTCAGTAATT TCCACTGCTA ATTCTTCTTT CATTTCACGA 3660

ATCGCACATT CCAGCGCTGA TTCACCAAGT TCTTGTTTTC CGCCAGGGAA ATTCCATGTG 3720

TCTGGCCGAT CTTTTAAAAT AAGAATTTCA TCAGATTGAT TTTTAAGAAG TACTCGCGAA 3780

AATTCTTTTT TCATTTCGTT TAACCCTCTT CTTCATTTTT TATTGAGAAG CCACACTTGG 3840

TAGCATAAAA ATATAATGCA AAATACGATC CGCATACGAC GGATTTTTTT CAAAGTCATT 3900

GACTTCTTCA TTGACTAACT CCAAATCATC GGTAATCACT CCAGCAACGT CCATAAAGAG 3960

CATTTTACTC AATACCTCTG AGTCATTAAC TGTCCAAGCA TAAACTGCTT TTTTCTGTTG 4020

GTCAGCTTTT AAAATGAAGG TATCATTCAA CGTAGTAGCT TCCATTGTAT ACAAATCAGC 4080

TTGTGTTTCT GGAAAAGTGA AATTATAGGG CAAAATAAAA CTAACTTTTA CTTTTGATTT 4140

GGCTTTTTTA AACGCTTTGA TCACATTGTA GTCGAGAGAT TGAACCTGAT GGTTATTCTT 4200

TATCAGAGGA CGTTCATATT TTTCAATAAA GTTAGAAAGC GCACCTTGAC TATCTTGTTT 4260

AGACGTTTTA ATTTCTACTA GTAATTTTTG TTTGGCTTGG TTTGCTTTCG CTAAATAATC 4320

ATCAAAACTG GCAATTGGTG CTTCTTGGCC ATTTTCTTTA ACGGTCATTT TTGTTAATTC 4380

AGCCAACGTA AATTCTTGCG GCGTGCCATC AACGCCGGCG AGTTCTTGAA GGTTTGCATC 4440

ATGCATCACA ACAAATTGAT GGTCTTTGGT TTCTTGAACA TCAATTTCAA TATAATCTGG 4500

TTTAAATTTA ATGGTTCTTT CCATAGCAGG AATGGTATTT TGTACGCCAT TACTATTGGT 4560

GACCCCTCGA TGCGAAATAA TCAAAGGTTT TGATTCTAAT AGCCCTGTTA AGTAAACAGC 4620

GTTGAAAATT ATATAGCCGC CAAAAATGGT GAATAGTCCT AGGCCCATCC CGATAGTCAC 4680

TAATTTATTA CGTTTCGTTT CTTTGTCAAA GGCAACTTTT GTCGTCGTTT CTGCTTGAAC 4740

ATTTAATTGT GTATATAAGA AATTAATCAG TAATACTGAA AGCCAAGCAT TAGAGACAAA 4800

CTGTAAAAAT TGGACAACGG TTAAATTTAA AATCCCACCT AGCAAGCTAA TGGTATCGCT 4860

CAAGGTATCT AACTTCAACT GTAGAAGATA AAGTAACACA TAAATAACAT ACGTTGAAAC 4920

AAATACCGCG ATCGTCACAA ATGCAATATT ACGAATAATG AACCATAATC GTTTGTTTGT 4980

CATTGACCAA CTAGCCTTAA CTGCCTCGCC CGCTTTTTTT CTCTCCAGAA TCATTAATGG 5040

AAGCGTGTAA ATGAAACGAA TAGCTAAATA CCAGACnnrt AACCCAAAGG CCAGTAACCC 5100

CACCAAGTAA GGAATTCGTT GGGACAAAAA TTCAACAATA AAATCTGGAA TCACAAATTT 5160

CGTCAATAGA TTACTTTGGA AAATCAGGTT ACCAAAAGGG ACAATGACAA CAAAATAACC 5220

GAAAAAGAAT AACCACGAAC GGGCACcTTG CTTTTTAAGA aCCTTAAAAG ATGCCTTGGT 5280

AACTCCTTTA AAATGAAAGC GATGGTCTTG CCGTATTTGA AAAATCCCTA ATAATAAAAA 5340

GGTAAACTGA TAAAAAACTG CACCTAAAAA AAGTAACAAC AAGAGAATTA ATAACACCAG 5400

AGCAAGCGGC TTTTCTAACA ATAAATTCAG GTTATTAAAC GAAAGATAAG GAATACCTTG 5460

AGTTTTTAGT GCGTTGGAAG TAGCCCAACT AAAAGCCCCA CCCACCAATA ATAATAAGAC 5520

ATTTAAAGTA AAAAATAACC ATAAATACTG CAAGATGTCT TTAAAAAATT GCCTTGTTCC 5580

ATTTTTAAAT GTTTGCCAAG CAGACATACA AACTCCTCCA TTCTAAAAGT ATCTGATTAA 5640

AGTTCTTCCA TACGAAGCCT AAATAAAACA ACGGCAATCC AAATTGAAAT AAATGATGGC 5700

AAAATAACAA TAATGATTTC GACTGGCTCA TCAATAGTTC CTTGTAACGT ATTTTTTACT 5760

TCTGAAGAAA CAATaAACTG ATCAAAAATC ACTTGATAAA TAGTAACATA AATCAATACC 5820

CATTGAATAT AATATTCAAT TATTTTCaTT AAAGCGATGG GTAAAACAAT TTTTTTCGTC 5880

GTTAAATTCA ATAAAAAATA TAACAAAAGA CTCGTACTGA TGATAACGAC TATCCCTAAA 5940

AGAAATAACG ACTCTAACCG CTGCCCTATT ACGTTTGCAA CGCCCATTGT TAATAATAAA 6000

TACATAGCTA CCGAAATTAA GATGCTCACA CTTAGCATAA CAGAAAACAA AAGTAATGCC 6060

TTAAGAAAAm sCCACTTATC AACTCTTTTA TTTCCAATCA ATAAACCTAA AAGAATCACC 6120

GACAAAAGTA AAATCAATTC AATCATTCGT TCCTCCTCC 6159

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GTAATAGCAG AAATGAGGAA AAGAAATGCA GAAAGAATCC ATTTATGGAC TGACGAGAGA 60

ACAGCTTGTG GACTGGTTTT TAGCCCATGG CGAGAAGAAA TTTCGCGCAA CACAAGTGTG 120

GGAATGGTTG TATACAAAAC GTGTTGCTTC ATTTAGTGAA ATGTCGAACA TTTCTAAATC 180

ATTGATGACT TTATTAGAAG AAAATTTTTC ATTAAATCCA TTAAAACAAG TCATTGTGCA 240

AGAAGCACAA GATGGTACCG TAAAATATTT ATTTGAATTA CCAGATAAAA ATATGATTGA 300

AACAGTCTTG ATGCGTCAAG AATATGGATT ATCTGTTTGT GTGACCACTC AAGTTGGCTG 360

CAATATTGGG TGTACATTTT GTGCTAGTGG GCTATTAAAA AAACAAAGAG ATTTAACTGC 420

TGGCGAGATT GTTGCCCAAA TTATGTGGGT GCAACATTAT TTCGATGAAC GTGGGTTGGA 480

TGAACGTGTT AGCCATGTCG TTGTGATGGG AATTGGTGAA CCATTTGATA ATTATGCCAA 540

TGTCATGAAC TTTTTACGAA CGATTAATGA TGATAAAGGC TTGGCTATTG GTGCCCGTCA 600

TATTACAGTT TCAACAAGTG GTTTAGTGCC AAAAATTCGT GAATTTGCAG ACAGTGGACT 660

ACAAGTAAAC TTAGCAATCT CATTACATGC TCCTAACAAC GAAtTCGTAC ATCAATTATG 720

CGGATTAATC GTAGTTTTCC AATTGAAAAA TTAATGGCAG CAATTGATGA ATACATTGAA 780

AAAACCAACC GACGTGTTAC ATTTGAATAT ATTATGTTGA GTCAAGTGAA CGACCGACCA 840

GAACATGCTC AACAATTAGC AGATTTACTA CGGAATAAGA AAAAACTTTC TTATGTTAAT 900

CTGATTCCGT ATAACCCAGT GAGTGAACAC GATCAATATA GCCGAAGCTC TAAAGAAGCG 960

GTTTTAAAAT TTTATGATGT ACTCAAAAAG AATGGCATCA ATTGTGTTAT TCGTAAAGAA 1020

CACGGAACAG ATATTGATGC GGCTTGCGGA CAATTACGCA GCAAACAAAT GAAAAAAGAA 1080

AAAGTCmAAA ACCAATAACG TAGTTAAAAT CGGATCAGAA AGGTTTCTTT TTGATTCGAT 1140

TTTTCGTTTA TTTAATAAAA AATCGTCGGT TTTTCAATTC TTGTTTaTAA ACaAAAGATG 1200

rATGCyCtAA AACtTTTATG aCAAwTTTyC TTTTtGTGGt TTTcaAnCTT GaAATyCTAA 1260

AAGGAAATAG CTATACTGGA AAGGAGATCC GTCnCCnGAT TTTTTCCTGG AAACCGCCTA 1320

TTATTTTCCG nTAnCCTTTT CCAAAAAGnT GGGAATTTTG GTACGC 1366

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CATTTCCGAT TATGCCGGCG TTTAGTTTTT TGAAAATCGA TTTTAGTGAT ATTCCGATTC 60

TACTCGGAAT GTTCTTGTAC GGACCGTTAG CAGGAGTAAT TACTGCTTTT GTTCGTTCGT 120

TGCTACACCT GTTCTTAACC GGACTAGCAC CGCAAAATAT GGTGGGAGAT TTCGCTAGCT 180

TTTTAGCAAG TAGTATCTTC ACCTTGCCAA TTTTTTATTT CTTTGGTAAA AAGAAAAATA 240

TCCGTACAAA TCGGATAGTG GGCTTAGTAA GTGGGATCTT AGCCTTGACA ATTTTCATGA 300

GTATTGCGAA TTATTTTGTC ATTACACCCA TTTACTTACA ATTATATGGT GTGACCACAC 360

AACAATTTTT AGGAACATCT TTAGCAAGCT ATGTGGCGAT TGGTATTGTG CCATTCAACC 420

TTATTAAAGG CCTCTTAGTC AGTGGTGTTT TTCTAGTACT ACATGCGAAG TTATTGCCAT 480

GGCTATCAAA AAAACAACAT ACTATTCAGA AAAAAACACC GTTAACAAAA TAAATGATAA 540

AAAACCTGCT GTTGAACAAT GTTTGACAGT GGGTTTTTAA AATTTACGCC TAAAAGAAAA 600

GAGGkTGTCA TAATCTGtCA TCATTCTGTT AAAAAATACT AAACCATCTG CATTGTAATT 660

TTAACTTTCC CTTGGTATGA TAGAAATCAT CAAAGAAAGA GGAGTTTTCC TGAGTGAAAA 720

AGTGTAAAAA TTGTCGTCAC GTGAATCGTG ATACGGAGTC CTTTTGTGAA GAATGCGGCG 780

CTCCGCTAAT GAATGAATCA ATGCATCAAG AGGAAAACCA AGCACAACCA TCAATGAATA 840

AAGGGGACGA TCTACTCCTC TCAGATCAAA AAAGAAGCTG GATCTGGGCG TTCCTTTTGT 900

GGTCCATCCG TCCTGGGGCC GGGAGCCnAT TTCCTCGGGA CCGCCATnAT TTTCCAAAGG 960

ACCACCAAAT TCCCTAATTT AATTGAAGCC GATTGAGGAA TnGGGGTGnC CCAAGGAATT 1020

AA 1022

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8145 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

TGGTTCAGGT AAAGGTCGTT TTATTTATGA AATGGCTAAA GCACATCCTG AAATTAATTA 60

TATTGGTATC GATATGCAAT TAAGTATTTT ATCGATTGCA TTAGATAAAC TAGTGGCCGA 120

TCCGTTACCT AATCTACAGT TATTGCGAGT AGACGGCGAA CATTAACAGA ATATTTTGCT 180

GAAAATGAAG TAGATTTAAT CTATTTAAAT TTTTCAGATC CTTGGCCAAA GAAAAAACAT 240

GAAAAACGTC GTTTAACGTA TAAAAACTTT TTAGCGACAG ATGAAATTAT TTTAAAACCA 300

AATGGAGAAA TTCATTTTAA AACGGATAAT CAAGGGCTcT TCGAATACTC ATTwAgtAGC 360

TTTTCTAAAT ATGGCATGAT TATTGAACGT GTGTGGCTAG ATTTGCATAA TAGCGAGTTT 420

GAAGGCAACA TTATGACAGA ATACGAAGAA AAATTTTCTA GTCGTGGTCA ACGAATCTAT 480

CGAGTAGAAG CACGTTTTGT TGCAAAATAA AAACAAGCAT TCCTTTATTT TAAGTGAAGG 540

AATGCTTGTT TTTTATTATT TAAGAAAGCC TAAGTTGTCG TTCTTAGAGC ATAGGCGTCC 600

AATAAAATTC TGGCCAGAAT GGATAATGGT AACCGTGAAC GCACTTCATA ATCGGGGAAA 660

AAGGAGCCTT CTGATTTGAA GCCTACGAAC GGAATTTCAA TGTATTTCAT TAAACTAGAG 720

TGTTTGCTTG CAGTTAAAAG GATAGTCCCA ATTTCTGAGT CGTAACAGTT TTTACCAGCG 780

ACAACTAATT CTTGGGTTTC TCCGTTTAAA GAAACAAAAA GAGCCACATC CTTTTTTGAT 840

AACTTTTTAC TAATATTTTT AATAATTTCT GGGTCCGTAT GCAGTTCACA GTATTTGCCA 900

GCCAATTGAA ACTTAACCAT CATTTCCTGA GCAATTAATT CTGAAAAACC TCTAGCAAAG 960

ATAATAATCC GTCGAGAAGC CTTGATTTTT TGGATCGCAT CTTCGATATT ACCAATTTCA 1020

ATCATGTTAA TCGTGCGAGT TACTTCTTCT TCATTCTTTA AAATGGCTGT CCGAATTCCT 1080

CGGTCTACTT TTTCTAATGC TGAAAAATTT ATATTTTGGT TTTCTTTATC TTTCAAGTGA 1140

TGCTTGAAGG ATGTGAAACC TTCATAGCCT TTCTTTTTCA TGGTTCTTAC AATCGTCGCA 1200

GTTGATACAT TGGCTCGTTC GCTTAATTTT ACAATGGAAT AATCAGGGAT TTCTAAAATA 1260

TGTGTTTCGA TAAAATGCCA GAGATATTGC TCTGACTCAC TCAATTTTTG TTCCATAATG 1320

ACCAGCCCTT CTTTCTTTCA CTAAAAAAAC ATTTATAAGC CTATTTTTAA TGAAAAAAAA 1380

TAAAAAAGCT AGAGAAATTA TGAAATTGTA AATGTTTTCT ATATTTTTGC GAAAGAATGA 1440

AAACCTTTAC ATGGCATTTT GAGACATAAT AAAGAGGAGA AAGGAGGAAC TACAGTGACT 1500

ATTTATACAT GTACATTAAA TTTAGCCATT GATTTATTTA TCGAAACAGA AGAGCTAGTT 1560

CCTTTTGTCG TGAATCGTAC GAAGGAAGAT GATATTCAAG CAAACGGGAA AGGAGTCAAT 1620

GTTTCCCTAA TTTTAAAGAT GTTAGGGATT GATAATACCG CTTTGGGAGT CAAAGCTGGT 1680

TTCACTGGGA ACTATGTCGA GGACTATTTA AAAGAAAAAG AAATAACCAC TGATTTTATC 1740

GAAGTCGCTG GTACAACGAG AATTAATGTG TTTACAAAAG TTACCCAAGA TCAAAAGGAA 1800

TACAAATTAG TCAATAAGGG ACCAAAATTA TCTGAAGAAC ATGTACAACG TTTTTTGAAA 1860

AAAATTTCAG AGTTACGTAA AGGGGATTAT TTGTGCGTAT CAGGAAGTTT ACCACAAGGG 1920

GTTTCGCCAA GTATTTTGAT TGAAATTAGC CGAATTTGTT TTGAAAAACA GGTGTTCTTA 1980

ATCTTAGACA GTAGTTATGA AGAAATTTTA GATTGTTTGC CTTATCAACC ATTTTTATTG 2040

AAACCAAATG AAGAAGAACT TCAAGAGTGG TTTCATACAG AAGTGCAGAC TAAGGACGAT 2100

TACATTTTTT ACGGACAAGA ATTACTGAAG CGGGGAGCCA AAAATATTTT ACTTTCTTTA 2160

GGTAGTGAAG GGGCTTTATT TATGAATAAT GAAAAGGTTC TTTCAGGTAA TTCACCAACT 2220

GGAATGGTTG TGAATACAGC TTGTTCAGGG GATGCAATGT TAGGTACCTT TTTAGCTGGT 2280

TGGCATCAAG GACTTTCATT GGAAAAAAAT TTGAAAAGAA GTATTGCAGC AGGTAGTTCA 2340

ACAGCATTTC GCAAAGGATT GACAGATTTT TCAGATGTTC AGGAGTTAGA GCAACAAATA 2400

AAGATTCAAG AGGAGGAATA AACAGATGGC TACGTATCAA TTAATAGCTG CTACAGGTTG 2460

TCCGACGGGA ATAGCGCACA CGTATATGGC ACAGGAGGCA TTGGAACAAG CTGCGAAACG 2520

TAAAGGTATT ACGATTAAGG TTGAAACACA TGGTCAGATT GGTATAGAAA ACGAGTTAAC 2580

ACCTGCAGAA ATCCAAGGAG CGGAGGCAGT CATTATTGCC GCCGACAAAG ACGTTCAAGC 2640

AGAACGTTTT GCTGGGAAAC GAATCATTGA TGTCCCTGTC AGTGTGGGAA TTAAAGAAGC 2700

AGATCGCTTA ATTGAAGAAG CGCTCGCAGG CAAAGGATCG ATTGCGGCCG AAAACCAAGC 2760

AGTGGATGAA CTTGAACAGG AAACACAGAT TTCTTCAGGA AATGTTGGAC ATAGTATTTA 2820

TAAAAACTTA ATGAATGGCG TCTCTCACAT GTTGCCGTTT GTAGTAGCAG GCGGCGTTTT 2880

AATTGCTCTT TCTTTTGCTA TTTGGGGCAT TTATTCATTT GATCCAGAAA GTAGTCAGTA 2940

TAATGCTACC GCTGCTATGT TAAAAAGTAT TGGTGATGCC TCAATGGGCA TGATGGTGCC 3000

AATCTTATCT GCGTATATCG CAGAGGGGAT TGCCAAACGA CCTGGTTTGG TTGTGGGCTT 3060

TGTCGGTGGT TTGATTGCTA ACACTGGTGG CACTGGCTTT TTAGGAGGGA TATTATCTGG 3120

TTTTCTTGCT GGGTATTTCA TTCTTTTATT ACAAAGAGTA TTTAAAGGCT TGCCTAAATC 3180

ATTAGATGGT TTAAAAGCAA TTTTCCTTTA TCCAGTCATT GGCGTTGCAG TTATTGGTAT 3240

CACTATGTCT TTACTAGCAG ATCCGATGAA AGCTGTTAAC GAAGGAATGA TGAGCTTTTT 3300

AGCTAGTTTC CAAAACTCCA GTCCGTTGGT TTTAGGAATT ATTGTGGGTT GTATGTGTGC 3360

CTTTGATATG GGAGGTCCAG TTAATAAAGC GGCCTATGTT ACTGGGACGG CACTCTTAGC 3420

TCAAGGAAAT ACTTCTTTTA TGGCAGGAGT TTCTGCTGCC TGCATAGCGC CACCTTTAAT 3480

TACAGGCTTT GCTACATTAT TCTTTGGAAA ATACTTTGAC ACAAATGAAC GCAATGCGGG 3540

GCTAGTGAAC TTTATTTTAG GCTCCACACA TATTACAGAA GGCGCTATTC CGTTTGCGGC 3600

AAAAGACCCC TTGAAGGTTT TACCAATTAT GATGCTCGGA TCTTCAATTG CGGCAGTCCT 3660

AACGTATATG TTTGGGGTAC AAGTGCCAGC ACCTCATGGA GGATTTCTTG TTCTACCAGT 3720

TGTTACTCAC GCTGTTCAAT GGGTTTTGGC AATTTTAGCT GGTTCATTGG TAGGTGGCTT 3780

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ATGAAATAAC AGGAATTAGG AGTGGATGGA ATGGCTTTTA TTAAAGAAAA TCATATTTTT 3900

TTAAATCAAC AGTTACAAAC GCAAGAGGAT GTTTTTCACT TTTTAGCAAA AAAATCAACA 3960

GAATTGGAAG TTGCTCAGGA CGCACAGGAA GTTTTCGATA AACTGAACGA GCGAGAACAA 4020

GAAGGAACAA CGGGGATGAT GAATGGATTT GCGATACCTC ATGCAAAAGC AGCAACGATT 4080

CAACAAGCGG CCATTATCAT CGTTACCTTG GACCAAGGTG TTGAGTGGCA GAGTCTTGAC 4140

AACCAATTAA CGGAGTTTGT AATTGCGCTG TTTATTCCAG ATGCCGAAGC TGGCACGACA 4200

CATTTGAAAT TACTCTCTTC TGTTGCGCGC CTCTTATTAA GAGAAGAAGT TACTTCTGGA 4260

CTGAAACAAG CAAGTTCGCC AGCTGAAATT GCTACGTTAC TAAATAATCA ATTAGGAGAG 4320

GGAACAGAAT GAAAAAAATT AGTGAACAAA AACGTAAACA TTTAGAAAAT CTGGTAGATG 4380

ATCAAGGGAT TATTGGCGCA CTAGCCATTG ATCAACGTGG GGCCTTAAAA CGCATGATGG 4440

GAAAATACAA AGAGGTGACT GCGCAAGAAA TCAGTGACTT TAAAGTATTA GTATCTCGTT 4500

GCTTAACACC AGAGACTTCA GCAATTTTGT TGGATCCAGA ATATGGCCTA GCTGCTGCTG 4560

AAAATCGAGC ACAGACTTCA GGTTTGTTAC TTGCGTATGA AAAAACGGGC TACGATGCTT 4620

CGACACCAGG ACGGTTACCC GATAGTCTTG ATGTTTGGTC GGTTAAGCGT TTAAAAGAAG 4680

CGGGCGCAGA CGCGTGTAAA TTTTTGCTTT ACTACGATGT TGACGAAAGT GAAGCAATCA 4740

ATGAGCGAAA GAAAGCTTAT ATAGAACGGA TTGGTTCAGA GTGTTTAGCC GAAGAAATTC 4800

CATTCTTTTT AGAAATTGTC TCTTATGATG CAAACAATTC GGATAGTGCT TCAAAAGAAT 4860

ACGCTAAAGT AAAACCGCAC AAAGTAATTG AAGCGATGAA AGAATTTTCA AAGGATCGCT 4920

ATAATGTTGA TGTTTTAAAA GTAGAAGTCC CTGTGAACAT GAATTTTGTA GAAGGTTTTG 4980

GCACTGAAAG TCTTTATAGC CAAGATGAAG CACAGGCCTT TTTCAACATG CAAAGTGAAG 5040

CAACACAACT TCCATTTATT TTCTTGAGTG CAGGGGTTAG TGCTACGATG TTTCAGGAAA 5100

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TTGAAACAAC TGGTAAAACA AATGTTGAAG AATTGAATCA GGTTTTAAGA GAGAGCGCAG 5280

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TGGTCATCTG AATTAAATTT TTTCAGAAAT CGTCTTCTTT AAGTGAACTC AATGTACGCA 5400

AACTCAAAAG ATATGATATA ATTATTTCGA TATCGATGTA TGAACACCCA AAAAGTAACA 5460

TTGCTTTACT TTATTTGGGG AAAGTTGGGG TATTATGGGA ATTCCTAAAG AAGGCGAGTT 5520

TGTAACCATT CAGAGTTATA AACATGACGG ACATTTACAT CGAACGTGGC GTGATACGAT 5580

GGTACTAAAA ACGAGCGAGT ATTCTTTAAT TGGTGTGAAC GATCACACGT TAGTAACGGA 5640

ATCCGACGGA CGTCGGTGGG TGACTCGTGA ACCAGCCATT GTTTATTTTC ACAAGAAATA 5700

TTGGTTCAAT ATAATAGCAA TGATTAGAGA AAAGGGGGTT TCGTATTACT GCAATCTGcT 5760

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TCGCCATATG TTTTAGATGA CGAAGCGTTG AAGTATATTG ATTATGATTT AGATATCAAG     5820
GTTTTTCCAG ATGGTGAAAA ACGTTTACTA GACGTTGATG AATATGAATT TCATAGCAAA     5880
CTAATGGATT ATCCAGAAGA TATTGACTTC ATTTTAAAAG AAAATGTCAA GACTTTAGTG     5940
GATTGGATTA ATAACGAAAA AGGCCCCTTC TCGCCCGAGT ATGTAGATAT CTGGTATCAA     6000
CGTTATCAAC AGCTATCAAA AAAATAGCCG ATGTAAACAG CCCACAAAAG GrGCTTGGAG     6060
CATTAGCCAA AATGGCTAAT GCTCCAAGCs CTAAATTTTC CGATTTAATT GGTGTTATAG     6120
TTCTTTGTTC ATTTCGTAGT GTTCAATGCC AGCATCCATA AAAGGTGCTC CTGTTTTTTG     6180
ATAACCTAAA CGTTCATAGA AGCCTACAGC GGTGACTTGT GCTCCTAGAG TAATCTTGTG     6240
GTAGCCTTGT TCTTTGGCAA AATTTTCCGC CGCTTCCATA ATCACTCGTC CATAGTCGGC     6300
GCCACGGTAA GCTTTTTCAA CGGCCATTCG TTGTAATTTC ATAACGCCAT TTTCTAGTGG     6360
AAGCAAGCGA CaAGTTGCGA CAGCTACATG GTTCGTGTAC AAAACAAAGT GAATACAATG     6420
TGCTTCATAT TCATCGATTT CCATCTCTTC TGGTACCCCT TGTTCCGCTA CGAATACGCG     6480
TTGACGAAGC CGGACAGCAT CTAAATAAAG ATCACTCATG GTATCTTTTG TTTGAGCTAC     6540
ATGCATnGAA AaaCCCCCAg TTCAGAAcTG tkTCTATTTT AyTATACCtG AAAAAGTTCT     6600
AGCmATGAAG TATTCTaCAA TGACTGAGGG GGGGAAGGTG TGATAAAtAA AACGCAACAA     6660
TTGAATAAAn ATAAAGGAGG AGCCGCTGTG ATTAATCGAT TTAAAGAATC GAAATTATTT     6720
TTCTGGTCAG TTGAATTACT TGTCGTGGCC AtGCTATtAt TTAwTGCTTC GAAAATTAAT     6780
TTCTTATTTG CACCGATTGG GACATTCTTT TCAACGTTGT TTGCCCCAGT CTTAGTAGCA     6840
GGCTTTTkGT ATTATTTACT AAATCCTGTG GTCAATCTAC TAATGAAGAC GAAAATGAAA     6900
CGAATTTATG CCGTCTTACT GGTATTTTTA TTACTAATCA TCGCATTAGT TCTGATCTTA     6960
TTAACAATTA TCCCTAAGTT GGCAGATCAG CTAGCTAGTT TAGCATCAAG TATGCCGGAT     7020
TTCTTTAAAC AAGTGGAGAC CTGGATTTAT GAGATTGCGG AGTTACCTAT TTTTAAACAA     7080
ATTGATTTAA CAAGCTATAT TGAAAAAATG GATATTTCTT ATGCCAATAT TATCCAACAA     7140
TTTTTAAGTA GTTTATCAAG TAGCTTAGGT TCAATCGTAT CAACGGTGGC GTCAACCACT     7200
ATTGTTTTGG TCACTGCGCC ATTTATTTTA TTTTATATGT TAAAAGATGG AGATAAGCTA     7260
GTACCAGCGA TTCAACGCTT TTTACCTGAG AAAAGAAAAG ATGATATTGT GGATCTTTTA     7320
GGACAATTGA ACCAAACCTT ATCCAGTTAT ATTAGTGGAC AAGCGATTGA ATGTTTATTT     7380
GTCGGTACAT TTACGATTAT TGGGTATTCA TTGCTTGGCG TTCGTTATGC CtTTTTATTT     7440
GGTGTCATTG CCGGCTTTAC GAATTTGATT CCCTATCTAG GACCTTATCT AGGATTAGCG     7500
CCTGCTGTCT TAGTGACCAT CTTTAATGAA CCCgTCaAAG CAGCCtTATG TTGTTTAgTG     7560
GTGCTAGTGG TTCaACAATT GGACGGAAAT ATTATTTATC CAAACGTTAT CGGAAAATCT     7620
CTAAAAATCC ATCCATTAAC GATTATTTTA ATTTTATTGG TAGCAGGAAA TTTAGCAGGT     7680
TTGCTAGGTA TTTTCCTCGG TGTCCCATTT TACGCAATCT GCCGGACCAT TATCTACTAT     7740
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GTTATTGATA TGGTCAAAGC GGGTCGTAGT GAAAAAGTTA CCAATGCCGT TCTTTTAGGG 7800

AATGAAACAA ATACGAAAGA AAATAACGGT TAATGATTGA ATCCGCTAAT CTTTCGTGCT 7860

ATGATTTTAT GGATTAGGAT AGAAAATAAC CTGTCATAAT ACTGATTGTG TCTGTTTCTA 7920

AGCCTAACCA TAAAAAGAGG AAGAACGTTA AAAGAGTACG AAAGTACAGC CTCGGAATTA 7980

TCAACAATTA AGGAGAGAGA GAACATTATG AATAATGCTG ACCCTGAGAG TCAGTCGCTA 8040

ATTGCGCAAC TTCTATTATT AGTCGTGTTG ACGTTTATCA ATGCCTTTTT GGCAGCGGCG 8100

GAAATTGCAG TCGTATCTGT TAACAAGAAT CGTGTGGAAC AAAAA 8145

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

AAAAGAGGCT TTAACAGCCA AGAACATCAA ACCTAGTGAT TTAGCGAAAA AAACTGGCAT 60

CGGTAAATCT TCGATCAGCG ATTGGCTAGC TGGTCGTTAC GAAGCAAAAC AAGACAAAGT 120

TTATCGCATT GCAGATGCAT TAGACATTAA TGAGGCCTGG TTGATGGGAC AAGAAGTTCC 180

CATGGAAAAA AATGCCTCAA CTATCGACCG CATTTATAAA AAATTAGAAC CCCAACGACA 240

AGCCATCGTT TATCAATTTG CCGAACAACA ATTACACGAA CAACAAACGC AAGCAGAAAT 300

TCTCTCATTC CCTCGCCGTG ACGAAATGAC ACTGGCTGCC CACGCTGGGG ATCCAGAAAA 360

GATATTTTCA AAAGAAGAGA TCGAGAAAAT TCACGATTAC TTGGATGAAA TTGATGCCAA 420

ATATCAACAA TCGATTTCTT CTGACAAAAA AGAGGATTAA CTTCCCATCT ACTCTTTTTA 480

TTAAGTAATG GCAGGTGAAT GGTAAAGTGA ATGATTATGA AAAACTCGTC AGTTCCATTC 540

AAAAGGATGT GACGGTTTTA GAAATTGATT TATACAATCA AACAGGTTGT TATGGGTTGT 600

ATCGAAATGG CAAAATTTAT ATTGAAAAAA CATTGAGTAC CCGTCAAAAG AAGAATATTT 660

TAGCCGAGGA ATACGGGCAT TATCAAACAT CCGTTGGCAC TATTTTAAAT CAAAATTGTA 720

CAGAAAATCG GAAGCAAGAG TTGAAAGCTC GCAATGTGGC CTTAGAGCAA TTAGTTACAT 780

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TTTTGGAAAT CGATGTTGAA ACATTAAAAA ATGTGATTAC GTACTATCGA CAAAAGTATG 900

GCGCCACTTA TCTTTATAAA GGACGGATTT TTGAATTTAG GGATTATTCT GTGATGGTAT 960

TAAATACTGG GTTAACTTAA AAaGCATGGA ACAAAATCAA TAAGGATTTT GTTCCATGCT 1020

TAAAAGTATT CTGGAAAATT CAAGAGCGTT TTTTGTACCA ATGGTTAATA TGTCCAACGC 1080

CAAGCATAAG ATTGGGGACA AGTATAAGGA CGAATATAAA TGACGGCCAA AATCCGATGA 1140

ACTGAATAAT ATGTTCCCGC ATACTATGTA GTACAAAGAA GAAAAGAAAA AAGTACAGGG 1200

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AACTCTTGCC TGAACCCATT TCTTTTAAAT AACGATCTCC ATTTTTATAG AAAACAACAA    1260
TTCTTTTCAT CTTTGCACCT CCATGACTAT TTTATCAAGA AATCATGAAA AGAAAAAGCA    1320
CACCATTCGT CTGGTGTGCT TTTTCTTTTT AATTATTCAC CTTGATTCAA CTTACGAATC    1380
AACTCATCAA TGTGATTTCC GTATTGGACA GATTCGTCTC TTTCAAAAAT CAACTCTGGT    1440
GTTTTATACA AGGTTAACCG TTGTCCTAAT TCTTTACGAA TCAGTCCTTT GGCTTTGTCT    1500
AAGCCTTGTT GAGCTTTTTG TTGTTCGGAA GCTAAATCAG ATAACAAGCT GTAATAAATC    1560
GTTGCTTGTT GTAAATCACC GGTCACACGA ACATCTGTAA TAGTGATGCC TTGGACGCGT    1620
GGATCTCTGA TGCGTTTGTT CAAGATATCA TTCACTTCAC GCATGATTTC TTGACCTACA    1680
CGACGGTCAC GATAATTTGC CATAGtGTCT TCCTCCAATT ACTAAAATTA TTGTTTGATT    1740
TCTTCCATAA TGAAGCCTTC AATCGCATCA TCTACACGTA AATCATTGAA GTTTTCAATC    1800
ATAGCGCCAC ATTCAAAACC AAGTTTGACT TCTTTCACGT CATCTTTAAA GCGTTTCAAG    1860
CTTGCTAATT TACCTTCATA AATAACAATA CCATCACGAA TGACACGCAC GCCACTATCG    1920
CGGCGAATAA AGCCTTCTGT AACATAACAG CCAGCGATTG TGCCAACTTT AGATACTTTG    1980
TACAATTCAC GAACCGTCAT TTGACCCGTA ATTTTTTCTT CAAATTCTGG ATCTAATAAC    2040
CCTTTCATCG CTGTTTCGAT TTCTTCTAGG GCTTTATAGA TAATACGGTG TAAACGAATA    2100
TCAACTTCTT CTTGTTCTGC TTGTTGTTTC GCTTGTGGTG TTGGGCGAAC GTTAAAGCCG    2160
ATAATAATCG CATTACTTGC TGCGGCTAAA GTTACGTCGC TTTCATTGAT GGCCCCAACT    2220
GCCGCGTGAA CAATTTTCAC ACGAACGCCT TCTACATCAA TTTTTTGTAA ACTTGCTGAA    2280
ACGGCTTCGG CAGATCCTTG TACGTCTGCT TTGACAATGA TATTAACTTC TTTTAATTCG    2340
CCTTCTTTTA GACTTTCAAA TAAGTTATCC AATGTCACAC GGCTACTTGC TGAACGTTGT    2400
TCAAGCAACG CACGTTTAGC CCGTTCTTCC CCTGCTTGAC GTGCTGTTTT TTCATCTTCA    2460
AAGACCACAA AACGATCACC CGCTTGAGGA ACATCATTTA ATCCGGTAAT TTCTACAGGA    2520
GTTGCGGGTC CTGCTTCTTT ATCACGGCGG CCCATGTCAT TGGTCATCAC ACGAACACGT    2580
CCGTAAGTAT TACCAACAAC GATTGGATCA CCAACATGTA AAGTTCCTTG TTGAACGAGT    2640
AATGTCGCAA CCGGACCTTT ACCTTTATCT AAGCGCGCTT CAATCACTGT TCCAATTGCT    2700
TTTTGCGTTG GATCAGCTTT TAAGTCTTCT ACTTCAGCAA TCAATAAAAT ATTTTCCAAT    2760
AGCTCATCAA TGTTTTGATT GAATTTCGCT GAAATATTGA CGAAAATCGT ATCTCCGCCC    2820
CATTCTTCAG GAATTAATTC ATGTTCACTT AATTCTTGTT TCACATGATC AGGATTTGCA    2880
CCAGGCTTAT CAATTTTGTT AACTGCTACA ATAATCGGCA CTTTTGCCGC TTTGGCATGG    2940
TTAATCGCCT CGATTGTTTG TGGCATTACT CCATCGTCCG CTGCAACAAC TAAGATGGTA    3000
ATATCAGTGA TGCTGGCACC ACGCGCGCGC ATACTTGTAA AGGCCGCATG TCCTGGTGTA    3060
TCTAAGAACG TAATTGGTTT GCCATCAATA TCTAACTGAT AGGCACCAAT ATGCTGCGTG    3120
ATACCGCCTG CTTCACCTGA AGTCACACGA GAATGGCGCA ATGTATCTAA TAATGTTGTT    3180
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TTCCCGTGGT CTACGTGTCC CATGATTGTG ACAACAGGGG GACGTGTAGT TAAGTTTTCT 3240

TCAACAACTG CTTCTGGTTC GAAGAATTTA TCAATGTCCG CAATATCAAC TTGAACTTTT 3300

TCTTGCGGTT CCATGCCATA GTCCACAGCT AATAATTCAA TTGTATCTTT ATCTAAGGCT 3360

TGGTTTTGGT TAACCATGAC ACCCATCATA AATAATTTyT TGATGATTTC CGCTGGTTCG 3420

CGGTGGATTT TTTTCGCAAT ATCCGCCACG TTCATACCTT CTGTATATTC TAAAACATCT 3480

GGTAATTCAC GGAATTTACG TGCTGGTAcT GCTGGgCTTC GCTGATTCTT GTTGGATGTT 3540

TGGCCTTTTT TCCCTTTTTT GGTTGGAAAC GATTGCGGTT TTGGnTTATT AAAAGTTATT 3600

CCGGGTTAAT TACGATTTGG AACCGCCACC AAAATGGTGG TTACGGGTTT GGCCGCCA 3658

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

TTTAGAATAT GGGCAAATTT CGTGGGCTTT TTTAACAAGT TCTTCTGCTT TAGCTTGATC 60

TACCCCATCA ATATGAACTT CTAATTCAGC ACCAACGCTA AACCCATCTT CTCCTTGGAA 120

TAAGGATACA CGTGCAGTTA CTGTACTTTT ACCTTCGACT TTTTCTTGAT CCATCACTAA 180

TTCTAATGCA CCGTTAAAGC AAGCACTGTA AGCCGCTGCG AATAATTGTT CTGGATTTGT 240

TGTATTTTCT TTCTTGACAC CTGGCGAAnA ACCGCATAAG AAAATGATTT ATCCGGTGAG 300

TGAACTTCTC CTGCACGTCC ACCCGTATTA ATGATAGTTG TTTCATAGAT TTTTTTCATG 360

TAAATTCCTC TCCTTTGTAA AGTTTTACAC TTCTGAGAAC TTGTTACTTA CATAATTATT 420

GTAGGAAACT TTGCCAGATA CAGCAAACGT TGTGCTTGTG rATAATAAAA AATaACATTA 480

ACGTgTAwTT TTGACGtGAA AAAGGACCCC ATCTATGAT 519

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TCAAAATTAT ATCCAACTAT AACAACAATC ATTTCATACC TTATTTCTTT TTATTTTCTG 60

AGTAAAACTA TGCAACATTT ACCACTTAAT ATTGCTTACG CAAGTTGGTC AGGTTTAGGA 120

TTAGTATTAA CAACAATTGT TTCAGTTCTT ATTTTCAAAG AACAAATAAA TTTAATAAGC 180

ATTATTTCAA TTATTTTAAT AATATTTGGT GTTGTTTTAC TAAACACATT CGGATCATCA 240

CACTAATTAC TTTATTCCAA TTTCCTTTTC GGTAGAAACT TTGACCCCTC ACACTCCCCA 300

AAGATGAGCC ACCAGGCAAA AAAACGCCCT GGTGGGCCCA CTTTGTTTAG TGTATATGAG 360

GGGTCTTTTC TTTCCGAAAA GTTTTCTCGG CATAAAAGAT CATCTGATGT TTTTTATCTA 420

AAAATCATTA TTTTTCTAGA AAATCGTATC ATTTTACAAC TTTTATTTTT GACTGTATAA 480

TCTAGTTAAA TCCCGTAAGG GCGCACTTAT ACGTCGATAA ATCGACGTGT GACGAAACTG 540

ACCTGcGTcA GTTTTTTAAA ATTAAATGGA ACGGcTTGAG TTaTyCCGAG CAGTTAAAAA 600

AATtAATATG kGtGAATATC GCTACTGCAT TCtTAAAAAA GTGGgGCAGA TTTTAGCCCC 660

ATAACTTTTT GGATTACATC GACGATACGG CGCGAAA 697

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

CTTCTGGTkG GCyGcTTTCt GCgGTTTcTG TTGtGCCgTT CTCtTCaGTk GTCaCAcTtG 60

GTTTTTCaGG TATGATTGGC TCaAtCGTGC CyaGTGTTTC aCTTTCaTCT GGATTTTCTT 120

CTtCtGTTGG TGAGACATGA ACTTCTGGTT GGCTGCTTTC TGCAGTTTCT GTCGTGCCAT 180

TCTCTTCAGT TGTCACACTT GGTTTTTCAG GTATGATTGG CTCAAtCGTG CCtAGTGTTt 240

CACCTTCATC TGGATTTTCT TCTTCTGTTG GTGAGACATG AACTTCTGGT TGGCTGCTTT 300

CTGCGGTTTC TGTTGTGTCT GTCTTTTCAC TTGTTTCTGT TGCCTGTTCC GAAGTAGGTG 360

TCTTTGGTTC CCATTCATCT ATTGTCTCTA AAGGAATGTC TAGACTTTCT TCTGTTGGCA 420

TTTCCACATT TTGATTGCCG CTTGCCTCGC CTTCTACAAA AACATTTTTA ACCTGTGATG 480

TATTTTTTTC ATTCGTTGCG TCTTGATTGT TTAGTTGATA ATTGATGTCA TAACTATTTT 540

CAAATGTTGC TTGATGTTGG CCTGCTTCTG TGATTGTCGA AGTGTAACGg ACGATAAAGG 600

AAGTAAAGCG TGCTTTATCC CGATAAAAAC GTAAGTTAAA GTCATTATCT GTTACGAAgT 660

CAATTTTGCC ATAACCTTGT TGCTCAAACT CGGCAAGTGA AATATATTTA GTTTCTTTGT 720

CATTCACAAT ATCAAATGTA AAACTCTCTT TATTTAATTG TTGACCACTT CCTTGTCGAT 780

CCGCAATTGA AATATCTTCT GTGACATCGG ATTTATTGAG GTTCACATTT AAAAACCAAC 840

GTACTTGATT TGACTCTCCA GCCAAATCGC CTACTTTATA AAAAAACGGA TAGTCTCGCT 900

CAATTTGGCC AGTCTCTGTG TTAGTCACTC CTTCAATCGT CAAACGTTGA GTCGCCGTTG 960

CTGTTCCGAA ATCCGTTTCT ATCACATTCG GTTGAGAACT ATTGGTGATA AGCGTTTTAA 1020

TCCCGAAAGA AAAATGCCCA TTCACATTAT GTAAAGATTC AACTTTTTCG TTAAATGTTG 1080

CTACAACATG ATCTTTATAG ATAAAAACTT CCCCTAAACC ATTTAAATTG ATTTTTCGTG 1140

GTGAACTATC GTTCTCGGTC ATTCCAACTA GTGCGTCTGG TAAAGTTAAA GTAATAGTAT 1200

CTCCAGGTTT TATTTTCTGA TTTTCTTTGT CACTAAAAGA TACTTTAATT GAGGTCATCT 1260

CTCCTTGATA TAAAGTAGTG TGATCTAATT CTACTTTGTC AACGATTGAA CTTTTGCTCA 1320

ATTCGGCGCC AAACGAAATT GGACCAATCA ATAACGCCCC CGCAATTGGT AGAATCATTA 1380

CCAACAGTAA CACTAAAAAT TTTACACTTT TTGTCATAAA AAATTATTCA CCCTTCTTTT 1440

CTCTTATTTT TTCCACTTAG TGGTCTTTTT CAGAAGTTGA CAATAGCAAA AAGATATATC 1500

TCACACAATA TTAATGCTCA TTTAAATAGC CTTTTTTTAA AATTTCTAAT TCACTTTCTA 1560

AGGAAAACGG TTTATTATGG TAGTTACATT AGATAACATT TGTTACAAAA TATCTAATGC 1620

TGCCAAATTT GAGTTGCATA AATAACATAT TTCACATCAA TAATGAATAA AAATACTTAT 1680

TTCATCCTCA TTTTGTTTCC CAGGCCATTT ATTCTTGTTA TAATAAAGTT TATGAGATAA 1740

GGAGGaAAAG AATGAAAAAT TCATATTTTG ACGGTGGTTT AGCAACGTAT ATCGGGACTT 1800

CAATTTTAGC AaCCTTGATT ACTGTCTTTA CATTAGGCAT TTGCGCACCT TGGGGAATTT 1860

GTATGATGTA CAACTGGAAA ATCAAGCATA CCGTTATTGA TGGTAAACGC CTTTATTTTG 1920

ACGGTACAGC TATGCAATTA TTCGGTCATT GGATTAAATG GCTTTTATTA ACTATAATTA 1980

CTTTAGGAAT TTATGGTTTT TGGTTGAATA TCCGTTTGCA ACAATGGATT ACAAAACATA 2040

CCCACACACT TTCATAAAAA GAGGAAGGAT GAACTGAGTT ACGGTCCATC CTTCCTCTTT 2100

TTATGAATAT CTAACAGAGT GTTATCCTAC TCTTTGAAAA AACAAGGAAT TTATGCTATA 2160

CTTTGATAAG TATCAAGGGA TACTTATGTT ATTTCGGGGG CGTTACGGAT TCGACAGGCA 2220

TAGTTGAGCT TGAATTGCGT TTCGTAGGTT ACGGCTACGT TAAAACGTTA CAGTTAAATA 2280

TAACTGCTAA AAACGAAAAC AATTCTTTCG CTTTAGCTGC CTAAAAACCA GCTAGCGAAG 2340

ATCCTCCCGG CATCGCCCAT GTGCTCGGGT CAGGGTCCTA ATCGAAGTGG GATACGCTAA 2400

ATTTTTCCGT CTGTAAAATT TAGAGGAGCT TACCAGACTA GCAATACAGA ATGCCTGTCA 2460

CTCGGCACGC TGTAAAGCGA ACCTTTAAAT GAGTGTCTAT GAACGTAGAG ATTTAAGTGG 2520

CAATATGTTT GGACGCGGGT TCGACTCCCG CCGTCTCCAT TTTTAGAAAA GTAGAGAAAA 2580

ACAAAAAAGA GCTAAAACCT TATAAAATAA AGGTTTTAGC TCTTTTTTTC TATAAGCAAG 2640

AGAAGGCTCG TTACCTCCTC TTACACTTCC TATCACATTA TCTTTCTAAA ACCACTTCAT 2700

TTTCTTTTTC TATTGGTGAT TTTGGGTATT GCaTAGAACa TGGCTAAAAA TATTATTGTT 2760

ATCAAAAGAG TTTTTAAGAT TTCAATTTCT CCTGAATCTA TCCAAGTATA CACAAAAGCG 2820

ATGATAAAAG TAATTACTAT TTCCGTAACA TGATCTTTTA AATTCATTAG CTTAGCCCAC 2880

ATTGAACTGC CCATAAAGCT AGTTGTCCAG CTACAATAAT AGCATTCGTC TTTAACCCAT 2940

TGGCTTTAGC GAAGCGTAAT ACAGTCACTG CTAATTCTTT cCAGGCTTTC TTTTGTGCAG 3000

CTTTTACAAT TGCGCTGATA CTAATCATTG CAAAAAACTC ATCTTTGATT TTGTTAGCAA 3060

CGCAACTTCC TAATGCATTC CAATTAAAAC GTGCTTGAAC TACTGTTGAA GCATCAGAAA 3120

TATTTACATT TAATTCTTCC TCAACTGAAG AAATCTCTTG CTGAGCAAAA TTATTTTTGA 3180

CATAGTTTTT AAAGTTATCT TCCGTCACTC CATTCGCATA CATTTCTTCC AGTCCTTTTG 3240

CTACAGCCTC AACTTCTGAA TCCTCTAGCT GGTCAGATGC ATAAACACTT GTACCAGCGC 3300

TGATAAAAAT ACCTAATGTC ATTAGTAATG CCATCGCCAA ACAAAAAAAT TTAGCCTTTT 3360

TTGTCACCTG TAATTCCATA AATAAATCCC tACTTTCTTT TTCCTTGTTA TAATCATAAC 3420

AAGGAAAAAG ATAATTTATC ATCGAAATCC CTATTTGATG CTTATATTTT CCTATATATC 3480

CTAGAGCTGA TTTTTCTCAC TAGTGATCAC ATCAATTTGa ACTAATGaTT CAAAAAAAGA 3540

CACAGGTTAT TTGAGGTACG TTCGAGGTAA TGCTAGGTTC TATTTTGAAA ACAACGCAGC 3600

TCTCTTGaAA TATTTTTTGa GCTTGTCTaA ACCTTCTGAA ACGAATATAG AAAATAAAAA 3660

AAGAGTCCCC TTTCTCAAGG AAACTCTCAA TTGCTAAGTC AAAATAACTT CACGktATCT 3720

AAATCTTTkA AATCAATCCT ATGGTtCGCG GrACAAAGGa GCTAAAAaCT TAATAGAATA 3780

AATCGCACAA ATTCCGACAA TAATATAGAT AATTTTTGCT AATGGTGTGn TTGCACCGCC 3840

ACTAATTGTT GCAACTAAAT GCAAAATTA 3869

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GGAGGAAnCG AATGGTAAAA AACGATTAAT TATTGAAGCT GTGGATTCTG ATAATGATTT 60

aACAATTGAA CAATTGTTTG AAAATTATAA AGAAGAGaAG GTGCATGTAA CTATTCAAGA 120

TTTAGGAAAT GCGGTAGGAA ATGAAAAATG GTAAAAGTTC CTCATCAAGG TGATATTTTA 180

TTGTTGAATA CGGCTCCTAG ATCAGGACAT GAACAAACAG GTAAGAGACC GTATATTGTT 240

TTAAGTCATG ATATTATTGC AGATTACAGC AATGTTGTTA TTGTAGCTCC TATATCAAGT 300

ACAAAAAGAA ACTATCCTTT ATATGTTTCT ATTAATCCTT CTTACGGAAT GAAAACATCA 360

GGTAAAGTAT TATTAGATCA ATTAACCACC ATCGATTATG AGGCTAGACA ATGCGTGTTT 420

TTAGAAACAG CACACGAAAA ATTAATCGAT GAATTATTGC TAAAAGTTAG AACCGTATTT 480

CAAAAAGTAA ATAAAACAAA TAAATTTTAA CTAATAAAAA GGCGAAAAAA CGAACAAGTC 540

AAAAGTTTCC GACTTGTTCG TTTTTTTCTA TCGATTAAAT GCTCCCACCA GAAAGTAATG 600

ATACAGGTAA AATATAATCC TTACTTATCT TTTCTCCCTT AATCTTTTTC AACAAAACAT 660

CAACAATTAG TTTTGCAAGT TCATCAATAG GTTGTTTAAT TGTGGTCAAT TGTGAAAAAA 720

ATTGTTCAAT AAATGATGTT CCATCGTAAC CAATAATTTT CACATCTTCT GGAATATTTA 780

AGTTGAGTTT TTTTACAATT TTCATAGTAA GAATAGCAGT TAAATCATCT GAAATAAAAA 840

TGCCATCTGG TTTATTAGTT GaAATAATCG ATTTAATTTC CATCTCTCGA CGAATTGTAG 900

ACAAACTATT AGGAACTTTA AAGACTTTTC CTTCTGGAAT TTGGAAAGAA AATCCTAAAG 960

CACGTAAACC TGTAGGAGAA TCTGTATTAT CATTTCCAGT aATCATAATA ATATTTTGaC 1020

AACCATTTTT CCGTAAAAcG CTTGCTGcCA ATTTACCACC TTCaAAATTA TCTGATGCGA 1080

TGATAGGAAC ATTTGGTGCT AAATTTCTAT CAAAAGCAAT AATTGGTGCT TGAACACGCT 1140

CATAGTCAGC AATCCCAAGA TTATGACTAG AAGAAATAAT ACCGTCGACT TGATTTGCTT 1200

CAAGCATTTC AAGATATTCA CGTTCTTTTC CAGGATCATT TTCGCTATTA CAAATAATTG 1260

TTTTATATCC TTGATTAAAT aATTCTATTT CAAGGGTATT CAATGAGTTC CGCATAGAAT 1320

ATGTTACTGA TATTAGGGAA AATGAGA 1347

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TAACCTGATA ATGTAATCGG GTATCGTCTT GACGACCTTC TAAATCAAAG GCGCGCTGAT 60

AAAACGTCTT AACTGCTTCA TTTCCATAAA CAGTTAAACG ATTGGGAATA TCTAATGCAT 120

AACCAGACAT TCGATAAGCC AAATCCTCGC CGTAAAAATG ATCGGAATGC CAATGAGAGA 180

TTAGTAAAGA GTCAAAGTCT GCAAAACACA AGTCGTACTG CAACAGGTGT AAATaAGAAT 240

CCCCTGGAAA ATcAATCAGC AGGACATCAT CAATAATTAA TTGAGTTTGT GTACGAATTT 300

CTCGTCCTTT TTTCTCTCGA GCGTACTTAC ATAATTTACA ATTACAAAAA ATTCCTGGAA 360

TCCGTTCTGC TGCACCCGTG CCTAAATAGT TGATTTTCAT TGGGAGtACC TwACCtTTcT 420

TTGaCATTCT TCATACTTAG TAGATAACGC TGAACCTTAA AGTAAATGGG CATGGAAACT 480

gAAACaTTTG TTGTGTCCAT CTTACCTTTT TTAGAGAAGA ATTGAAATGG AATTTTTTAA 540

GTAAATATGC GTAAAATrGA AAAAGCTAGA CGCCTTTTTT GATAAGCTGA ATTTACTGCG 600

AATGCTCGTA CTATTTCCGA AAAAAAGTTT TACCAAAGGC ACTTTCATAT CCATCTGCTA 660

TTAGTTATAG AAAAATAACA AGATGGACAT AGCTTATTAG AGCAAAAATA ACTACGCTAT 720

TGATAAAGAG TGAGGCGTGT TTTGAACAGG TTGCGTGGGC AAATGAATTT GAATAAAAGG 780

GATGACAAAA GATGACTATT GAAAAATTAG AATATTTTTA TACCATTGCA AAATATAATA 840

GTATTTCCAA AGCAGCCTCT GAACTCCATG TTAGTAAATC AACCTTAAGT GCGTCATTAA 900

AAGATTTGGA AAGTGAATTG GGCCATTTAC TTTTTAACCG TAACGGTAAT TCTTTGACGT 960

TAAATTCCTA TGGTGATAAA ATCGTCCAAT CTGTATATAT CATTTTAAAC GAGGCTAAGA 1020

AAATGAAACT TAATTTGCAT GAAATGATTG AGAATCCAGT GATGCGTTTA GGTTTTGGAA 1080

ATACGTCCTT GATGTATAAA GTGACAGAAA ATGAGGATCA ACTGAATCGT TTTTGGGAAT 1140

GTTACCATGG TTCATCGTTT GAGTTATTGA ATAAATTGGA GAATCATGAG TTGGATTTTG 1200

TGATTACTTC TGCAGATGTG AATAGTCCAG TTTTAAAGAA AGAACAATTA ATTGAACTAA 1260

AAATGTATCT TTGTGTTTCA AGAGAAATTA AACAAGAAAT TGAGGAAGAA GGCTTCAGCT 1320

GTTTGaCCAA CTATCCATTT CTATTTTTGC CGCATCACTT AGATCATTTA GAAGCTACCA 1380

AGAGTGTGCT AGAAATGTTG CAATTAACAA GTCCGCTTGT TTGTTGCTAC GATACGTTGA 1440

TGCTTACTCG TCTCATTGAA AAAAGTAAAG GAGTTTATGC GGTGATCTCT CTTCGGAAAG 1500

AACAACTGCA GGAAATTGAT TCTAAACTCT TCTTTTTACC GATTGAACGA AAACAAAAAT 1560

TTTATTTATA CCGAAATGTT TCCAGTTCGG TTTTTGTCCA ACCTGGTCAA ATCAAGGCAA 1620

CTTTACAAAA GTTGCTAGAG ACTTAGCCAT TAAAATTACT TTGGAATAGT TACCAAAAAT 1680

AGCTTTATTC GCTTAGATTT ACTTCTGCTG CGGATAAGGC TATTTTTGTT GTTCATTGTT 1740

TAAAAGAGAT GCTCAATTAT GGGGCTGTTC GATATTTCTG AACAGAATGT TCAATTATTT 1800

AATAACTTAA GAATCGATAA ATCGTATCTA TTACGGTTCA ATTTAAAGGG GTTCTGGTGT 1860

ATAGTTTGGC TATCTAAAGA TTTACTTTTT TAAATATAAA ATAACTAAAT GGCAAGGAAT 1920

ATAAAGAACT GTTGATACGT GAGTACTTGC GATAACTGTG TCGTTAGAAG TTTAAGTGTC 1980

ATTGTTGCTT TTCCTGTTTT ATGTAGTtGC TAGAAAGGAC TGTTTTTATG ATCGATAGAA 2040

AAAAAGTTAT TTTGTATACT TGTTGCATGA GTTTGTTTGT AGTGACCATG GATGTTACGG 2100

TTGTCAATGT GGCGTTACCA TCCATTCAAA GTGATTTTCA CACGAATCTG TCTACATTAC 2160

AGTGGGTAAC AGATGGCTAC ACTTTAATGG TAGCATCCTT ATTATTGTTG TCTGGGTCTA 2220

CAGCAGATCG AATTGGCCGT AAACGAGTCC TTCAATTGGG CTTAGCCTGT TTTGGTTTAG 2280

CGTCTTTCCT ATGTGGGATT TCGCAAACCC CAGGGCAATT GATCGCGTTT CGCATGTTGC 2340

AAGGGATTGG TGGTTCTATG TTAAATCCGG TAGCAATGTC TATTATTACA CAGGTATTTA 2400

CCGAAAAGTT AGAAAGAGCG AAAGCAATTG GCTTGTGGGG CTCTGTTACA GGGATTTCCT 2460

TAGGCATGGG CCCGATTATT GGTGGACTGA TTGTTTCTTA TTTTAGCTGG CGGTATGTCT 2520

TTTTTGTAAA TGTACCGATC ATTGCTGCGG CAATCATCCT TACACAAAAG TTTGTACCTG 2580

AGTCAAAAGT AGAGAAGACG GTGAAAAATG ATTTTGTTGG TCAAGCATTG ATGATTCTTT 2640

TTCTATTTAG TTCTATCTAT TCCATTATCG GACTACCTAG AAAAGGGCTT TTCGCGCCAG 2700

ATATTTTAAG TACTGGGATA ATCGGCTGCT TAGCCATTGT TATTTTCTTT ATTTATGAAT 2760

ATAACATTGA CAATCCGTTA ATCAACCCGC GTTTCTTTTT ATCTATTCCA TTTACATCGG 2820

CTTCTTTTTT AGCTATTTTT GGCTTTATCA TATATAACGG CTATTTATTT TTAAACACGC 2880

TATATTTGCA AGAGATGAGA GGCTTCAGCC CGTTGGAAGC TGGCTTATCA ACCATTCCTT 2940

TGGCTTTTGT TAGTTTTCTT GTTGCACCGA GAGCCGGCGA AATGGTAGGG AGAATAGGGA 3000

CGAAACGTCC TATTATGCTT TGTGGTATTT CAATGTTGGC TGTTAGCTTT TTACAATTAT 3060

TTGTAACTAA AACAACGCCT ATGATTATTT TATTTATTAT TTATATCTTT TTAGGCATTG 3120

GGTTTGGGAT GTTAAATTCA CCGATTACCA TTACAGCGAT TGAAGGAATG CCACTTTCTC 3180

AGTCAGGAAC TGCAGCAGCC ATTGCGGTGA CATGTAAGCA AATTGGCAAT TCTTTAGGGG 3240

TGGCGCTACC AAGTCTTTTA ATTACAAAGC CTATTACTAG TTCGCTTACT CGAACACCTT 3300

TTACAAACGT ATGGCTTTaT TTGGATGTTG CGCCATTGCG ATTATCtTTT TAAGTTATTT 3360

aTCCAATTCT CCGCTAGCGA AAAAGTCATT GCGCAGAGTT AGGTTTTATT TTTAACAAAT 3420

CAAGATTTTT TTGAAGGGAA AGGAAGACAA ACTTAGATGA AAAAAATAAA TAACCGATTA 3480

GGACTCTTTT TATTTTTTGT TTTACTCTTT TGGGCAAAAA CGATTCTGGC GTATTACCTA 3540

GATTTCTCAT TGGGTGTTAA GGGCAGTCTC CAGCGAGAAA TTTTATGGTT CAATCCaGTT 3600

GCTACTACGC TGTTATTATT TGGTTTTAGT TTGTATTTTA AAAAGCATAA AACATTTATG 3660

CTTAGCTTAA CTCTTTtAAA TGTTTTAAAT ACATTAATTT TATATTTGAA TATTATTTTT 3720

TATCGTGAAT TCACTGACTT TATTACCATC CAATCTGTTT TTGGCTTTTC AAAAGTTTCA 3780

GAAGGAATTT CTGGTGATTT ACTTGCCTTA ATGAGGGTCC ACGATGTCTT TTATTGGCTA 3840

GATACTTTAG TGCTGCTCGT TTTGGTATTT TACTCTTTTA AACAGCGACG GAATCATCAA 3900

GTCTTTGTGA CCAAACCTAT CAACAGAAGA TTGGCGATCT CAATTAGTTG TTTAAGTGTC 3960

TTGCTCTTTT CGGTTAACTT ATTTTTAAGC GAAACCGATC GTCCTCAATT GCTTCAAAGA 4020

ATTTTTGACC GTAATTATAT TGTAAAATAT CTTGGCTTGG ATGCATTCAC AGCCATCGAT 4080

GGTGTCAAAA CAGCCATGTC AAATGAGGTA AGAGCAGAAG CTAGTTCAAA CGAATTACCT 4140

GAAATCATGA AATTTACCAA GCAAAACAAT TTACCGCTTA ATCCACAGTA TGCCGGGATT 4200

GCCAAAGGAA AAAATGTATT TGTGATTCAT TTAGAAAGTT TTCAACAATT TTTGATTAAT 4260

ATGAAAGTCC AAGGCCAAGA GGTTACACCG TTTTTAAATC AGCTTTATCA AAACAAAGCG 4320

ACAATCAGTT TTGATAATTT CTTTCATGAA GTAGGGCAAG GAAAAACGAG TGATGCGGAG 4380

AACATGTTGG AAACAGGAAC ATTCGGGTTA CCGCAAGGCT CTCTTTTTAC ACAATTAGGA 4440

TCAGACAATA CTTTCGAAGC GGCTCCCGCA GTTTTAGGAC AAAAAGGCTA TACmACCGCT 4500

GTTTTCCATG GAAATGTGGG GAGTTTTTGG AATCGAGACC ATGTGTATAA AAACTTAGGA 4560

TATCAATACT TTTTTGATCG GTCATATTTT TCAAAAGATG ACAAAATGCT AGGTTACGGT 4620

ATTTTAGATA AACAATTGTT GCGTGAATCA GCTAGTGAGC TTGAACATTT ACAGCAGCCA 4680

TTCTATGCGA AGTTTTTAAC TGTGACCAAT CATACCCCTT ATTATACGGA TGACCAAAAC 4740

TTCCCGTTTC CTAAATTGAA CACAGGCAAT TCGATTGTGG ATGATTATGT TCGAACAGCG 4800

CACTATTTGG ATCAATCGCT AGAACAATTT TTCCATTACT TGCAAACAAC AAGTTTATAC 4860

AATCATTCTA TTTTTGTTAT TTATGGTGAC CACTTCGGTA TTTCAGATGC GAACAACAAG 4920

GACTTATGtA AAgCTTTCAA CCGCGATCCA AAAACGTGGA CAAACTATGA CAATGCGCAA 4980

TTGCAAAGAG TACCTTTGAT GTTTTACATG CCAGGCTATA CGCAAGGGAA AATCATGCAC 5040

GAATATGGTG GGGAAATTGA CGTTTTACCG ACACTGTACC ATCTTTTAGG TGTCGATGAT 5100

AAAAATTATA TCCATTTTGG CACGGACCTT TTATCTCCTC AATATAAACA AGTGGTTCCT 5160

TTTAGAAATG GCGATTTTGT AACGCCTCAA TTTTCGTATt AGGTGGGGAA ATCTACAATA 5220

ATCAAGGGAA AAAATTAGAC CAAGTTCCAG CAGATTTAAA AGCAGAAGTC ACGAAAGATA 5280

ACGATTGGGT GAAAAAATCG TTAAGTTTnT CTGACAAATT AAATCGGGGA AACCTTTTAC 5340

GnTTTTATAA ACCACAAAGG GTTCCAAGAA GTGCAACCAn AAGGG 5385

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CGTGTGGTTA TCTCTGCTCC TGCAGGCGCA ATGAAAACAA TCGTTTACAA CGTCAATGAT 60

GATACACTTG ATGCCAACGA TAAAATCATT TCTGCTGGTT CATGTACGAC AAACTGTCTA 120

GCACCGATGG CTTACTTCTT AAATAATGAA TTCGGTATTG AAGTTGGTAC CATGACAACT 180

GTCCATGCCT ACACATCAAC ACAAATGCTA TTAGATGGCC CTGTTCGTGG CGGAAATCTT 240

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ATTGGCTTAG TTATTCCAGA ACTTAATGGA AAATTACAAG GCCATGCCCA ACGTGTTCCC 360

GTTGTGGATG GATCCTTAAC AGAATTAGTT AGCATTTtAA AAACAAAAGT AACAGCTGAT 420

CAAGTAAATG AAGCAaTGAA AAAACACACC ATtGATAACC CtTCTTTCGG TTATGAwGAT 480

CGTGAAATTG TTTCTGGAGA CATAATCGGC ACGACAGAAG GTTCGATTTT TGACCCaACG 540

CAAACagAAg TAACGACaGC TgGCgATTTc CaAtTaGTgA AAAcTgTGGc TTgGtAtGAc 600

AATgAAtAtG GtTTTaCTTg CCaAAtGATT cgCTTatTGG aAAAAtTcGC tAATTTatAA 660

TTCCaATGaA taAAAAAcTg CCtTGcaTAA AtTaATgCaA gGCaGTTTTT TTAATGTTTA 720

CTTTGACAAC TTTGACAAAT ACCATGAAAA GTTAAGCGAT GATCTTTGAC TAAAAAATGA 780

TACCGACTTT CAACAATTTG CTCTACTTCA CCAAGCAAGT CTTCTTCCAC TTCCTCAATT 840

GTGCCACATT CTAAGCATAA CAAATGGTGG TGAAAGTGTT TGGCGCCTTC TTTTCTTAAA 900

TCATAGCGAG CTAAACCATC GTTAAAGCTC ACTTTATCAA CGACTTTTAA GTCTGTTAAA 960

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AAGTAAATTT CTTCTGCTGA TAAATGATCT TTTTCAATTT CCAATAATAC AAGTACGGGT 1080

GCCTCCCGGT GTGGGGGTAA ATTnAAGnCn GAATCCnGGA ATGGGTTTTG GCCTTTTAAA 1140

GCCGCC 1146

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

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GACTTTTATT TAGAGCCAAC AGGAGGCATT GATTTAGAAA ACTTTGAAGA AATTGTTCAG 240

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GCGAATCCAG AAGTTTTTTG AAAAAAATCA ATACCAAACA CCACGCCTAT TTAGTTACAG 1080

CCAGCACTTA GCTGATTTCA GAGCAATTGA AGAACAAATT TATACGAAAA TCCATAATCA 1140

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AAAGTCTAAT TGGCTATAGG CAAGATTCAA TGTAAAGCCC CCACCATGCA GGTACAGTAC 12840

AGCTTTCTTG GTAGGCGCAA TAACGGAGTT TGACATGCGA TACATCGTAG GAAATTGAGT 12900

CATTTCTTGA AGAGGAAAAA GATGACGTAA ATGTTTTGGC AAAGTTACTT GTTCATTTAG 12960

TGATCGTTGC CAATGATAAA AAGCCTTGGT GACTTTCGGA TTTCGTTCAA GGCGAGCAAT 13020

TTGGGAAAGA CGTAAAGAAT CTTCAAAAAG ACAGGCTTTT AAGGATTTTT GACGAGAACG 13080

TGCGTGAAAC AAATATGCGC TAGCTAACAA CAAACCAATC GATTTCTTTT TCAATTAAGG 13140

CCCTCCATTC AGCAAAAAGT AAATCATTTT TTCTACAGTA TAACATTTTA AAAGTAGAAC 13200

AACGAAATTT GTTGAAGGGG TGAAAGGACG GTTTAAACGA ATGTACGTAT TTATTTGTGG 13260

TTGCGTAAAG TAAATGATTG TAGTAAATTA AATGAGATTA AGAGGTCCGG TGAATGGGCG 13320

CGTTCACGGC AAGGAGAGAA GTAGGATGAC AAATAAAAAG GTTACAATTA AAGATGTTGC 13380

CAATGATTCA GGGGTCTCCA TTACTACCGT TTCACAAATT TTAAACGGGA ATGGGGCACG 13440

GTTTAGTGGG AAAACGGTCG AAAAAGTATT GGCTGCAAAA GAGCGATTAA ACTATCAGCC 13500

CGACTATTTT GCGCAACGTA TGGTGATGAA AAAAAGTAAG ACGATTGGCG TAATCGTACC 13560

TGACATTACC AATCCATTTT TCGCGCAATT GATTCGAGGA ATTGAAAGTG TTTTATACAA 13620

AGAAAATTTT ATACTGATGT TATGCAATGC GGACCAAGAT GTTACAAGAG AACATGAATA 13680

TTTAACAGAG TTGATTCGTC GTAGTGTCGA TGGCTTTGTG ATTGCAAGTT CTGAAATTTC 13740

CAATCAAACG ATTAATGAAA CGCTACGTGC GAAAAAGATT CCGTTTATTG TACTTGACCA 13800

AAAAAAAGCA GAAGGCTTTA GCGATGCTGT TTTGACAGAC GATTATAGAG GTGGGCAACT 13860

AGCAGCAAAG CATTTACAAG AGCAACGACA TGAACAAGTC ATCGTGGTAA TGCCGCCACA 13920

TGCGCCAGTC AATATTCAGC AACGGTTAAA AGGTTTTTGT TCTGTTTATA CGGAAAAGGT 13980

CCAGTTAATC GAAACAGAAT TATCAAAAAC CGGCGGCTAC CAAGCTGTCC CCGAAATTTT 14040

AAAAACAGAG AGCACCGGAA TTTTTGCTAT CAATGATGAA ATTGCTTTTG GTTTATATCG 14100

AGGATTAGCA GAAGCGGGCA AAAAAATTCC TGAGGATTAT A 14141

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

ATnATACCTA TTATCCATTA GGCGACATAC GTCCTTTTCC GTTTAAAAnA AnnTAAATCC 60

ATATTTCCAT TTTTACCAAT ATCCGAAGTC TAAATTAAAg TAmGAAGATA ATcCGTAAAT 120

ATTCCATATT TTGAATGAAG GGTAATTCTT CTTTTAGCaT TGAATCaTTT AATAATAATT 180

CaGTTGCAAA TATATTTGCT TCATTTTCTA AAGTAGCTTC AAAAGCTAGG CTGTGCATAT 240

CTATACAGAA TACATTTAAA TGTTTGTGTA AGAAATAATG TCCTAGCTCA TGAGCAATTA 300

TTTTATCTTG TTTTGTTTCA TCAGTAATAT TGCTATTAAT GTGAATGATG TAAGTGTGAT 360

TATAGTATTG TAGAAAACCT TCTACATTAC CTAAGTTAGA TTTTAAAACA TGAATTCCTA 420

AGAATTCTGA AATTCTTTTT GGATCATTAG ATGAATAAAA ATTAATTATA CCTTCAACTt 480

CGCTTTTTAT TTTTGAATAG ATGCTACGTA TCGGACTCAC TCCTTAGTCT TTTTTGTCAT 540

ATCGTCAACA GTTTTTATTG CATTTTTCAT TGCAATTTTT AAAAGACGTG CAGTTTCTTC 600

GTCAATATCG CCGTTTTTTC CCATAAATAG AAGAGTATCT TCATTTTTTA ATTCTTCAAT 660

AGTTTCTTTA ATAGTACTAT CCAATTTAGT GTCATTTTTA TCTGGTATAT CTAGCAAGTA 720

ATTTGCGCTT ACATTAAAAT ATTCAGCAAT tTTTTTATTG TTTCTGGaTT AGGAGtAGAA 780

CGATTATTTT CATAGTCACT AATTGAACTT TGTCTTAAAT GAAGAATTTC TGCAAGTTCA 840

CTTTGCTTGA TTCCTTTTTT CGTTCGTAAC TGTTTTAATT TATCGGAGAA AGCCATAATA 900

TCACCTCTTT TCTGCAATAA TATCACTAAA TGTTATATGG GTTAACTTTA TTTGTAAAAA 960

AAGAATATTA GTTGTTGACA AAACGTAAAA TACGATATAT ACTAAAAaCG TAATAAACGA 1020

TATGGTTTAA AAAAAGGAGG TAAAAAACGT TATGAAAATT AAGTTTTTGA CaGCAAATGA 1080

AGTTAGTGaA TTAATGAATT GTTCAAAAGC TAAAGCCTAC GGAATTATCA AAGAATTAAA 1140

TAGCGAATTG AAAGAACAAG GAATGAAAAC TTCAGCAGGA AGAGTGAATG AACAATTCTT 1200

TGCTAAAAAA TTTGGTTTTG AGCATGAGTA ATAAAATTGG ATATTTTGTT TTATTAGAGT 1260

ATCTGATTAT ATGTCGGATA TTCTCATAAG GCAAAAAGCC TTAATAAAAT TAAATAAACA 1320

AAAAAGCGTT CACGAGAAGA AAATGAATTT CTGTTTCGCA AACACTTAAA GTAATACCTA 1380

GACAATATTA TTTTAAGCGA TTTGACsTAA TAATACAAGA ATGAAATTTT TGTTCGAGGT 1440

TATAAGTCTT GTTGAGGTGG TGTGTGCCAG CCGTTGAATG GAACACAAGG TGGCAGTAGT 1500

ATCTTTAACT AGAGCCATGT TGATGACAGA TTAGTGCCGA GCTGTCAGAT TATTTCCGAT 1560

AACCATGTCG TGATGACACG TTGGGAATAG TTGCTGAATT AGATTGAATG AAAAAATCTA 1620

TGCAAGCTTA GCAAGAGGAG GAGAGCTGTA TACCGTATGT CGTAGGTCTA TATAACGTGC 1680

CGTGATGTAA TTTTAATTAC TAGCCGTTGA AAAATGATTC TATGAAACGA ATGGATAAGG 1740

GGCTATTTCA TAGCTAAGGC GAACTTTTAG TCAGTTATCT GCAGAAATGC ACATTCTACT 1800

ACGATGAATT TTAGAATCTA AATTGCTATA TAAGTAAGAT TGTTATTTGT AAGAGTGGaA 1860

AAGATTTTTT CTAAAAGGAT AACCAATCTT AGTTTAAGTA TGCACAGCTG GATTACTCTG 1920

GTTGTGCTTT TTTATTTGAA AGAATAGAAT TTGTTATAAA AAATAAGGAG GATAGGAATG 1980

AAAGAAGAGT TATTACTTTT TGTTGAGAAG TTTGTTGCAC GAATGAAACG TCAGAAAAAA 2040

GCATTCTCTA TTACTGATAT AGAAAAAAGC TATAATTTGG AACGTAAGAA GTTAGGTAAG 2100

AGTGCTGTTA AGTTAACAAA CATGGAACGT TTAACAATTG AAAGTCGATT ATTAAAAAAT 2160

CAGATTTTAC AACGrACCTA TAAAATGACA GGyTATCATA ArCCTTGTCA AGTTGTGTTT 2220

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TTTrTAyAAA AAtTAAkTGA AAGAAGGAAA TTATTTTGGC AAATAGAATT CArGAAATTG 2340

CATTAAswGA wAAAAATyTA GGAAGTAAAA TTAAAGCTrT TTATAAAACA GAACGTGATA 2400

TTTATGTrAA TGGkGCrCCw GTwCGyGGTC GTGTrTTyAC yGCTTCAAGC GAAAArCAAC 2460

GTGATTTTGA AATTTTTGTC CCTCATTTAC GAAAyTCACA AATGTTGAAT GGTCGTGAAG 2520

AAGTTAAATT AATTGATCCA GTAGCACGAA TyAATGTGAA aCGAAATAAC ATTGGTAATA 2580

GTCGCTCaAT TGATATGGTA GTTTATGCaA AACGTTTAGA AGTAGTTGGA GGTAATAAAT 2640

AATGGGATTA ACATTTGAAA ATAATACrAT TGAAAATTTT GACGTACAAG syACATTTGG 2700

TAyGATGAAT TTyTTAGAAG TAGTkGCAAT TAATGArCGT GATGGwGAAG rmAATGTCAC 2760

TGAmGAAGTT CGTGAACArC GwGTGACkGT TTATTCTAGC AAATTAAATG ACCAAGTAGA 2820

AATTGyGATT GAyCCAGATT ATGATGTyAG TGGTATyAAy TATGATGATG ArATTGAATT 2880

GACTGGAAAT GTGACTGCTC GTGGTTGGCT TAATACTTTy AAAGGsTwyA ATGACAATGT 2940

rCArACwGAA CAAGCyTTTA AAGTACGTkC rGCwGGTATT AAAAArGTAG GGGCTGTTAA 3000

ACmAACrCAG rCACCTCArC CAAaGgAAAA ACAAGAAAAT AAAyAATAGA AgTAArTmAA 3060

TATTGTATTC GGACrAAtCG GTAGCGCCGT TTAACAGCTG TrAAGGGCAT TCTGACGAGT 3120

GCCCTTTTTA TTATTAATTT GTGTCAACAA GGTTTGTTAA TAGACATTAA TAATAAAAAA 3180

TGAGGTGGTT AGTTAAAAGA TGAATCGATT AGAGGAATTA ATCAAGAACC CAACAAAATT 3240

CAATCTATCA AATGAAGCGA TTGATTCATT AAGGGAATTA TTTGTTACTT TTGAAACGAA 3300

TCCATTTTTC CCAATGAGTC GATATGATTA TGCTCGCAGA TACTTAACAC AACTATATTT 3360

TGCAGGCTTT ATTAGTAGTG ATTTAGTTCA AAGCATTTTG AGTGAGTTCA AAAAGAGTGG 3420

GTAAAGTTAA TAAAAAATAG GAGTGATTGG ATGAAGCAAG GGAAACGCCC AGTTAGAAAA 3480

GAAAAAGAGT TGTTGAAAAG TCGCAGATTG AATGCGAAGA ATTGGTTAGT GGAAAGACGT 3540

TTGAAGAGTA GTGTTATTTT TCTTCATAAA GAAAGTGGTA ATTTGAAAGA GATTTTTTAT 3600

TAAGAAAGGA AAAATGTTAG TGGAAAAAAA TAATGAAAGT ACTAAATTAT TGCAAAGAAA 3660

AATTAGGTAT ATGTGTGCGG TTGAAGGTGA AATGGAGTTT TATGTGTTAC GTCCATTATT 3720

TACTGATGAT GTTAATGTTC AAGCAGTAGT TATGACATTT CAAGATGTTT ATGaTAATTC 3780

TTTTyTCTAT GAAGGTAGTG CAGAGGGATT ATATCAAACG ATTGTTCGGT GGATTGAAAA 3840

GAATATAGCT TAGTAATTAA ATGTAAACTG AGAGGGGGTG TCTTGTAAGT TAATGAGTAG 3900

TCTGTCGGAA AAAATGGAGC ATAAACAAGT AAGGTATCGA GCGTTTTTAG AAAGAAGATT 3960

TTATTCATAC AGGGGGTGGC AAAGTTTTAA TTATTACCGT GACTTGTACT TAAAATTATT 4020

TGATGAAACG AGTAATGGTC TTATTCAATT CTTATTACTA GATGATTCTT TTTTTGAAAG 4080

TGAACAAGCT GTTTTGAAAT TGTTAGATAG TTTTTTGGAT CAATTAGTTC GTGCGTACGA 4140

TTTAAAGTTC CATGAAGATT TTGAAAAGAA AGTGTATTTT GAAGAATATC CATTAGGAAT 4200

AAGTGAGGTA AATTGATTGT GATGGTTTGA TGGCTTATAA TGGCTTTAGA ATAGACGTTA 4260

GAAGAGGTGA GACAAATGGT AATGACAATG AATGAAATTA AAGAGCGTGT GAAGCCAATA 4320

GCTGAAAGAT ACGAAATTCC TGTGATATAT GTGTTTGGTT CTTATGCTAG AGATGAAGCG 4380

AAGGAATCAA GCGATATTGA TTTTTTGGTT GGCACTACTG GTTTGCCAGA AAAATATCGG 4440

TGGTCTGTGT ATAGTGATTT TTTCGATGAA TTGAAGGAAG CCGTTGAACA TGAGATCGAT 4500

TTAGTAGAGC TTGAAGCATT TGAACAACCA ATTGATTCAG AATACCAGAA AGAGTTTTAC 4560

GATACTATGA TGAAGGAGAA AGTTAAAGTA TTTGAAAGAG AAAAATAGAG ATATTCGTGT 4620

TCTCAAGGGA ACATTGATTT ATTGTGAAGA TGTAAAATCG GCACTCAATC GTTGTAGCAG 4680

AAGCTTTGAA GTTTTCTCTC ACGATAGAGT GtTTTTTCAT GCAATCAGTA TGTCTTGCAT 4740

GCAGGTAGGA GAACTTGCTA ACTCTTTTTC TGAAGGGTTT AAGGAAAGAA ATAGTGGTGC 4800

GGTTGATTGG CGACAATTAA GGTCAATTAG AAATATTTTT GCACATGCGT ATAGTAATAT 4860

TAATAAACGG ACTGTTTGGG AACTTGCAAC AGTCTTTTTT CCTGTTTACG AAGAATTTTG 4920

TAGACAAGAA TTAGCACGAT TACAAAAAGA AGGTAGGTAA ATGTTTAAAA AATTATTTAG 4980

ATATAGAGGA AGGCGTATCC GTTATTCTTC AAGAAATTTG TTGGCACTCn ATCGAGTGTT 5040

ATTTTTTATG CCAATTTTTG TTTGTTTAGG CTATTTTGTG GGCTATAAAT GGCTTTATCC 5100

ATTGTATCTC TCAAATCCAC CTGAtTGGAA AATTTATATT GTGCCAGCGT TAATCATTGT 5160

AGGTGTTTCG ATAGGTGCCA ATGGGGnAAT 5190

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

```
CAGATAGAGA AAAATATTAC CCCGCATACA TTGCGGCATA GnTTTGCGAC ACATTTGTTG     60

GAAAATGGCG CAGATCTTAG AATCGTGCAA GAATTATTAG GAnATGCAGA TATCTCCACG    120

ACACAAATTT ATACACATAT TACCAAACAA CGAATGGCAG ATGTTTATAA GGAACATTTT    180

CCTCGGGCTT AATTTGCGAG AATGCCCACA AACGAATAAA TTTATGGTAA ACTAGGAAGT    240

CGAGAAAAGA AAGTAGGTGT CGTTTTTGCA AGAAATTAAT TTAAAACTAG ATGTCTTTGA    300

AGGACCACTG GATCTTCTAC TACATTTAAT TCAAAAATTA GAAATCGATA TCTATGACAT    360

TCCCATTACA GCAGTAACTG AAcAATACAT GTCTTATATT CATGCGATGC AAACCTTAGA    420

GTTAGAAGTC GCTGGAGAAT ATCTAGTCAT GGCTGCCACC TTAATGGCTA TTAAAAGTCA    480

GATGTTGCTT CCAAAACAAG AGCTTGAAAT CATTGATGAT GAAGATTTTT TTGAAGAGGA    540

AGACCCACGG GAAGCTTTAG TAGCTCAGTT ATTGGAGTAT CGGAAATTTA AATATGCAGC    600

GACTGTTTTA CATGAAAAAG AAGAAGAACG TAAACTCTAT TATACAAAAG AACCAATGGA    660

TATGGATGAT TATAAAGAGG AAGATACAAC ACTACCGCCT AATCAAATCA ATACAATTGA    720

TTTATTTCTA GCCTTTCATG CCATGTTAGA AAAGAAAAAA AATCGCCAGC CTGTTGAAAC    780

AACTGTTGCC AGTGACGATG TTTCCATCGA AGAAAAAATC TCCGCTATTT CAGAGCGTAT    840

GCGTCaAGTA CAGAAAGGGA AGGCAGTGTC GTTTGATTCT TTCTTCGATT CTTATTCCAA    900

ACAAGAAATT GTGACAACGT TTATGGCTCT TTTAGAATTA ATGAAAACGG GCgCGATTTA    960

TGCTGAACAA GAAAATAATT ATAGTGAAAT TTTGTTATTT AATACAGAAA CCCAGCAGGA   1020

AGATACAACA GAGGTGGAGG AAACACAGTG ACATTAGTTA GTCAAATTGA AGCAATTTTA   1080

TTTGTGGTTG GCGAaGAaGG AaTTGGCTtG GAaGAGCTtG CGTACTTATT AGAGAAGTCA   1140

ACAGCAAAAA CCTATGAAGA ATTAACGAAA TTGAAAGAAC ATTATGCTTC TGACAATAAA   1200

TCGGCGTTGA ATATTTTAGA AGTCGGCAAT CATTTTGTCT TAACAACTAA GAAAAAATAT   1260

GCCTCtTACT AAAAAAATAT GCGCAATCGC CTATGTCGAA CGCCTTATCA CAAGCGGCGC   1320

TAGAAACATT ATCCATTATT GCTTATAAGC AACCAATTTC GCGTATTGAA ATTGATGAAA   1380

TTCGTGGCGT ACAGACTTCT GGCTCTATCC AAAAGTTAGT TGCCCGTCAG TTGATAGAAG   1440

AAAAAGGCCG CGTAGATGGT CCTGGTAGAG CAATTTTGTA TGGCACAACG AAGTATTTTA   1500

TGGATTACTT TGGGTTGAAA AGTTTAGATG AATTACCAGA TATCCAACAA ATGGAAGATG   1560

AATTAGAAGA AGAACTACCA ATGGATCTAT kTTTTGATCG TaTCAAGAAm CGAACCCAAT   1620

GTCTGAAACA ACAGAAGGCG AGGAAGCTTA AACAaTGGaA AGtTACmAAa AggCAtTGCT   1680
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CATGCTGGGG tGACTTCgCG TCGCAAAGCa GAGG 1714

(2) INFORMATION FOR SEQ ID NO: 397:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

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TTCAATCACT GCAGAATGCA TCTCGTGGAC TTCCATTACT TGGCCATCTT TTTGTTCATC     60

GATGACAAAG GAACCGTTGG ATGTTCGTTC ACTGATTGGA TAGTTTTTCG ACTGAATAAC    120

TTCTTGTGTG CCTTTTTGCG TAGTAACTAA TAAATCTAAA TCGGTACTTT CAGACATAAA    180

GACAACACGA TGTGGATTTT TCTTCAATTC CCGCAAGACC ATTAGTCCAC GTTTTGCTCG    240

TCCTAATTGT GTTAATTCTT GGGCTAACAT GCGTTTAACA CCGCCACGTT GGGTAACGAT    300

GACAATCGGT GtATCCCCTT CAGAATGAAC CAGTAAACCA TTAACGACAT AATCGTCTTC    360

TTTGAGGTTC ATTGATTTAA CTCCAGCCGC TTTACTACCC ACGACTGGTA CTTCATATAA    420

TGGATAACGT AAGCCAAAAC CGCGATTGCT AACGAGGAAA ACATCCAATA AGTCTTGATC    480

ATTTGTTAAA TAAACATTGG TAATTTCATC TTGGtCTGAT TTTAATTTCA TACAAGATGT    540

CGGGCGGCTC TTATAAGTGC GCCAAGGCTC AAAATCAGCC ATTTTGGTTT GTTTAATCAT    600

GCCAGCTTTT GtAATGAAAA CAAAGGTTTT TGTCGGACTT AACTCTTTaT AAGGATATAC    660

AGCAATAATC GATTCATCGA TAGCaAGATT TAAAATGGkT TGaGAAATAT GTTCGCCnAT    720

TTCyTTCCAG CGTAAATCTG GCAACTCATG GACGGGGCGA TAGATCATAT TCCCTTTATT    780

TGTTACTAGT AAAAGATGAT CTAATGTATT GACTTCGCCA GCATATAATA AAAAGTCGCC    840

TTCTTTCATG CCGATTCTTC TGGTTTTGAT GCTGTATAAG AACGA                    885
```

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

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GCAGCCACAA TATCAGCAGC CGCAACAACC GGTTGCGcAc AACTtGGAGC TCTTGTAAAA     60

GCGCACTGCG TTCCTTTTCT TTATTCTTTT GATCTTGAGA ATCTTCTAAA AATGCCGAAA    120

AGAAATGTTG GGAAGAGAGC GTAATCAGTT TAGAAATGCT CTTGATGGTA GCTTTATGTT    180

GATCCATTCT TCTGCCTCCT TTACGAATAA AATAGAATAA AACTCAAATG ACTAATTACC    240

TGTATTTTAC CTAATTTTGT GATAAAATTC AAGAAAATAT GTTCGCCTTC AATAATTATG    300

AGAATTTACC AACGTTTCTG TTTTTCGAAA AAGAAAGTAG TATAATGTGT GAGCATATAA    360
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GAAATACATA AGATTATCGG ATGTAGTCAA TAGATAGAAA AGGATGAATA GTATGTCAAA 420

AAAACCATCA GGTTACCAAA AAAAAGTTCT CACGGTGTTG TTGGTATCGT TTGGCTTTGG 480

CGGGTTGTTA GCGCAGTTTT CGCCGATGAA ATCAGGTGGG TTTTCAAGTT GGTTTGATGA 540

TTCATATGTC AAAGCTAGTG CTGAATCAAG TAAAACAAAA GAACCAGCAC CAGTTAAAAT 600

TGAGAAAAAA GTCAAACCTT TAAGCTATGG ACAACAGGTC AATCAAGAAA TTGAAAAGAA 660

GCAATATGAT GGACATCTGG ATTTGCCGTT AGAATTGCAG ACAGATGCTA AATGGAAAGA 720

CACCGCATAC GGATTTGGCA ATGTGGATAA GCCGAATACA ATCGAAATTA ATGGCTGTGC 780

GATTGTATCG CTTGCAATGG TTGGTTCATA CATGGATCAC CAAGAAGTTA CCCCTCTGGA 840

TGTGTTAGCT TGGGCAAAAA ATGACTTCTT TATGGAAGGG CAAGGGACGG CGTGGTCTAT 900

TTTTAGTGCA TATGCTGAAA TGAAAGGCTA TAACTGTCAA GAAATTGGGG ATATTGAAAC 960

AGTGGCAGCT TTCTTGAAGG AAGGTCATCC AGTCATTATT TCTGTAAAAC CGGGCTATTT 1020

CACTACAACT GGTCACATTA TGGTGATGAG TGGTGTGGAT GAAAAAGGCG ATTTCTGGaT 1080

TAATGATCCA AACGATTCAG AAGAAAAGGG CCATTCAAAA CGGACATTTA CAGCCGAAGA 1140

AGTGATGAAT GAAGCGTTAA ACTTCTGGGC ATTTTATTAG GAATAAGAAA AGGTGTGGAA 1200

CAACAGGCAg TACCCTTTGT TCGCATCTTT TTTAGCAAAT AAAAGGAGGC AGGACAATGG 1260

AGCGATGTAC TTGGGCAACG AATACAACTG AAGAGATGCA AGCCTATCAT GmTGAyGAAT 1320

GGGGACGTCC AGTTCATGAA GAGCAACAGT TATTTGAGTT ATTGACCTTG GAAAGTATGC 1380

AAGCAGGCTT AAGCTGGGCG ATTATTTTGA ATAAACGAGA AACGCTTAGA GCAGCTTATG 1440

ATGCGTTTGA TTATCGGAAA ATTGCGCGAT ATGATGAGGA AAAAATTTTA GCTTTACTAG 1500

CAAATCCTGG TGTGATTCGT CATCGTTTAA AAATTCAAGC GACCATCACG AATGCGCAAG 1560

TTTTTCAAGA AGTTCAGGCA GAATTTGGGT CCTTTGATCG CTACCTCTGG AACTTTGTCG 1620

ATCAGCAACC AATCGTTAAT CACTGGCAGC ACCCAGAAGA GGTTCCAGCC TCCACGGAAT 1680

TATCGCAACA GATTAGTCGA GCGTTAAAAA AACGAGGATT TAAATTTTTA GGTGCCACGA 1740

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ATAAATAAGT ATAGAAGAAT TAAAAAGGAA GGAACTAGCA AAACGAATGG CTAGTTCCTT 1860

CCTTTTTTTG CAGTGATTAT GGACACTCAT TTAACATCGT TGAAACAGTT TTCGCCAACT 1920

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ATAATTTGCT AACGGGATGG GAAAAAAGGT GGGATACAGA AGCAGATAAA TTATAGATAC 2220

TGGAAAAATA AATTTCACCA AATTCAGCTA GGACTTTGGA CGTTCCTTCG CCAATAAAAA 2280

GAACAAATTC TTTTTTTGCC AGTAATTCCG CAGCTTGAAC AATCCGTCCT TCTAATAATT 2340

CTTCTGATGA GCGTTGCAAA AAATGAATCA GCATTGTTTC ATCTAAAGAT TTTGGTTGGG 2400

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CACACTCGAA TTTTTGACAA AAACGCCAGA TTGCCGTTTT ACTGAAATGA ATTTCATCTG 2520

CTAATTCTCG AATTGTCATA TAAGGAACTT TTTCAATATT GTGGCTAATA TACTTGTAAA 2580

TCTCTAATTC TGTTGGATTT AATTGTGGAT CGTAGGTTAA AAACAGCATG CTGATCCCTC 2640

CTGTCATTTG TGAACGTAAT GTCCTTTTTT AGGGACATGG TCTTATTTGT AGATTATAGC 2700

ACTCAATCAG AAAACTAGCT ATAAAAAgGC GCCACTTAGC TACAATCAAT TAGAGAAACA 2760

ACTAAAAATT CATGAAACAG AAGAGAGAGT GGGGAaAAAT GAGCAATAaA AAATtAATTA 2820

TCAACGCTGA TGATTTTGGT TACACGCCAG CGGTAACGCA AGGAATCATT GAAGCACACA 2880

AACGTGGCGT GGTTACTTCA ACAACTGCAT TACCAACTTC TCCTTAT 2927

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

AAAAGTTATT TCTGCTTAAT GATGGTCTGG TCTTTTAAAC AGTCAATTTC TAAsAACCCT 60

TAGTTATCTC CATAATTTTT TGGAAGATGT GAAGATAACT AAGGGTTCTT TTTCTGTTTT 120

CAATAAAAGA AAGCAGGATT CTATAGAAAA GGCTACTAAA AAAgAGCGGa AATATGCTAT 180

TATTATTAAG AAGTAAAAAA ATATAGAAAC AAAGGGATGC CGATGAAAAA GTCCTACCGT 240

GTCAAGAAAG AAAAAGAATT TCAACAGGTG TTTAATAAAA AACAATCTTG TGGCAAATCG 300

TCGTTTCGTG GTGTACGTTT TAGAGAAACC ACaACAAGCC CATTTTCGAG TGGGGATTTC 360

TGTTGGGAAG AAAATTGGAA ACGCGGTCAC AAGAAATGCT GTGAAgCGGA AAATCCGCGC 420

GAGTTTATTT CAATTAAAAG ACCGTATCTC TCCAGAAATT GATTTTATCG TGATTGCACG 480

TCCAGGATTG GAAAAGTTAT CGTCTGAAGA AGTGAAAGCT AATTTAACAC ATGTGTTAAA 540

TTTAGCTAAA ATATTAGATG TAAGAGAGGG AATTGAGTAG TGAAGAAGTA TAAGCGCTTA 600

TTATTAATGG CTGGGTTAGT GACCTTAGTT TTTGTTTTAT CCGCCTGCGG AACCGCGCCC 660

GTAAGTGAAA GTAGTACAGG AATTTGGGaT CGATACATTG TTTATTATTT TGCCCAAGCG 720

ATTAAGTTCC TATCATTAGG CGGCAGTGTC GGAATTGGGA TTATCCTATT TACGTTAGTC 780

ATCCGGATTA TTTTATTGCC GTTGATGCAT TTCCAAACGA AGAGTATGCG TAAAACACAA 840

GAGTTGCAAC CGCAATTAAA GGCCTTGCAA CAAAAATACT CTTCAAAAGA TCCTGAAACA 900

CAACGCTTAT TCCGAGAAGA ACAGCAACGT TTGTATGCAG AGAATAATGT GAATCCTTAC 960

ATTGGCTGTT TACCACTGTT GGTTCAACTA CCAATTATGA TGGCTTTGTA TCAAGCCATT 1020

TCACGCGTGC CTGAGTTAAA AGAAGGAACG TTCTTGTGGT TAAGCCTCGA TAAGCCGGAT 1080

CCGTATTTAA TTTTACCGAT TTTAGCGGCT GTCTTTACGT TTGCTAGTAC GTATCTTTCA 1140

AGTATGAGCC AACTAGAAAC AAATGCCTCA CTAAAAATTA TGAATTACGT TATGCCAGCG 1200

ATGATCTTCT TTATGGGGAT TTCATTAGCC AGCAGTTTAT CTCTTTACTG GGTGGTCTCA 1260

AATGCCTTCC AAACAGGGCA AACATTGTTA TTAAACAATC CATTCAAAAT CCGTAAAGAG 1320

CGGGAGGAAG CAGCACGTCA AGCCAAAGCA CGGGAGCGAG CGCTTGAACG AGCAAAAAGT 1380

CCTAAGAAAA AAGGGAAGAA AAAATAAAGG AGGTCGTTCA GATGCCGATT TATGAAGGAA 1440

ATACAATCGA AGAAGCAACG CAGAAAGGCT TACAAGCACT TGGTTTAACC AAAGAGGATG 1500

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AATGAAGCAG GCTTGGCAGC CATCAAACAA CTAAAGCAGG CAAATTATCG GATAACAGCA 30540

ACCGCTATTT ATACAGAATT TCAAGGTTAT CTAGCGATTG CGGCAGGTGC AGATTATTTA 30600

GCGCCATATT ATAATAGGAT GGAGAATTTA ACAATTGATT CTCAAAAGGT TATTGAGCAT 30660

TTAGCTGCAG AAATTAAACG GACGAACGCA AAGAGTAAGA TCTTAGCTGC TAGTTTTAAA 30720

AACGTGGCAC AAATTAATCA AGCCTGTCAA ATGGGGGCGC AAGCGGTCAC TATCGCACCA 30780

GAACTCGTGA CACAAGGCTT GGCAATGCCC GCCATTCAAA AAGCAGTAAC TGATTTTCAG 30840

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AAGGGTTATC TTTTGGGTAT TTTTTTTGGT AGCAGTATGA TGAGGGTATC AAATGATAGG 31080

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CAAAAGGTGT AGATGACAAG AGTGCCTATA TCGTTGGTGG TGGCCTAGCA GGTTTAGCAA 31200

CGGCTGTTTT CTTAATTCGT GACGGTCAAA TGAAGGGCGA AAATATTCAC ATTTTTGAAG 31260

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CTCGCGGCGG ACGCGAAATG GAAAACCATT TCGAGTGTTT GTGGGATCTA TTTCGTTCGG 31380

TACCATCATT AGAAGTAGAA GATGCCTCTG TCCTAGATGA GTTTTACCGG TTAGATTTAG 31440

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CTGAAGATCA ATTAATTGGC AAAAAAATTG AAGATGTTTT CGGCGAAGAA TTTTTTGAAT 31620

CCAACTTTTG GATCTATTGG TGTTCAATGT TTGCTTTTGA AAAATGGCAC TCTGCCATTG 31680

AAATGCGCCG TTACATCATG CGCTTTATCC ACCACATCAA AGGTTTGCCT GACTTTACAG 31740

CCTTGAAGTT TACCAAATAC AATCAATACG AATCGTTAGT GAAmCCATTA TTAAGCTTTT 31800

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TCAAAGGAGC TACTAAAGTT GCTCGGCGAT TATTGTTGAC ACAAGCGGGC AAAACCAAAG 31920

AAATTCCTTT AACTGAAAAT GATTTAGTCT TCGTAACGAA TGGCTCAATT ACTGAAAGTT 31980

CGACGCAAGG AGATCATCAT ACACCAGCAC CAATTACTCA TGAACTAGGG GGAAGTTGGA 32040

ATCTCTGGAA AAACTTAGCA AAACAATCCC CAGAATTTGG GCACCCAGAA GTTTTCTGTG 32100

AAAATTTACC AGATGAAAGT TGGTTTGTCT CAGCAACGAT TACGTGGGAA AATTTCGATA 32160

TTGAACCGTA TCTTTCTCGG TTAACACATC GTAAATTACG CACAGGAAAA ATTGTCACAG 32220

GTGGTATTAT TACTATCAAA GACTCTAATT GGATGATGAG TTTCGCTATG CATAGACAAC 32280

CGCATTTTAA AGAACAAAAT GATCAACAAT CTATAACTTG GGTATATGGA TTGCTTTCTA 32340

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AAGAGTTACT TTATCATTTA GGGGTCCCGG AAGGGGaAAT TGAACGTATT TCAGAAGAAT 32460

CGGCTACCAC TATTCCGGTT TATATGCCGT TTAtCACTTC TTACTTTATG TTAAGAGAAC 32520

CAGGCGATCG aCCATTAGTT GTACCAAACG GCTCTAAAAA TCTTGCTTTC ATTGGGAACT 32580

TCGCAGATAC TGAACGAGAT ACGGTGTTTA CAACAGAGTA TTCTGTACGG ACAGCGATGG 32640

AAGCTGTTTA TCAATTGCTA GAGGTTGAAC GCGGAGTACC AGAAGTGTTT GCTTCTGCAT 32700

ACGACTTGCG CGTCTTAGCA AACTCTGTTT ATTATTTATC TGACAAGAAA AAATTAACAG 32760

AAATGGAT 32768

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

ACCCCTTTTT AGTTCGTTCG ACAAACCCAn GGCTATATCC CAGGnTCCAA TGACCAAGTA 60

TTGGTAACGA ATTAACCnCC TATCCAATAn AATTGAAGGA AATGAACCTA CAACAATTAA 120

AAAAGCTGTA TCAAAAAGTC TTAAAAAAGC AAAAGGGTTG TTGAAATAGA AAGATTTTAA 180

AGGAGATTAA AAATGAACGA TTTATGGAAT TTTTTAGATA ATCATCCTGA AGAGAAAGAA 240

TTGATAAAGG CAAAAGCATT ACAAGGTTAT ACAGTTGATG GAATTTTAAA TGATCAACTT 300

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AGTATCCAAA TCCCAGAATT TAATGAATTA CTAAGTAAGA AGATGGTAGT ACTTTTTGTT 420

CCTGCGGATG GAGTGGGACA CTCTGGCGCC AAAGAAAGAT ATTTTGGATT GAGACAATGG 480

AATACCCTGT CTCAATCTGT TCGAAAAAAT ACCATCATTC TTAGAATAGC TGATGTTGGC 540

TTTGTGTCAG GATCCTATTA CACATTATTT GAGCAAGAAA TTTTGGATTT AATTGAAGCA 600

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GGAACGGGAG CGTTATTATT AGGTATTACA GGTAATTACA AAACAGTTAG TGTAGATCCA 720

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TATGAATTAG AAAACATTAC GGTGATTGCT TCTGAAGCAA ATAAAAAAAT GTATGAGAAA 900

ATTTACCCCT TATCTAATGG TTTTACCTTG AAAAAATTAG AATTAATGAT TGATTCTGAA 960

AATACAATTG GTATACACGG CCTTACGATA ATGGAAAGTA TTCATTTACA ATTAGCGTTA 1020

ATAAATAATT ATTTATTTGA TTAAGTAACA GAGAAAGTAG GAGCgGAAAA ATGAAAAAAG 1080

CAGCmATTAT GGGCTGGTGG TATAACCaAA ATTATGGATC AaTCTTAACA TACTATGCTC 1140

TAAACAAATA TGTACAGAAT AAAGGGTACG AGACGGTTAT GATTGATGGA CCACTAGGTT 1200

ATAAAAACAG AAGTAACTTT CGAGCATGGA TGCCTTTAGC GTATAATTTT TTTAAGAAAA 1260

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TTTCATTAGG AAAAGCAGAT ACAAGTAAAT ATGATCCTAA ATGGGTTGCA AACCGCAAAA 1500

AAGATATTAC ACAGTTTAAT CATGTTTCTA TGAGAGAAGA TTTTTCTGTA CAAATTATGA 1560

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AAGATATTTT TCAAGAAGAA GTTATTCAGG CTTTGGATCC AACCTATCTT GTTGAAAGAA 1620
GTGAATATGA TTCTTTAGCT GATCAAGCTA CGTTTAAACG ACAAGAATCA GGAGATTATA 1680
TGGCTGTCTT TTTCTTGGAT ATTAACAAGG AAAAAGTTCG TGTAGCACTA GCGATCGCAG 1740
AAAAATTGGG ACTGAAATTA GTGGTCCTGC CTAATCCTTT AAAAGGACGT GAACTAGCGA 1800
AAAAAACGTT TCCTAATACA GTAGAATATG TTTCTGAAGA TACACCAGAA AATTTCTTAT 1860
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AACAAGAAAT TGAAGAAAAT AAAAATATTA GTTTAGCACT TGACTATCAA AAGACCGCTG 2100
GAAAGATTGC aGAGAAAAAG AGATTTCAGA TAAGTGGTTA ACCGATGCGT TGACAAGTAA 2160
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TTTGGATTTT TATCGAGCTA AAACAACTGT TCCGATTTCC GCAGCAATTG TTTTATCGCC 2280
AAATGGTACG ATAAAAAATT CCAATCCTAA TGAAAGCTTT TGGAAGCTAA CAGATAAAGA 2340
ATTAATTTTT ATGAATAATC ATCGTGAAGT CACTACAAGA TTTAATCGTG AAAAGTTTAA 2400
GGGAAAGGAA ACGTTCAGTC CTTTTAGAAT CGTCGGTAAA TATGTGAAAG ATGAAAAAAT 2460
CGAACATGTT ATGTATTTGC ATCCGATACA AAAACCTAAG CCTAAACCGA AACAAGGCAC 2520
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AATTGTGCAA AATGAGAGAA TTCGTTCGTG GAAACAAGAT CTTTTAGAAG AATTACCAGA 2640
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ACACTTGAAA TGCGGTTTAG AATGGGCAGA TAATATTCCA GGAACCATTG GTGGCGCAGT 3000
TTATATGGaAT GCTGGGACAG TTAAGGATAT TAATAGCATG TTTCTTGAAG CTACGATTGT 3060
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GCACCCACTA ACACATCCAA ATCATGGGTC AACTTTTACT TGGGGACGGG CGCCTCGATT 3300
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TCCAGGTTTC TTTATCAATG TTGAACAAGC CTCTGCTCAA GACTATGAAG CATTAATTTA 3420
TTTAATTATT GCAAAAGTTT ATGAATTTTC TGGATTTTTA TTAAAACCAG AAGTGAGAAT 3480
TTTAGGTGCA AATATGTGGG AAGCAAGTTT AACTTTTAAA TAAACAGGGG AGTGTGTGAC 3540
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ATGAAGAAAA TAATCACAAT AATTGTGTCT TTAGCAATTG GTATCGGTTG TGGTTTTTGG 3600

TCAGGATATT ACATCAGTAA AAAATATTCA GAAAACCAAG AGACAACTAT TTCCAAAAGT 3660

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TgGAAAACAT TAGTTGTTAA AGATAATGTG TGGACATTGG ATGGCAAACG TATTTATGAT 3780

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AGTTGCTAAT TACAAAGGGG AGCTCTACAA CCTACCATTC AATATGAACA CGTTCTACCA 4320

AATGTGGGGG GTAAAAACAC CAGCTGAAGC ACAAGCAAAA ATTTCAGAGC AGCGGGAGGC 4380

AGCTGGAATT AAAGGCGCTC CmAAAAATTT AGAAGAACAA GCGATTCGTT TGATAGGAAC 4440

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CTTTAACCAT CGCTATCAAG GCGTwCCTGT CGACGGTTAT ACAGCTATGT TTGATAAATT 4620

GTTAGAGAGT GAATTAATTG ATATTCAATT GAATAAAGAC TTTTTGGCAG AGAAAGAAAC 4680

TTACTTATCA GAGTTTCCAA AAATTGTTTA TACAGGGATG ATTGATGCAT TCTTTGATTA 4740

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TTCACTTTTG TTTAGAAAAT ACAAAGAAAA AGCAAACGCT CAAGAAAAAG TTATTTTTGG 5040

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AGCAGTCGCT AAAGAATTTG GTGAAATGGC CAACTAGTGA ACGGTTAGAC TCGGAGGAAC 5160

AAATGGAAAA AGAACTGAAA GTTAGAACAA AATTACTTAC CAAAGAATAC AGTTTAGCGC 5220

AAACACGTAT TGACAAATTG AAGACACTTT TTAGTGTTTT TCAAAACAAA GTTCCCACAT 5280

TTTGGGCGTT AAAAGGTGTT AGCCTCGACG TATATTCTGG AGAAACAATT GGTATTATTG 5340

GTTTAAATGG TTCAGGCAAA TCCACTTTAT CAAATATTAT TTCAGGCATC ACCCCTCAAA 5400

CGTCAGGAGA ACTTGAAATA AATGGTGAAG TTTCAATTAT TTCGATTGGT GCAGGACTAA 5460

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TTTTTGTCTC TCATtCTATT CAACAAGTAG AGCAAATTTG TGATCGTGTC GCTTGGATGC 5820

ATTATGGTGA CCTACGTGCA TTkGGkGAAA CTAAGCATAT TTaAAGGAtA TCGTGCTTTC 5880

TgCAcCGTaT AAyCATTTCm CTGAACCGCA AAAAGAATCG TATCAGAGAG AGGCAAGGCC 5940

AAACAGAGAA ATTTTCCTTG 5960

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

AAAAGTTCAA AACCTTTTTG TTTAATCACA TTTTGTATGG CGGCGACGAC TTCTTCAATC 60

GTCAAGCCTG TTGTATCGAT TTTCACAGCA TCACTTGCTT GGACAAGGGG TGATACTTCT 120

CTGGTTGAAT CTAAATAATC CCGACGTTCA ATCTCCGCCT TCAAGGTTTC AAAATCCGTC 180

TCAATCCCTT TTTCTTGATT TTCTTTAAAA CGACGTTCTG CACGTTCTTC AACGCTAGCC 240

ACCAAGAATA TCTTTACTTC GGCCTTTGGT AAAACTGCAG TACCAATATC TCGACCATCC 300

ATGACAACTC CGCCGGCTTG ACCAATTTTC TGTTGTAACG CCACCATTTC TTCTCTAACT 360

TTTGCATGTT TTGAAACAGC TGAAACAGCA TTCGTTACAT CTGGCTGGCG AATCGCTTCG 420

GTCACTTCAT GACCGTCGAT AAAAACACGT TGGCCATTCT CTGCTTGCTG AAAAGAAATA 480

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TGTTTTGCTA AAATTTTTGC AACTGTACTT TTGCCTGACG AAGCTGGTCC GTCAATAGCA 660

ATACTGATTT TCCCCATGAA AAAACTCCTT AACTGATATG CATCTTTTTA AATGCGCTTC 720

TTCTTTTATA TTAAAATCAG AAGAAAAGAA CTTGGATTTA AACTGATGAC GAGTCTCTAA 780

CGAAAAAGCA ATAAGCCGAA ATCCCTCGAA AGACGCAAAA CATCTTTCGG AAATTTCTGC 840

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CTCTTTTTCT GGATTATTTA ATACGTAATG GTTGTCCTGG ATAAAACACA GATGTATCAA 960

TCCCAGGATT TAACGCTAAA ATTTGTTCTA ATGTCATTCC GTTACGTTCG GCAACTTGAC 1020

GTGCCCCTTC GCCACTTTGA ACGGTATCAT AAACAGGTTG TTGGTTCTGC GCTTGTTGCT 1080

GTTGTTgATT TTGAGCTTCT TGTTGTTGTT GCTGCTCTTG TTGTTGCTGT TGCTGTTGTT 1140

GTGCnTGTTG GTCCTGTTGT TGCTGTGCAG CnATGCTTGA ACTTGAAGGT GTTGTATTTT 1200

CAGCTGGTTG GCTGCTTGCT GGTTCTGAGC TTTCCACTGA TTTTGGACGT ACTTTCTTTG 1260

TTTCnTTC 1268

(2) INFORMATION FOR SEQ ID NO: 402:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

CTTTTGTGCC ACAATCCGTT CCTCCCACCT TGGCGTGCCC AAACAAGGTT AATGATTTGT 60

ATAAACAATT TCCAACATCA ATAGTTGGGA CCACTAAAAT ATCTGCATCC CCCATGATAG 120

GACCGCTGTA ACGTTTATGC GCAACCGCTT CTTCAGAGGT CGCTAAATCA AGCGAAAGTG 180

GCCCAAAAAC CGTAGCCTCT TGTTGATCAT TAAAATGTGC CGTGACTTCT TTTGCTAAAA 240

CAGACGAAGG CATTTTAGGA TTGAAATTTT CCGCTGCGCT TAACAAAGCA ATTTTCGGGT 300

GATGCAGTCC CAATTTTTGG GCGACTTCTT TAGCATTTTC AACAATTTCA ATGAGGGTCG 360

CTTGAGTGGG GGCGATATTC ATCGCACAAT CGGTTAACAA GAAGGTTTTT CCCGCAGGCA 420

GCTCCACCAT TGCTACATGG GAAAGAATCG GTTTATTTTT TAATTGATGC TCACTTTTCA 480

ACATTTCTTT CAGTAATGTG TGGGTCTGAA TAATTCCTTT CAATAAAATT tGTGCTTGAC 540

CGGTTGCAAC TAAACTGACA GCTTCCTGTG CTACCGCGGC CTCATCTGAG CAATGAACAT 600

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GTTGCTCGGC TTCTTTTAGT GCTTTTTTAA CTAACTGTAA AATCTCTGGT TGTGAACCTC 720

CTGCAATTGA AACAGTGATC ATTTTCTCAC CTCATTTTTT CTTCTTTACA CTTTAAATCT 780

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TGTTTATTTA TGTCAGATCC TAAAGCATGT TATACTTTAG ATACTTATTT TTAGGAGGAa 1020

TTAAATGGCA CTACTACTAT TCTTTTTGTT TATCGCCCTA CTAGGATTTG GTATATTAAA 1080

AATTAATAAC CGCAGtATCC TCGGCGGTAT CACtCTGGCT tCCGGCACCT TATtGTCATt 1140

AGtCaCCTtA CTATTTATCG GATTAGACAA AATTTATTTA CATTTTAAGA ATGGCGACCT 1200

AATT 1204

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4996 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

ATAACAAAAC ACTACTCTTC TATCmATAAT TGaCTTAATA aTTGAATTTC TTGrTTCTTA 60

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TTAGGAAATA ATnCGACAAA TTTyCCTTkG yCCATTtGkA CATATTTTTt ATCCAATAAT 180

AAACGCTCTT CAAAAAAAGT TTGAAGCATT TGCTGCAATT CTTCTTCATA ACCATGTGCT 240

TTCATAAATA ACGCCGTATA GATTTTTTGA TGTTTTTGGG CAAATAATAT AAAGTTCAGA 300

CCCAATGCAA TCACTGGGTC TGAGGCACCG ACATCTGCTT TATAAAATAA TTGCATACGA 360

TGAAATAACG ATTTAATTAA GGTTCGTTTT AAATCGTCCA TGTTGACAAA TTCTAAATAA 420

ATTGGCTGCG TAGAAATCCC CATAGCATCT GCAATATTTC TAGCAGTTAA ATTAGAAAAA 480

CCTTTATCTA CTAAAATTTT TTCAGCTACG TTTAAGATTT TTTCCTTTGT ATATACCTTC 540

GTTCTAACCA TTTTCATACC CCTTTTCTCT TTTAGTTAAC AATAACTTTA TTATGTTCAC 600

ACAAAAGAAA ACCATTTTCA TTATATATAT AATATTTTAC ACTTTTTTAT GCGTTTCTTT 660

TCTCAAAATT TTCTATACAT TTCAAAAAAA TTGAGAATTT TCATCGCCTA TAAACAAATA 720

GGTCCAGAAC AAAAGGTCAT CACCTTTTGT TCTGGACACT AAACGGCTGC ACTCTTTATT 780

CTTCTATTTG TTTGCCTTGT TCTTTGGCAA GCTCATTTTT ATCATAAGCT ACAAAGAACG 840

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CGCCGCCTGT CGCCATAAAG GCGCCAATTG GTCCTGGTAA GGTCCAAGGA GCGGTAAAGA 960

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CGCCAATGCC AAAAGTCGCA TATAACGCCA TAATGTACAT TGTCATTCGG TAAGGCAATA 1860

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GATTTTCAAT CCAAACAGTC AGTTTATCTA ACATAAATAA CACTCTCCTC TGTTTTTCTC 2100
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ATCGTCTTCA CCATTTAGCG CGGcATAACT AATCGTcAGT GgCATCAGCA ATCTTTTGAA 3060
AATtGTTCAG TTwATtGCGT tCTtCyAACA ATTGTTCTTC TTCGCCAGCG ACTAACTGTG 3120
CACTAGCAAT TtCATCACTT TGAAAaTGAa GCATGTCCAT tCTTTGGGCA AATTCTTTTT 3180
CATTTTTTtG tCGCTTTCTG ACTTTGGCTT CGAGTGCGCG ATACTCTTGA TACGCCTGTG 3240
TATATTTTTC TTTGACTGCT AAAAGTTTTT TCCCACCAAA TTCATCTAAC ATATCAATAT 3300
GGCGTTCACT TTGCATCAAT TCTTGATGTT CGTTTTGGCC ATGAATATCT ACTAAATATT 3360
CCCCAATTCT TTTTAAATTA GTAATGTTGA CAATCCGTCC GTTGACACGG CAAACATTTT 3420
TACCAGAAGC GGAAATATCT CGTTGAATCA CTAAAGAATC TTCTTCTGTT TCAATACCTA 3480
ATTCTTCTAA TAATTTCTTT AATTCTTGAC TTTTCGGCAT TGAAAAAAGT CCTTCTAAGG 3540
TGCATTTATT TGCTCCTTGA CGAATATAGT CACTGGAGCC GCGTCCGCCT GTGAGTAATC 3600
CCATTGCATC AATAATGATG GATTTCCCCG CACCCGTTTC TCCCGTTAAA ACGGTCATAC 3660
CCATTTGAAA CTCTAATTGT AACGAAGAGA TAATCGCAAA ATTTTTCACG GAAAGTTCTT 3720
GTAACATCTT GTTCACCTCA TTCTTTATAG ATAGCTTAAC AGCTCTTTAT GAAGTTTTTC 3780
TGCTGCTTCC TCAGTTCGTG CAATCATGAG GACACTATCA TCATCGTTGA TGACGGCAAA 3840

AAGTTTCTCT TGGTAATTCT TTTCGATTAA ACTACCACAC GCCGCCGCAT TGCCAGGAAT 3900

GGTTCGTAAT ACGACATATT TTTCCATTTG TTCTGCAGCT ACAAAGGCAT CTTTTAAAAG 3960

CTTTGCAAGT TTAGCACTCG TATTAGCTTG TGTTTCTAAT GGAAGGCTAT ATCGATAACC 4020

CCCTTCTGCA GATGGAACTT TGATCAGTTT CATATCTTTA ATGTCGCGAG AAATTGTTGC 4080

TTGTGTTaCA GTACGCCCTT TTCTTGTAAG TAGTTGACAA AATCTTCTTG CTTTTGAATA 4140

TTTTTTTCAG TCAATAAACG TGTAATTAAA CGGTGTCTAT CTTGCTTTCT CATGGCGCCG 4200

CTCTCCTTTT CAGTTTACTC TTGCCCTCAT CATAGCTTAT TTTTATGCAT TTTAAAAGAT 4260

GAATTACTAG ATTTATACAA AAAAGAAGCT TTCACCTATA GGCGTCCACT TCTTTCTTCT 4320

AACTTTTCTC ATCATTCCGC TAATTTTTGA TGCGCATGCG CGaCAACTTC TTCAATGGAT 4380

TCTGGCGCTT GATAGGATCC TTCCCCTTCA ACAGAAACTA AATGTGCCAA AAATTCAATG 4440

TTTCCTTCGC CACCAGTGAT TGGTGAAAAA TCTAAGTTTT TCACATCATA ACCGTTATTC 4500

ATGGCAAAGC GTGTAATTTC CTCCACAACC ATTTGATGGG TTTCTGGATC ACGCACGATT 4560

CCTTTTTTCC CAACAAACTC TTTGCCAGCT TCGAATTGTG GCTTAATTAA CGCCACCACA 4620

CTACCGCCTT TTTTCAAAAT ATCATGAAGA GGTGGCAAAA TTAAGCGTAA TGAAATAAAG 4680

GAAACATCAA TCGTTGCAAT ATCCGGCACC CCTTCAGTGA AATCTTCAGG TTTACTATAG 4740

CGAAAATTGG TACGTTCCAT TACCACCACG CGTTCATCTT GCCGAATTTT CCATGCTAGT 4800

TGGTTATAGC CAACATCTAA AGCGTAACTC AAACGAGCCC CATTTTGTAA AGCAACATCG 4860

GTAAAACCAC CTGTGGAgGA aCaATATCTA ACATTGTTTT GCCTTGAACG TTGATTGCAA 4920

AAACATTTAG TGCCTTCTCT AGTTTTAAGC CCCCACGAGA AACATAAGGC ATTACTTGGC 4980

CTTAnTATGT AAGGGT 4996

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1926 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

CACCGTGGnG AACTCTTTTT TGGGTAACCn GGATGGTTTT TTTTGGACAT ACTATTCCnC 60

CCTTGTCTAT CTAATTGACT ACCnTCCGAT AAATCTTATG TATTTTCTTA TATGCTTCAC 120

ACATTATACT ACTTTCTTTT TCGAAAAACA GAAACGTTGG TAAATTCTCA TAATTATTGA 180

AGGCGAACAT ATTTTCTTGA ATTTTATCAC AAAATTAGGT AAAATACAGG TAATTAGTCA 240

TTTGAGTTTT ATTCTATTTT ATTCGTAAAG GAGGCAGAAG AATGGATCAA CATAAgCTAC 300

CATCAAGAGC ATTTCTAAAC TGATTACGCT CTCTTCCCAA CATTTCTTTT CGGCATTTTT 360

AGAAGATTCT CAAGATCAAA AGAATAAAGA AAAGGAACGC AGTGCGCTTT TACAAGAGCT 420

CCAAGTTGct GCCGCCCAAA AATCCTTAGT GGTCTTACAA TTGAAAGAAG TCCCTACAGC 480

GCATAAATTC GAAACGGTGA TTGGCTGGAT TGTCTCAAAA AATATTTCGG ACAATATCGT 540

TGTTCGTTTA CAAACGGATG AACAACAGTT GCGCATGATT CCTGTTGCTT CTGTCATGAA 600

AGTCAGCACG TTAGCCAATC GTCACCAACG TCAAATTCAC TAGAATATTG AAGTCTTTAT 660

AAAATAAATG GAAACCACCA ACCCTGGCGA TTGCAGGTTG GTGGTTTCTT TTATTTATGA 720

CTTTAGTCAA AATCCCATGA AACTTCTGAC TTAGGACTCA ACTTATTTCT TAGGAACAAA 780

TAATTGCGGT GCTACTTTTG CCAATAAGCC TAGAACTAGA CTTACATACA AACAATTGAC 840

GACGGTACTT GTACCGTTTA GAACAAmGGA ATAGAGATAT GGGCTCATTC CTTCTGGTGC 900

ATACATGcCC CAAACCAATA CACCCGCCCA AAAATGCCAA AACCAGCGGG CGAAGACTGC 960

CACAACACTT CCTAAAATAA TCGTACGAAT GGCTGATTTT AAACGATTCG CTTGAAAATA 1020

CAGTTGAATT TTTCTAGCGA ATACGCCACC CATTCCTCCA AACGCAAAAG CAAAGGGATA 1080

TTCAAAAATA ATCTGTGGAA CGGACAAGAA ATTTTTCATG GCTGTACCGA GAATAATATT 1140

TAACATGCCC CAAACAAAGC CTGCTGCAAC TCCAGGAAGC AACCCACGAC GAAACGAATA 1200

AAGAACTAAT GGGACCATTC CCAACGATAG GTCCAAGCCA CTATTGGCAA ATTCAATCGG 1260

TAAAAAAGAG AGGGCCATTG CCATTGCTGC GACGACTGTT CCTTCTACCC AAATACGTAA 1320

ATCCATTTTT CTAGCCAAAC AAATTTCCTC CTATGTtCTG ACGCTCTCAA CCACTAATAC 1380

ATCGTTATTT TACCATAGGG ACTTTAGAAA AACACGTTTG TCGAACAAGC AAAAAAATAG 1440

CTGATCAGCA TTTAAGGGAA TCAACTCCTA CTCAAACGCA TGCCAGCTAC TTTTTATCCA 1500

TTAATCGTCC CGCTCAGTTG TCAAAATTTT ACCAGAATGA GCATCGATTT TTACCTCTAT 1560

TTTTTGTTGG CCCTCTTTCA CTTTCACTTC CCAATAGGTG ATTCCTAATT CTTTCTCTAA 1620

CTTCCAATCT GTTGCCTGGC CGACTTTCGC TGCTTTTTCA GCCAAGGTTG TGGCTTGTTC 1680

TCTGGAAATG ATATTTGTTA AATCAAGTGC CTCTTCTTGC ATTTTAACGC CATTTTGTTC 1740

ATCGGCATCC AAGGTTTCGA CTTTTTCTTT TGTGAATTCG CCTGTTTCTG CGTTCACTTC 1800

AACTTGATAT TCTTTTTGCT GATCCACGCC TTCTATTTCA TAAAAATAAC GTCCAAAATC 1860

TGTATCTAAC TGCAGACTTG TTATTTTAGC TTCTGGATAT TTTTTCTCAA ATGCTGTCGT 1920

TACTTT 1926

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1479 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GATTTCTGCT CACTCTTTTT GATGGGAAAA GTCATCaGGA CACGGTTCGT TACATCAATC 60

TCGAAGGAGG CGAAAATTTT GAGTAGTGCT GTGGAAACTG TAACAAAGTT AGTCACACCA 120

ATCTTAGAAG AACAAAATTT TGAACTTGTG GAAGTAGAGT TTGTTAAGGA AGGAAAAAAT 180

TGGTTTTTAC GAGTATTTAT CGATAAAGAA GGTGGCATTG ATATTGAGGA ATGTGCCTTT 240

GTCAGCGAAA AATTAAGTGA AAAACTAGAT GCAATGGATC CAGATCCAAT TCCGCAAGCG 300

TACTTTCTGG AAGTTTCTTC TCCGGGAGCA GAACGTCCGT TAAAGAAAGA AAGCGATTAT 360

GAACAAGCGG TAGGTAAGTA CATTCATATT TCTCTTTATC AAGCAGTTGA TGGAGAAAAA 420

CAGATTGAGG GTACCTTAGT CCATCTTGAT TCAGAACAaT TAACATTAAG TGTAAAAATT 480

AAAACCAGAG TGAAGGAAAT GACTTTTGAA CGTAAAAATA TCGCAAAAGC TCGTTTAGCC 540

ATTCAATTTT AATCAACAGA CTCGAATGTA AAAAAGGGTC CACTAAAAGT TTTACTTTTA 600

GCTAGGCCTG TGACAAGTTT TAACGAGAAG TTTTTCCCTT GGAAGAAGAA CCACTCGTTC 660

AGCTTTAACG AATCCATAGG AGGAAAAGAA AAACAATGAG CAAAGAAATG TTAAATGCAT 720

TAGACGTATT AGAAGCTGAA AAAGGGATTC CTAAAGATAC GGTGATTGAA GCGTTACAAG 780

CAGCTTTAGT TTCTGCATAT AAAAGACATT ATGGACAAGC AAGCAACGTC GAAGTTGAAT 840

TTGAACCAAA AAAAGGCAAT ATTCATGTGT ATGCTGTCAA AGAAGTAACA GAAGAAGTAT 900

TTGATTCACA ATTGGAAGTT TCATTAAAAG ATGCCGTTGC ATTAAATGGT GCATATGAAA 960

TCGGCGACAA AATTCGTTTT GAAGTTACGC CAAAAGACTT TGGCCGCATT GCTGCCCAAA 1020

CAGCAAAGCA AGTAATTTTA CAACGTGTCC GTGAAGCAGA AAGAACAATT ATTTATAATG 1080

AATTTAGCGA ATATGAAAAT GACATCATGC AAGGaATTGT TGAACGTCAA GATCGTCGTT 1140

ATATTTATGT AAACTTAGGT AAAATCGAAG CAGTCTTATC AAAACAAGAT CAAATGCCAA 1200

ATGAATTTTA CCAACCGCAT GrTCGGrTTA AAGTTTACGT ATCACGTGTT GAAAACaaTt 1260

CAAAAGGcCC ACAAGTTTTT GtAAGCCGTA GTCaTCCAGa TTTaCTAAAA CGkCTTTTTG 1320

AACAAGAAAT TCCAGAAGTT TATGATGGAA TTGTTGAAAT CGTAAGCGTC GCTCGTGGAA 1380

GnGGGCGATC GTTCAAAAGT AGnCCGTTCG TTCAACAGAT CCnAATATTG GAnCCCGTGG 1440

GGTACCCGTG GTTGGTCCAA AGGGCCACGT GTCCAGGCG 1479

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

CAGGTGCAGT AGGAATTGCT TTTTTTGCTG GAAATATGAn ACAAGACAAA AGGATAGCAG 60

ATAGGCAAAA CAAaaAAAGT GAGAAGAaGT ArGGAGAATA TTTATGCCAG TTAATAAAAA 120

TGGTTTACCT TTTTATCTCG ACAGAAAATT AGATGTAATA CGCTTTGGAG TTGATCCGGA 180

TAATCATGTG AAAGAACAAC AACTTTTTAA ATATCCGGTT AAAACGGATA AGCCAAATAA 240

AAAAGAACGT TTCATTGAAA AAGAAAGTGA ATCTTTAATT CAATTAGGAT ATAAAATTGT 300

AGTTGATACA GTTACTGGTG TTAATTATTT AGAGAGCCCT AGAGGAGGAA TTACACCTTT 360

GCTTGATGAA ATTGGGAAAG TTTGCATCGA TAAAATTAGT AAGTAAATAA AACCCACCCC 420

TGAAAATCTT TTTTTGGGGG TTATTCTATA TTCAATTATT AATGATAATt ATaGTGATGA 480

GAGAGCAATT CTAAGCCATT TTCACAAATA TTGATCGGTA GTTATGCAAT GAAGAGATTT 540

TAACGTTCGC TCTTACAGGA TTAAATATGA TATGTAGATG AAAATAAAAA aaTCTCTAkT 600

TAAaTACGAA TAATTGTTCA tACCAGGCAt GTGGCCAaCC ATCAAAAGAC GAATAACTGG 660

TTTCGCTTTG CTCAACkGGC CTTCAACGTT TTGTATAGTT TCCCTCTCTG CGTTCAGTCC 720

AACTATGCCA AAAGTTTACA GGTGTATAAA AAAATACGGA AAACTGAATT TTACTAGTTG 780

CAAAAGAGAA CATTCGTTCG TATAaTGGGT TAGTAGAAAG ArGGGATTTk GGATGaATTT 840

GACGTTCGAT TATACGAArG AACCCAGTCG TGATGTGTTT TGTATCGACG TAAAAAGTTT 900

TTATGCTAGC GTGGAATGCG TAGaACGTGG ACTTGATCCA TTGAAGACAA TGCTTGTGGT 960

CATGAGCAAT TCTGgwAAAT TCAGGTGGCC TGGTACTCGC TGCTTCCCCT ATGGCAAAAA 1020

AAGTATTAGG TATTTCCAAT GTTACAAGGA AAAATGAAGT TCCGGACCAC CCAAACTTAA 1080

TTATTGTACC TCCACGCATG AAATTATACA TGAAGAAAAA TCAAGAAATT AACAATTTAT 1140

ATAAACGCTT TGTTTCTGAT GAAGATCATT CTGTATTCAG TGTCGATGAA TCGTTTCTTG 1200

ATGTGACTGC TTCGCTGACC TATTTTAAGT GTGACACCGC CTATAAACTG GCCAAGATTA 1260

TTCAACGTGT GATTTATAAC CATATGGGAT TGTATGTGAC AATCGGAATT GGGGAAAATC 1320

CGTTGCTGGC CAAGTTAGCA TTGGATAATG AAGCAAAGAA TGCACCAGGC TTTGTGGCTG 1380

AATGGCGCTA TGAAGATGTG CCAGAAAAAG TTTGGCCAAT CTCCCCTCTT ACAGAATTTT 1440

GTGGGATAGG AAATCGCATG GCTGCTCGCT TAAAAAAGCT AGGTATTCGG TCCATTTATG 1500

ACCTAGCGCA CATTGAACCT TACATGTTAA AAGAGCGTTT TGGTATCATG GGGCTACAGC 1560

TGTACGCGCA CTCATGGGGC ATAGATCGTA GTTTTTTAGG GCAAAAAGCG GGACGGCCAA 1620

CAGAAAAATC ATTTGGCAAT AGTCAGGTTT TACCCAAAGA TTATGCAAAT AAAGAACAAA 1680

TAAAATTGGT TTTGAAGGAA TTGTCGGACC AGGTTGCTAG TCGcTTACGC ATGGCATCGT 1740

GTCAGACAAC CTGTGTCTCT TTGTTTGTTG GCTACTCAAA AGGTCAGACA GACAAATACG 1800

GCCAAACAGG CTGGCGTAGA CAAATGAAAG TAGAACCAAG TAATAATACA AAAGTTTTGA 1860

CTGAACATGT ACTGCGTCTT TTTGAAGAGA ATTACGCACC AGGGGTCGAC GTACGAAATT 1920

TAGGGGTATC TTATGGCCGT CTTGTATGGA ACAAAAATTT ACAGCTGGAT TTATTTTCTG 1980

TTCCGGAGGA GCAAATTCAT GAAACGGATA TGTATTTTCT TATTGATAAA ATACGTCAGA 2040

AATTTGGGTT TAAAGCTCTG ATACATGCTT CTTCACTGAT GGAAGGCGCC ACAGCAATTT 2100

CACGAGCAAG CCTTGTTGGT GGCCATGCAG GTGGAACTGT TGGCTTAGGT ACAACCAAAT 2160

GAAGCAAAAT AGAAAAGAAT TTTCTTCTTA TTTTTCTCGC TCAATCAAAC AAAATAAGCC 2220

ATTATATTTA TTACTTATGT CTTCAGAAAC CAATCCTTTT CCTATACCAG TtATAGGAAC 2280

TTTTCGAGGA TATGCGGAAG AAAACAAAAT AATAATTGGT GAAGATTCCT ATAGTATAGA 2340

AGAAATTGAC TCCGTGTGTA TGTATCGTCA TTCTAGCAGA ATAAAACAAG AAGAAAGAGT 2400

AAATTCAAAC CCTTTTcAAG GTTTGGTCTC CCCTCCTTTT TcAAAAAAAG AGCAGAAAAA 2460

GTTAGATGAG TATTTTAGCG ATTGGGGGTT TCGTAATGAA GGCATATGAT TATAATGGTA 2520

CCATTATTCC TCTAGGAGAT AGCGCCCGCC AAGTGGCTTA TGTAGAATGC AGCTGTGGCT 2580

GTCTAGCAAG CAGAGTTACG AATGACTCAA GCAAGTATAA ATGTTCCTGG TGTAAACGAG 2640

TTTACACGCT TAGAAAAGAT CATAAAACAG CTAGATAAAT TGTTGAAGGT TTTATTATTA 2700

AATTGGCAGA ATTTCAAATT ATGATATAAT TmATGCGGCA GCTCGCCTCG ATTGGAGGTG 2760

TGTTATTTGT GAAAGATTTA ATGTCGTTGG TTATCGCACC AATCTTTGTA GGATTGGTTC 2820

TGGAAATGAT TTCTCGTGTG TTGGACGAGG AAGACGATAG CCGAAAGTAA GCTGCTATCA 2880

ACACACACGC TAGAAGTCGC AACTAGTGTA AAAAAAAGCA ATCCTATTCG CCGTAGGATT 2940

GCTTTTTGTG TTATCTGTAC GATTTAATGT CGTTTCGCAC TTTTAGTATA GCATATTTTT 3000

ATTTTGGGTC AAGTTTTGTG ACTATGCAGG AATTGGTAAA gAATACAGTG GTAGCAATTT 3060

TCATCGATGC TATTTTATTA ATAAAATAGT AGTAGAAAAA TATATTTATT GATAAACTTA 3120

TAGTTATGAA TCTGTATAGT TAGTTATAAT AATTGGTATT TTTTTAGGAA AATTTGAGCT 3180

TTTGAATTGA ATAAGAAGGA GTGATTTTAT GGATTTAAAG TACAATGTTT TTGGTAATTC 3240

AATGTATTCT TTGAAAGAAA TGGAGCTAAT TCAACTAGCT TCACAATGGT TTTATGATGC 3300

AGGAAGGTTG CCTAGTAGTG CATGGGCGCA AGTAACCTAT GGGGATGTCG CTGTTGATAG 3360

TATACGGAAA ATTTTATCTA GTCAAAGtGA GCCGTATCAC TTTGGAGGAG TTGATAATAT 3420

TTTTCCTCCC TATTTACATG CTATTAGATC AGCAGTAGAA ATGTATAATG ATTTTTGTAG 3480

ACATGCACCA CCGTATTTCT TTAATAAGAC TTCAGATGAA GAAATAGAAA AAGTAATGAA 3540

TATTTCAGCA AATTTTGGTA TTGAGTTAAA GAAAGAATAT TTTACACGTT TCACAATGCT 3600

AGAGGAAATA TTAGTTAAAA TAAAAGATGA TATTGATTTC TTTGAAAATA ATTCAAAACT 3660

GATGGAATAA TAAAGTGCTA ATTATACGGA CAATACTTTA TAATTAATTA TACAGAGCTT 3720

TTAAGGCTAT TTCATAAAAA AACAAGTAGT AAGGGGCACA AGCATTTCCT TTATTGCTTG 3780

TTTTTTGATA ATATATTACT GCAAACGCAT TAATATATTA AGAAAGGAAA CTTACCCACC 3840

ATGCCTAGAA AAACCTTTGT ATATCCACAC CCAATCAATA CTTATATCAT TAAGCAACTA 3900

GGGATTACTG TAGAGGAATT TTGCGAACTA CACTCCTTCT CTCAAGGAAC TATTTCTTCT 3960

TGGATCACTC GCAACAAAAA AATGGAAACT TTACCAGTCT CCTTTATCTA CTCTCTTTCC 4020

TTATCTGCTA GCAAGACTAT GGACCAAGTC TATTCAGAGC TTTTAAAACT GCAAGACGAT 4080

TATTTGCTAC ACTTAGAACG CCACAGACGA ACTAAAAAAA TTATTGAATG AAAATACTTT 4140

TTTACTATCT TACTATTTTA CTACAAAAAA TAAAAACACA AGAGCAATGT TTGTACAGCA 4200

TTTCTTGTGT TTTTATTTTA TTAAACAGTA TCTTTTATTT TTGTTTCTTT TTGTCTCGTG 4260

ATTCATAAGC TTTCATATAC ATTTCAAACA TTGTACGTTG TTCTGGTTCT AATGTGTTAT 4320

CTAATCTATC TAACATGAAC GATACAATGT CGTCTTGTGT TTCAAAATCT AAAGTATTCT 4380

GAAACGCATT TATTCTATTG ATGTTACTCT TTTGTATCCT AATTGTACTA TATACTTTAT 4440

TTTTAGCAGG TCGCCCAATT CGTTTTGATC CTGAATCACT TGCTGAACTT TCTTCTTTTG 4500

AAAAACTACT TAAATCAAAA GTAGTTTCAG GTTCTGAAAT TTCAGTTGCk TTAATTTCTT 4560

TTGATTGTTT ACGTTCAGGA TCCTTATGAA ATGTATACTT ACTCATTAGC AGTCGTCCCT 4620

TCTGTTCGkT CAATTATTTC ATCAGATAAT TTGTkATACA ATtCATGAAC TTTTCTATCA 4680

TGAAAATCAT ATAATTCCGT ATATCCTTCT TCTGATATAC CTTTACGATC ATAACGTTTT 4740

AACCGTTCCA TGTGTCTAAC AATTGTATTA AACAAAGTCT CATCACCAAA AGCGTCTTTG 4800

GCATCTTTAA TTATTTGATT ATCAATTCCA GAATCGTTTT yCAACAGCAC TGGAAGTACC 4860

CCAGCGATAT CAAAGTCAAT GTTTTTATAA GTATCATACA AGGTTTGCAA GTATTCCCCA 4920

AAATGCTTCT GCACCATCAA GGGAGCGTTG CTGCGTTTGC AAAACAATTA CAATGTAATT 4980

AGAAGAATAA AGAGCTGTAT CGGTAAATAC TGAAAGTGTA GGAGGAACAT CAAATATAAT 5040

GTAATCATAA TCATTTTCAA TTGGTTTAAG TAATTCACTA AAAAATGCTA TTCGTCTCTC 5100

TTTGTAGTTT TTCTCTGTCG GCATAATTGT TAGCTCAAGA AAATCAGGAT AATTAACAAA 5160

GTCTTTGTGT GAAGGCAATA AATACAAATT AGGCATTACA TTTACAACAG CTTTTCCTAA 5220

ATTTCCTTCT TGAATTGCTA CCATCATCGT TTCTTTTATA GGTAGTTCTT TATTATTTTG 5280

TAATCCATAT GTTCTTCGCA ACAATTGCGT TGAATTTGCT TGTGGGTCTA AGTCACAAAC 5340

TAAAACTCTA AAACCTTTTT TAGCTAATTC ATAGGCTACC ATTACAGAAT TAGTAGTCTT 5400

CCCAACGCCG CCTTTGAAAT TTCCAAATAC AATTTTTTTA ACCATACAAT GACT 5454

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

ATCCCGGGGA ATGAGCCAAT CTATCAGCAA GCTGCAGTAG CGTTACCGCT TGGATGAAAG 60

AAAATCACTA TGATCTAGTT TATGGCGGTG GCAATGTTGG TCTAATGGGT ACGGTGGCTG 120

ACACGCTTTT AGCAGAAGGT GGAGAGGTAA TTGGTGTCAT GCCCACTTTT TTAATGGAAC 180

GAGAGATTGC ACATAATGGC ATTACAAAGA TGCATACAGT CAGTGATATG CATGCGCGTA 240

AGAAAAAGAT GATTGAATTG GCAGATGTGT ATTTAGCTTT ACCCGGTGGT CCCGGCACGC 300

TAGAAGAAAT TAGCGAGGTG ATCTCTTGGG GCCGAGTCGG TGAACATATG AATCCTTGTA 360

TTTTATACAA CGTGAATGGT TACTATGATT TACTAGCTGC TTTTTTTGAT AAAATGGTAG 420

AAACTAATTT CTTAACAGAA GCGGATCGAG CTAAAATTTT CATTTCAGAT TCCTTAGAAG 480

AAATTGGTGC ATTTATTGAT TCCTATGAAC CGCCAATGAT TCGTCAATAC AAAAAATAAC 540

AAAAGAGGCA GTCACTCTAA CCAGAATGAC TGCCTCTTTT TTACTAGTTT TTCGTTAAAA 600

TCCGATGTAA GAACTCTTTT GTCCGAGCTT CTTTTGGATG GACAAAAATA TCTTCAGCGG 660

TCCCTTCTTC GGCAATGACA CCTTTATCCA TGAAAATAAC ACGATCGGAT ACGTCCCGCG 720

CAAATTCCAT TTCATGTGTT ACAATCACCA TTGTTAGCCC AGTATGGGCA AGATTTTTCA 780

TCGTTTTTAG CACTTCGCCA ACCATTTCAG GATCCAATGC AGAAGTTGGT TCATCGAAAA 840

GTAAAACATC TGGATCCATT GATAATGCTC GAGCAATGGC TACCCGTTGC TTTTGTCCAC 900

CAGACAATTG aGCAGGTTTG GCATCAATAA AACGAGCCAT GCCAACTTTT TCTAAATTTT 960

CTAAGGCAAT TTTTTTGGCT TCTTCTTTGT TTCTTTTTAG GACAGTCATC TGACCAGAAG 1020

TACAGTTTTC TAAGACATTC ATGTTATTAA ATAAATTGAA TGATTGGAAA ACCATACCTA 1080

AATGGGTCCG ATATTTGGGC AAACTATAAC CACGTTCTAA AACATTTTTA CCATTATAGA 1140

TGATTTTGCC ATCTGTTGGT TTTTCTAACA AATTAATACA ACGTAGTAAC GTTGATTTAC 1200

CAGAACCAGA AGAACCGATA ATGGTGACAA CTTCTCCTTT GTTGACGTTC ATATTGATAT 1260

CTTTTAATAC TTCGTTTTCG CCAAAGCTTT TTCGTAAATG TTCAATTTCA ATAATTGCAC 1320

TCATCTGTTT GCCTCCTAGC TTTCTTTTCC TTCTTCAGTT AATTCTTCTA CTTTAACGTA 1380

AGCAGAAGGG CCATCCATTT TACGTTCCAC AACACGTAAG ATTCGTGTGA TCACAAAAGT 1440

CATTACCAAG TACATGATGC CGACAATTGT AAAGGTTTGG AAGAACTGGA AGTTTGCGCC 1500

AGAAGCAGCA TTCCCTTGGA AGAATAAATC TGCAACACCG ATAACACTTA ACACGGCCGT 1560

ATCTTTGATA TTAATGACAA ATTCATTCCC TGTTGCAGGT AAAATATTAC GTAATACTTG 1620

GGGaATAACG ACTTTACGCA TTGTTTGTCC ATGGGTCATC CCAATCGCTT GTGCTGCCTC 1680

GAATTGTCCT TTATCTACTG CGAAAATACC TCCGCGAaCA ATTTCAGACA TATAGGCACC 1740

AGTATTCACA GAAACGATAA ATAATGCGGC CACTGTTCGG TCTAAAGAGA TGCCAAAAGC 1800

TAGAGCTAAA CCATAGAAAA TAACCATTGC TTGAACCATC ATTGGTGTAC CACGGAAAAC 1860

TTCAATATAA ATAGAAAGAA TTAAATTTCC TAATTTTTGG AAGAAACGAG CGACTGGGTT 1920

TTCAGAATCT GGAATTGTAC GGAAGACACC AATyAGTAAA CCAAGGGTTG TTCCGACAAC 1980

TGTCCCAATT AACGCGATAA ATAGCGTTAA ACCAGCACCA CGTAAAAACA TGTCGCCATA 2040

TTGATTCCAA ATATTTTTGA AATCGTTAAT AAGTCCTGTT TTTTGTTCAT CACTATCTGT 2100

TGCTGCAGGT TGATCCTTGA TTGCTTGGTC CATAATTTTT GTCCGTTCAT CTTGAGAAAT 2160

ACCTGCTAAA ATTTTGTTTA CTTTTTCAAT GTCTGGATCG CCTTTACGCA TGCCGACTGC 2220

TACTTGCGAG TCTTCAGCGC TAGCATCAAA GCCCTTTTCT TTTGGAAATc TAACATTTTT 2280

AATTCTTTAT TGACACTAGT TGCTGTTATG CCTTCAGGGC GTTCACTAAC ATACCCGTCA 2340

ATCATGCCAG AAGCAAGTGC TGTTCGCATA GCTGAAAAGT TATCCATTGC TTGCTGTTTA 2400

TTGACATTTG GAATTTGATC AATTAATCCG TAGTGGAATG TATTTAGTTG AGCCGTAATT 2460

TTAGCATCAG CTAAATCTTT CAAGCTTTTT GCATTAGCGT ATTTGCCATC TTTTTTTACA 2520

ATTACGACAA ATTGTGATTC ATAATAAGGG TTTGTAAAAG CAATTTCTTT TTTTCGTTCA 2580

GCGGTTGGGC TCATTCCGGC GATAATGGCA TCAATTTTTC CAGATTGTAA GGCGGGCGCC 2640

AAGCCATCCC ATTTGGTTTG GACGATTACT AATTTACGAC CTAAACCATC GGCAATTTTT 2700

TTAGAAATTT GAACATCATA GCCGCCTGCA TAAGAGTTGC CTTGAATAGG CACTGCGCCA 2760

TGTGCGTCAT TTTTcTGTGA CCAGTTAAAA GGGcGTAGCC AGCTTCCATG CCGACACGAA 2820

ATTCACCATT TTCCTCCGCC GAAGCGTTGG TTGTCATGCC AAGTAACGAA AATAGCGTGA 2880

CAAGTAGTAG ACTGAATGAA AAAACTTTTT TGTTCATCTT TTTCTCTCCT TTAAmTTTCT 2940

TGTCTGATTG ATCGTTTTGT CTTTTTTCAA TCAACAAGCT TTGATAATCA GCTGAGcAAA 3000

AGCGATTCTG TCTTTTTAAA GGAGAATACT TCTGTCACAA CCTATTTTTG AATACAAAAA 3060

AACAACCAAA CAGATGTAAG GTTGCTAGGT AATGTCGAAA AAAATTCCTC AACGAAACAT 3120

AGCACAACTT AGCATCACTA CTAAGACAGT CCGCAAGCTC TTAACTTACG TCCCAACACA 3180

CAACAGAAGA GGCTCCGTTA TGCATTTCGG CGATTGATCC TAAACTTGCT TCCCAGTGTC 3240

CTCTCACTCC ACAAGCGTAA TAAAAACCGC GACCTCTACC TCTTTTTTGA GGCACTATTC 3300

AGTTATTAAA TTCAGTTATT AATTTTaGGA TAAATCCAGA AGAAAGTCAA TATGTTCCAG 3360

CAAAGGAATT TATCAAGAGG ACACAAACAC CATGAAtTAA CGTAACATTT TCCCTACGAA 3420

ATAGAAACTA ATACGAAAAA AGCAACCATT CCTAAAGGAA CAGTTGCTTT TTACTTAAGC 3480

TTTGACAGCT TTTGGTTCAC GACCTAAAAT AGCTTGAAGA ACAGTCAATA CACCTAAAGA 3540

AGCTAAAATT GTATAAATTA GACTTGAGTA AGTTAAGATA CCGAAATCCC AAGTTTTGTA 3600

AACTAATAAA ACAATTGCTA AGGCGATAAT AGCGATAACG TTGAAGAACG CAAAAGCCCA 3660

AAGATTTCCG TTTTCTTTAC GAGAAAGATA AAAAACAGAG AACCAAATGC TTAAAACGCC 3720

CCAAGCGATG CAGGCAATAA TTGCAGCCCA ATAAATAATA AATGCGACCA TTGTTGTTTC 3780

ACCTCACTTT TACTCATGCA TATTTTACCA CGAGTTGAGA AATTTGTCAC AAACTCTTTC 3840

AAGATAAATC AATATATAGG TAAGAnGTTT tCmAAAAGTG GAAAAaCTTT tGGTGCTAAT 3900

GTTAAAATAC GTTATAATAT AGAAGATTAG GAGCTGAATC GATATGCAAG ATATCACGCA 3960

AGCCGAGGCA ATTCATTGGT TGGCAACCCA ACAAAAAATC ACATTTnTAA CAGGTGCGGG 4020

TATCTCGACA GCCTCAGGTA TGCCAAATAA TGC 4053

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

TAAACATATT CTTTACTTGT TAAAGGATCT GTTATTTTTA TTTAAAAATT GTTAGCTAGT 60

TAGAGCAAAT GGTTCGTAAT CATTCGGTTG ATTGTTCGAA TTTATCATAG TAGTTAAAAC 120

GAAATTATCT TGTGTATATA GAAAACACCT ACTGAAGACG CACAATACTT CCCCAAGTTG 180

TGTATGTTTA GTAGGTGTTT ATTTATAATT GTATATTTGA ATTATAAATA AAATACAATT 240

GTTTTGTAAA ATGAAAACTt GAAATTTAAA AAaGAAAGCG GTAAAATATC TTaCCAAACA 300

ATTTTATTTT TCATTTTATT ACTACCTCTT GTCGCCTTAC CCCAATGAGG CGGcTTTTTT 360

TACATAAAAA TATTGAACTC AAAAAATAGA TATTGTAAAA TATCTATACA TATTTAAACT 420

CTTATTTTTT CACGCAGACC GCCTTTTCTC AATAAGGTGG TCGTTTTTTT GTTGAAAATT 480

GAAAATCAGT AAAGTAAAAT TGTTATATAT TAAGCTATAA CTAGTAAGAA CTATTTTATC 540

CCCAATAAGC TAGTTATTAC TTGGACCATT AGCTCAGCTG GTTAGAGCAA ACGGCTCATG 600

ACTATTCGGT CGATGGTTCG AATTCATCAT GGTCGATAAT AGAATTAGAC AGGTAGTGAA 660

TTATTTTGAA AAGAACAGGA ATTCTCTTAG TGAATTTAGG AACACCAAAA GATTCTTCCA 720

AGACGGAAGT AAGGAAGTAT TTAAAAACTT TTTTATCAGA TAGAAGAGTA ATAAAAATAC 780

ATCCTATAAT TTGGAAACCG ATTTTGAACG GTATTATCTT GAATATACGT CCAAAAAAAT 840

CAGCAAAACT CTATCAAAAA ATTTGTACTG AAAATGGATT TCCTCTTTTG GAATATACTG 900

AGAAACAAAT GGAAAATTTG AAAAATATAT GTCCAGAAGT GGAAGTTACA ATCGGAATGT 960

CATATAGTGA ACCGAGTATA GAAACTGCTC TAGATACATT ATTATCmAAA GAGATTGAAG 1020

AACTCAATGT CATACCAATG tATCCGCAAT ACTCTGGGAC AACGGTAGGA TCGGTGTTTG 1080

ATTCCGTTAT GAATTATTTT ATAAAAAGTG ATAGGATAGT GGATATTAAA TTTATTCGAT 1140

CATTTTACAA TAATCCACAG TATATAGATT ACTTTTCAAA AAAAATAAAT GAAGCTTTGA 1200

ATGAAAGTCC AATAGATGCT ATCGTTTTTT CATACCACGG AATTCCTATG TCTTATGTAA 1260

AAGATGGGGA TAACTACCCG AAGGAATGTA CTAAAACAAC AAAATTAATA ATGGATAAAT 1320

TAGGAGATAT TCGTTATTAT CAAACCTATC AATCGAAATT TGGGCCATCT GAATGGTTAA 1380

AACCAGCAAC TGATGATACC TTGAAAAAAT TACCATCAAA AGGTATTAAA AATATATTAA 1440

TTGTTGCmCC AGGTTTTGTT GTAGACTGTC TAGAAACAAT AGAAGAATTG GAACACGAAA 1500

ACAGAAACTA TTTTTTAGAA AATGGCGGGG AAGTCTACAA ATATGTTCAT CCATTTAATG 1560

GAGATATTGA AtTTGCmAAA TTAgTAAAGG aCATTAtTTC TTTGTAGTAA TTTGTTTTAG 1620

TkTTTTATTT TAGTTTGAAT TTGTTAAACA ATTTATTCAG GGTTTGCACG AATATATnTA 1680

CTGGnATACA TATAGGTAGA ATTAAGCCAA AATTAAACGG CCTATCCCCC GGTCCAGTTT 1740

AnGGAATAAG CCGCCTAA 1758

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1091 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

ATGCTGGCGT TTCAGCTACT AAATTTCTAG CAAAGAAATT TAAAAAAGAT ACGGACGTAA 60

CAATCACATT GATTGATCGC CATTCTTACC ACACTATGAT GACCGAATTG CATGAAGTAG 120

CAGGCGGACG TGTTGAACCA GAAGCAATTC AATACGACTT ACAACGTTTG TTCTCACGCA 180

AGAAAAAACGT AAAATTGGTA ACAGATACTG TTACTGGAAT CGACAAAGAA AACAAAGTTG 240

TGAAAACTTT AGCAGGTTCT TATCCATTTG ACCAGTTAAT TCTGGGTATG GGTGGCGAAC 300

CAAACGACTT TGGAACACCA GGCGTGAAAG AAAATGGTTT CACCTTATGG TCATTTGATG 360

ATGCAGTGAA AATTCGTCAT CACATTGAAG CAACCGTTGC TAAAGCAGCC ATCGAACCAG 420

ATGCTGAAGT ACGCAAAGCA ATGTTAACAT TCGTTGTCTG TGGTTCTGGT TTTACTGGGa 480

TCGAAATGGT CGGCGAATTA ATCGACTGGA AAGATCGTTT AGCGAAAGAT GCCAAAATTG 540

ATCCAGACGA AATTACATTA ATGGTTGTTG AAGCAATGCC AACCATCTTA AACaTGTTAT 600

CTCGTAACGA TGCTGCCAAA GCAGAACGTT ATCTAGAAAA GAAAAATGTT CAATTATTAk 660

kGAACTCACC AATCGTTGAA GTTGCAGCAG ATCACATTAA ATTAAAAGAT GGTTCTGAAG 720

TACCAACGCA TACGTTAATC TGGACAGCTG GTGTGAAAGC AACTTCTGAT GCCGCTGACT 780

TTGGTTTAGA AGCAGCACGT GGTAGTCGTT TAGTTGCGAA TGAATACATG CAAGCAAAAG 840

GTTACGAAGA CAAAAACATT TATATCATTG GTGACTTGGT TTATTACGAG GAAACACCAA 900

ACACACCAAC TCCTCAAATC GTTCAAGCAG CTGGAACAAA CAGGTCATAC TGCGGCTGCC 960

AACATCGTTG CAGATATTAA AGGCGGCGAA AAAACACGCC TTTTAAGGGG AACTACCCAG 1020

GGATTCCTGG GTTTTCCATC GGCGGCGAAA TGGGGGCGTT GGCCAACTTA TTCnGATnAA 1080

AATTCCATTT G 1091

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

TCATCTATTA ACTCTCCATA GGTTTCATTT AAGGATTTTG GGGAAACTTT ATAATTTTGA 60

ACTTTTCTTT CTATTACTAA TTTCATGACC CAGTCAACTG CTTCTAACAC TTGACTGTTC 120

TCTAATTCCA TTTCTATCAT tAATkCCTCA TCGTTTATGT TAGTCTGAAT TGCACTCGGT 180

ACTATTmCAC TCTTCAAATC ACTTAGATTA AGAAAGTTAA CAGTCATATA ATTTCGATCG 240

TTTATTTTTA TAGACTGTTT TTTTAAGTTC TTATCCTCAA GAACCTTTCC ATGATTCATT 300

AAAATATATC TATCAGCATA TTTTTCAACT TCTAAAATAT TGTGTGTGAC CACGATGATT 360

ATATGCCCCT TATTAGATAA TTTTTTCAGA TATCTCCATA TTTTTTGCCG TCTAATAGGA 420

TCCACATCAT TAGTAGGTTC GTCAAGGACT ATTATTGGAG AAGGATATAC AACGGCCATT 480

GCAAATGAAG TGAGCCTTCT AAGTCCGCCT GAAAGTTTCT GTCCTGGTAT ATCTTTCCAT 540

CCATCTATTT TTAATTCTTT TAAAATTTTA ATACACTCTT CTTCAGCTAT TTTCTGACTG 600

CCTCCTCTTA TTCTTATTAT TGACTCGACA GATTGAGCCA TCGTTATACC TGCCAAGGGA 660

GCATGTAGTT GAGGCATCAT AGAGACATAT TCTCTTGcAA TTTTACTATC TCTCGCAAAT 720

GATAGACCAT TAAATGTTAT AGAGCCCTTT GTTGATTTCG TTATACCTAT AATCTGATTC 780

AACATTGTTG TTTTACCAGC GCCGTTATGT CCAGCTATGG CAGTTATTTC ACCTTTATTA 840

AAGCGCAAAT TTATATTATC ATTTGCATAG CTCTCTGATT TCTTGTACTT TTTACTTAGC 900

GAATGTAATT CTAACTGTTG ATTCAAAGCA AACCTCCTAT ATTTAGACTT AATTAAATTG 960

ATTGATAACA GGTTGGAACC ATAACCAAAT TATCATTACT AGCACACTTA TGCTTATTAC 1020

TTTAATAATG ATTAATTTCA TAATTGCGAC CTCTTCAAaG TAGAAaGGAT TATCAACCAC 1080

AAAAGAAATC AAAaTGTTAA TATCTGTTTT TTGTATAATG ATAAATTGCC ACAATATCCT 1140

TGTTATAAGT ATTGATGCCG CAATAGAATT AACTCCAACA CTTTTATTAT TCATAATCAA 1200

AAAAACTAAC AAGAATATTG CATCCGACG 1229

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3721 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CATCAGTATT AGTTGGTGTA GGnCTTGTTT TTGGGGCAAC TGGAATAGTT AATGCACAAA 60

TGGGTGAAGG AAGATTAGTA AATTATTCTG CTTCAGGAAA TACGTTTCAA GAAAATCCGG 120

GATATACGAA GAATTATAAT TTCTCGGATT TACAATTCAA CCCTAAAGCA ATAACTGGTG 180

ATGTGTTACA AGGAAATACA ATTGATTTTG AGGTTTATGG GAAACATAAT ATTGCAGCTT 240

CAACTGCAAA CTGGGAAATT CGTCTTCAAT TAGATGAACG ATTGGCCCAG TATGTTGAAA 300

AAATTCAAGT TGATCCGAAG AAGGGCGTAG GAAATAGTAG ACGAACTTTT GTAAGAATTA 360

ATGATTCGCT TGGCAGACCT ACAAACATTT GGAAGGTTAA TTACATTCGA GCAAATGATG 420

GACTATTTGC TGGGGCAGAA ACAACTGATA CACAAACTGC TCCTAACGGT GTGATTACAT 480

TTGAmAAAAA TTTAGATGaA ATTTTTAAAG AAATTGGtGc AGATAATCTT aAAAGCGACC 540

GTTTaATGTA TCGTATCTAT TTgGtAAGTC ATCAAGATGA CGATAAAATT GTACCTGGAA 600

TAGAAAGCAC TGGTTACTTT TTGACAGATC AAGATGATTT CTATAATAAG TTAGATGTAT 660

CCGAAAATAA TTCTGATCAA TTTAAGCATG GATCGGTAAA TACTAAATAT GAAGAAGCTA 720

ATATCCAAAC AAAAGACGGT TCTGGGTCTA CTGGTGCTAA TGGAGCTATA ATTTTAGATC 780

ATAAGTTAAC GAAAGAAAAG AATTTTTCTT ATTCAACTTC TGCAAAGGGA ACGCCTTGGT 840

ATGCTAACTA CAAAATCGAT GAACGTTTAG TACCATATGT ATCTGGAATA CAAATGCATA 900

TGGTTCAGGC TGATAAAGTG GCATATAATG TTGCTTTTGA ATCAGGAAAA AAAGTGGCTG 960

ATTTAGCAAT TGAGCGACGT GAAGGTCATG AGAATTATGG TATGGGTTCA ATCACTGACA 1020

ATGATTTAAC TAAACTTATT GATTTTGCTA ATGCTAGTCC ACGACCTATC GTTGTTAGAT 1080

ATGTTTTACA ACTGACTAAA CCTTTAGATG AAATCTTAGA AGAAATGAAA GCAGCGGATA 1140

AAATCGAAGA AAATGCGCCA TTTGGTGAAG ATTTCATCTT TGATTCTTGG TTGTCGGATA 1200

CGAATAAAAA ATTAATCCAG AACACTTATG GAACAGGTTA TTATTATTTG CAAGATATTG 1260

ATGGTGATGG AAACCCTGAC GATAAAGAAG AGAGCGGAGA CACGAATCCA TATATCGGGA 1320

AACCTGAATT AGAAGAAGTA TATGATGTTG ACACAACAGT TAAGGGGAAA GTATTCATCC 1380

ACGAGTTAGC GGGAACAGGT CACAAAGCGC AACTTGTTGA TAAAGAAGGT ACTGTATTAG 1440

CAGAAAAAAC TATCGCTCCA AATGAAAAAG ATGGGGCTCC AATTTCAGAT ACTGTAGAAT 1500

TTGAATTTAC GGGTGTAGAT TCAAGTAAAC TAATCGCGAA AGATGAATTA AAAATCCAAA 1560

TCGTTTCTCC AGGTTTTGAT AAACCAGAAG AAGGTTCAAC CGTTATTAAG GAATCACCAA 1620

AAGCGGTTGA TAAACAAACC GTGGTAGTTG GATTTAAACC AGATGCTAAA GAATCAATTC 1680

GGAATAATAA AAACTTACCT GAAGATGCAG AGTATTCATG GAAAACAGAG CCTGATACTT 1740

CTAACGTTAC TGATAGTACG AAAGGTATTG TAACTGTTAA GATAGGAAAT CGAACTTTCG 1800

ACGTGGATGT AGAGTTTGCT GTAAAAGCTT CTCAAGCTAT GGAAAATGAT GCAACATACG 1860

TACCTATAAC AACAACCCCA GAAACGACAA TTCAAAGTGG TAAACCTACA TTTGATAAAC 1920

CAGATGTTCC TCTAGCTAAC GATGCCTTTT CAGTTTTAGA TGTTTATAAT AAGGACTTCG 1980

GCAATGCAAG TGTTGACGCA AATACTGGTA TTGTTACATT CACTCCAGCT AAAGGTGTAG 2040

GAGAATCGGA GCCGATTACT GGAACAATTC CTATTAAAAT TGTTTACCAA GATGGTTCTG 2100

TAGGCACGAC CGATTTAGCA GTAACTGTAA GTAAAAATAT TTATGAAAAT CCAGGAGAAA 2160

ACATTCCTGC AGGCTACCAC AAaGTAACCT TCACCGCAGg AGAAGGAACA AGTATTGAAA 2220

GTGGAACAAC AGTCTTTGCA GTGAAAGACG GCGTAAGCTT ACCAGAAGAT AAACTTCCGG 2280

TGTTGAAAGC AAAAGATGGT TATACAGATG CGAAATGGCC AGAAGAAGCA ACGCAACCAA 2340

TTAAAGCAGA TGATACAGAA TTTGTATCAA GTGCAACAAA ATTGGATGAT ATCATTGAAA 2400

ACCCAGGGGA TAACATTCCT GCAGGCTACC ACAAAGTAAC CTTCACCGCA GGAGAAGGAA 2460

CAAGTATTGA AAGTGGAACA ACAGTCTTTG CAGTGAAAGA CGGCGTAAgC TTACCAGAAG 2520

ATAAACTTCC GGTGTTGAAA GCAAAAGATG GTTATACAGA TGCGAAATGG CCAGGAGAAG 2580

CAACGCAACC AATTAAAGCA GATGATACAG AATTTGTATC AAGTGCAACA AAATTGGATG 2640

ATAAATCTGA TGCTGACAAA TATACTCCTG AAGGTCAAAA AGTGACTACA GAATTGAATA 2700

AAGAACCTGA CGCATCTGAG GGAATTAAAA ATAAGAAAGA TTTACCAAAA GATGCTAAGT 2760

ATACTTGGAA AGAAAAAGTA GATATTAGTA CAGCTGGAAA TAAAAAAGGT ACGGTTGTAG 2820

TGACATATTC AGATGGATCA TCTGATGAAG TTGAAGTAGA TGTCACAGTA ACAGACAATC 2880

GCTCTGACGC TGATAAATAT GAGCCAACAG TAGAAGGTGA AAAgTAGAAA TCGGTGGTAA 2940

AGTrGATTTA ACAGATAaCG TTACTAACTT ACCAACGTTA CCACAAGGAA CAACAGTAAC 3000

AGATGTTACT CCTGGTGGTA CAATCGATAC TAATACACCA GGTAATTACG AAGGTGTCAT 3060

TGAAGTAACG TATCCAGATG GTACAAAAGA TACAGTAAAA GTTCCAGTAG AAGTAACAGA 3120

CAATCGCTCT GACGCTGATA AATATGAGCC AACAGTAGAA GGTGAAAAAG TAGAAATCGG 3180

TGGTAAAGTA GATTTAACAG ATAACGTTAC TAACTTACCA ACGTTACCAC AAGGAACAAC 3240

AGTAACAGAT GTTACTCCTG GTGGTACAAT CGATACTAAT ACACCAGGTA ATTACGAAGG 3300

TGTCATTGAA GTAACGTATC CAGATGGTAC AAAAGATACA GTAAAAGTTC CAGTAGAAGT 3360

AACAGACAAT CGCTCTGACG CTGATAAATA TGAGCCAACA GTAGAAGGTG AAAAAGTAGA 3420

AATyGGTGGT AAAGTAGATT TAACAGATAA CGTTACTAAC TTACCAACGT TACCACAAGG 3480

AACAACAGTa ACAGATGTTA CTCCTGGTGG TACAATCGAT ACTAATACAC CAGGTAATTA 3540

CGAgGTGTCA TTGAAGTAAC GTATCCAGAT GGTACAArAG ATACmGTAAA AGTTCCgTAG 3600

rAGTAACAGA CAATCGCTCT GACGCTGATw AATATacaCs TArAGGTGAA AAGTAGAATC 3660

GGTGGTAAGT GnTTTACnGA TACGTTACTA CTTACCAACG TTACCACAGG nACCACGTAA 3720

C 3721

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

nCAAAnGAGG GCTAATTAAT GGAnAAAAAT GGATTGAaAA AAACmAATAT TTTGTTGGAG 60

CAATTGGAGT TATTCTCaTT GCTCTTTTTT CATTCCtTCT TTTTGAAAAC CAACAAAAAG 120

AAGAAGTGAA AGAAGCTATA AATACAGTGG TATCaAGTGG CTTAGAGGAA GCGGAGAAGC 180

CAAAAAAACA TGTAGAGACA AAATCTAGTG AAACTGTTCA AAGTAATCAA GTAGATGTTA 240

TTACTGGTAC GGAAGCACAA GAAGAaACmC CTATTTCAAC AGTGATTTCT TTAACCGAAG 300

GCGAACGTCC GTCTGTTAAA ACGATTCAAA ATGCCCAAGA AAATTTTAAT GAAGTGTCGG 360

ATTCTGTTTT AGGGTCTATT GAAATTGATT CTATTCAATT AAAATTACCT ATTTTAATGG 420

GTGATAGTTT TGACAATATG CTTTATGGAG CGTGTACTGT TTTATCAAAA CAAACGATGG 480

GAAAAGGAAA TTATGCTTTA GCTTCTCACA ATGCTGGGTA TGAAGGATTA CTTTTTACCT 540

CGTTAAATAA AGTTTCTGTA GGAGATTTGG TCAAACTTAA TGATCGTGAA GGACATTCGT 600

TCATATATAA GGTAAAAGAG CAAAAGCATG TTGATATGAC TGATACAACT ATGTTGAATC 660

TAACAAGAAA GCCAACATTA ACTTTAATAA CTTGTGACCA AGCCACAAAA ACAACAGGAA 720

GAATTATTGT GATTGCGGAA TTAGTTTAGA GGAGGGAAAA AGTTGGTTGA AAAAATAAGG 780

GAATTGTCAA AAGAAGAATT TGTTAATCAA TACATGTTTG ATTTTAAGGT ATTGATTTTT 840

AAATCTAAAA ATCCTGAAAA AATAACTGCC AAGCAAGAAA GACTTTTAGA ATGTGAAAAG 900

AAGATTGCTG TGTTGTTTTA TGAAACGTAT AAACGAAATA AAGGTTATCT GCCTGATGAA 960

AAAGAACTGG GGAGGATTGT TCAAAGAAAT TTTCTTGACC GTTTAAAGTT ATTTCGAGTG 1020

GAATATGATG TGATtAGTGA AGAAAAATTT tGTGGTCTAC ACGTACAAAT GGTCAAACAG 1080

CAAATGCCAT TAGAAAAGTA TCGAACAGAT GATTtATCTT ATATTTTAGG TCGAGAAAAG 1140

AAGATAGCTA TTAATTATTT TATCGCACAT GATGATTTTC CTATGGGTTA TGAAGAACTA 1200

ATGATAAGTC GTTCTAAACA AGCAGTTACC CAAGGcTTGG AAGAGTTAAG GGGAGAATTt 1260

ATGGAAAGAT ACCATAAATA TTACAGAAAA ATGGAAAGGA GTTGTATTTT ATGAATCAAC 1320

ATATTATGCC AATTTTTAGA GAGCATAGTA AATTTTATCA AAGGTATTCA AATGTACCAG 1380

TTCCTGAAAT GCTTCGCTTG CATGGATTCA TAGTTGATGA AATGCCAATT GATGAAGCAG 1440

ATATTGTTTA TATGGAAGAA TATAAAAATT CTTTACTTAA AATGGGGATT ATTATTGATG 1500

AAGTGCCTTT TAAGAAGGAA TTTGTTGCGC A 1531

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2760 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

ATTGTAGGAG ATAATGGTGG CTTGGCACGG GTCTCTGAAT CGTTTATTTT AGGTTCGGTC 60

TCATTAATTT TTTGGACATT GACTATCTTA ACCACGATTA AATATGTAGT TATTGCTTTA 120

AATGCTGATA ACCATGGAGA AGGTkGGATT TTCTCTCTTT ATACATTGGT TCGTAAAAAA 180

AGTAAGTATT TGATTATTCC cGCAATGATT GGCGGTGCCG CTTnacTGgc TGATGGCGkk 240

TtGACCCCAG CTGTGACAGT GACGACAGCG ATCGAAGGCT TACGGGGGAT TCCAGCATTT 300

TTTGAACGTT TTGGCAATGA CCAAACGATT ATAGTGGTTA TTACGTTGAC GATTATTTTA 360

ATTCTTTTTT CTGTTCAACG ATTTGGAACA GAATTGGTCG GGAAAGCTTT TGGGCCGATT 420

ATGTTCTTGT GGTTTACTTT TTTAGGCATC ATTGGTTTAA TGaATTTTAG CCAAGATTGG 480

ACGGTTATTC GTGCaTTAAA tCCATATTAT GcTTTGcAAT TACTAGTCAG TCCAGAAAAT 540

AAATTAGGTC TATTTATTTT AGGGAATATT TTCTTGGCTA CAACTGGTGC TGAAGCTTTA 600

TATTCTGATT TAGGGCATGT AGGAAAAATG AATATCCGCA TTAGCTGGCC GTATATTAAG 660

ATTTGTTTGA TTCTTAATTA TTTAGGGCAA GCTGCGTGGT TGTTAACGGT CAAAGAAAAC 720

CCTGAAATGC AGGCATTAGC TGAAATTAAC CCATTTTTCC AAATGaTTCC ACGAGGTATT 780

CTCGTATTTG GCGTTGTTTT TGCaACAATC GCCGCAGTGa TTGCTTCGCA AGCGTTAATA 840

TCAGGTTCGT ATACTTTAGT TTCTGAAGCG ATTAAATTGA AGTTATTACC AAGACTTAAA 900

ATTATTTATC CTGGGAGCAA TATCGGTCAA ATGTATATTC CAGCGGTAAA TTTAATTTTG 960

TGGTTAGCTT GTTCAGCAAT CGTGCTGGCT TTTAGAACAT CGACACACAT GGAAGCTGCG 1020

TATGGTCTAT CGATTACGAT TACGATGTTA ATGACAACCA TTTTATTGTT GTTTtATCTT 1080

TtGGATAAAA TTCCAGCTTG GTCTGCGTAT CTAATTTCCT TGTTCTTTGC TGCCATTGAA 1140

GTTGTCTTTT TCTTTTCAAG TGCTGCGAnT TTTTCCATGG TGGATATGTT GCTGTGGGAA 1200

TGGCAGTCTT CTTGTTATGC ATCATGATTA TTTGGGAACG CGGCAACGAG ATTAAGGAAG 1260

CGACGGCGGa ACAAGTGTCG TTGAAAAAAT ATGTACCACA ACTTAAAGCT TTGAAAGAAG 1320

ATACATCTGT ACCTATGTAT CAAACCAACG TGGTCTTTTT AACCTCCGAT CGAGTGGATG 1380

GCGAAATTAA TCGTAATATT ATTTATTCGA TTTTGGACAA ACAGCCAAAA CGAGCGAACG 1440

TTTATTGGTT TGTTAATGTT CAGGTAACAG ATGAaCCCTT TACTCAAGAG TATTCTGTTG 1500

ACATGCTAGG AACTGATTTT ATTGTGCAAG TTCAGCTATA TTTAGGCTTC CATATTTCTC 1560

AAGAAGTGAA TGTATATTTA AGACAAATTG TTCATGACTT GATGAAAACA GGCCGCTTGC 1620

CAAAACAGCC ACAACGTTAT TCATTAACGC CAGGAAGAGA AGTTGGCGAT TTCCAATTTG 1680

TATTAATTCA AGAAGAATTA TCTAACGTTT CTGAACTGAA AAAATGGGAT CGACAAATTA 1740

TGCAGGCAAA ATTAGCTATC AAAAACTTAA CTACCTCTCC TGAAAGTTGG TTTGGCTTGG 1800

AATACAGTGA AGTCAAATAT GAATCCGTTC CTTTAATCAT TGGCCCACAA CGGAAAACGC 1860

ACTTAGTCGA ACGAAAGAAT CGTTCATAAA TAGAAGAAAT TTAACTAAAA GATTGAGCCT 1920

AAGTCCTTGA GATACATGGC TCAATCTTTT TTGTAGAATC AGAGTAAATA CTGTAATTCC 1980

ACAAAGAATT CATTTAAAAG CGTTTGGTCT TTAAAGGAAT TCATCCGCTT AAAGATGGCC 2040

AGTAAGACTT CTTTTTGAGG TTCAGTTAAT TGATCTACTT TTAACAAAGG AAGAAAAGCG 2100

ATAATCAGAG AATAATCCAA TTCTGGATTT TGAGAATGTG TAAATAATTC ATGGAGTTCT 2160

GACAAAATAA ACGGATGATA ATAAGATTGG TCAGACTGTT CTTCTGCAGT TGTTGGTTCA 2220

TAAATAGAAA TACTCTCTTG GGAATGAGAG GGGGCTTCTA CTGTTAAAGG AAAAGCATAA 2280

AAGGACTGCT GTAACTTTTG CGCTTGAATC ATAATTTTTA AGGAATCGTG ATAGGATAGC 2340

TGTTCTTCAG ATAAACGTCC CATCAACTGA GTAAAAAAAG GTGGTTTTAG CAGTTGTTTA 2400

TTTTGAAAAT TTtCTTTTAA TAGCTGGCGC ACAAATCGAT CGAAATCACC ATAAAGTAGC 2460

CAATCTACTG TTGTGTCACA GGCTTTAGCG ATTTTTTTTA AGTATCGTTT ATtGGGTAAA 2520

TTCAAACCTA GTTCCCmGTT ACTAATkGkA CyTCCACTrG ATAAmCCAaT TTTATkGGCT 2580

AAATAACGTA AAGTGTACTT CTTCTTTTTT CGAGCTTCAC GCATGCGTGC CCCGACTTGC 2640

TTTGTAGTAA TTTTCATTGA AACACTCCTT TTGTAATAAA TATGAGGATA AGGTGTTCTT 2700

AAAATATACA TACGCAAAAT TCGGCTCTTT TTnTTCTAAA CnAAAAAAAG TnATTTATTC 2760

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

TTCGGCTACC CCTAATTTTA TCGGCtTAGA tAGAaATAGT GAATTAAGAG GTTAGCAGAC 60

AACAAAATAA GAACCGACTG kCaTAGGACG GGAATCCTAG AGGACAGTTA AACAATTCtG 120

ATACAGCATG AACTATACTt CGGTTCTCGT TTGTTGCAAC ATTAGTTACA ACGTATAGTA 180

TAACAATTTT TAATGTAAAA TTCTAGGCTT TTTTAAACTC CTTTATTGGC CTAGGTAAAG 240

TTTTTTACAA TGAATTGTTT TAATTAGTTG TATAAATGTT GGGACAGCGG GGAATGTATA 300

CAGTTCATGT ATATGTTCCC CGCTTTTTTG TTGTCTGTTA ACTTGTTGAA AAAATAAAAA 360

AACCAAGTAG CAAGCATTCT CATTTTCTAA AAATGGCCCG CTTGTGGAAT AATTCAATGC 420

TTTCACGCAT TGTTTGTACT GGAACTACTC GTAAGAGCCG TGCAAACAAC GTGTTGCATG 480

GCTCTTTTTC TACTTGGTTC AGAAAGTAGG TGAATCAATG ATTGAACTGA AAGCAACAGA 540

TTTGCACCGT ATTACGTGTC AACTGACCTT GTTTAATCGA CAAAGGTTTA AATTGTATAA 600

CGGCACAACA GAACGTATCG TATATGATTT TTCAGGAAGA AATCTGTTGA TCAATCCTGT 660

GAGTTTTGAA ACGGAGCAAG ACATGGAACG TTTCTTTCGA CAAGTAAAAC TGATTTATTT 720

TGATGGAAAA GTGGTCGGTT ATCGTGGCTG CTCGGAACTT CCGTTAAAAC TTGAATGTAG 780

AGCGTtCAAA AAAATGGnTA AcGACaAAAG ATGTTACTTA ATGCACCGTT CAACTATAAG 840

GTTTTTGAAG AAAATGAATT TAGGGAATGG TGCAAGAAAA TGAGAAGCTA TAAGTAGTGA 900

ATTTGGTTTT TTATACTTGG TCTTTTTGTT TGTTAGTTTT AACTAACATG TGCAATTTAC 960

CAATAGCTAG GTTAGCTATC GAAAAAGGAT GCAGAAAAGC ACACGGACAC GAAGGTGCAA 1020

ACTGGCTACA CGTCAACTTT TTTGCAGATT TGGGAGATCC TAAAAAATGA ATACCACAGG 1080

nCTTATCCAG TCCATCAGCG TGCCTTAAAA GTCTAGGnAA GGGnAACCAn CCTAAGAGTC 1140

CG 1142

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CTTTAGTTCA GGCTGGGCCT TTTGAAAATT TAGATGAAGG ATTTGATGTC TACGCCACTC 60

AAGCCTTTAA TGCGCCAGAT GGTCGTGCAC TTGCGGTCAG TTGGATTGGG TTGCCAGAAA 120

TCACTTACCC AAGTGATGTG GAGGGTTGGG CAAATGGCTT AAGTCTGGTT AAAGAACTCA 180

CAATTCACAA CGGGAAACTA TTTCAATATC CAGTTTCTGA AACAGAAATG CTTCGTCAAT 240

CCGCTACTAC TTTATCAAAT GGCTGCCATT TCTTATCTAC TGCTTCTTTT GAATTAGAAG 300

TGGATATTCC CAAAAATGAG ATTGCTTTTA TTCGGCTTTT AGCGAACGAA ACGGGTTCAA 360

AAGGACTTTT AATTACAATT GrTACGATTC ATGGTAAAAT AACCCTTGAT CgAACATTTG 420

CTGGCCAATC TTTTGCTGAA AAGTATGGCA CAATTCGTGA AACTAAAATT AGGAAAAATA 480

AGTCAGTTCA GTTAACTATT TTTGTTGATT GCTCTGTTGC AGAAATCTAT GTAAATAAAG 540

GTGAAAAAAC GATGACTGGT CGCTTCTTTC CAGATAAAGC GCAACAGTAT CTTCATCTAT 600

CCAAGACGGC AAAAGCTTGT TTTTATGAGC TGGAAAATAC GAATAATTAG GAATGATGGT 660

GAATTTTGAT GGTGGTTAAA TTAACGGATG TAGCAAAGCT TGCTGGGGTG AGCCCGACAA 720

CGGTAAGCCG CGTGATTAAT AATTATGGTT ATCTTAGTCA AAAAACAATT GATAAAGTTC 780

ATCAAGCGAT GGAAGAATTA AATTATCAAC CTAATGGATT AGCCAGAAGC CTCCAAGGAA 840

AAAGTACGCA GCTGATTGGT TTAGTCTTCC CTTCTGTTAG TCATCCATTT TTTGGTGAAT 900

TAATTGAAAC ACTGGAAAGA AAGCTCTTTG TTCAAGGATA TAAAGTGATT TTATGTGATA 960

GTGAAAAAGA TCCAGAAAAA GAGCGCGCCT ATTTACGAAT GCTCGCTGCA AATAAAGTGG 1020

ACGGTGTAAT CACTGGTAGC CATAACTTAG CTATTAACGA ATATGAAAAT GTTTCACTAC 1080

CTATTGTTTC CTTTGACCGT TTCTTGGCAC CTGGCATTCC AATTGTCTCT TCGCAAAACT 1140

TTCAAGGGGG CCAAAAAGCC ACTGAAGCCT TATTTGCAAG TGGTGCACAA AAGATTGCAA 1200

TTATTACTGG TGCTAATAAC ACAGGCGCAC CTAGCGATTA TCGATTGGCT GGTTATAAAC 1260

AAACAATGGA AAAATATGGC GCAGAAAAAA CGATTCTACA AATTGATAAT GGGACCTCAA 1320

CAACATTAAA AAATCTAGAA ATCGAACGTT TGCTTCAAAA TAAAACTGTA GACGGCATCT 1380

TTTGTACAGA TGATTTGACA GCAATTACAG TTATGAATAT TGCTCAAAAA TTGAAGATAT 1440

CCATTCCTGA AGAATTAAAA GTAATTGGTT ATGATGGGaC AAAATTAATC AAAAGAATTG 1500

CCCCACAACT ATCAACCATT GTGCAGCCAA TCGACGAGAT GTGTGACGTT ATGATTGACT 1560

TACTGCTTCG TAGAATGAAG GATCCTGATG TTGCACTTGA GGAAAATTAT CCTATTCCGA 1620

TTCAGCTATC ATTGTCTGAA TCCTGTTAAA AAAGACACCT TTTCAGGTGT CTTTTTTTAT 1680

TCTTAATTCC TCATTTGCCT ATTTTCCCTT AATTCCAAAG CACAGAGATT AAATAATACA 1740

ACAACATGAT CCCTACAAAT ACACCGAGCA TTAGTAAAAC ATACCACCAA TTTTTGGCGC 1800

TATAGGTTTC ATTTTTATTT TTTTCGGTTC GTTTCCCGGC AGCCCATTTC CATAAATCGT 1860

AATTATTCAT CTCTCTCACC ACCTTTAATG GGTTTATTAA CTTAAGCCTA ACACGGAATG 1920

AGAGAACTTG AAAACAAAAG GATCACCCGC TTATGCAATG GATGATCCTT TTTTGGGCAC 1980

TATTCTTCTG ATAACCCATT ATTTTTAATA ACTGATTGGT ACCAATAAAA ACTATCTTTT 2040

TTAATGCGTC GTAAATCTTT TAACTCATGG TCTTCACGAT TAACGTAAAT AAAACCGTAG 2100

CGTTTTTTGA ATCCTTGATG GGAACTTAAA ATATCCATGA CCGACCAAGG GCAATAGCCA 2160

AACAACTCAA CACCGTCAGA AATAGCCGCA TGACAAGCAG CAATATGATC ATGCAAATAC 2220

GCAATTCGAT AATCATCATG AATTTTTCCG TCCTCTGTTA GGTGATCTGG TGTGCCTAAG 2280

CCGTTTTCTG TAATGATTAA CGGCAAACGG TATTGACGAT AATAATCATT TAAAACTAAA 2340

CGTAGACCAG TTGGATCAAT TTGGGCACCA TACTTAGAGG TTTTTAAATG TTGATTTTTT 2400

TCGATTTTAA AATAACCGTA TAGATCAAAA TCAATGTCCT TTTCTTTCGT ACCCAATGGG 2460

TGTTGCTCAT CTGTCGGTAA ATAGCTAGCG ACTAACGTCC GATAATAATT AAGAGCGATA 2520

AAATCTGGTT TAGCGGCTTT CAAAATTGCT TGATCTTCTG GCTGTGTTTC GGGATAAATG 2580

CCGCATTTGG TTAAATACTC TTGATAGTAA CCAGGGTATT CGCCAAAACA ATACATTTCT 2640

AGAGCGTAAT TCGTTTTAAA GTTATCATTC ATACGAGCTG CCCAAACATC TTCAGGCTTA 2700

TTAGAACTAG GATAAGTCAT CGTTGAGGAA ACAGAGGGAC CGACTTTTCC CCCAGCGACC 2760

AATTGGTGAC AATCATTCGT CGcTAACGCA TGGGCAACAA ACATATGGTA ATCCATTTGT 2820

GCACGAATTT TTTCAACATT TTCTGGTGCA ACATCGTACA TATTCATTCG TTCATCAACA 2880

CGAATCATTA AGTTTTGTTC GTTCGTAACT TGCCAATTTT TGACTCGATC ACCAAATGCT 2940

TGATAACAGA CTTGCGCATA GCGTTGAAAT GCGGAAACGC AGCGACGATC CGCCCAACCA 3000

TTGTATTTTT CCACCAACGC AAAAGGTAAA TCAAAATGAT AAAGTGTGAC AAACGGCAAA 3060

ATATCGTTTT CTAAAAGTGT ATCAATGACA GCATTATAAA AATCGATGCC GGCTTGATTG 3120

ATTTCGCCAT CACCTGTTGG AATGATTCGT GCCCATGAAA GAGAAAAACG ATAGGTTTTT 3180

AAGCCTAATT CTTTCATTAA CGCAATGTCC TCTTTGAAAC GATGGTAAAA ATCGCTGGCG 3240

ACTTTCGTAT CTGCTTGTAC AGCTGACTTT TTAAAAGAAT TGTAATCAGC GACTGTTAGG 3300

CCTTTGCCGT CCTCATTCCA AGCGCCCTCA ATTTGAAAAG CGGAGGAAGA AGCGCCCCAT 3360

AAAAAATCGT TCTTAAATTG TTTAACCATT AGTTTTGCTC CTTTACTTGC ATGAAAAATA 3420

AATTTGTTTG TGGTGTAATC TCTGTTTGTT TGGTTGTCTC AATTACAGCC ATTTCCGCAG 3480

TATTTGTTAC GATGACTAAG ACGGTTGGAT CATAACCAGC AGCTTGGATG ATTTGTTTAT 3540

CAAAAGAGAG CAGCTTTTGT CCTAGCCTGA CTCTTTCTCC TACTTTTACG AACGTTTCAA 3600

ATGCCCGCCC TTTTAATTCG ACGGTATTGA TTCCAATGTG AAGGAGGATT TCAGCACCAT 3660

TGTCTAACTT TAAGCCAATT GCATGATGAG TTGGATATAA AGCCGTCACT TGCCCATTTC 3720

CTGGTGAAAC AATTTGTTCC TCTGTCGGAT AAATAGCTAG CGTTTTTCCC ATTTGTTGAG 3780

AAGCAAAGAC TTCATCGTTG ATTTGGTCTA AAGATACGAG TTGTCCTTGA ACAGGTGCTT 3840

GAATCCGTTG TTTTTCTTTG ACTGTCCCTG CCTCTGTCTT GAAGCTGGGT TCTTGACGTG 3900

ACTCGTCAAG CGGTAAATCA TTAAAGCCTA GAAAAATCGT TAATAGAAAT GCACCAAAAA 3960

AGCAATACCA CAACCTAATA AATAACAAAT AAAGGCTTTG GTTCCTGCTT CTGCGTAAAC 4020

TGGGATGGTC AAGAGTCCTT GGTTAGCGAA GGCTGTCCCG TAGGAACCGC CCCAGCCCAT 4080

TAAGGCCCCG CCTGCTGcTC CGCTAGCCAC CGCATAAATC ATCGGTTTTT TTAGCCGCAA 4140

GTTTGCACCA TAAATGGCTG GTTCTGTGAT ACCAAATAAT GCAGTCACTG TTGCAGAGGC 4200

AGCAACAGCT TTCAAGTCTT TATTTTTTGT GCGGACAAAC ACGCCAAATG CGGCGCCCGC 4260

TTGAGAAAAG TTTGCTGCAC CAGCAAACGC TAGCAAATTT TGCCGTCCTG TTCGAGCGAC 4320

ATCATTAATC CCAATTGGCA CAAGCCCACG GTGAGCCCCA AAAATGACTA AGACACACCA 4380

AATTCCCCCG ATAAAACCGC CTAACAAGAT GGGACTCAAA TTCATTATAT AATAATACAA 4440

CCAATTCACG CCGTCACCTA AATAAATCCC TATCGGTCCA AATAATAATA AAGTGGCTGG 4500

AATCATTAAA AGTAATGACA GCGTAGGAAC CATAATAATT TTTAGAACTT CTGGAATGAC 4560

TTTTTCCAAA AAGCGTTGCA CATAAGCTAA CATAAAAATT GCAAGAATAA TAGGAATTAC 4620

TGTGGAAACA TAATTGGCTT TGGTCACATG TAATCCAAAC AAGGTAACCG CTGATTCTTC 4680

AGTCATTAAT GAAACGATGG TTGGATAACA TAAGGTGGCA CCAATTACCA TGGCGATATA 4740

TTCGTTTGTT TTGAAAACCT TAGCAGCTGA ATAACCTAAA ATAACTGGCA TAAAATAAAA 4800

AAGTGCATCG GAAGCGGCGC TTAAAATAAT ATACGTATTC AAAGGTTTTA AATCGACCTG 4860

GTAAAAATTG TTTGCGACCA TCACAGCAAT AGCTAGAATT CCTTTTAACA TGCCTGAAGC 4920

GGCAATTGCT GGTACGACAG GTGTGAAAAT CGCCGCAACA GTATTTAAAA TTCGATTACC 4980

TAATGAATTT TTTTCTTTTG TAGATGTTTT GGTCGTAAGT TGCTGAGCCA ACAAAGGTTC 5040

TAGAGCATTA TAGACATGCG CGACTTTATT GCCTAAAACC ACTTGATACT GCCCGCCGCT 5100

TTCAACAACA GAAATGACAC CTTCTGTTTG TAGTAAGGCT TCTTTGTTCG CTTGTTTCGT 5160

ATCTTTCAAT ACGAAACGCA ATCGTGTATA ACAATGTGTG ACATCCACGA TATTGTCTTT 5220

GCCACCTACG TCTTTCAAAA TTTCTTTTGC TATTGCTTGG TAGTCCATGG TGACCACTCC 5280

TTATCTATAA AATAACAGCT CAATaAAAAA GACCAAATCA CACATGCACG TTTCAGCAAA 5340

CACACTCAAT ATTTGCTCGT CGTGAATGTC CCTTTGATCT GATCTACGTA ATAACTATGT 5400

TTCTCACGAT AGAATAGCTG ATTGAATTTA TTTTTAATTT ACCATTATTT AGAGGGATTA 5460

TCAATGAATT AGGTAGAGCA ACTCAGTGTT TTGTTACTAA AATCAGCAGT GAAAATAGTA 5520

GTTTACTACA TTCACTGCTG ATTTATTTGA TTACAAGACT GGGGACAACA AGCGTGAAAA 5580

GTTTTGCTTG AATCGTAGCC AGTACCCTTG TTTTTTAATT ATCTCGTCGG TTAGTAAGAC 5640

ACTTTTTTCT ATATCTTCTT CAAAGACTTG CGCTAACATC CACGCAATGT CGGGATTGTA 5700

AATAAACGTA CTTACCTCAA AATTCAATGA ATAACTGCGA ATATCTTGGT TTGTTGTCCC 5760

AACCATAGCT AATTCATCAT CAATCACCAT TGTTTTTGCA TGAATAAACC CACTATCATA 5820

AATATAAATT TTAATGCCGC GTTTGTGTAA GTAATTTGCG TAATATTGTG TCGCGCGGTA 5880

AATAAAGGGA TGGTCAGGCA TACAAGGAAT CATAATTCGC ACGTCGACAC CTGAACGAAC 5940

CGCCACTAAC AACGCATTAA TCATACTATC ATCAGGGATT AAATACGGTG TTTGAATCCA 6000

GACACTCTTT TCTGCAGAGA AAATCATCCG AACAAACCCG CTTTTCAAAA TTTCTTCTTC 6060

TGAATCAGGA CCATCTGAAA CAACTTGTAA GGACAAATGC TCCACTTCAT GATCTTCTGG 6120

TAATTTAAAA TATTTTTCAT GATACGTCAT ACGTTCTTCA GGATATTTGA CTGAAGCATT 6180

CCAATCCATG ATAAATATCT CTTGCAATGA AAATACGGCC GTCCCGACCA AACGAATATG 6240

GGTATCTCGC CAGTAACCAA ATTTTTCGGT GACATTCAAA TATTG 6285

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

AAATTATTnG AnTTTCTTAC CCGCCATTAT CCATAATCCT TTAGTTCTCT CTTGGTTTCg 60

GGATTCGAAG TAGGCGTATC aCAACTACTA AAaTGGTTAG tATGGAATGG AGGACTgCAG 120

CATTATTTAC ATGTTTTACT TTAGCTAATC CTTTAACAAT TTTAACTTCT TTTATAATGG 180

CTCCAGTTGG CGCACTAAGT CCsGTATTAT CmGTAGGAAT GTTTTCAGCC CTAATGGAAG 240

CTAGTATAAA AAAACCTACG GTCAATGATT TTATGAATGC ACAAGACGAT ATTTCATCAA 300

TTAAATCGAT TTACAAAAAT AGATTGTTAA AGGTGGGTTT AATCTTTGTG TTAGCTAGTG 360

CAGGTGGGGC AATAGGTAAT ATTATCGGGG GAATAGAATT ATTTAAGAAT TTAATTTAAT 420

TAATAAACTA GGAGGAATTT AATTTATGAA GAAGAGAACG ATGCTTTCAT TTTTTTGTGT 480

AAGTGTGCTA GTTTTGATTT TAGGAGCTTG TAATGGAAAA GAAGGAACAA AAAATAACTC 540

TAAATCAAAA GAAGTTGAGC AAGTAGCTAC TTTTTCAGCT ATGACACCTG TTCAAAGTTT 600

AGACCCAGCA ACAGCAGTGG ATCAAACAAG TATTACATTG TTGGCCAACG TAATGGAAGG 660

GTTGTACCGA TTAGATGAAA AAAaTCmrCC mCmACCmGCm ATTGCmGCyG GGgCAmCCAA 720

AAttCCmATA AtGGTAAAAC ATATACAATT GTGATTCGAG ACGGTGCAAn ATGGGCCGAT 780

GGTACAG 787

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

CTACGTTAAA TGAATGGAAA AAACGATTTC CGGACATTAA GGACACCATA nAAAGAGGTA 60

AAGAAGTTGT AGACCGCCAA GTGGAAAaTG CaTTGTTTAA AmGTGCGGTG GGTTACGArT 120

ACACTGrAAT TACTAAAGAG TTAACTGACT CgGCATGCAA AGTAACTAAA CGAGTAACAA 180

AACAAGTGGC CCCTAACCCA ACATCTGCTA TTTTCTGGTT GAAAAATAGA AAACCAGATG 240

AGTGGAGAGA TAAGAAAGAA ACTCAAGTTT CTGGTGAAAT GTCTGTTAAC AATCCTTTTG 300

CTGGTTTGTC TGAAAAAGAA TTAAGAAAGT TAGCTGAAAG TGATGAATAA GATTGTTTTG 360

GGTGCGAAGT TAGAATTATC CCGTCGTTAT TTTTGGGAAT ATTGCAAATT AACGGCATCT 420

GACTTTTATA AGCAAGACAG AGAGTACTTA AAAGAGTTAT GTGATGACTT GCAAGAATTC 480

ATTTATGATA GCGATAATGA CGTTCTAGTT ATCAACGAAC CGCCGAGACA CGGGAAATCG 540

AGAACTGCTG GTAAATTCGT AGAATGGTTG TTAGGGAATG ACACTCGAAA AAAAATAATG 600

ACGGGATCAT ATAACGAAAC GTTATCTACA ACATTTTCTA AAAGCGTAAG GAATACTATT 660

CAAGAAATAA AAGCTGATAA AAACAGAGTT GTATTTTCAG ATGTATTCCC TGGTGTAGAG 720

ATAAAGTCTG GTGATGGAGC CATGAACTTA TGGAGTTTGA CTGGCGGATA TAACAATTAT 780

CTAGCAACGT CACCAACTGG CACaGCTACA GGGTTTGGTG CAGACATTAT TATCATTGAT 840

GATTTAATTA AAAATGCTGA AGAAGCAAAT AACGCTATGG TATTAGAGAA ACACTGGGAG 900

TGGTTTGTTA ATACGATGCT ATCTCGTTAG GAACCnGGCG GCAAAATCAT CATCATTATG 960

ACCAGATGGG ATTCnAATGA TTTAGCCnGT AAAAGCTTAA AAGGATTGCC GCAATCCAGG 1020

CTATAAAGTA AAACCTTATT TAGCCTGGAA GGCATATTAC CGAGGAAACC GGCCACCAnG 1080

CCTTGTGGAG TC 1092

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3709 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

GTTTTCGCAA TGTCCATGTT TCCCCAAGTG TCATACCAAA TATAGGTATG CGCACGTTTA 60

CCTTGGGCAA TAGCACTTGC TACTTGCGTT TTATATGTGT ATTGTTCATA AATACCGCTA 120

GCATTGTAGC CGCCAATCTG AGCAATGGCG AATTTATCAT GTGCATAACC AAAACGACCC 180

TGTTCGCCTT GATAAATCGC CCAGTCAACG CCTTGGTCAC CTTTTGCAGC AAATACATTT 240

AAAGGCATAA AAAATAGAGC GACAAGCGCT CCTACTAAAA TTTTCTTTTT CATTTTTACT 300

TCTCCTTGTC TTTTAAATTA TATGCTGACA CACCTGTTAC TACTCCTAAA AAAGTTGCAA 360

TGGCATTGAT AGTTAAAACA GCCATATCTG TTTGTTGCCA ACCGTAGGCT TTACCTAGCG 420

TGGCAATCAA AACAGaACTT GCAGGAAGCA CAGTAAGCAC TCCCCACTTG ATGATTTTGT 480

AATACTTGTC TGGTAATATC ATTTCTAAAT TCCTCCTAAG TATTTCGTGA TTAAATAGAC 540

AGCAACAGAA ACCCCAATTC CTGCAATTGT TCGCCACGTC CACTTTTGAT TCTCTTTTAT 600

TTCCGCAATA TCGCCTTCAT TGTTTTTGGC CATTGAGAGC GCTATGTCTG CTTTCTCTCT 660

TAATTGTTCA TGATTATCCA ACTTTGTTTC AATCCGTGCC AAACGATCGA CGATTTCAAT 720

TAAAGGATCA TCTTTCAAGT TATCGTCTCC ATCCCTCTAA CAAAAGAACC GCCTAGCTTT 780

TGCTAAACGG TTCACCTGTC ATTTTAGTAA ATTCATCTTC TGTAATACAA CTAGGCACAA 840

ATTCTGCAAC CTGCTCTGGA GTAAATAGTC CCCAATCATA CATCAGTTTA ATGTCATCAT 900

ATGAATACAT TATTTTGCAC CTCCGATTTG TTCTTTAATA GCATCAATTT CTCTTGTATT 960

TTGAAGAGAA GTAAGCATCG TCTTAGAATT GATTTGTGCA AGTGATTCTG CTTTAGCAGT 1020

TAGCTTTTCA TTTGCTTGTT TTAACTCACT ATTTGAAACT TCTAAGCCAT TAGCAAGATT 1080

TTCTAACAAA TTCAATTTTT TTGTATAATC CTGTGTCACT GCTTCTTCCC ATTTTTGTTC 1140

TGAAAAGTTA AAGAATTGGG ATTGTTCATT CACTAAATTT TCTAGTGGTT TCTCCTCTAC 1200

AAATGGCAAG GCTACAACAT AATCATCTTG AACTTCGAAA ATTTGAAATC CTACTGGGTA 1260

GAGCACTTTA TATATTTTTT TCATTTTATT ATCCACTCCT ATTTACGACG CATAACGCCG 1320

ATTTCTCTAA AAACAATTTT TTTATTTGCT TCATTTAATG TGTTTGCAGT ATCTCCTGTA 1380

ATCACTAAAG ATGTACCAGA TTTAGAAATA GATATTTTTT TATACGCTAT TGTTGGGTCT 1440

GTTGAAGCAG AACCTACCCA TGCAACTGCT GGTAATTCGT ATTTTAATTT CGTAATATTC 1500

GGAGTAACTG GTATTGAGTG AACAATACCG CCACCGTTAT CGTTGTAACG CGAGAATATC 1560

AAAACAATTT CATCCACATT GCTGCTATTT GAAATTGTTA CTGATTGAGA TTCTGTCAAA 1620

TAAGCTCCAG TTCCATCCCA GTAGTCTTTC ACCACCTCAT AGGTCGGTTT TGCATTAACC 1680

GATACAGATT TACCACCGAT TTGAATCCCA TCTTGAAAAT TCTTTGTCCC TAAAACAGTC 1740

TCATTTCCAA CGGCCTTTAC TAATTTTCCT TCCACGCCGT CAATAGCATC TGCATGTGTT 1800

TTCATATACT TTACAACACC ATTTTCTTTT AGCTGAACGA TATCTGCCAT TACGCTTCAC 1860

CTACCTTTTC AAATGTAAAA ACTGGTAATG CATCCAATTT TGCTTTATCC GTTTTAGACA 1920

TTAAACCGTC TTTTTCAGAA GTGGCATTGC TAGGAAGCGT TGGAATAACA GTTGTGTCTG 1980

GCAGTGCTTT TACATCAGAA GCAGTTAAAA TAACTTCACC TGTATGACCA TTTACAGACG 2040

AGACAGTGCC TGCTTCAGCA CCACTAATTT TTCCATCAAC AAATTCATTT AATCCAACAA 2100

CGCCAGCTGT ACTAGTTTGT ACATCAATAG CTACGCCGTC TTTTTTCACT ACATATAAAT 2160

CAGGCATTTA TTTCTTCATC TCCTTTTACT TTTTCAAACT CAACACCAGA ACCACCTAGT 2220

TTTCCATCTT CATAATCGGC TATGATTTTT AACATTTTGT CATACTCCTG TTTCGAAATC 2280

ATAATCCCAT CAATAGGTAA ATCTAGGTCT GCACGCGTAA TAATGACTGC GCCTGTATGT 2340

CCATTTACTG AAGATACTTT TGAATTACCA GCCATTATCT CTGTTAATCC AAGGATTGCC 2400

GATACGTGTG TCATAGGAAA AAACTGACGT TTAATCCCAT TTTCATCAGT TTCCATCATT 2460

CTTTTAGCAT CAACCATTGT CTACACCTTC AATCGTAAAA ACATTTTGTT TTGAATCATC 2520

AACTGTCGCT ATAATTAACG CCCCTTCTTC aATTGGATGA TTAACTGTTC CCAATACTTC 2580

AACTTCATGA TTCTTAGAAA ATGAATCATC CTCTAAAATT TCTAACGTGT TTACATTACC 2640

GTATTTGATG GTGTATAGCC GTTCCTCTAA CCGATGATAC AAATAGTTCA TATCAGCCAA 2700

TAAACGCTCA GAAAGTGAAT TATGACGTAC TCCTTGTATG TCTACACGTG CATCCATTAG 2760

CTCGGCTAAC ATTGTTCCGC CTGGATCAAT AGTTTTTAAA ATATCTTTGA TTGATTCGAA 2820

CCATTTTAGA TAATCTGTTT CTTGGCCGTT CCGCCAAGCT TCAAAAGTAT CTTGTTGATT 2880

TTTACGCCAT TTTTCAAACT CTTCTTTTCT AGCGTTCATC CACGCTGTGA AATCGCCCTT 2940

GTTTTCATTA ATAAAAGCAG TCATATCAGC TATCAAATCC TCGATTGACT GCCAATATGA 3000

CCCCATTTCA CCTTCTGTTT TAGAAGCAGC ATTCACAACA AAGTAAGAAA AGTTCTGCGT 3060

TGAGCCAATT AGATTGTCGC CTTTATGAAT ACTGAAGTAT GCTTCCTGTC TATGCAATGA 3120

CTGCATAGAA TATTCATCAA AGGTATACTG GATAATCCCT TTTTTGGCAT TCACAATTTT 3180

TGCTGCTCGT TGAATCGGAT ATTTATTATC AATAACTGAT TCAAAAAAAA CTTCGCAACC 3240

TGTTAAATCA AGTGGCAAAG CATTTTCAAC TAGTATGGCT TCTAAGACTT CTGTGTTTCG 3300

ATTTCCTTGT CGTACATTCT GAATCCCAAT GTAATTGTAA GGTTCAGTTG TACTTAGCGT 3360

TGCTTGCCAT TTAACCATTG AAAAATCCTC CTCTCGTTAT TTTGGTGGAA TAACAATCGA 3420

TTGAATAGAA TTAGCAAAAT ATAATCGGTC ATATTTTGCG ACAATTTGTC CTTGCTCGGC 3480

ATTCTGTTCT ATCGTTTGGA TACGTCCGTT ATTTAAGCCG TAAATCACGC CCGTGTGACC 3540

ATATGTTGGG TCTACTGTCC AACCTGgTTC CCCATTGGnC ACTCGTCTAA TATTGACGAT 3600

GCCCCTACnA CTAAAnCTGA TACGTGGATT GGATACTCGC CAACTACGnA TCCAATCAAA 3660

GCTCACCATA TTGCAGCAGA GATGATCACC ATACAGTGAA AGCATAATG 3709

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

AAAATAAATT CCCTGTAGGT TCATCTGCAA AAATAATTTG CGGATTATTA ACTAAAGCAC 60

GCGCTATACA TACCCGTTGT TTTTGGCCAC CAGATAAATT ATTCGCTTTA TTTTGAACTT 120

TATCTTCCAA ACCGACTGCT TTTAACGCAT CTAAAGCCAT CTTTTTCCTC TTGCTACCGG 180

AAATCCCACC AATTTTTAAT GGTAAAAGAA CATTATTTAA AACTGTATCC TTGGCATTCA 240

TAAAGAATTG TTGAAAAACA AAACCAAATT CTTCATTTCT CGTTTTATTC AGCACTTTCT 300

TTCTAATACT AGTAACATTT TTACCATTTA AATAAATATC TCCTGAAGTT GGTTGATCTA 360

ACAATGCCAA AATGTGCATA AATGTTGATT TCCCAGAGCC ACTTTTACCA ATTATGGCCA 420

CAGATTCACC TTTTTCAACT TTTAAATCAA CACCTTTTAA CGCGTCAAAT TTTGTtTCGT 480

tCTTTCCATA ACTTTTTTTG ATATTTTTtG CTtCAATTAC CGCCATGTTA CCCCTCCATT 540

TTTCATTCTT TGTCGTTTAC TTATTTACAA AGTTTTTTAC TCTTTTCATA CTCCTTTCTT 600

CTGTTTCTAT TTTGACGGAA GCCCTTTCCT TTGTCATGGT ACTTCCGATG TATCTCTCAA 660

TTAAAACAAT AAGAACATGT TCCAAATTCA CCTCATTGAA CATGTTCTTA TTAATTAGTT 720

ATGCATTTAC GCGTTTAATT TCACGATGTT TATTCAATAA ATAGGCCAAG CCAAGATTAA 780

TACCAACAAA GCAAcTGATT GTCAGAAGAA GTGGTAGGAC AGTAAAACCA GTGGATTGAT 840

AACCAACCAT TGTTTGCAAG ATGTGGAGCA TTCTCAGGCG CATTGGTGCC CCCCCTAATT 900

GTGCAATCGT GCCCAGTAAA ATAGGAATCA TTAATAACAG CAATAAAACA ATGAGTTTTT 960

TTACGCCATC TATCCGATCA TTAAAGACAC CTGCTAACAA GCCAAGTGAG CCACTAAGCA 1020

TTAGTAAGAT AAAAAAGAGC AACCACGACA TGAAAAAGTT TCCTTGTGCA TAGACATCAA 1080

TTAATTTCAT TGaTAATTgA AAATGAGAAA TGAAATTGcC GCTAAATACT TTAATCAGTA 1140

CAAGTACAGC CAAGGrTCCA ACCAAAGATA rAaTwGCATT aCTTACmAAA TTCmCCAAAA 1200

AAATTGTCCA GCGGGAAAGC CCGTTTTGAA TAAACAGTTT AAAATCTGTG TTCATCCCCA 1260

AAAATGATAG TATCCCCATA AAAACCAGAC AAGGAATTAC TGCATCAGAG CTGACAGTGT 1320

TCACGTCGTT AGAAAAGAGC AACCCAATAA GAGGAAAAAG AATGCCGAAC AAAGCmTAAA 1380

AGCCAAAATA AATTGCTAAG GrACGGrCTT GATAAATAAC ACGGTACCGC AAAGCTGTTT 1440

TAAATTTCAT TTTACTTTTC CyTCTTTCTA TTGGTTAATk GTmCAAAATA TGTTTGTAAA 1500

TTTAGCGGCG CAATTTGAAC CTCTGCTTTT TCAGTCGGCA AGTCGCCGTA CACGTAAGCC 1560

GTAACTGCTC CACCTAAAGT GTCCATGCCT AAGATTTCCA ATGACTGAGT ATAGCGCTCT 1620

ACTnGTTCTT TCGGCCCnGA AACAATGCG 1649

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

AGGGTAGCAC AGAAAAGAGG GAGGTATGAC AATGGAACAT CATCAACTAA AAGCATTTCC 60

GCAAGATTTT TTATGGGGCT CTGCTTCGGC AGCTTATCAA GTGGAAGGTG CTTGGAATGA 120

AgACGGCAAA GGCGCATCTG TTtGGGGATG AATTTGTTCG GCTACCAGnA AAAACGTTCA 180

AAGAGACAAC TGGCGATTTA GCCGTCGATC ATTATCATCG TTTCAAAGAA GATGTGGCTT 240

TAATGAAACA ACAAGGTTTA AAAGCATATC GTTTCTCGAT TGCATGGACA CGAATTTTAC 300

CTGAAGGGCG TGGTCGAGTA AATCAAGCGG GACTGAAATT TTATTCAGAT TTAATTGATG 360

AGTTATTAGC GGCAGGAATT GAACCAATGG TAACTTTGTA TCATTGGGAT TTGCCAGCTG 420

TTTTGCAAAA AGAATATGGT GGCTGGGAAT CAAGAAAAAT TATTGATGAT TTTGTGGCCT 480

ATGCGAAAAT TTTATTTGAC GCTTTCCGTG GCAAAGTTCG CTATTGGATT AGTTTAAATG 540

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AACAAAATGT GTTTACTTCG TTAGGTTATC AATTAGCCGT GCATCCTCCC GGCGTAACAG      600
ATAATAAACG GATGTATGAG GCCAATCATA TTGCTAATTT AGCCAATGCA GCAGTGATTA      660
ATGCGTTTCA TGAATTAGAA ATGCCTGGCA AAATTGGCCC TAGCTTTGCT TATACGCCTG      720
TTTATGCCGT TGATGCGCAT CCTGCCAATG TTTTGGCGGC AGAAAATGCA GAAGATTTGT      780
TGTCGCATTT TTGGTTAGAT GTCTATCTTT GGGGAGAATA CCCAATTGCC GCATTAAATT      840
ACTTACAGGA GCAAGGTGTG GCCCCAACGA TAAAAGAGGG CGATTTAGCG TTACTACGTT      900
CAGCCAAACC TGATTTTCTA GGTATTAATT ATTATCGGAC GGATACGGTT GCTGCTAATC      960
CATTAGATGG CGTCGGAATA GGGAAGATGA ATACAACGGG TGAAAAGGGT TCTGAAACGG     1020
AATCTGGGGT ACCGGGTTTA TTTAAAAAAG TAAATAATCC ATATGTTGAA CGGACGAACT     1080
GGGATTGGGC CATTGACCCG CAAGGTTTGA GAATTGCCTT ACGACGATTA GCTAGTCGCT     1140
ATCAAGTCCC TATTTTAATT ACTGAAAATG GGTTAGGCGA ATATGATACC TTAACAGAAG     1200
ATAAACAAAT TCATGATACG TATCGCATTG ATTATTTGCG AgCCATaTCC AAGCGATTCA     1260
AGAGGCGATT ACGGATGGTG TTTCAGTTAT TGGTTATTGT ACATGGAGTT ACACCGATTT     1320
ACTGTCGTGG CTCAACGGCT ATCAAAAGCG TTATGGTTTT GTCTATGTGG ATCAAGATGA     1380
AACACAAAAA GGTTCCTTAG AAAGAATCCC GAAAGACAGT TATTATTGGT ATCAAAAAGT     1440
CATTGAAACA AATGGACTTA TCTAATTATA AGAAAAGAGT GTGGAAAATA TGACAGTAAA     1500
AATGGGGTTT ATTGGATTTG GTAAAAGTGC CAACCGCTAC CATTTACCTT ACGTAATGAT     1560
TCGAGAAACA CTAGAAGTGA AAACGATTTT CGATTTACAT GTTAATGAAA AAGCAGCAGC     1620
GCCCTTTAAA GAAAAAGGCG TAAATTTTAC CGCTGACCTT AATGAATTAT TGACGGATCC     1680
AGAAATTGAA TTGATCACAA TCTGTACACC TGCGCATACA CATTATGATT TAGCCAAACA     1740
AGCCATTTTA GCTGGTAAAT CAGTGATTGT GGAAAAACCA TTTTGTGATA CGTTAGAACA     1800
TGCAGAGGAA TTATTTGCTT TAGGGCAAGA AAAAGGGGTA GTAGTGATGC CTTATCAAAA     1860
TCGACGTTTC GACGGCGATT ACCTAGCGAT GAAGCAAGTA GTAGAGCAAG GCTTTTTAGG     1920
AGAAATCAAT GAAGTGGAAA CACATATTGA TTATTATCGA CCAGGAAGTA TCACGGAACA     1980
AGGACCTAAA GAAAATGGTT CGTTTTACGG ACTAGGCATT CATTTAATGG aTCGCATGAT     2040
TGCTCTTTTC GGGCGTCCAG ATCAAGTCAC TTATGATATT CGTAATAATG AAGTGAGCGA     2100
GGCAGTCGAT AATTATTTTG ACGTTGATTT ACATTATGGT TCaAAATTAA AAGTAAAAGT     2160
TAAAACGAAT CaTTCTGTCG CTAGTCCgTA TCCaCGTTTT ATTGTTCATG GCAGCAATGG     2220
CTCGTTCaTC AAATATGGTG AAGATCAACA AGAAAATGAT TTAAAAGCCG GAATCATGCC     2280
AGATGCACCA GGCTTTGGAG AAGATTCACC AATGTATTAT GGAGAAGTGA CCTACCGTAA     2340
TGGCAATGGC GACTGGATTA AAAAACAAAT TAAAACGCCT GTAGGTGATT ACGGTCGTTA     2400
TTATGATGCC GTTTATGAAA CGTTGAAAAA TGGTGCACCG CAACTAGTAA CTAAAGAGCA     2460
AGCATTAACT AACATCGAAA TTTTAGAAGC AGGTTTTCTT AACCCAAGTC CAAGTGTTTA     2520
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TCATTTGAAA GAAAACTAAA GCGTATTTAA ATGACTTGAA AAGsGCCTGC CCTACAGTCC 2580

AGACAACTGT GGGGCAGGCG CTTTTATTTA TAAAGAATTG TGAATTTTAA TATAAGAAAC 2640

GTATATTGTT AGTAAAAATA AaAAAAGGAA AGACATCTTA GTAGCACTAC TTCCCCAAGA 2700

ATTGCTACTA AAATGTCTTT TGTGATGCTC GCTCAATTGA AGAGCCTTAA ATAGGATATC 2760

GAATATCCAG TATAAATGCA AGTAAACTAC TTTATAGTTA ATATTAGTAT ACTTCATAAA 2820

ATAATTTTTC AAAGAGAAAA AGGCTTGTTA TGAGAAAAAA TTAATTTTTA ACTCGTTTTT 2880

TCTAAGCAAG ATTCGGGTGA AAAAGACAAT AATTACTGAA GCTGAATGGT AATTAAAGAG 2940

GTTCTTTGCT AAAATAGGAA AGACAAGAAA GTTTGGTTAA CGAAAGAACC AAATCAGAAA 3000

GGAGGACAAC CAGTGGAGAG TTGGCTTTTT TTACTACTGA TTGCCTTGAT TGCGTTTGTT 3060

GCAAAAAATC AAAGTTTATT AATTGCGTCA GTTGTTGTGC TTGCTTTAAA AGCTTTACCA 3120

AATAGTGCGA AAATCATGTC GTGGTTGTCA GATAAAGGCA TTAATTTAGG CGTCACAATT 3180

ATTTCAATTA CCATTTTAGT CCCGATTGCT ACAGGACAAA TTGGCTTAAA AGATTTAATC 3240

CAATCATTCA AAACACCGAT GGGATGGCTG GGGATACTTT GTGGAATTCT GGTGGCTGTT 3300

TTATCCTCAA AAGGAGTAGG TTTAATTAAT CAATCGCCTG AGATTACGGT GGCCTTAGTT 3360

TTTGGAACGA TTCTTGGCGT CGTTTTTTTA AAAGGAATTG CAGCTGGTCC GATTATTGCA 3420

TCGGGGATGA TGTACGTAAT CATTACTACC TTTCAAGCCT TTCAACACTA AAAAAGCAAA 3480

CAAAACGCGT AAACGTTTTG TTTGCTTTTT TAGTGTTGAT AAATGTCCAC ATTACTATCT 3540

AATATGCCAC TTTCATTTTT TAAAGTAATG GTTCCCGCAT TCGGATGAAT CACTAGCTGT 3600

AAATGCCCTG TTAAAAACAT TTGGTCATAC GTCGAAGTAT AGACGTGAAA AGAATCATTA 3660

GCAATTGTTT CGGTATAAGG CGCTTCTGCT TGATCAACAG GAACGATAAT GAAACGATCG 3720

CCAATCATAC AACAACCTTC TGCGGAAGAA TAAGGATTAG AGCCGTCATT TGCTACCAAC 3780

AAGAAGGTGT TCGTTTCAGT TAAGAAAGGG GCTAAACGTT GTTTTACTTC TTCAGAAATA 3840

GTCAGAGACA TTTGCCTCAC TCCTTTAAAT AGTATGTAAA AGGAAGAGGG TAGCTTGTCG 3900

CTATGCCGCT CTTCAAAGGT TTTGTTATTT GCTTGTTTCT TTACTGCTTT TTTTGAAAAG 3960

AGCAATAGAA AAGGCGACAA CTAAGACAAC TGTTGCAGCT AAAACAAATG GATTTTTTGT 4020

TGCTGaTGTG AACCCTAGGa CTGTTGAAcC AATCGCACCT ACGTAAGATA AAATAATCGC 4080

TGCTTyCTTt GGkGTTGAAA GTTCTGTCAA AGTG 4114

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

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ATGnAGGCCA GATCCCCTCC AAAAAAAATG GTGGCCnnnT TACATTACCC CGCGGCATTT     60

GCCTTTGACT ATCAGAACTG AAGAACTTCA AGGAATTTTA GTCCTGTTGC CGACTCACCC    120

ACGGACATTG GAAATCGTAA ACATCGCTGT CTCAGAAGAA AGCCGAGGGC GGGGCATCGG    180

GCAAGAATTA TTACATTTTG CCATTGATTT TGCCAAAAAA GAAAAGTATG ATTCCTTGGA    240

GATTGGGACT GGGAGCACAG GCTTTCAACA GCTATATCTC TACCAAAAAG TCGGTTTTCG    300

AATGACACAT ATTGAACCAG ATTTTTTTAT CCATCATTAT GATGAGCCTA TTATAGAAAA    360

CGGCTTGCCT TTAAAGGATA TGGTTCGCTT ACGGTTACAT TTAAGTTAAA AAGAGGTCGG    420

GACAGAACCG TTTAGCTCCG AGAAATAAGA AGAAATTTCC GAAAATTGCT CTTTAATTTT    480

TGGAGAATTT CGGCTTATTT CCGAAGaGTT GGTTCTGTTC CCGCCGTTTA TCAGTTTTTG    540

AGCGTGGAGC AAAAATCCAA AGTGATTTTT GTCCCACGCT CTTTTTAATG CCCAAGAATT    600

GGTAACAACT CATCTAGCTG TTGAATCGTA TAATTGGGTT GAATGGTTGG TGTTGCTGGA    660

GCGGAGGTCG GATTGAGCCA AACAGTTTGA ATTTTCGCTT GTTGACCTCC TTGAATATCT    720

GAATGCAAAG AATCGCCAAT AATCATTGTT TTTTCTCGAC TAAAATTAGG AATCCGTTCA    780

AAAACAAAAT CAAAATACTC TTTCATCGGT TTTTGATAAC CCACTTCTTC TGAAACAAAA    840

ATATCTTTAA AATAAGGCAT TAATTTCGAA TCTTCCAACC GACGATACTG TGTTTTTGCC    900

ACTCCGTTTG TCACAATATA TAAATCATAA TGGGGTGCTA ATTTTTCCAA GATACGTTGA    960

CTATTGCCAA GCAAGTCATG TCCTTGACTT AAATATTCTC GGTAGTTTTC TCCCATTTTA   1020

ACGCTATCAA CTTCTCGATT AAACGCGTCA AACAATAAAC CAAACCGTGT ATCAAGGAGA   1080

ACATCTTTTG TTATTTTTCC TTCTTCAAAT GAACGCCATA ATCCTTGATT AATTCGGTGG   1140

TATGTTGACT CGACTTCAGA TGTAAATGGT ACATTTTCTT CTTCAAATAA GGCATGTAGC   1200

GCCTTCTTTT CAGCCAATTT AAAATCTAAC AATGTATCAT CAACATCAAA AAGCAATGTT   1260

TTCATTTCCG TTCCTCTTCT CTTTTCAAAT TACTCGGTAA CGCTTTGCTT GTTTGTTGTT   1320

TTTCAATAAA AAAATAAGGC AATAGCAATT GTAACTCTTC TCTTGTTAAT GAACGATAAG   1380

CACCTAAAGG TAATTGCGGA TCTAGCCGCA ACGGCCCCAT AGTTTGGCGT TTTAAAGCAG   1440

TCACTTTTTT CCCCACGGAT AAAAACATTT TTTTCACTTG GTGAAATTTT CCTTCTTGAA   1500

TAGTCAGGAA AACATGACTC TCCGTTTCAG TCGCTGCAAG AACAGTTATT TTTGCTGGCT   1560

TACATTGAAT GCCTCCTTGC AAAACAATCC CATCTTTAAA TTTAGCACAA TCTTCTGCAG   1620

AGACCAAACC ATTGACTTTC ACTTCATAAC ATTTCGCTAC TTCTTTATTT GGCCGAATTA   1680

ATTGATACCC TAATTGTCCA TTATCTGTTA ATAGAAGTAA CCCTTCCGTA TCGCCATCGA   1740

GTCTGCCCAC TGGATAAAGA CCAGGGCGTC TGTCTTGTGG CGCAATCAAA TCAATAACTG   1800

TTTTTTTAGA TGCATCTGAG ACAGCGCTAA CCACACCTTT TGGCTTATTC AACATATAGT   1860

ACACATGGGT CTTATGCGAA ATTAATTGTC CTTTTACTTT AATCATTTGT AATTGCGCAT   1920

CGACATTTTG GCTTTCATTT AAAGTCACGA TGCCATCCAC AGTGACCTGC TTGCCTTTGA   1980
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TTAATCGTTT CACCGTTTTG CGTGATCCAA ACTGAAGTTC TTCTAGTAAT TTATCTAATC 2040

GCATTGTTCA GCTCCATTCT GGTATAAGTA TAGTGGAATC CGTTAAAGAT GAAAAGTGGA 2100

AAAAGGTAAT TCCTTGACGT ATAAAAATAT AAGTGTTACG GTTAATAAGT AAAGTAAATA 2160

AAGGTTcTCA aAAACAGCGT AATGACCTGG GAGAGAACac GATAACatGA ACCATTCCCa 2220

TGAGTGTTGC CTGGCAATAT TTGTGGGGAT TTTGTATGTA CATTTCAGCA GACACGAAAA 2280

GGTCT 2285

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2974 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

ATCGgTCAtT GAAAcGGTTG ATCAGrATGa TCAAACmACG CTGTGCCTAA CTCAGATTCC 60

ATTTTTTTCA ATGCTAAAGA AAGTGTTGGT TGGGTGACAA ATAAATTGCG AGCGGCCGCC 120

GATAAACTGC GGGTATTAAC AATTTCaATG AAGTACTTTA AAAGCTGAAT ATTCATCAGA 180

AACTCCCTTT CTTTTTAAAA GCGCTTACAC AAATGTGCTT GGATAAAAAA TAACAAATAG 240

ATCACTTATA ATATAACATA TGTTTTGCCT TTTTATTGCT ATAAAAGTAA GAGATAGAGA 300

TTTTCTTAGC AGATTTTTAC CTAAAAATAA AAAATTGAAC GGAGGAAAAG AAATGAAGAT 360

TATTATCGCA GGTGCTGGCG CTATGGGCAG TCGCTTTGGA CTAATGTTAC ATCAAGCAGG 420

AAATGATGTT ATTTTTGTCG ATGGTTGGCC AGAACATATT GAAGCAATAA GAAAAAACGG 480

GTTAGTTGCT GATTTTAATG GCGAAGTGGT GACCGCTAAA ATTCCTATCT ATCCTCAGAC 540

AGAAGTAGCA AGCATCGATT TTACAGCAGA CTTAGTTATC CTATTTACAA AAGCAATGCA 600

ACTGGCAGGA ATGCTTGAAG CATTAGAACA TTTCCTTAAT AAAAATACGA AAGTTTTATG 660

CTTGTTAAAT GGAATTGGGC ACGAAGATAT TATCAAAAAA TACGTGCCTT ACGAAAATAT 720

TTTATTAGGA AACACAATGT GGACCGCTGG GTTAGAAGGA CCGGGCAAAG TAAAATTATT 780

TGGTAATGGT TCGATTGATT TACAAAATTT AGGGGCGCAA AGTGAACAAG CAGCAGAAGC 840

AGTCATTAAG GTATTAAATA ACGCTGGCTT AAATGCTCGT TATTCTGAGA ATATTTTATC 900

ATCCATTTAT AAGAAGGCCT GTGTGAATGG AACAATGAAT GGTTTATGTA CTTTGTTGGA 960

TTGTAATATG GCAGACTTTG GCGAAACAGA GCAAGCAGAT CAAATTGTTC AACAAATAGT 1020

TAATGAATTT TTAGCAGTCG CTGAAGCGGA ACAAGTTACG TTAGATAAAC AAGCAGTTCT 1080

TCAACAAATC CGCTCGTGTT ATAATCGAGA AACAATTGGT TTGCACCATC CATCGATGTA 1140

TCAGGACTTA ATAACCAATC ATCGTTTAAC CGAAATTGAT TATATCAATG GAGCAATTGT 1200

TCGCAAAGGG AAAGTCTATG GGATTGCTAC ACCGTACTGT CAGTTTTTAA CAGAGTTAAT 1260

TCATTGTAAA GAAAATTTAC TTCATGCTAA ATAACAAGTA AAAACAGAAA TACTCTTGAG 1320

TCGGTCTTGA GAAGAGCTTG ACCTACTTCT TTCTATACTT TGCCAGTGTA CAAGGCTGAG 1380

ACAAAATCCA AAGTGAGTTt GGCTCAGCTT TTTTGTTTTT TAAAGAACAC TGCAGAAAAT 1440

AAATCAAATC CGTGaAAmAT ATGTTAAACT AGAGAAGGTG TTTTTTCGCA AGAnTCTACG 1500

CGGaACACAG GACTCGTTGA AGAATTGAAT CAAAGAAACA ATGTGTTAAA GAAGGGATTT 1560

GAACAGATTA TGACCATTCA ATGGTTTCCC GGCCATATGG CCAAAGCAAG AAGAGAAGTT 1620

TCTGAAAAAA TCAAATATGT CGATATTGTA TTTGAACTAG TTGATGCGCG GTTACCGCTT 1680

TCTTCCCGTA ACCCAATGAT GGACCAAATT GTCCAACAAA AACCACGATT AGTCCTTTTA 1740

AATAAAGGGG ACTTAGCAGA TAACGACCAA AATAAAAAAT GGCAACATTA CTTTCAAAAG 1800

AAAGGGTACC AAACCCTAGT TATCAATGCC CAACAAAATA AAGGAATCAA TAAAATTGTG 1860

CCAGCAGCCA AGGAAGCGTT AAAAGAAAAA TTGGCTCGTG AACAGGCGAA AGGCTTGAAA 1920

CCGCGTGCGA TTCGCGCCAT GTGTATTGGG ATCCCCAATG TTGGTAAGTC AACCTTAATG 1980

AATCGTTTAG TCGGAAAAAA AATTGCGCAA ACTGGGAACA AGCCAGGTGT GACAAAAGGA 2040

CAACAATGGT TACGCTCTGG TTCCCAATTG GAATTACTGG ATACACCAGG GATTCTCTGG 2100

CCAAAATTTG AAGATGAAGA AATTGGAAAA AAATTAGCTT TAACTGGCGC TATAAAAGAT 2160

CAATTATTGC ATCTAGATGA TTTGGCGATT TATGGATTAG AATTTTTTGC ACGTTTTTAT 2220

CCGCAACGTT TGACGGAACG ATATGGTTTA ACAGAGGAAG AGCTATTTTT ACCTGCCCCA 2280

GAACAGTTGA TGTTAATTAG CCAAAAACGT GGTTTTAGAG ATGATTATAA TCGAGCCAGC 2340

GAAATGATTA TTTTAGAAAT TCGCAGTGGA AAATTAGGTA CGTATACTTT GGACCGCTGG 2400

GAAGAACTAG GAGACGAATA ACATGGCAAA AGAGTCGATT CAGGCAATCA AAGAAGCGTT 2460

GTTAACTGTC ACTGATGCAA CCGATGAACG ATTAGCAAGC TGGCGAGAAG ATGAACGTTC 2520

AGGAGTGCAA CAAGCGATCA AACAATGGGA ACGTCGCCAG TTAGCCAAAG AAAAAGAGTG 2580

GCAACTTTTT AAAGAAATGA GTCAATTTGA GGAAGCGGCC TATAAAAAAG GCCATCGTTT 2640

AATTGCAGGA ATTGATGAAG TAGGCCGCGG ACCATTAGCT GGCCCTGTTG TGACAGCTGC 2700

AGTTATTTTA CCGAAAGATT GTCAGTTATT AGGCTTAAAT GATTCAAAAA AACTATCTGC 2760

TAAAAAACGG GAAaCGTTAT ATAACCAGAT TCmAGAACAG GCTGTCGCTA TCGGGTTAGG 2820

TATCGCTGAT CmAGGAGTCA TTGATCmAtT AATATTTATC CAGCCACTTA ACCAGCGATG 2880

GAATGGGCAT TGACGATTTA GCTTTTTACC CnGATTATTT ATTAATTGAT GCCATGCnGT 2940

TAGCGTTCCC CCACCnCAGA AGTTTGATTA AGGG 2974

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3078 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GCCCTGTTTG ACGCTCTATA GAnCTTTGGC TCTCTTGTnA CGTGTCCATA AAACCTCCTT 60

GGTGTGAAAA GAGCCGCAGC TATTCCGTCT GCGGCTCtAk GTAAGTTTaC ATCaGCCCtT 120

AAgCGGTAGG cCAGTTTGTG TCCGCCCCGC TGCTGGCTGT TGTACTTTTC CAGAATGACG 180

CGGGCAAAGC GCAGGGCGGC TTTATTGGTG GAGAAGTCCA TCTTGCCGCG CCGGATGATT 240

TCTTCCGGGT CAACCGCTGA CAGCCGCTTA ATGAAAATGC GGTCGTTCAG TTCGGTTTCA 300

TAGGTTTTCA GAAACAGCGC CATGCCGGAG AGCATCGAAG CACGGAGGGA AATGGATGCG 360

CCGTGCCAGG TGCTGTCTAA GAGTACCAGC AGGCGGGAAA AAGCTGTGCC GCCAAGCAGA 420

CGGTAGGCGT TGATGATGGC GCGGGTAGAA AGGATTTCGT AAGCGTCGCC GCTCTTTTTA 480

TCCAGTATCC AAACAAAGCC CGCAGCTTCC ACTAGCCGCT TGATTTCCAG AACCTCCGCA 540

TCCGTGCCGG ACTCCAGCAG GGCTTTTGTG GCGTGGGACA GACGAAGCCG CCCTTTGGAC 600

TGATCCAGCT TAAAATACAT CTCGGCTTCC TGCTCATAGG TCATGCCGGT GTAAATCAGG 660

CAGGGGACGG TCACgTTgCC GCCGTCTGCC ATTTTCCGCA TTGnGGCGAt CCGGTGCTGG 720

CCGTCCACCA CATTAAACTT TCCGTCGCGG AAnCTGACCA CCAGCGGGGT CaGgGCGGTC 780

GTCCCATTTG GCAATCAGCC GGTCAACGTC CTCCGGCTCC ACGGGCCGCT GGTAGGGCAG 840

GCCGGAAGTA AGCTGGTTGC TGGATAAGTC GCGGGGGACG CCGGGGTTGG CGTACTGGAT 900

TTCTGTTAAA AGGGTTTGTT GATCCGTCCG CTCGTTACCT GGCGGACGGC GTTTTTTTCG 960

ATTGCTCATG TCGTTATTGT CCTTTCCATT TGATTTAATA ATTCCTCCAT CGCAGTAGAT 1020

ATGCTTTCAA AGCGCTGCCG GACAAATTCA AACTGTACCT TGGAAATGCG CGGGAACACG 1080

ATAGTACAGA ACGGGTCGTG ATACCATGCG AACCCTTGTG AAAGGTCTGC ACAAAGCCGT 1140

CGATGTCTGC CAGAAGCGTG TCCGGCGTGT AGCTGCAATC CTTATCCGGG TTTTTCAGGT 1200

CGGCTATGGA TTCCTCCAAA GTGTCATAGT GCTGATCGCy cwGCGTATAG GGAACGGAGG 1260

GCTGCGAGGG AAGTTTTGTA ATCGGCTCTG AGGTCTGCCC TTGTTCCTGC ACCGGTTCCG 1320

TTTGTTCTGG TTTCTGTGTC AGTTTGGACT GTTCTGGTTT CTGCGTTTGC TCAGCCTGcT 1380

CCGGGATTGG TTCGGGCTGT TTCGGTTCCG GCATTGGCTT GGGGTACTTT GGCTCCTGCC 1440

TTGGTTCCGC CTGTTTCAGT TTCGGTGCTG GTTTGGATTG TTCCAGTTTC CGCGCCGGTT 1500

TGGGAAGTCC CGGAGGTTCT GCCGGTTGAA ACTCGTCTGC GGACTTGATT TTACCAGCCG 1560

CCAACTGTGC GGCGGCGTGT TCCTGCTGTT CCGGCTCCAT GCGGGACAGC TTCAGCAAGT 1620

CCTTTTTCTT GATTTTGCGG TCGGAACCCT GAATGACTTC CTGCGCTTTk GGGGTtATAT 1680

CCCTGGCAAT CTGGATATTT yCTtCCACCG AACGGGCGGA AATGCCCAGC TTTTTTGCTG 1740

TGTCCCGTGT AAAGGACTTT GACGTGGACG CGCCGCGCTC GCTCACGTTG TTGCCCTGGG 1800

CGCGGTTCAT TGCGTTTGCC TGCGACACGC CGCACCTTGT TTCCGGATGC AGGATTTCAT 1860

AGATTTCTTT CCGCCGCATC AGCAGCTTTC CAAACTCCAC CGTTTCCAGA TCGGTGCGTA 1920

CAAAGTTTTC GTCAATCTCA GCAAGTTCCG CCTGCAAGCC CTCCAATGTG CTGATATGGC 1980

ACTCGATTTC CGACCAGCCA AGCAGCTTTG CCGCTTCCAG CCGGTGCAGT CCGGCAATCA 2040

GGGTATAGTC CCGGTCAACG GTGATCGGAT TTAGCAGCCC TACCGCCGAA ATACTGTCCG 2100

CCAGTTCGCG CACGGCTTCC GGCAGGGCTT CCCGCCGCCC GGAATTGACC TGGATTGCGT 2160

CAATGTTGAT CTGCATTTTC ATCACCTCTT TCGGCCCTGG CCGCCTTATT TGTTTTCTCC 2220

TGCCGGATGA AACACGTTGC GCCGCAGGAA TACTACGGCG TAAGGTCTTG CATCCCGCAG 2280

GAAAGGGAAA GCCCGCGCCG GTTTTGTTTT GCGCCCTcAT TCTGTGAGGA AATATGACCG 2340

GCGTGGGTTT CCGCTTACTG CATTTCTTAA AAATCTGTGC CGTATTATCA GGCGGCATGA 2400

CCGCCTTACT GCCCACCCCC GGCACGGGAA TATGTAAGCC CAACATGGCA CGTCGGCGCG 2460

ATACCAACAG ACGGCGGCGG CAGGTGACGA AGCTGCCCaT ACCAATCCCT CAGTATCTCC 2520

CTTTTACCCT GCGATACGGG TTTTTGCGGT GCATCCCGCG TCTGCGGCGC TGCCATGCGC 2580

CGGACAGCCA TGCCGGTATC GCTCGTGCCT TTGATGTGAT CGGTTTGACG GGCAGGGACA 2640

GAGGTTTACA CCCCCTTTCG CTGGCCCTGT CCGCAGGCAG TCCTGGCGCG GAATGGCTGA 2700

TGCAGGATGC AATCACTTAC ATACTGGATA TGAACAGGCG CTTGTCCTGC TGTTTTTCAA 2760

GGTGCTTTGG TTCTTACGCT CAGGGAGCAA ATTGGTGGAG AATACTGTCC AGTGTGGCAA 2820

GGTCATCACC GGTAAGTTGT GCGCTCAATT TGACAAGCAG CGCAGCCTGC CGTGCCGTCA 2880

ATTTCCTGCG ATAAAGGTAA AACCCATCCG CAACCTTGAC GCCGCCGCCA TACCGTCCGC 2940

GTACCGTTTC AATGGGATAG GAACACATAA GCACGGCAAT ATCcTGACGG ATGGTTTCTC 3000

TGGAAACTTG AAATTCAAAT GCCAGATTGC GGTAGGTATC GTGCyGCCTT ATGCACAGCA 3060

CTTCCAGAAT CGCTTACT 3078

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

AAATATTACG ATaTTCmAGG GGCTTAAAAG CCCcTTATyC AtGCaAGTTA TTAAGTCGCt 60

AAAGGACAAG TGGTGTGGGT ATTkGCACAm CCTGTTAGTT TAyCCTATCT CCTAATTCTA 120

TTCTTAGGGA TTGTGTTAAC TGGCTTGTTT TGGAAAGAAG TACCATTACC ACAAATTTTA 180

GGAATTAACT TAAATTTGTT AATCATGGTG TTGGTGCCGA ATAAAGTTGC TCGTTGGTAT 240

TCCGAAAAGG AATTCGAAGG AAAAACAGGC TTTGGTTTTT TAAAAGATGG TTTTGTCTAT 300

GTGAAAAATT ATGTGTTAGA TAGTAGACCA ATTGTAGCTT TCGAACGAGT AAAAGAAATA 360

GAAGAGTTTT CATTTAAACG TTAGTACAAA AAGCGCACTA TATCTATGAA TATAAAAAAA 420

CAAGGAGCGC ATAGCATTAG CTCCTTATTT TTTATGTCTA AATTATGAAT TTTTATATTT 480

TAAATAAAGC ATGACTGCAC AGACTATTAT TCCGATGACT AAAAGTAGCA CAGTAACAAT 540

ACTTTCATTT TTATTTATTT TTCTTTCAGG TCTATAGCTA GGATTAATTT GTTTTGCGTT 600

AAAATCAGTA ATTCCAAAGT CTAAAGTAGG AAGTAAAAAC AGTAATAAAA TAATATATAT 660

AATTCCCGCT ATAAGGAAAA TAGGAGCGTT GGTGAAAAGT GAAATAATGG TACCTATGAT 720

TATAGGAGTT AAAATGTATA AAAAGGATTT GATAACATTT TCTTTTCTCA TTTTAATTAC 780

CAAATTTTGT TATTCATGTT TCCCATATTT CCTAAAGGAA CACAATAACC ACCGCTCATA 840

TTTTTTCCAC CTGTAGACCA ACCACCTTTT TTAAAATAAA AACCACCAGG GCAAGAGCTA 900

CCAAATTCAG CTTCTCTGGC ACTAGCTTCT GAACTAAAAA TAAAAGGTGT TACCATTGCG 960

AAAATAGTTA AAGCTAAAAA AACTTTTTTC TTCATACACT TTCCTTCTTT CCAATTATTA 1020

TTTAAAAGCT ATATTAAATA TAGCTTTATT TTATAATAAC TGAATGAAAA AAAGTTGTCC 1080

AATAATATAT AGAAATTTCT GAAAAATCAT TTTTAATGTT AATTACTAAA ATAAAATCAA 1140

CAAGAAAGGA AAAAATATGC AATTAGAATA TCCATTAACG AATCATATGA AAGGAAATAT 1200

TGTTTTAACA CAAGAAAAAA CAGCGATAgC TTACTATCGT GTTCGTTCTG AAACGGTAAT 1260

GTTGACTGAT GTTGAAAAAA AATTAAAAAC GAAAAGAAAA GTTGCTCGTG CGTTAAATCG 1320

CTTAAAAGCA AATGATGGAT TTGAAATTAA CCTTTTGCCA GTTAATGCCG ACATTCGAGG 1380

GAAAATGGGT GCTATGCGTT CTTTAATTGA TTCTAATAAT TATGAAGTAG GCGTAGATAA 1440

ATTGATGAAA ACGGCAATGG TTTTAGAACA AGAAATGGGT ATGGTTTACG AATATACGTG 1500

GATTATTGGT GTGCCTTTAA TCAAGAAAGA TCTCGCTGTT GATTTAAAAG AAACCGTTAC 1560

TAATTCAATT AGCAACGTAT CGGAAAAATT TGTTAAAGGG CTAGGTTTTG ATGTGGAACT 1620

AGCAGAATAT TGGGAAAAGG ATTACCGAGA ACAAGAATTA GAAGTTTACC AAAATCTATC 1680

TGAATTGTTA ATTGAACGAT TAACAGAAGA TGAATTGTAT TATTACCAAG CGTACCAATT 1740

CTTGaAAAAT ATTCCTCATG AGCGACAAGA TGTTCTTTCT AGTCAAAATT TAGaTAATTT 1800

aATGGCmACa AAAATTAAAC CGTTATTTGG CgGGGGATTG CATTTAAATT GTGATTATGG 1860

CGAAAGCTAT ATATCCTATC TTCCAATGGG AGATGTAGGT GTTTTTCTTG ATGGTAATCA 1920

TTTTTTAGAG GTCGT 1935

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 767 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

TTTGTAAAAC TTTTCTTTTG GCAAGCAAAC TATTTTGTAG AAAGCGGTTC ACTCTGTTAT 60

CATAATAGTT GTATGAAAGA CGTATGTTAC ATACTAAAAA ATAGGGGGAT TTAAAAAATG 120

ACTTACACAT TACCAGAATT ACCATATGCT TATGATGCAT TAGAACCTTA CATTGACGTG 180

GAAACAATGC ACTTACACCA TGATAAACAC CACAACACTT ATGTGACTAA CTTAAACGCA 240

GCGATTGAAA AACATCCAGA ATTAGGCGAA AAATCTGTAG AAAACCTAAT TTCAGATATG 300

AATGCTATTC CTGAAGATAT CCGCACAGCT GTTCGTAACA ATGGTGGCGG TCACGCAAAC 360

CATACATTCT TCTGGGAAAT TATGGCACCA AATGCTGGTG GACAACCAAC TGGCGCTATT 420

AAAGAAGCAA TCGATGAAAC ATTTGGTAGC TTTGaTGAAt GAAAGCTGCT TTCAAAACAG 480

CTGCAACTGG CCGCTTTGGT TCAGGTTGGG CTTGGTTAGT TGTGAATAAC GGTAAATTAG 540

AAATCACTTC AACACCAAAC CAAGATTCAC CaTTAATGGA TGGCCAAACA CCTGTTTTAG 600

GTCTTGACGT TTGGGaACAT GCGTATTACT TAAAATATAA AAACGTTCGT CCAGATTACA 660

TTGAAGCATT CTGGaACGTk GTTAACTGGG aTAAAGTAAA CGAACTTTTk GCtGCAGCAA 720

AATAAGTTTG CCAAtGGTAA AAGGAAAGAG TCAAATGACG GCCGnCA 767

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GCAGGTACTG GGATGGCCGT TTTCTTCGCA TTACAATTAT ACCTTGACTT CATCAACTTA 60

TTCTTAGCTT TCTTAAGAAT TTTTGGTAAA AACAACTAAC ATGAACGTAA AAGAGGTnGG 120

GACAGAAGCG TTTAACTCCG AGAAATAAGA AGGAATTTCC GAAAATTGTT CTTTAATTTT 180

TGGATAATTC CGGCTTATTT CCGAAGGAGT TGCTTCTGTT CCCGCCGTTT ATCAGTTTTT 240

GAGCGTGGAG CAAAAATCCA AAGTGATTTT TGTCCCACGC TCTTTTTTTA ACCCATTCCA 300

ATAGCGAAAT TCAACAGTTT ATCGGAGTAT GTTGGGTTTt CyAAATCGGT TTTCATTGTT 360

TCGTTCAGTA GACTGAGCTG ATCGGTAATG ATGCCATCGA CGCCATAAAA AATCATTCGT 420

GTCATAACAT CTTCATCATT TGCTGTCCAA GCATAAACCT TTTTCCCATC ATGATGAGCG 480

GCATTTACAA AGTTACGATT CATTGTACTG TATTCCATAG TAAAAAAGTC AACTGGCATT 540

TTAGGCGGTC CCACAATGTT GAAAGGAATA ACGTAGCCTA CATAAAAGCG TGGTTCTTCT 600

TTCTTTAAGG CCATCGCCGT ATCATAGGTT AAGGTATGAA GGATATGGCC GTTTTCAAAA 660

ATATTTTCAC GGTATTGTTT GACAAAGCGC TGTACTAAAT CAGGGCTATC TTGAGGCGTG 720

GTTTTGATTT CAATTAATAA ACGTTGTTTT AATTGATTGG CTTTGGCTAA ATAATCATCG 780

AAAGAAACCA TTTTAGCAGT TTGACCATTT TCTGTGACAT TCATATTCGT TAATTCTTTA 840

AGTGTTAATT GATTCGGTCG TTTATTAACG CCCGTTAACG CCCGTAAATT AAAATCGTGC 900

ATGACAATAA ATTGATGGTC TTTGGTTTCT TGAATATCCA TTTCAACATA ATCAGGTTTT 960

GCCTTATTGG TCTCGATTAA AGAGTCCAAG GTGTTTTGAA CGCCATTGTT ACCATTAACA 1020

CCACGATGGG AGATGGTAAC CGGTTTTCgG TCAGGTGTAT GACTTAGGTA ATcGTATTAT 1080

AgGTGCCTAC ACCAATnCCG AAGATGAnTG CAATCaAACm AAAAAGAcGA CtCtGAAGGn 1140

GGtCCATCnA CCcGAmCcyG ATTTCGGGGT GAACCATTCT GGCGTGTCAG GCAAAATCCC 1200

TTCATCTTCC ATATCATCna CaATwaTGtA AAAaATAGCm ACaCTwGaCA ACACCAAGTT 1260

TaAGAGCATC ATAmCCTGAA GGAGTGTCAT AGCGATGACa GCGCTAGGTA AAGACCACTC 1320

AGGTTTAAAC GTTTCGACTG CGGTTTGACC TAAAAATATC AAGAAATAGC CAGCCGTAAA 1380

AATCCCTAAA ACAGTTCCTC CAATGATAAT AAATTGCCCT AAAATCTGGA AAAAGCGCCG 1440

CTTTGTAATT TGCCAACTAC GTTTTAAAGA CTCACGAAAc CAACATCACG TAAAATCAAC 1500

TCTGGAAGGG CAAAAGCAAG TCGAATCGCT AAATATAAGA TAATCAGTTC TAACAATACG 1560

AAACCAATAA TAATAATGAC GCGATTTGCA AAAATAAAAT CTAAGATAAA GGCTGGAATC 1620

TTAACTCTTG TTAATAAATA AGAGCGGAAG GTTAACCCAC TTAATGGTAA AATCAAAAAG 1680

AAATATGCCA GGAAAAACAG AAAGGTAATT CCTCGAACTT TTTTGATCTG AAGCAAGGTG 1740

CCGTGCAATA ATTGCGTTAG AGTAATTGGT TGCTTTTTCT TAATAAAATA GACACTAAGC 1800

AATAAAAAGG TAAATTCAAA AAAGAGCGCC AGTAAAATTA ACAGCCCAAT TAGTAGAAAA 1860

GTCAAAAGGA CATAGGGATG TTGCGTAGca ATTGCCCCTA AGTTATCGTA GGAAATATAA 1920

TCAATCCCAC CTTCTTTGAG TACCAATTTG GaCAAACTTG TCAATAAAGG CAATAGAACG 1980

AATAACATAA ATCCGTGCAT CAAGAGCACA TCGCGaAAAT ACGCCGTTGT CCCTTTAAGA 2040

AAATCTAGCG TATTCACmAT ACTATTTTTA AAATAACTAA ACATCmAAAG TCCCCCAGTT 2100

TCtACCmAAA TTCC 2114

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAATTGTCTG AACACATTTA GCGCCGTCCT GAATTAATTC ATGGCAGCCT GTTGAAAAAG 60

ACTGGAAAAT ACTTCCCGGT ACGGCAAATA CCTCGCGCCC GTAATCCATC GCCGCTTGTG 120

CAGTAATTAA AGAGCCACTA TTCTTACGAG CTTCCATCAC GCAGACCCCT AAAGATAATC 180

CAGCAATAAT GCGATTACGT GCAGGAAAAT GATATTTTTT CGGCCCACTC CCATTCACAT 240

ATTCTGTTAA AACAAGCTGA TTCTGCTTCA TAGTTTGCTG TAATTCTTTC TTTTCATACG 300

GATAATATAC ATCTAATCCA GTGCCTAAAA TTCCAATTGT CTGACCCCCG TTCTGGATGG 360

CCATCTCATG GCTACGACTA TCGATACCTT TGGCAAGACC ACTGACGATT GTGAACCCTT 420

CTTTGACTAT TTTAGGAACC AGAGCTTCAG TCACTCTTAA CCCATACGAA GTGGCATAGC 480

GAGCGCCGAC GATGCCAATT TTCCTTCTAC TTAACAATTG TAAATTTCCT CTATAAAAAA 540

GAATtGCTGG TGGATTATAA ATTTCTCGTA ATAATTTAGG ATAGACGGCA TCTAAAATTG 600

TCATAAATTG GTGTTGGCAT TGTCGTATAT ATAACGCTTC ACTATGAATC GTATGGTGTA 660

ACCAAGATTG TTCAAATAAT TCACGATATT TCTTGATTTC AGCAATTCTA ATAATTTCTG 720

TACTGGAAAA ATCAACACGC TTTTGTGCGA TAGCTTCTTG TAACACTTTT AAGATCCCTA 780

AATTGCCAAT TCCTTGGCAT ACCGCTAATT TAAATAATAA TTGTCGTTGT AAAATTTCCA 840

ACAAAAAACA CCTCTTTCAC ATCTTCTTAA AATAAGAATA CGTAAAAAAA GTGTTTTATT 900

TTTAAATCAT ATCTTTTATT GGCGCAAACG TACGTCGATG AATGGGCGTT ACACCGTATT 960

TTTCTAACCC GAGAgAkGTT CTTtTGTTCC aTAACCTGCA TTGynTTTAA ATCCATATCC 1020

AGGATATAAT CCATCATATC CTTCCATTAA TCGTCTCTGG TACTT 1065

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

CTGACnAGTG CACACAGTTG TTGGCGCGAT GCTGGACGCC CtCGtTTTTG awcTTaAgyT 60

TgGGCtCtct TctGtTkGtT AGCCAGTnCA GCTCTTTTGC TGCTGGTcTT TTTCaGCCTT 120

tGCTTTTycC rCTyCCGcAt TTTtCGcTAA tyCTTmAAgC TTGGCTTGTT CTTGtTTCGC 180

AGCTGTTAcT GCTTGTTGAT CTTTATCATT TTGyACTTTA GCAGCATTCG TTTCTTTTGC 240

TTTTTCTTCG ACAACAGCTT GTTGTTGGTT AACGTCTGTT TGAGCTTGAT CyACTACTTT 300

TTGTTGGTCA TCAACwGCCT GTGTATcCGT AGCCACTTGC TCTTTGGCTT TTTCAATGGC 360

TGAAGGTGTT GCTTCATCCA CGACTTTTTT AGCTTCGTCT ACAACTGCTT GTTGGTCAGT 420

CACTGCTTGT TGACTTTGAT CCAATGCGTC TTTGTTTTGA TCGACCACTG CTTGTTGGTC 480

TTTAACAGAT TGATCAATGG CGTCTTTTTC TTTTTTCGCA GTGTCAGCGA CTTGTTGTTT 540

TTGATCGACA ATTGCTTGTT TCTCTGTTAC TTGTTGCTGT TTTTCAGTAA TAGCTTGCTC 600

CGTTGTTTGT GTAGCTTTCA CTGTTGGTTG TTCTGTAGAA CTGTTTTCAG GTGTTTTTGG 660

TTGCGCTTGT TCTGCTGCCT GTACTTCATT TCCCCCAATA CCTGCTACCC CTGTTGCGAC 720

TAAAATACTT AACCCTGyAC TTGCGATCTT TTTCATTTTA TTTTCCTCAC TTCCGATTAT 780

TTTTGTTGTA AATGGGATAC CCATTGTCTT TACGCCATTG TTGTAACGCT GTAGTTGTTA 840

TrTGGAACTC TTCCGCTATT TCTTTAAACT GTAArCCCAT TyTTTGATAG GCTTCAAATC 900

TTTCCTTGCT AATATGAGAA GAAAATTGTC TGGTGCTTGC TGTTTCTATC TTTTTTGCAA 960

GTTCTTGTAT TCGTTTAAAA CGCTCGGTAT CTTCATTCCT ATACCAGTCT GCGTCTTCAT 1020

TCATCAATGC CAACATCTCT TTACGCCAAA TACTTTGCTC TTTTTTTGTC ATACCCCTCT 1080

CACCTCAAAT TAATAGTAAA AAAATAACAT TTATTAAAAA AATACTATCC TTCTTTTGTC 1140

TtCTTGGACT TACCAAAAAA TAAAAATATT TTCGACTAGT TTATGGCGTC CGGAACTAGA 1200

AACCCTAATA GACAACGGTA AATGTAACAA AATTATTGTT ACAAGTGCCT ATATGCATTG 1260

CAGCACACAA CATATCTTTT ACAGATATGC GCTCTCCCAT TACGAAGAGC CTATTAAATA 1320

TTACTTAATA ATAAGTGTTT TAGCCTAAAT CCCTTAGTAG CTGCTCTGAT TAATTTAGGC 1380

GCTATAAATT GCTTCCTCTC TGGTTCAAAA TGTTTGTTTA CTAACTATCG TTATCATAGT 1440

TATTCATTTG CAAAAGCTTA TGATTACGAC GTTTGCTTAC ACTAACCAAT TTTTTGTTGT 1500

TAATGTACTA AAACAATCCT TCGTCCGAAA TAAAGGAGGG CCACTCCACC GCTGAATCAT 1560

TAAGCCTATC TTAATCTTCC ACTCTCTCCA CATTCTTCTT ACAGAGATTT CACAATTGTT 1620

TTTTTAAGCA AGTCCAAGAA GACmAAATCT ATCTTATGAT TTTTTATCGT AGTCCAAAAA 1680

TTTACTCATT CCTCTACCGG TAACTTTTAA CGGACCACTA GGAGAATTTC TTCTAGCGAT 1740

TAATACCCCA TTATGGTCAT AAACATGTTT AATTTGTTTA TAGACACTGC GCAAAGGAAC 1800

TTGACCAACT TCTCTTTCGC ATAACTTTTT CCCTTTAAAA TACTTCTCTA TTTGAACAGC 1860

AAACATCCCC TCAATTCTAT ATGTTTTTGT CTTTCTAACA AACTTTGATG TAGCATTGGG 1920

TAACTTACGC TTCTCTCGTT GACCAAAAAC AATAATTCGG TTGCCGTAGT ACCCAACATG 1980

TTCAATTCGT AATACTGAAA AGCAACTCAT TTACATTCCC CCAATCGAAT ATTTTTTAAA 2040

TAAAAATAAG AGCCATGCAA CACGTTGTTT GCACGGCTCT TACGAGTAGT TCCaGTACAA 2100

ACAATGCGTG AAAGCATTGA ATTATTCCAC AAGCGGGTCA TTTTTAGAAA ATGAGCGTGC 2160

TTGCTACTTG GTTTTTTATT TTTTCAACAA GTTAACAGAC AACAAAAAAG CGGGGAATAT 2220

ATACATGAAC TGTATACaTT CCCCGCTGCT CCAACATTTA TACAACTAAT TAAAACAATT 2280

CACTGTAAAA ACTTTTCCTA GACAAATAAA GGAGTTTAAA AAAGTCTAGA ATTTTACATA 2340

AAAAATTGTT ATACTATACG TTGTAACTAA TGTTGCAACA AACGAGAACC GAGTATAGTT 2400

CATGGGGTTC TGTTGCAAAG TTTTAAATAA AGAATAAAAT CCCTTACGGT ATCTATGATT 2460

TAAGCTGGGA TTCCCAATAA TACCTTGATT TCAGTACAGA CCGAAAACCC GAAGAGAGTG 2520

CCTTCTTTTC GGGTTTTCTT ATATAATCCT CGAATGGCTT CCATGCCTTT AATCGTGGTA 2580

GAGGCAGTGC GTAAACTTCG ATAGAATTTA TTGCGTCTCT TTACTGGACG ATGGTCTTGT 2640

TCAATCAAAT TATTCAGGTA TTTAATGGTA CGATGTTCTG TCCCTTGATA AAAGCCGTAT 2700

TCTTTTAGTT TCTTAAAGGC ACTTGTAATA GAGGGGGCTT TATCTGTGAC TAcAACtTCG 2760

GTTCATCAAA CTGCTTCACT AACCGCTTAA GAAAAGCATA GGCTGCTTGT GTGTCCCGTT 2820

TTTTACGTAA CCAAATATCC AAGGTTAAAC CATCTGCATC GATGGCTCGA TACAAATAAT 2880

GCCATTTTCC TTTAATTTTG ATGTACGTTT CATCCATTTT CCATGAATAA AAGGATTTTT 2940

TATTTTTCTT TTTCCAAATT TGATAGAGTA GTTTGCCATA TTCTTGCACC CAACGATAAA 3000

TCGTCGTATG AGAAACGTTA ATGCCACGAT CATATAAGAT TTCTTGAACT TCACGATAGC 3060

TAAGGTTATA ACGAAGATAG TAGCCCACGG CTACAATAAT CACATCCTGC TGAAATTGCT 3120

TTCCTTTAAA ATGATTCATC GTCATTCCTC CTGCTATCTT TTTCTATTAn ACCACACAAT 3180

ATATTTCCAA TTACCTCTTT CTAATACTGG CA 3212

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

ATTGAGTGAG GTATTACnGG AnATTATGGT TCGCTATGGC GAATTATCAA CTAAAGGAnn 60

AAATCGTAAA ACGTTTATCA TGCAGTTAGC ACAAAATGTG AAACGTGCGT TAGCTGATTT 120

TCCAGCATTG AAAATCCATG CAGATCGAGA CAGAATGCaT ATTTTaTTAA ATGGGGAAGA 180

TAGTGAAGAA GTGATTCCGA AACTAAGTAA AGTGTTTGGA ATTCAAAATT TTTCGCCAAG 240

TATTCGTATT GAAAAAGAAA TGCCAGCGAT TCGTGCAATG GTTCAAGAGG TTGTTCGGGA 300

AGTTTATACG CCAGGTAAGA CGTTTAAAAT TACTGCTAAA CGCTCGGACC ATTCATTTGA 360

ACTTGATTCA AATGGCTTGA ATCAAGAATT AGGTGGGGCC GTTATTGAAG CCATTCCGGA 420

AATTCAAGTA CAAATGAAAA AGCCTGATAT TAACTTAAGA ATTGAAATTC GTAAAGATGC 480

GGCGTATTTA TCTTATGAAA CGATTCGCGG TGCGGGTGGA TTGCCAGTGG GCACCAGTGG 540

TCGTGGTATG TTGATGTTGT CAGGAGGCAT TGATTCACCA GTTGCTGGTT ATTTAGCTAT 600

GAAACGTGGC GTGGAAGTGG AAGCTGTCCA TTTTGCTAGT CCGCCTTATA CAAGTGAACA 660

AGCGTTACAA AAGGCTAAAG ATTTAGCTGA AAAATTAGTC CCTTATGTAG GAACTATTCA 720

ATTTATTGAA GTGCCCTTTA CAGAAATTCA AGAAGAAATA AAACGAGTTG TTCCCCAAGG 780

CTACTTAATG ACCATTACAC GACGTTTAAT GTTACGCTTA ACAGATGCAA TTCGTGAAAT 840

GCGGAAAGGT TTAGTCATTA TTAATGGTGA ATCGTTAGCA CAAGTGGcTT CGCAAACACT 900

TCAAAGTATG GTAGCAATTA ATGAGGTTAC CTCAACACCG ATAATTCGAC CCGTTGTTTC 960

AATGGATAAG ACAGAAATTA TCGAAATTGC CGAAAAAATT GACACGTTTG AATTAGCCAT 1020

CCAACCCTTC GAAGATTGTT GTACAATTTT TGCGCCACCG CAACCGAAAA CACGACCTCG 1080

CTTGGATAAA GCGCAAGAGT ATGAAGCGCG CTTAGACTTG GAAGGTTTAA TGGCTCGGGC 1140

CTTAGAAGGA CTCAAAATTA CAGAGATTTC AGCAGAAACA GCGAAAGATA AACAAGAAGA 1200

CGAATTTGCA GATTTCCTAT AAGArATAAA TACAGTGACG GTCGCTTAGA CGTCACTGTA 1260

TTTATTTTGT ACTTATTTCA CmAACAAGTT GCTCGGAGAG GGGAACCGTG ATAAACTGAA 1320

TATGTGAAGT AGGTAACAAG GAGGACAGAG GATGGAGAAA AAAATGCCTA AAGCAACGGC 1380

AAAACGTTTG CCGGTTTATT TACGTTATTT AAAAATGTTA GGGgATTCTG GTGTTAAaCG 1440

CATTAAaTCA CGAGaGTTTA GTGAAATGAT CCAGATTCCT TCTGCAAC 1488

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

ACGATGGTAT GTGCCCTTTT CCGACGACCT GTCAACnCnA AAACCTTGTA TCCTAGCAGA 60

CTGTTCGTCT TTTCCGATCT GATCTCTTGA TTGTACTTGC CATTCTTTCG TACTTCCTCG 120

TTCATGGCTA AAGATCAATG TATTTnCCTT TTAGTTTTTC TGTATCTAAC TGAGAACTAT 180

CGATAGCACC GTCAGTCATT GAnCTGCGAC AGCGACAATA TATTCCATCA TATCTGTTGC 240

TAAATAGAGT TTTGGCTCTT TGCCCTCGTT ATCTAACGAT CCAACCAATG AAATCGGTAC 300

ATCCATTCCC ATCGCTTTTA ATTTCATCTC TAAGTTGAAT GCTTTTTCTT TTTTGGCATC 360

TACTTGAATC TTCCCCAGAA AGCGATGCGT CTTTGATTTG CGTGATGAGC ATCCCAATCA 420

TAGGATTCGT TTGTGCACCA TCTTCTTGTG AAAATTTCAT GTCACTAATT GACATAGAGA 480

AATCyCAAaC CCCAGATTCT TGTGCGTTyT GATTGCCGAT TCCTTGAATG AACTCATCTT 540

TCGCACTTTT GCCACAACCT GTCAGTAACA AAGCTGAACA GAAAACGCCT GCGACAATCC 600

CCACTTTTCT TTTTAACACA CTTTTTCCCC CTCATTATAT AAAAAATTAA TTCCCTTTTA 660

TTAAGAATAG CAAACATTGC TTATAAATAG CAATGTTTAA TTTTAGATTT CCTCTCTTTT 720

AATAAATGGG ATTGATTTAA TCTTTTAGGT TTGAATCATT AAGCTGTATT ATTTTTAAAA 780

TAAAATTGCT TTTCGCCAAA AAATACTGGG AAAAGTTCTG CTAAACTGCC AGCTAAAGGA 840

CCTTCTCGCA ATTCTTTTTC AGTGACCCAA AACAAGGGTT GTTCCGTTTC TTCTGGTAGT 900

TCATCCGCTG TTTCTGCAAT GAATAATGTG GCTAATTCCC GCGCACCTGA ACAATCATTC 960

AGCCATTCTG CAACACCTAC TAATTGTGGC TTCAGCACTA ATCCTGTTTC TTCAAGGAGT 1020

TCGCGAACCA TGGCTGTTTC CATGcCCTCG TTTTTTTCAA CATGTCCGCC AGGGAACGTC 1080

CAACCAGGCC AATCCTTTTT TTGTCGTTCT TGCACAAGGA TTTCATTTTT CTGATTCTAA 1140

TCATA 1145

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

CAGAAACACT CTTTTTTTGT AAAGGATTAA ACTTTAAAGA AATCTATTTA GAAAATGCTG 60

TAAAAGACGG CCTAGAAATC TATGTTTCTG AGGTGCCTTA TGAGGTTCCG GCGCAACTAG 120

GAATTATCGT GACTGACATT AAAAAAGCAA TGGCTGTGTT AAGCATGGCT TTTTATGATT 180

ATCCACAAAA TAAATTAAAA CTGATTGGCT TTACTGGAAC CAAGGGTAAA ACAACAGCGG 240

CTTATTTCAC CAAATATATT TTAGATGTTG CTACACAACA AAAAACAGCC TTGCTTTCTA 300

CCATGAATTC GACATTAGAT GGCAAAACAT TCTTTAAATC TGCCTTGACT ACACCCGAAT 360

CTTTGGACTT GTATCGAATG ATGGCAACCG CTGTTGCTAA CGGGATGACT CATTTTATTA 420

TGGAAGTTTC TTCCCAAGCC TACAAAACTA ATCGTGTCTA CAAGTTATTT TTTGATGTCG 480

GCATTTTTTT AAACATTACC CCCGACCATA TCAGTCCAAT TGAACATCCA ACCTTTGACG 540

ATTACTTTTA TTGCAAACGT CAATTGATTA CACATTCTAA AGTCATTGTG TTGAATCACG 600

AAGCTGATTA TTTTCCATTA CTTAAAGAAA CTGCACAACA GCAAAAAGTC CCAGCCATTG 660

TCTATGGCAG TCAGCCGGCT CCAGAAGTAG ACTATTCATT CGCTGTTTCT TCAGAGGATT 720

CCTTACGTTT TATCGTTGAA AGTCCTGCAG ATGCGTTAGG ATTGGCCGGC TCTTATCACC 780

TTCGTTTAGG TGGTGATTTT AACAAAGGTA ATGCGTTAAG TGCGGCGATT GCTAGTGTCC 840

TTGTGGGAGC TTCAAAAGAA GAGTGTCAAC AAGGAATCGC AGCAACCACC GTCCCTGGCC 900

GGATGGAATC TTTAACGAAT ACCAACGGTG CAACCGTCTA TGTTGATTAC GCTCATAACT 960

ATGACAGTTT GAAGAATCTT TTAACCTTTG TCCGTGAAGA ACATCCTGAC GGCCGCTTAA 1020

TTGTTCTTGT CGGTAGCACG GGAGACAAAG CGATTTCTCG CCGCAAAGAC TTTGGTAGGG 1080

TTCTTTCTGA ATTGGCTGAT GTTGCAGTCC TAACAACCGA TGACCCAGCC AGTGAAGATC 1140

CAGCAAAAAT TTGCCAAGAA ATTCAAGCCC ATATTACCAA AGAAATGCCT GTTTACACCG 1200

TTTTAGATCG TGGCGAAnAA TTGCTCACGC ATTATCTTTA AGCACAACGG CTGATGATGC 1260

GATTGTCTTA GCTGGTAAAG GCGCCGACCT TTATCAAAAA GTAAACGGCG TAGATGAACC 1320

TTACGCaGGA GACTTTGCCC TTGCGGAAGC TTTCATTAAT AAAAAGrACT AAATCATTTA 1380

AaCaCACATG AAAAAAACAA GCTGCAACCA CTTATCAGCA AAGGTTGCAG CTTGTTTTTT 1440

AAAGAACTTC TTTTATTTTC GTTACTTCTT CTTCTGATAA GCCATGACCG CCATCCACTA 1500

GTAAAAAGTC GACTGGAAAA TGTTTCTTTA ATTGATTAGC TAAAGAAAGA ACTTGTCCCG 1560

GAATACTCAA CTCATCCTGA GCCCCTGTTG TGACAATCAC TTTTGTCGCA AACTCACCAG 1620

ATACATATTG ATAGCCTAAA TTGCTTGGAT GCAGTAAAAT AACAGTGTTA GCAATAGTTG 1680

GGTTCTTTTC TAACAGGCCT AAAATAAAAT TGGCACCGTT AGAGTACCCT ATAAAAATAA 1740

CTTCATCGTA TAACTTTTGC GGTTGCCAAA CTTCTTCTAG AAACGCCGTC ACTCGCTCAT 1800

CAAAGTTAGC ACGAGATAAT GCTCCATTGA CTAATGGCGC AAAAAAGCGT CGCTGTTCGC 1860

CTACACCTTC TGTCCCTAAG TAACTTAGAA CACTCGCTTC TGGATAAAGG GTTGCGATGG 1920

TGGTTAATAA TTGATATTCA TTGCCACCAG TACCATGGAA AGCGACAACT AATTGATTAG 1980

GTTTCGACCC TTTTTGAAAA AATTGTTTCA TTTAATAAAC CTCCAAGAAA GGAATTTTAC 2040

TATGTATGCA CAAATTCATC ACATCTCTAT TTTAAATCGA TTGATAAAGC CTACATTTGA 2100

CTTCTATCAT AATACACTGG GATTAAAATT ACTAATGAAA ACGATCAACC AAGATGACCA 2160

CACCATGTAT CACTTGTTTT TCTCAGATAA TGAGCAACGA ACAGGTACCG AATTAACTTT 2220

TTTTGAATTG AATGATGGCC AAGATCAATC CTTTGGGACA AATACGATTG AACGAACTAT 2280

TTTAAAAGTA CCAACGCGCG CCTCTTTGGA TTTTTGGGCA GAACGTCTTG AGCAAGCGGG 2340

TATCTGCCAC TATGGTGTGG AAACATTTAA CCAACACCCA ATTTTGCGTT TTGAAGCGCC 2400

CGATAATACG CAAATGGCGC TTGTTCCGTT ACGTGAATTT GAAAATGCGG AAGATTATTT 2460

TCCAGCTGAG CATTCCGAAA TTCCAGTAGA ACATGCAATT TTAGGCATTG ATGCAATTCA 2520

ATTACGCGTC CAATATGCCG TAGCTACCAA ACAACCTTTA GTGGATTATT TACATTGGCA 2580

TGAAAAAGAA ACAGTACCTT TTTTTGAAAC TGCGCATGAA GTAACCGTTC TGGAAAATCA 2640

TCATCCACAG TTTTATCAAG AGGTGCATAT CATTGATGAC CGTACCAATC CGCTTGCCAT 2700

TGAAGGAATT GGTGGCGTTC ATCACGTCGC CTTTGGGGTG GAAGATACGC AAGAATTAAC 2760

GCAAGTTGAT AGCCTGTTAG AGGAAAAGAA TTTTACAAAC TCAGGAATTA AAGACCGCGA 2820

ATTTTTCAAA TCATTGTATT TTAGAGAACC GAACCACTTG TTATTTGAAG TAGCCACACA 2880

AAAAGGCCTG CTAGATGCCG AAGCCTATGA AAATCAAAGC TCAAACTTTG ATGAAATCCC 2940

CCTTTATTTG CCTCACTTTT TGGCAGATCA AAGAGAACGA ATCGAAGCGA TTTTAGCACA 3000

ACAACGCCAT GAGTAAACAA AAATAGCGGT TCTAACCGCT ATTTTTGTTT TTTAATATCC 3060

TATTATTGCC CTTTTTTGAA AAAAAGGAGT ACACTAATAG TAGATGAACT GCGCAAGGAG 3120

GTGAGTACAT GTTATCTAAG GAAGAAGTTC TACACTTATT GAACGAAGCA AAAAAAGAAG 3180

TCGATCGTTT AGAAACAAAC CGCCAAGAAG ATTTAGGTAA TTCAATCAAC TATATTGAAA 3240

ATGAATTACA GCTCCAACGT GTCTTATCTC AAGTGGAAGC TTATGAAAAA GTACTTGGTT 3300

AATTGATTAC GCATTAAATG AGAGAGGAGC AACCAGATTC AGGTGAATGA ATCTGGTTGC 3360

TCCTCTCTCa TTTTTTACTA GACTAATTCG TAAGCAAGTT CTCGTGCAAT AATTTTTGCG 3420

GTTGTTTCAG CGATTTCTCC AGTAAAGCCA ATGCATTGTT CCATATGTTC AGGTGAACCC 3480

ATCGTCATTT TACTTGTCAA AATACTGCAG CAAACCACTC GATGCTTTTG TCGAAAACTT 3540

TGATGCAATT CGTTGGCTAA AGCCATCGTT TTATTTACTT GTTCTCCTTT GGCTTCTGTC 3600

CGACCAAAAA AGTAGCCCAG ACACATAACC CCGCCTGAAA GAGCACCACA AATACACTTC 3660

GCTCCTCCAA CACCTACAGG AAACCCAGAA GCCATGGCCA CAGCTTCAAT GGGAATCTCC 3720

GCATCGAAGT GTTGCCGAAT GGTCGCCACA ATCGCTTCCG AGCAATAAAA ATCACCGTTA 3780

CGATAATAGG CTTCCGCTTC TTCCCTGATT GCTTGTAAAC AAATTCTCTT TTTCAAAATG 3840

CCCTCCATTC TGTATCCGCT TTCATTTTAT GAATAAAAGG ATGCCAAGCA TCCCTTTATT 3900

TTATAGATTT TCTGCAGAGG TAAATACTTC TGACACATCA TCATCGTCTT CTAACTTGTC 3960

AACCAAGCGC TCTAATTGCG CTTTTTGTTC ATCGTTCAAG GTTAGTAAGG TTTGCGGAAC 4020

CATTGTTAAT TCAGCTTGTG CTAATGAATA ACCTGCTTGT TCTAAAGCAT CGCGAACCGC 4080

TGTAAAATCT TCTGGTGCTG TGTAAATTTC AAATACTTCT GGTGATGTTT CTATATCCTC 4140

GCCGCCTGCT TCCAAAACGA CTTCTAGCAT GTCGTCTTCC TCAATTGCAT GATCTTCTCG 4200

CTTAATGACA ATATAGCCTT TACGATCAAA CATATAATTC ACCGAACCCG TTTCACCTAA 4260

AGAGCCACCA TTTCGAGTAA ACGCGACGCG AACATTGGTG GCCGTTCGGT TGCGGTTATC 4320

TGTTAGTGCA TGAACTAAAA CTGCCACGCC ACCTGGCCCG TATCCTTCAT AAGTTACCTC 4380

GTCATAATGT TCCCCTTCAC CAGCACTACT GGCTTTTTTT ATGGCGCGCG CAATATTATC 4440

ATTGGGCATA TTGGCTGACT TAGCTTTATC GACTGCTAAA CGTAAAGcAG GATTCATTGC 4500

GGGGTCAGGG CCACCTGCTT TTGCCGCCAT ATAGATTTCC CTTGAAACTT TTTGGAAAAT 4560

TTTCCCACGT TTGGCATCTT GCGCATTTTT ACGCCCTTGA ATGTTGCTCC ATTTGCTGTG 4620

TCCTGACA 4628

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

AAATTATTGA AGTTATTACA GAnAAATTTG AGAGTAGTGG AGaAATCGAT ATATTATTTA 60

ATAGCTTTGA TTTAGTCTCA TATTGGTTGG wACAATACTT TTCAATAmAT GAACTTTCTG 120

AAAATCATGT AATATATTwr CGCATAGAAG AAATTTTAgA AAAATATTAT TTAGTGGATG 180

AAGTTAATAC TGAGGAACCC GCAATAAATA TAAGCAAGAC mGrAAACaTT ATTATATGgA 240

ATATTACTyC ACCaATTaTC mAAAAATwGG rATgGCAAAA ACAAGTAGTT ATGAACGGAg 300

CTCATTAGTG AACTCATTGA TACGCTTGAA ACTTCTGATT TGGATACTTT AGAtCGAATA 360

TTTTATCCTG AATATAAGAA AAAAATGACT GGTTTGCTTA TTGaTGATAA TGGTAAACTT 420

AGAGTTCCTA CTCACGGATT TCAACTTTTA AAAATTAGTG AGTACGAGaC GAACCAGTTG 480

TTGGATGAGT TAGGAGAATA CTTGAAGGGA CAAGGCTATG TATATGGTGC GATTCCTAAA 540

AAAGACAATC TACAATTTTG TAATAAAATA GTTGGTTTTT TGTATTCTAT TTTAGAAAGA 600

GAAGCAAATG TATTCAATAA AAATCAATTG TTAAAACTTT TAATAGCTCA AATTGAAACC 660

CTTCTTCCTG TACAATTAAG AGGAGAATCA TCCTATAATA ATGATATAGC TCTTTCAGTT 720

CAAGAGAAAG ATCGTTTTTT TGAGCAGTTA AATGAGGATA ATAGAAATTC AATAGCGACT 780

AAATTTTTGT TAGAATATGT AGTTGCATCA CCAATTACTG GAGAACAAAA TGTAGGAAAG 840

TGGGAGATTG AGCGACTTTT AGCAATATGT TCATTAATAA TTGAATGGGC ACACCGGAGT 900

GATTATTTTA AATATAATTT TGTAGATACT ACAATGAATT TTTTACAATC AAATAGAATT 960

GGTATTAAGA AGAAAGACTT TAAAAATGTA AATTCGGCAA TGTTAGCTTC TAGGAATCTT 1020

CAATTGGCAA ACTCTAATTT ACCTATTTCG GAGAACAGAA GATATGTTGA AAGAGTGAAC 1080

CAACTTTTTA AATCTAAGTT AGATAGTGCA TTTGTTGAAG CATTTGGATA TTCATATGAG 1140

GAATTTAATT TAGTGATAGG AGGTCTAAtA GATACACACA ATAATTTAGA GAAAATAGTA 1200

TGGATTGAAG AGGAAGAGGA GTTAGTTCGC AAAATATTTA ATGATTTAGA CAAAAAAATT 1260

AGTGAGATTA AAATAGTATC AGTATTAAAT TCTATTGCTC TTGTAGAAAG AGAAAAATAT 1320

TTAACTCCAC CAATAGGATT TGAAAAACTA GATATTTTCC CTTGGAGATT CAATCGTCGA 1380

TTGTCATTCA TTAGAAGACC TCTAGTAAAG TATGAAAATA AGTATATGTT TGGAATTAGG 1440

AATGTAATAC ACGCTCATAA ATATTTAATG CGACTGATTT GGGGTGGATG TTTAAAAACA 1500

AATAGTCGTA AGATGAAAGA TGTTATGTCT AAATTACGAA ATATACTAGG TGATGAATTT 1560

AATGATCGGG TAAAAAGTAT ACTCGAAACA TATCCTAACT TACAAGTAAT GAAAGGGGTA 1620

TCTAAAATTG GAAAGAAACG TATTTCTGGT GAAAATAATA ATACATTGGG CGATATAGAT 1680

GTTTTCGCTA TTAATCGAAA ACAAAAAAAA TTATTTGTTA TCGAAACCAA AGATTTTAGC 1740

TTTTCAAGAA ATCCCTATGA ATTAGCTATG GAGCAAGAAA AAGTATTTAT AGGAGATAAA 1800

GCTTTTTTAA ACAAGCACTT AAAAAGAAGT GATTGGATTC GCAAAAATTT AAAATATGTG 1860

ATTGATAATT ATGATTTAGA AGATGGAAAG TGGGAAATTG TTACTATGTT TGTTGTTTCA 1920

GAACATTTGA TAACAAAAGA CTTGGTAGAT ACTAAAGGTG TTAAATTTAT TTCATTGAAA 1980

GAGCTAGATT ATAATATGTT CCATTAATTG GAAACTAGTA AAGTTTTAAA GTTATAAAAA 2040

ATAGTATTGT TCTGATTCAC GCATATTTTT GGGTACGTCT TTAGGTACGA TGGTCTTAAA 2100

ATGTGGTGAA ATTCATTAAA ATCGTACCCG TTGAAAAGTT ACTCAGTTTA TTGCTGTTAA 2160

AAGGTTTTCT AACTCGTTCA AAATCTCTGT CACAGAACCA GGTCTTAAGA AAGCTCGTAA 2220

AGCTTCACAG TTCTCAAAAC GTTAATTATT TGGAGTCGTT GCGAACGTGT TCGCTTACGA 2280

ATCAATTACA ATGTTTCAAG ACACTTTCCA TTTTTTGGAA GGTGTCTTTT TTTATGGTAG 2340

CGACAGTGTG TGTTCTGTCA TAAACCAGTA TATAAAAATT CACATACTGA CAATATGTTT 2400

ATCTTTCTTA CCAAGAGAAT AATTGATTCC GATTTCAGCA AGTATCCTCA TTCCGAATAA 2460

CGCACTTACG CAAATGATAC ATTTCTTTTT AGTTGATTTC CTCATTTTGA TCGCCGCTAT 2520

TTCTTTTTTC TTTGAATTCA TTATACGTTT TTGGGAGATA TTTCTTTATT AACTTTTTCT 2580

CTCTTGCGTT TTGGAGGGAG TAAGTTGCGG TTTTTTGAGA GATTAGTATG TTTAAACTGA 2640

AGAGTTATTA A 2651

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1966 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

nAAGGCCCGT GTGGTTGGAA AGCCGnTACG CATTGCGAAT TAGTCGnACA AAAGGCAAAT 60

ATTTTGACGT ATATCAAAAc aATTAGGTCT GACAAwGGAA GGTGAGTCGC GTGGCTAGAA 120

ATACGTTTGA TGTAGATGAG ACTTTAGAAA AAGAATTTAA TTGGTCCCAC TATAAACGAT 180

TAGGCGCCTA TATTAAGCCT TACAAAAAAG CTGTTTTTAA AACATTATTT GTCATCATAT 240

TAGCTAATCT GGCAAGTATG TTAGGCCCTT ACTTTACTAA AATTGCGATT GACCAAGTAA 300

TTCCACAAAA GAATCTCTCG TTACTCTTGA TACTAGGGGC TATTTTCCTA TTTTCCTTGG 360

TGATTATTGG TTGGTGTATG CGTTATCGGA TATATGCCAT CACAGAAATT GGACAAGATA 420

TTTTAAAAGA TATGCGTTTT TCAATTTTTG AGCATCTACA AAAATTACCA TTTTCTTACT 480

TTGACAGTCG GCCGCATGGA AAAATCTTAA TTCGGGTGGT CAATTACATC AATACGTTAA 540

GTGATTTATT AAGTAACGGA TTGATCAATT TAATTTCTGA TTTATTTAAT GTGATTATCA 600

CCTTAATCTT CATGTTATTT ATTGATGTGA AATTAACCTT ATACAGTTTG CTGCTATTGC 660

CTGTGTTGTT CGTGATGGTT CTATTTATCC AAGGGAAACA ACGGAAAGCT TACCAAGAGC 720

TTAGCAATAA ACAATCAAAC TTAAATGCCT ATATTCATGA AAGTATTTCA GGAATTAAAA 780

TTACACAATC TTTTGCACGA GAAGATGAAA ATTTCCAGAT TTTTAACGAG GTAAGCGAAG 840

AATATCGTCA ATCCTTTATG AAAGCTGTGC GTGTCCAGTA TTTATTATGG CCAGCAGTGC 900

AAAATATATC CGTCATTACG ACTTGTTTTA TCTATTTCGT AGGAATCCGT CAATTAGGTG 960

TGTCCGTTAC CACTGGGACG CTAATTGCTT TTATCGGTTA TATCAATAAC TTTTGGAATC 1020

CAGTCATCAA TATTGGTAAC TTCTACAATT CTCTGATTAC TGCAACTGCC TATTTGGAAA 1080

GGATTTTTGA AACGATGGAT GTTGTTCCAG AAATTCAAGA TGCGCCGCAC GCTATTGAGT 1140

TGCCGCCAAT TAAAGGAACC GTCGACTTTC AGCATGTTTA TTTCCGTTAT GAAGAAGGAA 1200

AAAATATTTT GACCGATGTT AGTTTTCATA TTGAGCCAGG ACAAACAATC GCCTTGGTTG 1260

GGCCAACAGG TGCGGGTAAA ACAACAATCA TCAATTTGTT AAGTCGTTTT TATGATGTGA 1320

ATGAAGGGGC CGTTAAAATT GATGGTTATG ATGTTCGCGA TGTGaCACTC CGTTCGTTAA 1380

GAAAACAAAT GGGGGTAATG CTTCAAGATA CGTTTATTTT TTCAGGAACG ATTATTGAAA 1440

ACATTCGGTA CGGAAATTTA GCAGCCACAG AGGAAGAAGT CATCCAAGCC GCAAAAAATTG 1500

TTCGTGCGCA CGACTTTATC AAGGATTTAA AAGATGGCTA TGAAACAGTT GTGGAAGAGC 1560

GGGGTAGTAC ACTCTCGGCA GGACAACGCC AATTAATTTC ATTTGCTCGT GCTTTACTGG 1620

CAGATCCCAA AATTTTAATT TTAGACGAAG CAACCTCCAG TATTGATACA AAAACAGAAG 1680

AATTGTTACA AGAAGGACTA CAACAACTTC TGAAAGGACG GACATCGTTT ATTATTGCTC 1740

ATCGACTTTC TACCATCAAA AATAGCGATA AAATTTTCTA TATTGATGGT GGTCGTATTG 1800

TGGAAGAAGG ATCTCATGAT CAACTAATGG CAAAACATGC GTTATATCAT CATTTATATC 1860

AATCGCAATA CGACTTATTA mAGAGCTAGA TGATAAAACA GAGAAAATTC TTAGTTGAAT 1920

CGTTCTCTGn nTTTCTGTAT CGTAACCTTA ACAAAGGnnA AAATGG 1966

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

CCTTCTATAA ATATATAGTC AAACTTAAAg TTcTGaCCTG CTTGTTnnaG TTAGAAATAT 60

AACGCAACTA GCTTGTGTCA TATTCAACAT ACCATGACTG TACTCGAAGA ACTGTTTAAA 120

AAGATTTGGT CTACTCTTTA ACCCAAGCTT CCGTTTCAAC TTCTCCaTAA TTGCTCGCCA 180

CAATGTATTC ATAAGGTAGG CTGTCTATAA TGTTAGGAAT ATCGCGTACT TTTATTACTT 240

CCGTTCCATT AAATTTTGTA GAAACAATAA AGAATTCTAT TTCTTCATTG TAATCATTAA 300

GAAGTTGTAA CATATCTTTA TCTTTACTAA AAACATAGTG ATCAAAAATT TGGGGTTCTC 360

CATGATTGAC ATCTGATACA GAGATTACTT CAGCCATTGA TAATGCAATT TCTTCATTGT 420

ATTCTATTAA AAATATTCCA TGAGCTTTAT TACCCTTGTA AATTTTTAAA TTTTGAATAT 480

GAGTATCTAT GTTTTTCTTA CACGACTTTA ATAGGTTTTC CTTTAAATGA TTATTAGAAT 540

ACGTTAATCT ATGTCTAGCA AAAGTATCTT CATCGATCAG TCCTTCTTTT ATCTCATTAC 600

TTCGACTCTC GAACATTCTT TGTCTTTTTA TATGCTCGGC TCCTTTTTTC AAAGTTCTAC 660

ATTCTTGTTT TGTTTGTTGT TCTTCATTAT TCATTTTCTT AAACTATTCT CCTGTCTTTT 720

TTTAATATTA TGCTTTTACT TTATTTTGCA CGATAATCTT ACTCCACAAC AAATTGTTAA 780

ATTAGCATTA TTAAATGTAA AAATTGAGTA TACTCATATT TTACACAAAT GACGTATGCC 840

CAACTTGAAT GTCCTACTGT TTACCTAGTA ACAATTGGAA TATGAAAAAr AACCAACACG 900

GCATACCCTG TTGGkTCTTT TAGTTAATAT ATTTTAATAG AAAATTTATT TATTACATCA 960

TGAAATACTG TATAAAAATC GTAGCAAGCA CACATCACTT TTTTTAGCCT ATCATTTTAC 1020

GTCGACAGTC TAGCTGGTTT CTTATCTCAA TTTTGAACCC ATTGTTTTTC TGCTATAATC 1080

ATAGTTGACG TTTGATCTGA ATAATTTTTw ATGATATTGy TAAATTyTGT CATTGATTGG 1140

CTTAyTTCAT CATCAGCACT TTTTGAkCAT TTAAAATTTA GATATTTAAT TCTAGATCTA 1200

CTAATTGAGT CTAGATTTTT TAAATTAATT TTTTTAAAAG TTTGTTTATT rTCTACAGAT 1260

AAGATATATT CTATCATATA CAAATTAGCT AAATAAAAAT TCTGTAAATA ACTTTTATTA 1320

TTCAGTATCT TGTCTTCTTT ACTAAGTATT GGGTATATTA GTTTTAATTT CCTATTATTT 1380

TTGTCTATTA AATACTCATA TATAACATAC AGTAAGAATG TATTTAGCAC ATATAATGGT 1440

AATTCTTTAT TTTTTTTTAT TATTTTGCAT ACCTCATTGC TATTTAAGAA AGTTGACTGA 1500

TTATATTTAT TAAGTAAGCT ATTTGATACA ATATAATACA TTTCGAAAAT ATAATCCTTA 1560

GTAACTAATT TATATATATT GTATCCATCA TTCATAAACC CGTTAAAATT AAAAGGAACT 1620

ACAGTAATCA AGAATATTGA AAAATTAAAT AAAGAAAAAT ATTGAAAAAA GTCAATTTTT 1680

ACAAAAAAGG TTAATGTAAA AAAAAAGACT AAATATTGGT CCTCCGGTTA ACAACCTCAG 1740

AATTTTCTTA TTATTAAACG TAGTTGGCTT ATATCTAAAT AATCCACCAA AAAATCCCCA 1800

CTGTGTATTT AATCTAAyCT TAAACTGwTT TTCCCACGAA AGTTTTATAA ACCCAAATAT 1860

TAATGACTCT GGTCTAACTT TATTAAATAA TCCAAAArCT AAATGACCTA ACTCATGTAC 1920

AAAGATAGAC AATAACAAGG AAAAGTATGC AGTAGACACT AAATTTAATT CAAAAACAAG 1980

AGTAAAGATT ACGAGAAGTA ACGTAAAGAT CATCGGAGAT ATAAATTTCA TCTATTTTAT 2040

TCTCACCTCT TTGTATTTAA GCATGCTATT TTTATCTATA AAAGAATCAG CATTTTCAAA 2100

TAAAGTATTT AATACTTCAT TTGAATCTTT AGAATTATCT ACATTCTTTG ACATAATAGC 2160

TGCTAAAGtG CGCTTACTTC TGGAGTTGCT AAACTTGTTC CAAAAGAAAG TGTATwACCA 2220

TCTGGgAAAG TCAGCAGCTT TGCCTAGTGG AGAAACTAGC GATGTAGGGT AATAAGTCAT 2280

CATCATTtCA CGAGCATCAA TTTGtCCTGT TAwTtTGtAA TkGTCACCAT ATCCTCCTGc 2340

AGGACCATAT ATwGAgTrCA TTAGACCCAT AATTAGAATA GTCAGCAATA TCACCACTCT 2400

TTTTTGTCGC TCCGACGGTA ATTACAGACT CTAGTCCTCC TGGTATATGT TTTTCATTAC 2460

CAGTGCTTAT ATCACGCGAC TCATTTCCTG CTGATGCAAC AATTAGAATG TTATTTTTTC 2520

TTGCATAGTT AACAGCTTTT CTGAATGCTT CTACAGTAAA TCTTTCGTCG TCTATTTCCA 2580

TATTTTTATA TGATCCAAGA CTCACATTTA TTATATCTAC TTGATCATTT GTAGCATCAA 2640

CTATAGCTTT AAGCATATTT ATAGAGTTTC CATCTGTCCC ATCCATCACC TTATAAGAAT 2700

TTAAATTTAC TCTTGGAGGC AATCGTGTCT ATTACTCCAG CAACTTGTGT ACCATGACCA 2760

TATTCATCTA ACTCAATATC ATTAACATAn GTTTTTTAAT CTTAnGnTA 2809

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

TTAATATCTn TCTTATTTAT TGACATAAAT TTATTACCCn TCGCAAGTAC AGTTAGCGTC 60

TCAAGAACAT TTTCTTTTAA TATTAATGAA CTTTTTATAG AGTCTTCTAG AAAAACTTTG 120

GCTTTTATTT CTTGATATTG TGTATTTTGA AGCAGCTCTC CAGATAACAT CATTGTATCA 180

ATAATAAATG TATAGATAAC TGGATCAATT TTAGTACTAA TTTCTTTTTC ATTTTGTAGT 240

TCTTTAACAG TACTCCAGTA AACGTCAAAA AAACTTCTAT TATTATAGAA TTGTTTAACC 300

CATTCAGTTA TCATTTTTTT ATCACTAGGA ATTTTATTAT AAAATATGAT GAGTTCAGGA 360

TGTTGCTTTC CTAATTTTAA AATCATTTCA AACATTATTT CTAAACGATC TTTTAGTTTT 420

AAAGGAGCGT CGTTTATAGT ACTAACaTAT TCATCTAAAA TAACAAAAAC GTGTTCTATC 480

GCGACTGTTA ACATACCTTC TTTATTGTTG AAATACTGAT ATAATGATCC TACACTTAAA 540

TCTGCTTTAC TGGCAATTTT ACGAACAGAA GTTGCTTCAT AACCAACTCT CCCAAATTCA 600

TCTAAGATGT AGCATAAAAT AAGTTGCTTT TTTTCTAATT TTAGTCGATT AAATAATTCA 660

GTTGcTGTTT TATACATAAC TATCTCCTCA AAAAAGATAT TkTAATTTAG TaTACCATAT 720

TTATTATAtA AAAACGACCG CTCaTTTTTT TGCGATCCTT AATTGAAtCT TrGcTTGayA 780

AAAATTAAAT TACATATAAA ACAGTTAACC TCTGTAAGAG AAAATTGCCA AACTATCTAC 840

CTTCTCAAAA GTCTATTATC CTTTATCAAA AATAGCTATA TATTTATACT TCTTTATAGA 900

AGAATAGTAG AAGTAATAGC CTAACTGATA TGATAGATTT AAATGACTAA ATTTGTAGAT 960

TGCGTCATTT TTGCGCAATT TTAAGTCTGC TAGTCCATCA ACCAGTTTTT CCGTATATTC 1020

CGTATATAAG GATACTATTA CCTTAATAAT TATATTTTTA GAGATTTTAA TATACAAAAT 1080

GGAATGGTAA CGTTCTTTTT GACAAAAATT ATAAGGTGTT GTGAATGCCG TGATGTTATT 1140

GCTCTGATTG CTTTTGACAA TGAGCCTCAT CGGATCTGAT TCTCTCCGGC AGAAGCGCAA 1200

TCATTTAATT ACGCTGCCTC TCCAAAGATA TCAGACCCGA GCTCATTATC AAGGGCTCGC 1260

TTTGCCAATC TCTGTTGTCG AAATTGTATC GGTGTTTCAT ACCCAATGTC CCATGCAATC 1320

GCAGGTAGTT CCACCAATGC ACATAATCAA ACAATTCTAG GCGTAGTTGT GCCAATGTTT 1380

TAAATTGGTA TTGATGCACG AATTCTACTT TGACAAATTT ATACGTtGAT TCCGCAACAG 1440

CGTTATCATA CGGAAAGCCT TTCTTACTCA AAGAGCGCGT GATCCCAAAC CCATTTAAAA 1500

TATCATCGAT GGATTGATTA TCAAATTTTT TTCCATGATC TGCATGAAAA AGTTTGACGT 1560

CTGTTAAAGG ATAGGGAATC CGACCAAAGG CTTCTTTTAC CAATGCGGTA TCTTTTTTTC 1620

TCACCACAAG AATAACCGAT GATTTCTCGA TTAAATAAAT CAAGAATTAA GAAGATATAA 1680

TGCCATTTTT TCCCTACGCG AACATAGGTA AGATCGGTGA CAATAGCCTC CAATGACCGT 1740

TTCTTGTGTA AATGTCCAAT CTAATACAAT TTCAATACAT TCGTTGTCTC CGCTTCATTA 1800

CAAGCTGTTC GTTGGGCATT AAAATGAGCG ATCGTATAGG TGAATTTCAA CCTGCGTTGT 1860

TTCATGATCC GACCGATTCT GCGACGACTG ATTTGAAGCG CACGCTTGGC TAAGTATTTC 1920

TTTAATTTCG GGGTGCCGTA AGCTTTTCGG TTACGGATAA ATTCTTCGTG AATAAGTTCT 1980

TTCAGATCTT CTTCGCTTTT AATGGGTGTT GCCTGATTAA TAATAGGTCT GAAGAGAAAT 2040

CTTTAAGATT TTATACAGCG CTGATATCGA GTATTTGTGT TTGTTGACAT CAATCACTTG 2100

TCTTTTCGTC CGAATATCAA CGACGCTTGC TTTAAAATAT CATTCTCCAT TTCAAGCTAC 2160

TTATTTTTCT TTCGTAGTGC GATCAATTCT ACTTATTCCG GGGTTAAGGT ATCTTTTTTC 2220

TTGAACGATT CTGTTGAATG TGTTTGCTTC ACCCATTTAT CGAAGGAAGA AGGCGTAAGC 2280

TCATGTTCTC GAATGATTTC TACACGCGGC TTGCCTGCAA GGTAAAGATC GACGACGTGT 2340

TGTTTGAATT CTTTTGAATA GGTTCTTCGT TGACGTCTTG ACATAAAAAA TCCTCCAGTG 2400

TGTTTTTTAT TATTCTACAC ATCTTATTTT TTCTTTCTAG TGTAGCCGAT TCAGAAAAAG 2460

AACCGATAGT TAATTCGACC ATATTCATTA TAGTTAAAGA CATGTAAATG AAATGATCTC 2520

TCAAAGAATA TGTATTCCAT TTTTCTCTTA ATGAGAACTT ACTAAATAAA AATTGACAGA 2580

TTGTCTCATT GCATTACTTT ATTGTACATC TTAAAATTAT CTGCCTTATT TTGTTTGACC 2640

ATTCACTTTT TTTTTAGATC CTAAATATAC TTTTATCCGT TCATAAGAGC AGCCTGAATA 2700

AACACAACCT ACAATAATAC CCAAAACTAC TGCTCCAATA AGATTGTAGA AAAAGCCAAT 2760

TTTTTTTACA AATGTTTGAT AAAAATTTGT CATTATTATC ATCATGACTA CACTGTTACA 2820

CAAGTCATAC ATAAAAAATA ATTTAAGAAA GAGAAAAGAG ATCATTCCTT TTTGATCAAT 2880

TCTTCTATAA AAATTATATA TCCAATACAA ATAAAGAAAC ATACTTCCTA CCAATAAAAG 2940

TAATTTTAGT ACAAACCACC ACGaAAAATG TGGATAGAAT AAAAAATCAA TCAAACATAA 3000

TAACGGAATA AAATAAAGGA ATTGATGAGA GTGGGTTAGA TATTTCCAAA AGGTTTCTTG 3060

TTTTAATCGT TCCATTTGTT GATAAAATTT TTGGTCATCT ATTATTTCCA TTTATTTACT 3120

CCTTATCTTA ATATCATACA TAGCAACATG TACAACCTTA TAAAAATAAA TAATTTACTT 3180

ATTTATTTTC ATCGcAATCG ACATTCATTA GTAGATATGT TkGTTAGTAT TAAAAGAACT 3240

TGTGATTATT AAATTAGTAA ATGTTTTATC ATATAGAACT TATTGATGGT TATTAAAAAA 3300

AAGCTTCTTT TCTATAATTT AAACACATCT ATAGGTAGAT AGATATAGAA ATTTATACAA 3360

CATTCAAGTA AGAATTTATT TATTAAAAAT GTGGTCTTTC TAGTAAAAGA AACAAAAAAC 3420

CAGTTAAGCA TTCTATCTAA CTGGTTTTTT ACTAAATTTC AGTTGTATCT TTCTATATTA 3480

ATTAAGTTGT TATTTTACGC GAGGTTCAGT TTCTTCTTTT ACGTTTTGTA CACCATCACT 3540

TACTTTTTCA CTTGTACGCC TAAAGCTTCT TTTGATTTTT CAAATtGTTT kGAAGCAAAT 3600

TCTCCAGTAG CAGAAGCTGC ATCGGAAAGA TGATCTTGTA GAGTAACTGA ATCATTTTCA 3660

TGTTGTTCTT TCGTTTTTAC ATCTACGACG TTTACATTAA yCyCAATTAC ATCTAGGCCA 3720

GTCATTTTCT TAACTTCATT TGAAATAACT TGCTTCATTT TATCATAAAT TGTAGTTACA 3780

TCTTTACCAT ATTCAGCCAC TATTGAAAGA TCTACTGCGA CTTGTTTTTT TCCTACTTCA 3840

ACATCCACTC CAGAAGTTGT GTTATCCGTA TTTACTAGTT TTCCAGCTAT ATTTGAGAAG 3900

AAGCCTCCAT CAATCGTTAG AAGACCATCA ATCTCATCTA ATGCAATACC AATTATTTTT 3960

TGAATTACTT TATCTTCAAA AAATAGTTCT CCTTTAATAG TCTCAAAAGT TTTTGACATG 4020

TCCkTTTTTT TGAkCTCTGT TTTTGTATTA TTTGTTTTGT TTTCCATTAT TTTTCCTCCT 4080

AAAAATATAA AATTTATTTT TACCGTAAAA ACGGTTATTA ACTAATTTTG TTTGTCAAAA 4140

AAACCAACA 4149

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

CCTCTATGGA ATATTTTTTT CCTCAAGAAA TCATTTTTTT ATAAAAACCA TCCTTAAATA 60

TGATACCAGT GGCTGGCTTT ATTTTAAATA GACAAAAAAG AGTATGAGAC AAAAATCACT 120

TTAGATTTTT GTCTCATACT CAAAATCTGA AAAACAGTTC GATCCCGACT TCTTCGTTTC 180

TATTGTTTGG TTCTGGCAAC AACTAACAAG TAACTAATTT TACGAAATCC ATGACAATAT 240

TCATTATTGA GCATATTCAA TCCTTCTACT AATTTTCGTA TAAGATAAAT ATTGATTGAA 300

TGTGTTGACA CAACGAAAGG CCGTCCTATT CGCATATTGA TCATAATAAC GCTTGGTATA 360

CCACTGAAAT TCTTTCGTCC AAGGTTTGAC ATGGCCAGTA AAGTGGATAA TGGATGGTGC 420

TCTTCTCGTT TCTTCATATT GTTTTTCTCC ATAAATAGTT GGATGTTTTT TCGCTTTTGA 480

CAGAATATAA CCTTGGGCGT TCCACTTAGG ATGCAACAGG GTCCAACGGT CGTGTAAAAC 540

CGCATTCAAT GCATCTTGAT CATGGAAACG TAATTTATCT GGATTTTCTT CAATAAATCT 600

TAAGACTTTA GTGGTTACAT CTAAATTCAA CCATTTTTTA ACATCGATTA GCAACAAGCC 660

TGAGTTAAAA TAACACATAG ATTCTGCAGG AATCGCCATT TTTTCCaAAC GTTGATGGAA 720

CCCTGCATCT TCCaCAGCGG CGATGATATT TTCACCTAAA TCAACTGTCC ATAATTTTGC 780

GACATCATCT AAGGCAATCA TGTCACAATC CATATACAAC AGCCGTTCGA TCTGGCTTCC 840

TCTAAACAGC TCTGGAATAG CAATCCTGTA GTAAGCTGTT TTGGGAATTC GTTCACTGGT 900

TACAACATTT TTGAAAAAAt GGGGGTTGAT TTTTAAAAAT GTTAACTCTG CATTGATTTG 960

GGTATGTTTA ATCGTAAAAT ACAGTAGTTG CTTGCTTTCA AAATTGATAT TGTCATCAAT 1020

CACATAAAAA TGAACAGCTG CCGCTGAAGG ACTATTTTCT AAAATTGAAA CAAACATAGC 1080

AGCAAGATGC GGTACAAAGT TGGTATTGCA ACAGGAGACA ATCGCTAATT CTTTTCTATT 1140

TTCCATTTCT TGCACCTACT TTCTTTAACT TGTTTAGATA AAGAGCTGTA TAAGGATGAT 1200

TTTCTAACGT ATTCCAAGGT TTATCGTGTC CAGTAAAATG AATAATCGCT GGCTCTTGAT 1260

TTCCCGCTGT ATATAATTTT TGATAGGCTA CATTAGGCGC TTCATGACGA TTAAAAACTA 1320

AAGACGTCTG CATATTCCAT CTTGGTTCTA GAGCTAGCCA ATCTTCATAA AGAACAGCGT 1380

TTAAAGCATC TTGATCATGA TAAACTATGC GGTCCCCATT TTCTTCTAGA TACTGAATTG 1440

TTTTTTGGGT GATTGCTTTC TCGTTCCATC GGTCAATATC AATAATCATA ACTCCTGAAT 1500

TAAAATAATA ATGCGGAGGA AkGGATGCCC AAACGTTCAA nGCATAAGCT GACCAGGATC 1560

ATAACCGCGC CAATCGTTGG TTCAC 1585

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

CGAGCTCGGC CCCCCGATGT nAAAGTGGGC GACACTGTTA AAGTGAAATT TAGTGTTGAT 60

GCTTGGGCnA CTGGCGAAAG CTATTCCGCA ATGGGTAAAA GGAAACAGCT ATAAAGTACA 120

AGAAGTAACT GAGAGCAGAG TATTGCTTGA AGGTATCTTG TCATGGATCA GCAAAGGCAA 180

TATTGAATTA TTGCCAGATG CGGCAACTGT TCCTGATAAA CAACCAGAAG CGACTCATGT 240

GGTACAATAC GGCGAAACAT TATCAAGCAT TGCTTATCAA TACGGAACAA ACTATCAAAG 300

ATTGGCTGCA TTAAATGGAT TGACAAATCa AATCTTATTT ACCCTGGCCA AATTTTGAAA 360

GTAAATGGAT CAGTAGTAAG CAACATTTAC ACAGTTCAAT ACGGTGATAA TTTATCAAGT 420

wTTGCAGCTw AGCTTGGTAC GACTTATCAA aCCTTAgCTG CATTAAACGG ATTAGCAAAT 480

CCTAACTTGA TTTATTCTGG TCmAACaTtG AGCTATtGGA TTTTTkGCCA AAaTCGGkTG 540

aAATTTAGAG GtACCTCATT tACaATAGAG TTACCTTTTC ATATTATGAC TCTTTTCGAT 600

TTAGAAAAGA GGTGCTCCTA TCTTATGcCc AAGTCCTTAG GTAGGAGCAT TTTAATTTTA 660

CTCATACGTA GCTTAGTTTA AAGCTATTGT ATTACATAAG AAAACACCTA CCACAGATGC 720

ACGTACTTCC CCAAGCAGTT GTCTGTGCGG TAGGTGTTTT TTTAGATTTT ACTTGTTAAT 780

CATAACCGAT TTTCTTTTTT TATAACAAGG TTAAGCTTGA ATTTATGAAA AGGATAATGT 840

GTACGGAATT TATCCTAATA AAAAATAGAA TTAGCCTATT TCTAAGCTAC TATTACTTGA 900

GAACAGTTTC CTTTTAAATA AGTGGAAAAT TGTAGTACAG CTACTTTAGC GATATTCCTT 960

AATATCCCAG TTCTAATTTA AAGTCAAACA CAATTTTGTT AATAAGTTGT GAATAATTTT 1020

ATTGGTTGAA TTAACAAAAC TAATTTGCTA GAATAATAAA GCAATTACTT GTAGTAAAAG 1080

ACTACAGGsC CCTTGTATCA TAATTGTGCA aGGGGGTTTT TGTATCGTAT ATTTATATTT 1140

CATGTCTAGA GTAGATGGAT TATAACCTTT TTATAGTATT GGTcCCATCA TGtTTTAATA 1200

CACTCATTtG CTTTATAGGA AaTAGTATGG tATTATAAAT AAGTAATCAA TTTTGACATG 1260

TAACGAGAGC GCTATACATA AGACTATAAT TCTCCTTTTG CTTATCAAAC ATTTTTTGCA 1320

ACAAATCGCA TACAGGGTAT GCACAAGGAG GAAACATAyA TGAACAACGG TACAGTAAAG 1380

TGGTTTAACT CAGACAAAGG TTTTGGATTT ATTACAGGTG AAGATGGCAA TGACGTATTT 1440

GCTCATTTTT CAGCAATTCA AGCGGATGGT TTTAAGTCAT TAGAAGAAGG ACAAGCAGTA 1500

ACTTTTGATA TTGAAGAAGG ACAGCGCGGT ATGCAAGCTG TTAATATTTT TAAAGCATAA 1560

TAAAGGTTTT GGTAAAACGT TCCAATTTAA TTGGAACGTT TTTTTTATAA GATTAAATTG 1620

ATAGGCTCTG AATGTTGAAA GCGAAAGGAG ATCATCATAT GGGATTTGGA AAATGGAAAG 1680

AAaTTATACC ATCAGATAAA AGTAAACAGT TTGAAGAAGG ACAGAAAGTA TCATTTATTT 1740

ACAGAAAgAA tTAGAgGkaT AATAGCgTTT TATTAATTAA TcAGCAGaAT TAATATTATA 1800

GACAGTTCTA AGCCAGAAAA CnnAAAAGAn AAAACAGT 1838

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GGATTTGGGG TCTTAAGCGT TCTCTATTTT GTGGAACCCT TTGAGAACAA TCTCTTGGTA 60

TTGTATGTCG GATCGGCTGT TTTAGTGACG ATTTTAGAAT ATGTCACTAG TTATGGCTTG 120

GAAAAATTGT TCCATGCCTC TTGGTGGGAT TATCATGATG TACCTTTTAA TTTAAACGGT 180

CGCGTGGCTT TACCGGTTTC TCTTTTTTGG GGATTGGGGT GTGTCTTGAT TGTCAAAGTT 240

ATTCAACCAG AAATCGCCAA AGTTGTCAGC TTTTTACAAG CAACCTTTGG CAACTACTTA 300

GCACTTTGCA TAGTGATTGT AATGGGGCTT GACTTAATTT ATACGTTGCT GAACATGCAA 360

GGTTTCAAAA AACTTATTAC CGAGATGGGC CAAACGTTGG AAACGAACCA ACAAGAATTT 420

AAGCAACGGT TGAACACAAA AATGGAAATC GCTACAGCTG ATTGGCAGAA GTTAAAAGAA 480

CGAACCAAAA AAGAGCATTT CCAAAATCGG TTAAATTTCC AACAACGTCG TTTTATTAAC 540

AATTACCCAA AACTAACTTT AAAAAACATT AAAAATTCCA AAGAAGTTCG GCATCTCTTA 600

GAAGATTTGA AGAAAAAGGG CCAATAATTA ACAAAAAATA TTACAAAATA TTTCAATCAA 660

TGGTCTAATG GGATGAAAAA AAGAAAAATC GTCAAAAGCT AGTTTTTAAk GCGTCTTAAG 720

AAATTCTTAA AGAATTGAGA TAGAAATGGA CTAATGAATA AACGCAGGAT AAAAAAAGAG 780

TTGCATTTAA ATTGTAACAA ATTGTAACAT AATTGAAATA AAACAAGCCC TCCTGACTAG 840

TATAATGAGT AGGTGTTTTA GATAAGTTAG GAAAGGTGTT GGATTTAGTG AAGGTTAAAA 900

AGTTGATACC ATTTTTAACA ACAATGATGC TTATCAATTT TGGACTTCCA GTCGCTGCGG 960

CAGCAGAATC ACTTGATTCG TTGCAAGAAA AAGAAGCGCA AgCGrAACAA TCTGGGGAGT 1020

TAATTAGTAA AGAaATCAAT TCAGCCTTAG ACGATGTAAA TGCTAAATAT GCGGAAATCG 1080

AACGTTTAAA AACGCAAATT TCAAAAGCGG AAGATACGTT GAAAACTTCG AAAGAGGAAA 1140

TAGAmAAmAC AGAArAAAAT ATTTCTCGTC GTAAAGAAGC TGTTGGCGAT CGTaTGwaGG 1200

ATaTTCAATT AAaTGGCGAC CAAcGTACTT GGCcAgCCT 1239

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2025 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TTGAAAAATC CCAAATTAAA GTGGAACCAG CAGGCTTTGA CTGCGACTAT GTGGACATCC 60

AATGGTGATT AAACTGGGTC GCTACGGAAA ATTTTATGCA TGTAGTAATT TCCCAGATTG 120

TCGGAATACA AAAGCGATCG TTAAAGrAAT TGGCGTkACg TGTCCTGTGT GTCACGAAGG 180

ACAAGTTATC GAACGCAAAT CAAAGAAAAA TCGGATTTTC TATGGCTGTA GTCGGTACCC 240

AGAGTGTGAC TTCACTTCTT GGGACAAmCC aGTAGGCCGA CCATGTCCmA AATGTGGGCA 300

aTATTTAGTA GAGAAAAAAG TTAAAgGCGG CAAACAAGTC GTTkGTATCa ATGGcGATTA 360

TGAAGAAAAC GTCCAAAAtT AAGAAAAATT GAGACCGAAG AATTTACTTC GGTCTTCTCT 420

TTTAGTAAAA TGAATTGAGT TTGTAAGAGA CAGCTCTTAA CTTCTTGATA TAGAAAGGAA 480

TTTTTATACA TGACAAAAAA AGTCACAATT ATTGGTGCCG GTTTAGCCGG AmGTGAAGCG 540

GCATGGCAAG TGGCCAATGC TGGGGTACCA GTTGATTTAT ATGAAATGCG CCCTGTCAAA 600

AAGACACCAG CGCATCAAAC AGAAAATTTT GCAGAGTTAG TTTGTTCTAA TTCATTACGT 660

GGAaATAGTT TAACCAATGC GGTAGGTGTT TTGAAAGAAG AAATGCGCCG TTTAAATTCA 720

ATCATTATTG GTAGTGCAGA TCAAACCGCT GTACCAGCTG GCGGCGCCTT AGCAGTTGAC 780

CGTGATTCTT TTTCTGAAAC AATCACTGAA AAAATTAAAA GTCATCCATT AATTACAATC 840

AAAAATGAAG AGATCACCGA TATTCCGGAA GGGATTGTAA TTATTGCAAC GGGTCCTTTA 900

ACCTCTGAAA GCTTATCTCA AAAAATTCAA GAATTTAATG GTTCTGAAGG CTTTTATTTT 960

TACGATGCAG CAGCACCAAT TATTGATAAA TCAACAATTG ACATGGATAA AGTTTATTTA 1020

AAATCTCGTT ATAACAAGGG GGAAGCGGCT TACTTAAACT GTCCGATGAC TGAAGAAGAA 1080

TTCAATGCTT TTCATGAAGC ACTAGTCAAT GCAGAAGTGG TTCCTTTACG CACGTTTGAA 1140

AAAGAGAAGT TTTTCGAAGG CTGTATGCCC ATCGAAGTAA TGGCGCAACG TGGCATTAAA 1200

ACCATGTTGT tTGGCCCAAT GaAACCTGTC GGACTAGAAG ACCCTAAAAC AGGTAAACGC 1260

CCTTATGCTG TAATTCAATT ACGTCAAGAC AATGCTGCAG CTTCTTTATA CAATATTGTT 1320

GGTTTCCAAA CGCATTTAAA ATGGGGCGAA CAAAAACGAG TATTCCGTAT GATTCCGGGA 1380

TTAGAAAATG CTGAATTTGT TCGCTATGGC GTCATGCATC GTAATAGTTT TATGAATTCT 1440

CCAGAGTTGC TAAAACCAAC CTACCAATCA AAAAAACGTG ACGACCTGTT TTTTGCTGGA 1500

CAAATGACTG GTGTTGAAGG ATATGTTGAA AGCGCGGCAA GTGGTTTACT CGCAGGTATT 1560

AACGCAGCTC GTCTTGCCAA AGGGGAAGAG CCGATTGAAT TCCCTCGCGA AACGACTTTA 1620

GGAAGTATGG CTTATTATAT TACACATGCA GAAGGCAAAC ATTTCCAACC AATGAATGCA 1680

AACTTTGGgC TTTTCCCAGA GTTACCTGAA CGAATTCGTG ACAAAAAAGA ACGCTATGAA 1740

GCAATTGCTA ATCGGGCCTT AGATGTTCAA GCTCAAGTTA TCCAATCTTT AGATTAAATT 1800

AGAAAAAATA TGAGAAAAGA CCGAGCATCA TTGCTAAGAA ATGCGATGAT ACTCAGTCTT 1860

TTAATTTTAG AAAAAAATAA CAAAAGCTAA nGAATGGTAA AATTGTGACC ATATTTAGAA 1920

ATATTGGnTA ATTCCTGACC ACCTTAATTG TCTTTTGAAA AAnGGTTATG CCTAAAGTTA 1980

CTTTGTAATC GAATGGGGAG GGCTATCACC TGGGAGGAAA AGAAT 2025

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

CATCATGGAA TGGACTGGGG TTCATTAGTA TTAGGAATTC TATTTGTTCT GACTGCATTA 60

ATTTCTTTCC AAAATCCTGC CGGTAATTTA ATTGCCATTG TGATGGTTTT TGCGATTTTT 120

GCTATTATTA AAGGGATTTT CGAAATTTTT GTACGTAATC GTATGAAAGA ATTGCTAGGC 180

TACAAAGCTT ATGCACCAAT CATCTTAGGG ATTATTGATA TCCTCATTGG TGTTTACTTA 240

TTGTTTAACT TAAATATTGG TGTCGCTGTG TTACCATTkG TTTTTGCAAT TTGGTTTTTA 300

TTCGACTCAA TTTTCGGCTT ATTTACTTTA GATTTTGCTA AACGAGTAAG CACAGGTTAC 360

TTCTGGTTCA CATTAATTGT TGACGTTTTA GGGATTATCT TAGGTGTAAT GTTATTATTT 420

AATCCATTGT CTTCAGCACT AACTTTAAGC TTCTTAGTTG GCTTCTACTT TATGATGTTT 480

GGTATTAGTA ATATTGTATA TGCTTTTAGA TAAAAGAAGT AAAAAAACAG GTTTTCCGAA 540

AAGGAAAACC TGTTTTTTTT TAATAACGAC GGTGGCAGTT GCCATTATTT CCCGAAATTG 600

TTCGAACAAG CCACACGATA ATCGCTACGG GAACTAAAAT TTTTACTGCT AGCCACAATA 660

AGCTTCCCAC GATACCGACA ACGGCACTAA AGAGTGAACC GACAACTAAA AATAAAAgGA 720

CCACTAAAAG AATATTTATA AACATTGGTC GTTGATTATT CATACGTACT ACCTCCAAAT 780

TTTTCCTGTT TTCTATATAC AGAGTATAGC AAGAACGCGC aACAAGCACC TCCATCGGAA 840

GGCTGATTTT TTTCTCTGGC GAATGATGGA GCCGCTGTTG GTTATTTTGG ACTTTCTTAT 900

TGArATAATC AGAATATTCT GGTGTATATT ATAAAAAATG ATTTAAAGTG AGGGATTGGA 960

TGTCGACTGA GGGATTAATC GCTTTgTTAG AAAAGAAACG AAATCATTTA AGTAAAATTG 1020

AAAATCAAGT ACTGGATTAT ATTTTGACGC ATATGACGGA AATTAGTTCA CAAACCATTT 1080

ATGAGGTGGC GCAGGCGTTG TTTGTCTCAA CAGCCACTAT TTCTCGGACA GCAAAACACT 1140

TAGGTTATCG AGGCTTCCAA GAATTAAAAT ACGCAATCGT CCAATCGGTG CAGAGCGAGA 1200

GCACAGAAAG CGATAGTCGT AGTTTTCaAG CTATTaCGCA ACAGTTGATT GCCaATGTGC 1260

aAGATAGTTT TCAACAAATG GATGAAGCCA AAGTCGCGGA AATGCTTAAA ATGATTGAGC 1320

GTGCGAATAC GATTGAAGTG TTCGGTGTTG GTGGCAGTTT TCCTATTTGT ACTGATTTTG 1380

CACGAAAGCT AACATTTTTA GGAAAAAAAG CCTATGCACG ATCTGATTGG GATGAACAAG 1440

CGGCAGCAGT TAAGAATCTG GATGGACAGG ATTTAGCCAT TTTTGTCAGT TATACAGGAG 1500

AAACTAAGGG GATTTTAGCG TATGCACGTG TAGCGCAGGA ACAGCAAGTG CCGATGATTA 1560

GTTTGATTTC GACTAAAGGA AGCACCTTGG AAAAATTGTC GACGACGACG TTATTTGCCA 1620

AAGGGACGAC ACGTTATCAT CAGCGCGTGG ATTTAAGTTC AAGAATTGCT GTCATTTGTT 1680

TGTTCGATAC GGTTTTATTA ATGTACGCAG AGGCAAAGCA ACCGCGGTAA TTTTATGCAA 1740

CACCATACTA AATGATGTAA GGGGATACAG AAAGAGTGTA GCCTCTTTTT TCTTTGTTTT 1800

GGGCTAGTTA TAATGAGGGC AATGAATGTA AACGCAATCA TTTTTAGTTT TGTAAAGAAT 1860

GAATGGAGGA GTTAAGAAAT GGCAGTAAAG AAAAAGAAAG CGACTTTCTG GGAGTTTTTC 1920

CAAGGATTAG GTAAAACGTT TATGTTGCCA GTGGCTTTAT TAGCTTTTAT GGGGATTTTG 1980

TTGGGATTAG GAAGTTCTTT TTCCAGTGAA TCCATGATTG AAACGATCCC GTTTTTAGGA 2040

AAGCCCGCAG TGAAAATTAT TTTCCAATTT ATGTCGACAA TTGGTGGTTT TGCGTTTGCC 2100

TATTTACCTG TCATGTTTGC AATGGCCATT CCGTTGGGGT TAGTTCGGAA AGAAAAAGGA 2160

ATTGCTGCGT TTTCAGGTTT CGTAGGCTAT ACGGTGATGA ATTTAGCGAT TAATTTCTAT 2220

TTAGTGCAGA CGAATCGCCT CGTGGATCCT GAGCAGTTGC GGGAAGCCGG CCAAGGAATG 2280

GTTTTTGGGA TTCAAACGAT TGAAATGGGT GTTCTTGGTG GAATTATCGC TGGGCTTATT 2340

GTCTATAAGT TGCATAATCG ATTTTATACG GTGCAACTAC CAGATAGTTT TGCCTTCTTT 2400

TCTGGCGCAC GGTTTGTGCC AATTATTACT TCATTAGTAA TGGCATTCGT GGGCTTAGTA 2460

ATTCCGTTAG TTTGGCCACT TTTCGCGCTA ATGATTATGG CGATTGGCCA ACTTATCCAA 2520

CGTTCTGGTA TTTTTGGGCC TTTTCTGTTT GGTTCAGGGG AACGTCTACT GTTACCGTTT 2580

GGGTTGCATC ATATTTTGGT TTCCATGATT CGTTTTACTG AAGCAGGGGG TTCAGCGGTG 2640

GTGGCTGGCA AAGAAGTGTT TGGCGCGTTA AATATTTTCT ATGCAGAATT GCAAAATAAT 2700

TTACCGATTT CACCAAGCGC AACAGCTTTC TTGTCACAAG GGAAAATGCC GACCTTTATT 2760

TTTGGCTTAC CAGCGGCGTC ACTTGCGATG TATCATACTG CAGCTCCGGC GAATCGACAT 2820

AAGATTAAAG GCTTACTCCT TTCGGGTGTA ATTGCTACGG CTATCACTGG CATTACAGAA 2880

CCAATTGAAT TTTTATTCTT ATTTATTAGT CCATTATTAT GGCTGTTTCA TGTCATTATG 2940

ACTGGTCTAG GTTTCATGGT AATGGCTTTA TTAGGTGTTG TGATTGGGAA CACTGATGGC 3000

GGGCTACTGG ACTTTGTTAT TTTTGGCTTG TTACAAGGAA CTTATACAAA ATGGTGGTGG 3060

GTTCTCATTG TCGGCGCTAT CTGGTTTGTT GTTTATTATT TCGTCTTTAA AACAGTCATT 3120

GTAACCTTTG ATTTAAAAAC ACCTGGACGA GACAAGGTCT TAGATGAGAC TGAATATACC 3180

GATCAAGAAG TTCAATATAA GAAAACGGGT GGCTATGATG CGCCTGGGAT TTTAGCGGCT 3240

TTGGGTGGGC AAGAGAATAT TCAAGCTATT GATAATTGCA TTACGCGTTT ACGTTTAGTG 3300

TTAGCAGATG CTAATAAAGT AGATGATGAC AAATTAAAGC AATTAGGGGC TTTAGGCGTT 3360

GTACATTTAG ATGCGCAGAA TGTACAAGTG ATTATCGGAA CCAAAGTGAC AACGGTCCGT 3420

AATCAATTAG AGATGATTTT AGGTTAGAAA AAAGACAGAA GGTGAAGAGT GTGTCGTTTG 3480

ATAAAGCAAT TGATCGACGA GGAACGTATT GTACACAGTG GGATTTTGTA GAAGACCGAT 3540

TTGGGGAAGC GGACTTGCTT CCCTTCACTA TTTCCGATAC GGATTTTGCT GTGCCAGAGG 3600

CAGTTCTGGC AACATTACAG GAGCGTTTGA ACCATCCAGT ATTTGGCTAT ACGAGGTGGA 3660

ACCATCCGCA ATTAAAAGAA GCAATTCAAA CGTGGTACCA GACAAGATTC CAGACGAAGA 3720

TTGAAGAACA CTGGATTATG TATACCCCGA CCGTTATCTA TGGTATTTCT GCTTTGATTC 3780

AATTATTGAC TAACGAAGGG GAGGGCATTA TTTTACAAAC ACCTGCCTAT GATGCATTTT 3840

TTAAAGTTAT TCAGGAAAAT AAGCGGCAAG TAGTGGCGAA TGAACTGCTT TATCAAGAGA 3900

AGCGCTACAG CATTGATTTT ATTGATTTAG AAAAAAAACT AGCGCAACCA GAAAATCGCT 3960

GTTTGCTTTT ATGTTCCCCG CATAATCCAA CAGGACGTGT TTGGGAGCAA TGGGAATTAG 4020

AGCGAATAGT TTCATTGTGC CAACAGTATG ATGTGTTTTT ACTTTCTGAT GAAATTCATA 4080

TGGATATCGT TAATAAAGGC CATGTTCATC GACCAATTAC GCAATTTGAT TATAAAAAAT 4140

CTGCCATTAT TACCAGTGGC ACGAAAACCT TTAATTTTCC AGGGCTGATT TTTGCTTACG 4200

CCTTAATTCC AGATAACGAA TTGCGTGACG CTTTTCAGCT CAAATTAAAA AACGCCGATG 4260

GTTTATCATC AACAAGTATT TTGGGAATGC TAGCAACCAT GACGGCCTAT CAAAAATGTG 4320

GTACTTGGGT TGACGAGTTG AATGATTATT TAGCGGAGAA CCAACGTTAC GTGAAAGATT 4380

TTTTACAGAC ATATTTGCCA AAAATTAAAG TGACGGAGCT GGAAGCCACT TACTTAATGT 4440

GGTTGGATGT ATCAGCGGCA GTTCCAGATG TGGCCCGCTT ACAAGCGGCT TTAGTTTCTG 4500

TGGGGAAAGT CGCTATTATG GACGGCTCGA TTTATGGCGG TAATGGGCAA CGATTTTTAC 4560

GGTTAAATAT TGGCTGTTCG CAAGCAAAAC TACACGAAGG ACTTGAAAGG ATGCGCCAAG 4620

GTTTTGAAGC TGTTTTACAA AAGGATGGCA CAGCATCAGC GCTTAGGAAT AATTGAGAAA 4680

AGATAGCATT CCGAAAATGG TTGCAGTACA ATGGAAAAAT AGAAACAAAT AAAATAACAA 4740

AAAGTAACAA CTTGTCATTT ACTGGGGGAA AAGAAATGAA AACAATTAAA ACAAAGCAAG 4800

CACCACAAGC AATTGGGCCA TATTCACAAG CAAAAATTGT GAATGGTTTA TTGATTACTT 4860

CTGGTCAGAT TCCACTGGAT CCTGAAACAG GCAAGGTGGT TGGGACAACG ATTAAAGAAC 4920

AAACCAATCA AGTACTGAAA AATATTCAAG GGATTTTAAC AGAAGCTGGT AGTGATTTTG 4980

CTCATGTAGT CAAAACGACA TGCTATTTAC AAAATATGGC GGATTTCACG GCATTCAATG 5040

AAGTCTATGC TGAGTATTTT AGTGCGGAAT ATCCTGCACG CACAACGATT GAAATCTCTA 5100

AATTACCGAT GGATGTGTTG GTGGAGATTG AGATTATCGC AGAAGTAGTG GCGTAAAAAA 5160

TACAGTTAAA AGAGTGAGAA AAAATCGTCT TAGATTTTTT TCTCACTCTT TTTTTCAATA 5220

AAACAATACG ATTCAGCCAA AATGTCTAGC CGTGCTGGAA AATTTTCAGC AAATAGGCTA 5280

CCATGGAAGA AAATCGATAA AACGAAAGTT AAATGAATAG AAAAGAGATA TGAAAGAGGC 5340

TATAAGATGA AAAAAAATAT TAGCCAACTA ACGCAtGGTT GAAAGAACAC AGTTTATTAT 5400

TGAAACTAAT TTTTCTTGGT TCTGTATTAG TTTTCGTGGC TAACCAAGTG ACACATATCG 5460

CTCAAGGCAT GAGCTGGGCG GATATTTTTT CCACGATGGA ACAACAAAGT ACGGGGCGTT 5520

TAATTGGTAT GGTCTTGGCA GGACTATTAG GGGTTATTCC gATGCTCCTT TATGACTATG 5580

TAGTCGTTAA ATTATTGGAA AAAGAAGGTA AGCCACCAAT GAAACGAATG GATTGGTTAA 5640

CTTCGGCTTG GGTCACCAAT ACCATTAATA ACTTAGCGGG TTTTGGCGGC GTGGTTGGGG 5700

CAACGCTACG GATTAATTTT TACGGAAAAG ATGTACCGCG GGGCAAGGTT GTAGCAACGG 5760

TCTCAAAAGT TGCTCTGTTC TTGATTTCAG GGTTATCTAT TTTATCTTTT GTGGCGTTTG 5820

TTGATTTATT TTTTATTCGA ACCCAAAATG TTTTTCGTGA ATATTGGGTT TGGTTATTAT 5880

TGGGCAGCCT GATTGCGCCA GCGCTCTGGT TTTTCACGTA TTTAAAACGG CGAACATTGT 5940

TTAAAACATT TTTTCCAAAA GCAGTGCTCC TATTATTCGG CGCTTCATTA GGTCAATGGC 6000

TAGGTGGGAT GTTTGCTTTC TTGATGATAG GTCGCTTGAT GCAGGTGCCA GTTTCGATGG 6060

TTTCTGTTTA CCCAATGTTT GTTATCGCTA CGTTGATTGG GATGTTAACT ATGGTTCCTG 6120

GTGGTATGGG AACGTTTGAT GTCTTAATGA TTTTGGGCTT ATCACAATTA GGGATTGATC 6180

GATCACAAGC GATCGTCTGG TTGTTGTATT ATCGTTTGTT TTATTATGTG ACGCCTTTTA 6240

TGACAGGAGT TATTTTGTTC TTGCAACAAG CAGGCATGAA AGTCAATCAA TTTTTTGATA 6300

ATTTACCTCG GTTATTTTCA CAAAAAGTGG CGCATTTTAT TTTGGTGGCG GCGTTATATT 6360

TTGCAGGGAT TATGATGGTT CTATTGTCGA CTGTGACGAA TTTGTCGAAT GTCAGTCGTT 6420

TATTCCAAGT GTTACTTCCC TTTTCTTTTA ATTTTTTAGA TCAAACATTG AATTTATTTG 6480

TAGGATTCTT GTTATTAGGT TTAGCTCGAG GCATTTCTAT GAAAGTGAAA AAAGCTTATT 6540

GGCCTACAAT TATTTTACTA GGATTTTGTA TTGTAAATAC GGTGGCACGA ACGACTTCGT 6600

GGCAGTTGAT TGCTGTTTAT GCTGTTATTT TATTGGCGGT TATTTTGGCT CGTAAAGAAT 6660

TTTATCGTGA AAAGTTTGTT TATTCATGGG GCGCTTTAAC GGTAGATAGT ATTTTGTTTG 6720

GCTGCTTGTT TATCGGTTAT GCGGTTGCTG GCTATTACGC CGCACGACCA GCTGGTGGCA 6780

ATCAAGTTAT CAATCACTTT TTGTTGTTTC CGTCAGATGA TGTTTGGTTT AACGGATTGA 6840

TTGGATTAAG TATTTCCTTG ATTGGTTTAT TCTTTTTGTA TCAATATTTA GCCGAAACAA 6900

CTGTTACTTT AGGTGAGGGA TTTGAGAAAG CGCGGTTGAC ACGCTTTTTG GAAAAATTTG 6960

GTGGCAACGA AGGCAGTCAA TTTTTGTATT TAAAGGATTA TGGTCATTTT TATTACCAAG 7020

AAGAAGGCGA AGATCAAGTA CTTTTTGGGT TTCAAATGAA GTTTAATAAA TGCTTTGTCT 7080

TGGCGGATCC GATTGGGCAA CGAGAGAAAT GGACAGCGGC GACACTGGCG TTTATGGATC 7140

AAGCTGATTT GTTAGGTTAT CAATTAGTTT TTTATCGTAT TTCGGAAGAA TATGTTATGA 7200

ATCTTCACGA TTGCGGCTTT GAATTTATGA AAGTTGGGGA AGAAGGCTTG ATTCAATTTG 7260

ATGAGCCGTC AACAGTGAAT CAAACAGCCT GGACGGAAAC AGTGACTGAA AAAATAGCAG 7320

CGGAAGCAGC GGATTTTCAG TTTGAATTTT ATCCCGAAAC GATTAGTGAT GCCTTATATC 7380

AAGAGTTAGA ACGAGTTTCT GCGGACTGGT CACGGAATCA AAAAGAGCGC TACTTTATTG 7440

GTGGACGGTT GGATCCCGAG TACTTGAAAT GCAGTAGCGT GGGCTTGGTG AGACAGAAAC 7500

AAACGGTCAT CGGTTTCATT ACTGGAAAAG AAATGGAAAA AGGCAAAAGT ATTTCGTATG 7560

ATTTGTTACG TATTCGTTCA GACGCACCTG CTTTTACTAG AGAATATTTG TTCACTCATT 7620

TTATTGAAAC CTATCAACAG CAGGGCTATC AATTAATTGA TATTGGGATG GCGCCGTTGG 7680

CTAACGTAGG GGAGAGCAAG TACTCTTTCT TAAAAGAACG CTTTGTTAAT ATTTTTTACA 7740

AGTATAGTTA TCAAATTTAT GCGTTTCAAG ATACACGCAA GCGCAAAGAA CAATATGTCA 7800

CTAGTTGGCA ACCACGTTAT TTTGCTTATC CTAAGCGGAC CAGCGTACTC TTTGCTTTTG 7860

TGCAACTTTC CTTGTTGATT ACGAAAGGAA GACATCAAAG TGTTTCGCTT GTGGAAGAAG 7920

CAATGACTGA AATTTAAAAA AATCACGCGA TGACTTAGCC ATCGCGTGAT TTTTTATTTG 7980

TCTTCTTTTT TACGGTTTCG TCTAGCAGGA ATCAAGGTTA CGTAGGCAAC GAAACCACCA 8040

GTACATAGAA CGAATAACAC GATGCCAGGA ATCAATCCTT CTGGTAAATA AGAGAACTGA 8100

ATAGTATGGG TTCCAGCGCT GACAGGAACG CTTAGAAAGG CATCTTTAAA GGCTTTTGGG 8160

GTAACTTTTT TGCCATCAAT TTTGACACGC CAACCTTTGT CATAAGGAAT TGTAGTGACG 8220

AGTACTTGAT CTTTGTCGGC GGTAAAGGTA CCTGAAGCAG AGCGTTTGCC AGTTGTTAAA 8280

TCAACGCCTT TTTCTTGCAC GGCGGAAATG GCTTTTTCAA ATGCATTGGT ATTTAAGCCA 8340

ACCACTTGCG GCTGAACAAA ACTTACTGCT TTGGTTCCAT AAAAACTTAC TTTGAAGTTA 8400

ACGGTTGTAT CTTTGGGATA GTAACCTAAG TTATAATATT GGCCAGTAAT GCCAATTTGT 8460

GATTGCTGAC TTGAGCCGTT CACGGTGACC GTCGCAGTGG AACTTTCCAA TTGAGCAAAA 8520

TCCGTTGGGA ATAAACTCAA ATAAGCTTGC GTATTGGCGG GCACATTGAC TGTATAAGAA 8580

ATCTCTTTGG CTACGTTATG TTGTTTCTCC GTAAAAGTTA CGCCAGCTGT ATTTTGCGTA 8640

ATTGTCACGT TATTTTGAAG CGTCATCGTT GGTTGATAAA AGGTAAAATA CCGTTCATTA 8700

GTATTGGCTA AAGCATTTAG TAAATTTGTT TGACTACCTA AATTATCATT GAGAGGTTGC 8760

CGGACATTGT AAATCTCTTT GTCTGCTAAA AATCCTAACG GCAAAGCATT TTCGTTACGA 8820

TAAAGCTGAT ATTTACCAGC AGCAGCTTGT CGCTCAAAGC CGAATTTCAT TGGATTGTTT 8880

TCAGCAATAT TGTATTTAAT GCCCATCAAA GCATCCATTA ACAAGGTATT ATTTTGGTAA 8940

CGAATATTTA AATTCGTGCC TCGTGAGCGG AAACCTAAGG CGTTTAGGTA TGTTGAAGAA 9000

TGTCGGTTCC GTACGGAAGA AAACATGCTA ATGCCACTGT AGCCATAGTT AATGCCGTCA 9060

TTGGCCGAAA CACCATTTAA ATTTTCCAAG CGGTAAAAGG TATCATTTTC TTTTTTTGTT 9120

TGATCGACTA GATTTTTTAA GTCAGGATAA GGCTCAGAAT ACAAGCTGCG TGATGCGTAG 9180

TTCCAATCAT CTAAAATACC AGTGACCATC GCCCGTGTGT TAATGATTGC TTCACCAGAA 9240

ACGAGCAGCA ATAACAAAAT CACTAAGTAT TGCATAGGCG CTTTTTTCAA TTGATAAAAA 9300

GCAATCCCGA AAAAGTATAA TAGTAAAAAA GTTGCCGTTA ATACGAAAGA GGTTAAAGTC 9360

ACATACGTAT AACTAGTAGC ACCTTTTGTG CCCATTGCAA GAGCAAAAAT TGCTAAAAGA 9420

ATCAAAATCA AGCCGCTTAA GACACCGAGA TCATCCTTTT CAAATTTCTC CCAACCATAA 9480

CCTGCAAGCA AAATAACTAA GAATGAAAAG AGGAAACTAT AGCGGAAAAG AAACATGTTC 9540

GGCGCATGCA TACCGTGCCA GAATAAATTT AAGGGCGTGA TGTAAAAGCT AGCAATCAAT 9600

AGGACAAACA AACTGCCAAA AAGTAGTTTG TTTTTCAATG GAACTTCTTT CGTAACGAAA 9660

TAGAAGAGAC AAAAAATCAA AGGCAACAAC CCAATGTAAA TAAAAGGAAT GGACCCATAT 9720

TTGGTTGTAT CGTAAACGCC AATCATATTT TTCATAATAA TATCTAAAAA GGCAGTCGCT 9780

TCTGTTTTAA AGGTTGTAAT TTCAGAAAGA GTTTCACCAT TGGTTCGTAA ATCTAAGACA 9840

GCAGGTAAGA CCATAATCAT GGATGCTCCA CCAGCTAAAA GAGAAGTAGT AAAATACGCA 9900

ACGATTCGAG ATTTATATCG TTGCCAGTCT GTAAACGTTC GTGCAAAATA GTACAGGAAG 9960

GAAAACAACC CAATCATAAA GCCAAAATAA TAATTTGTAA TGAAAAGCAA GAAATAACTG 10020

ACAAACAATA ATGTCGGTTT TCGTTGGTCC ATTAAACGAT GAATTCCTAA AATTACGAGT 10080

GGCAGATAAA TAAAGGCATC CAGCCACATA ATTAATTCTG AATGGGCCAC AATGAAGGAC 10140

ATTAGCGCAT AAGACACACT TAAAGTCACA TGGGACCATT TAGGAATCTT AAAGGTTTGT 10200

TTTGCCAAGA ACCAAAAACT CAAGCCAGCA CTCCCAATTT TCAACAACGT TAGGAAATAG 10260

AGCGCATCAG GCATGTTTTG ATTGTTAAAG AAAAAGACGA GCGGCGTAAA TAAGCCACCA 10320

AGATAATAGG AAATTAAGGA CAAGTAGTTT AGTCCCAAAG AAGCATTCCA CGTATAGAAA 10380

AGACTTTGTT TTCCATGAAG AACATTGTTA AAGCTTGCGT GAAAATTTGA AAATTGAGAA 10440

AAGGCATCGC TGGCTAAAAC ACTGCGACTA CTTCCTGGAT AAATCCCAAT ACTCAAATAG 10500

ATAATTGCCA TAATTAAAAA TGGAaTGAAG rAACTgscTA ACATATAAGG CCAGTTGTtT 10560

TTTAAAAACT GCcTACTtTT AtTTTTCATA AATA 10594

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1087 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

ATGAATTAGA GCCTTTAATC GAGTTGGGCG TAACTGGCCT CCGGnTnCnn TAGCGGCATT 60

ACGATAGAAC AAATGGCTCA TGCTTCACAT AAGATTGATA TAGGATTGAA TGCTAGTACC 120

ATTACACTGG AAGAAGTGGC TGAGTTAAAG GCTCACCAAG CGGACTTTTC TCGCTTAGAA 180

GCTTGGCATA ATTATTATCC AAGACCTGAA ACCGGCATTG GAACAACATT TTTTAATGAA 240

AAGAACCGCT GGCTTAAAGA ATTAGGCTTA CAAGTTTTTA CTTTTGTACC AGGAGATGGG 300

CAAACAAGAG GCCCAATTTT TGCTGGTTTA CCAACATTAG AAAAACATCG GGGGCAAAAT 360

CCTTTCGCCG CTGCCGTTGG TTTGATGGCT GATCCTTATG TCGATGCTGT TTATATTGGT 420

GATCCTACAA TTAGTGAGCG AACCATGGCT CAATTTGGTT ATTATCACCA AACTAATCAA 480

TTTCTGTTAG AAGTAGCACC TAGCGAGAGC CGCTATTTGA AGCGAATACT TGGGACTCAT 540

ACCAATCGTT TAGATGCTGC AAGAGATGTT TTGCGAAGTG AATTATCAAG AACGAGTGAA 600

ATGTTCAGAA AAGATGAAAT TGCaACGATT GAGTCAGAGC AGACTGAAGC ACGTCCAGTG 660

GGaACCGTAA CGATTGATAA TGaAAAATAT GGTCGCTATA TGGGaGAAAT TCaAGTCACA 720

CTTGTnGGAC TTGCCGAAAG ATGaAAAAGT CaATACGATT ACACGAATTA TTGaAAAAGA 780

TCmAACGATA TTGCCGTTAA TCcAAGGCAG GCnATCaATT TACGCTAGTC ACGGAAGGnA 840

CGATAGAGAA TGAATTTAGA AAACTTAACA ACTGAACGTA GAAATGAAAA TACAATGGGC 900

TTAGATGAGA TGAGTGTCAA AGAAGCTTTA CAAAAAATGA ATCAAGAAGA CCAAAAAGTT 960

GCAATGGCAG TGGGTCAAGA ATTAGCAGCC ATTGAACCAG TGGTAGAAGC CATCCATCAA 1020

AAGCTTCAAT CAAGGGGGCC GCTTGATTCT CCnTGGGCCC TGTACCAATT GGCCGGTAAG 1080

GGGCCTA 1087

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

ATTGTGATTT TTTCAATTCA GATTCTTCAT CGTTAAGATG TCATTAAAGA CACTGACTAA 60

GTAATCGkTG ACTGTTTCTA AATTAGGTTC CATTCTGTGC ACCATCCATA TACTTTGATT 120

ATCAAAACAT TTGATGTTCA AACTATATCG TAAATAAGCA AAGAATGCAA GAGAATTTTC 180

TATATTTTTA ATGAAATATT CTTCAAATAT TTCAAAAAAG GCGCATTTTC AAGGGACGAG 240

GCTTTTAAAA AAAGGATCAA TTACTTTGAT ACCCAAACTA TTTTCACAGA AAAAGGAAAG 300

AAGTGCAACT AAAAAGCATC ACTGGCACTC CCCTGATTGA GAAGTGCCAG TGATTTTTGT 360

TATATAATTC TTAAATTCCC ACTAAGCTAT TGCTACAACT TGACTGGATA ATACGAGAAG 420

AGAGTGAACC AGAAGCTTTG GTGCTTCTAC TCCACTCCCT TATTAAAATG TAGGACGATT 480

AATTATTGAA TTAAGTCGTA AATTTCCATT GCTACAATAT CGATGTTATC GAATTGATAG 540

CTTTGGTGCG TATCAGATTC TGTTAATTCA AATGTTTCTG TTGATTTATC AAAACTTACA 600

ATACATTTCT CTACGCCTTC ACGTTCAAAG CGGCGTACTT GTACTTCATT ATCTGCTGCT 660

TCGATCATTG CTTCCAGTCT CTTAATAATC GCCACAAGTT GTGAATGTTT CATCAGTGGG 720

cCTCCTTTTG CAAACTAGTT CTGTACCATT GTAACAAAAC AT 762

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2012 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

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CAnnACACCT GCTTCTGTTG nATAAGGAAT GATTATCTTG GACAAAATCC AAAGTCTAAC     60
CCATGTTCTG CAAATTTAGC TTTGGAATAA CTnTCTGTAA AAAAGCCACG ATGATCCACC    120
GAAAACATCC ATTTCGATAA TTTTGACATC TTGTAATTTT GTATCAATAA CTTTCACGTT    180
TCTTCGCTCC TATTCTGCTG CTAAACGTAG CAAGTATTGG CCGTAGCCAT TTTTCTTCAA    240
TGGTTGTGCC AATTCTACCA ATTGTTCTTT TGTAATATAG CCCATTCGAT AaGsAATTtC    300
TTCcAAACAa GsGACTTTTA AATTTTGACG TTTTtCAATk GTTTCAATAA ATGkTGACGC    360
TTCTAATAAG GATTCGTGTG TGCCTGkATC TAACCAAGcA AaGCCACGGC CCATTACCTC    420
AACAGAAAGT TTATTTTTTT cAAGGTAGAC TTTATTAACG TCTGTTATTT CTAATTCCCC    480
ACGTTCTGAC GGTTTGATCC CTTTTGCAAT TTCAACCACT TCATTGTCGT AAAAATACAA    540
ACCTGtCAcT GcGtAwTTkG ACTTCGGTTG TGCTGGTTTT TCTTCAATAG AAAGCGCCCG    600
CATCTCTTCA TCAAATTCTA CCACACCGAA ACGCTCTGGA TCATTTACAT GGTAACCAAA    660
GACTGTTGCC CCTGATTCTT TAGAAGCCGC TCGTTGCAAC ATTTTTGATA AGCCGCCACC    720
ATAATAAATA TTGTCCCCTA AAACTAAGCA GACACTGTCA TCACCAATAA ATTCTTCACC    780
AATAATAAAT GCTTGCGCCA AACCATCTGG GCTTTCTTGT ACCGCGTATT CGATATGAAT    840
GCCTAAATCA TGGCCATCGC CGAATAAGCT TTCAAAACGT GGTGTATCTT CTGGTGTAGA    900
GATAATCAAA ATTTCATTAA TTCCCGCCAA CATTAACGTT GACATTGGGT AATAAATCAT    960
TGGTTTGTCG TAAATTGGCA TTAATTGTTT TGATGTTGCT TTTGTTAACG GATATAAGCG   1020
TGTCCCGCTT CCGCCTGCTA AAATAATTCC TTTCATGAAC AATCTCCTTA AATACTTCTA   1080
TTTTTAGTTT CTATAAAACC AAATATCCTT CCCTATTATC GCATTAAGCA TAGGGtTTGT   1140
CATGTTTTTT ACGTAAATTT TACAAATCTG TAAAAGTTTA GCGTTGTTCC TTTAAACGCT   1200
GATGTAAAGC TTTTAATAAA TTCACACGCC AATTTAATTT TTGTTGGAAA CTTGTTTTGG   1260
TAATAATAGG GCTGACATTC GCTCCATGTC TTCGGTAAAG CACTAATGGT TCTTTAATGA   1320
GACCCGTTTG CTTTTTCCGT GCAGCTAATA AGCCAATCCA CATATCATGC ATAGGAACTT   1380
CTGGCGGAAT GGGTAAAATG ACGTTTTTCA TCTCTTGACG AAAGGCCATA CCTGCCCCAA   1440
TATAGCCACT TTTTATCGCA TTTCGCCAAA ACCCTGGTTT GACTTTTCGA AACTTAAAAT   1500
AAGAGGGATT GGTAACTTGT AAATCCGCAT CAACAATTTT CAAGTCACTA ATAACCACTT   1560
GGATGTCAGG GTGCGTTTCA AAATATTCTG TCACTGTTGT TACTTTATTT GGCAACCAAA   1620
CGTCATCTTG ATCTGCTAAA AATATCACTT CGCCTTTCGT ATGCGTAAGc GCAAATGcAA   1680
AATTAGCAAT CACTCCTTGC CCTGGaCCTT GTAACAATTG AATTTGGGGA TAATTCGCTG   1740
cATACGTTCT CAAAATTTCC AACGTATGaT CAGTAGaAcC ATCaTCTGAA ATAATTAGtT   1800
CATCyTCtTC ACTGACyTGT AAAAGAATAC TATCTAATTG TTCCGCGAGA TATTTTTCTC   1860
CATTATATGT CGCAATACAA ACTGAGATCA TAGATTATCC TTTCATGAAC TTGAGAAATT   1920
CTGCCAATGT TTGCCGCCAA ATTTGGCGAT TTTTGACAGT TAnAAATnGC TTACTACTGC   1980
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GTAAAAATAG ATGGCGTCGA TGnGGGAAAA CT 2012

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACATTGGTG TTATATTACT TACAAGTTGT TTTTTCATTG GTTTTTATCA GGGTCCTGTT 60

CTGATAAAAG TTAGTGAAGA GACCTTCACT AACGTAACGA CTCGCCGTGC TAGACACCGA 120

GACGGTACGT TTTTTTTATT GGTTAAAATA GCTGCCGCTT GACATCATCG CGTCATGCGG 180

TTTTTTTTGA AAATAAGTAT TGTGGGCGCT ATTTATTTTG AATTTATGCT AAAATGAACA 240

CGATTGATAT TTGAGGAGCT GAAGATAGTT GACGAACCAT ATTGTTTTAT TTGAACCACA 300

AATTCCAGCA AATACTGGAA ATATTGCACG GACATGTGCA GCGACGAATA CACCGTTGCA 360

TTTAATTGAA CCTTTAGGAT TTTCAACAGA TGATAAACAC TTAAAACGTG CCGGATTAGA 420

TTATTGGAAT GATGTAAATA TTACGTATCA TAAAGATTCG GCTGCCTTTT TAGCCCATGT 480

GGCAGGCAAA CACTTGCATT TAGTAACCAA ATTTGCTCAC CAAACATACA GTGAGGTCAA 540

TTATAATGAT GGCGAAGACC ATTATTTCCT TTTTGGAAAA GaAACAACGG GCTTACCAGA 600

AACGTTTATG CGAGAAAACG AAGAAAAGTG TATCCGAATT CCTATGAACG ATGAACATGT 660

GCGCTCATTG AATCTTTCTA ACACTGCCGC ACTAATTGTT TATGAAGCCT TACGTCAGCA 720

AAATTTTCCG AACTTAGAAC TGACGCATCA TTATGAAAAT GATAAATTGG ATTAAAAAAA 780

GTTAAAACAG CAGCGCTTTT TTCAAAAATG TCAGAAGAAA GTGGTTTTAT TTTTACTGTT 840

GCCCAATTTC CAAGCCTAGA ACAAAAAACA ATTTAGATTT TTGTTCTAGG CTTATTTTGC 900

TTGGATTACT AGAAACTTCC ATGGATATTT TCGCAGGGAA GTGATAAACT AGAAAGACAT 960

ATGAAGAGAT AAAGAAGTTT GGAGAAGTTA CATGAAATTA TATTTTACAC GACATGGAAA 1020

AACTGAATGG AATCAACAGA AACGATTTCA AGGAATGACA GGAGATTCGC CGTTATTACC 1080

AACTAGTTAT GACGAAATTA AACAATTAGG CCAATATTTA CAAGATATTC CGTTTGAAAA 1140

AATTTATTCT AGTCCGCTAT TACGTGCCAA AAATACTGCG CGGGGAATTC AACAAGAATT 1200

GACTCATCCA GTTGAAATTG TTTATACAGA TACCTTAAAA GAATTAGGTT TAGGTCGTCT 1260

AGAAGGACAA TATATTGAAG AAATGCGTAA TTTTTATGGA GAAGAATTAG ATCATTTACG 1320

GCATCGTTTA GATTTGTATG ATCCAACAAT TTTTGATGGT GAACCAATCG AGCAAGCGAT 1380

TCAACGGATT TCAGAAACAG TTGCTGAAGC GGCGAAACAG CACGAAGGTC CAGTTCTATT 1440

TGTCGGACAC GGAGCAGCGC TGACGGCGGC AATCCAAGCG ATGGCTGGTA AACCATTATC 1500

AGAATTACGG ACAATGGGCG GGCTGTTAAA CAATAGCCTC TCAATCCTTG AAACCAAAGA 1560

GGCATCAAGG AACATGCCGT ACGACTTAAC GTTATGGAAT GATACGTCTT TTTTAGCTAA 1620

AGAAAAAGCA CAATAAGCAC ACAACAGAAA GGAGGGCTTG TAGTGGTAAC ACTTTTTGGT 1680

GAGGACGAAG AAAAAGCCTT TATTGTTGGA ACTGTACAAG CAATCTTTTT TGAAAATCCC 1740

AGTAATTTTT ATAAAGTCGT TCTTGTAAAT GTGACCGATA CAAATACAGA TTATTTAGAA 1800

AAAGAAATTG TAGTAACTGG AAGTTTTGGC CAAGTTCAAG AAGAGGAACC CTATCGTTTC 1860

TTTGGTCATT TTGTGGACCA TCCTCGTTAT GGCAGACAGT TTCAGGTGGA TAGTTATCAG 1920

CAAGAAAGAC CGACTTCGGC TAGTGGGGTG GTTAACTATT TATCAAGTGA CAAATTTCCT 1980

GGCATTGGTA AACGAACCGC TGAAAAAATT GTTGAAGTAT TAGGGGAAAG TGCGATTGAC 2040

CGAATTATTG ATGATCCTAG TGTTTTGGAA GAAGTTACTG TTTTAAATGA AAAAAAACGT 2100

CAAGTAATCG TCGAAACAAT TCGCTTGAAT CACGGGATGG AGCAAGTGAT TGTGGGACTA 2160

AATCGATACG GCTTTGGTAG TCAGTTAGCT TTTTCAATTT ATCAAACCTA TCAAGAAGAA 2220

ACCCTTTCTG TGATTcAAGA AAATCCCTAT CaGTTAGTTG AAGATATTGA GGGAGTCGGA 2280

TTTAAACGAG CGGACAATAT TGCTGAACAA ATCGGCATTC AGGCGGATTC TGCTGTTCGA 2340

ATTCGAGCGG CGATTTTACA TGAAGTGTTT GAACACTCTA TTCGTTCAGG CAATACGTAT 2400

GTTCAAGCAG ATGTTTTGTT AGAAGAAGCG ATTCGGACCT TGGAAGCAAG TCGCCCAGTG 2460

GAAATCTCAC CTGATCAAGT GGCCAATGAA ATCATTACGT TAgTCGAACA TGGAAAAATC 2520

CAACAAGAAG AGACTAAACT TTTTGAGAAC AGTCTCTATT TTTCTGAATG GGGCATTGGT 2580

ACTTCGATTC AACGTTTACT TTCTCGTAAA AAAGAAATTC ATTATGAGGA AGAAGAAGTC 2640

CAAAAAAATA TCCGAATGAT TGAGAAACGT TTAAATATTC AGTATGGCGA CTCGCAACAA 2700

GCAGCGATTG AAGAAGCGAT TAAATCGCCG TTATTTATTT TAACTGGAGG GCCCGGAACA 2760

GGGAAAACAA CTGTTATCAA TGGGATTGTC TCGTTGTTTG CGGAACTAAA TGGCCTTTCA 2820

TTAGATCTCA AAGACTATAC GCAGGAGATG TTTCCAATCT TGCTAGCGGC GCCAACTGGG 2880

CGAGCAGCGA AACGTATGAA CGAAACGACA GGTTTACCTG CAAGTACCAT CCACCGTTTG 2940

TTAGGCTTGA CAGGTCGTGA AAAAAATCCG AGTTTAACCG CCAAAGAATT AGAAGGTGGT 3000

TTGCTAATTG TAGATGAAAT GTCCATGGTG GATACTTGGT TAGCCAATAC GTTATTAAAA 3060

GCTATTCCGA CAAACATGCA AGTGATTTTT GTTGGTGATA AGGATCAGCT ACCGTCTGTC 3120

GGTCCAGGTC AAGTCTTACA TGACTTATTG CAAATTAACG AAATTCCCAA ATGTGAGCTA 3180

AACGAAATTT ATCGTCAAGG AGACGGTTCA AGTATTATTC CTCTTGCCCA TGAAATTAAA 3240

GAAGGAAAGT TGCCTGCTGA TTTTCAAAAA AATCAAAAGG ATCGCTCGTT CTTTGCAAGT 3300

GATATTGGTC ATATTGAAGA ATACATTCGA CAAATCGTCA CAAAGGCAAA AGCAAAAGGG 3360

TTTACGCCAC AAGATATCCA AGTTTTAGCG CCAATGTATC GTGGCGCAGC CGGCATTGAT 3420

GCCTTGAATA AGATGATGCA AGAAATCTTC AATCCAAATG ATGGTAAGAA AAAAGAAGTC 3480

AAATGGAATG ACACCGTCTA TCGGATCGGG GACAAAGTTT TGCAACTAGT CAATACGCCA 3540

GAATTAAATG TGTTCAATGG AGATATGGGA GAAATCGTCG GAATTACTTT AGCCAAAGAC 3600

TCAGAGGACA AAGTGGACGA GTTGGTTTTA CAGTTTGATA ATAATGAAGT AACGTATAAA 3660

AGAAATGAAT GGAATAAAAT TACGCTATCG TATTGTTGTT CGATTCATAA AGCGCAAGGT 3720

AGTGAATTCC GCATGGTGTT ACTGCCAATG GTTCATCAGT ATAGCCGAAT GCTGCAACGA 3780

AATTTGcTGT ATACAGCAGT GACACGTAGT AAAGAATTAT TAATTCTACT AGGTGAGGTT 3840

TCTGCTTTTG AAACATGTGT CAAAAACGAA TCGGCTAGTC GCATGACGAT GCTAAAAGAA 3900

CGAATCGTGA ACGCAGAACA AATGACCTTA ACGACTAGAA CTCaGTTAGA AGCCTATGAA 3960

GAAGGTTTAA CGGCAGACCA TCCATTTACT GAAACGGAAA CAAAAGCTGT CTTTTATGAA 4020

ACTGAACAGC AATCAACGAA AGCCGATCAG ATCAAAGAmA CAGACGAGCA ATTAGTTGAC 4080

ACAACGGTAC AAGAGGTTTC ACTATTTGCT GATGAAGGGG AAGAGTCAAC CTCACCAGCT 4140

GAACCACAGA AAGAAGAACA ATTACCTGAA AATCCTGTAT TGTCAATTCA AGAAATTCAA 4200

GAAAATAAAA TTAATCCAAT GATTGGTATG GCTGGAACCA CTCCATATCA GTTTATGTGA 4260

AAATAAATAA TTAATTATGT TTGTCTGTTT AAGAAGTCAA TTTATTTTAT TTGATTCAAT 4320

ATTATTAAAT AGTTTTGAAT GTTTGTTTAA GCTTTGCAAC AGTTTTACAA AAAAATAAAA 4380

AAGTGAGACG ATGAATAAAT ATTTTTTACA GATATTTATT CATCACTTAA ACTGATAGAG 4440

AGGAATTAAT TGTAAAAATG AAACGAAAAA GTCTAAAATC ATTTATATAT GTAAGCGCAT 4500

TACTTGTTTT TTTGAGTGGT TTTGTTGGTG TTAGTTTATT CGTTAAGTCA GAAGTAGTAG 4560

AGGCTACAAC GATAGGTGAT GACTATCCTG TTAAATGGAA AAATCTTCCT TTAGGCGGGG 4620

CGATTGATGA TTGGAGAATG TATACTAGAT ATTGTACCTC ATTTGTCGCT TATAGATTAA 4680

GCACAGCTAA TAACTTTGAG CTTCCAAGTG GCTTTGGAAA TGCTGATCGT TGGGGAACAG 4740

AAGCAATGGC GAGAGGTTAC AAAGTAGATA AGAATCCTAA AGTAGGATCG GTGGCTTGGT 4800

GGACATCTAC GCATGTTGCG TGGGTAGCAG AAGTATCTGG CGACAATGTT AAAGTTGAAG 4860

AGTACAATTA TGGATTCGAT GGTAAATACA ATACTCGTTG GATTAACAAG AATTCCGCCA 4920

ATGGATACAT TCATTTTAAA GATATGCCAC AAACACCTGT AGGTTGGTAT AACAACGGTC 4980

ACTATGATTA TTACTATTAT GCAGACGGAA CAAAGGCGAT TGGTCTAACT TGGGTAGGTA 5040

CGAAACGCTA TAATTTCGAT AAAAATGGTG CCATGTACAA GAATGCTTGG ACAAACAGCG 5100

wTAAATATTC ATATTATAGT ACATCAGATG GCTCATTAGC GGTTGGTTTA ACTTGGGTAG 5160

GTACGAAACG CTATAATTTT GATAAAnATG GTGCCATGTA CAAGAATGCT TGGACAAACA 5220

GCGTAAATAT TCATATTATA GTACATCAGA TGGCTCATTA GCGGTTGGTT TAACTTGGGT 5280

AGGTACGAAA CGCTATAATT TTGATAAA 5308

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

GCTAAGCTTC CTGTTAAAAC CACGTTATTC GGAGATTTTG TTAGTTTTCT TTTCATATGT 60

TTTCACCTCA TCTACTAAAT TTTACACTAG AAAGGCTGAT TCGTCAGCCC ATCTAGCTTA 120

AAATTGTTAA TTATTTATCC GTATCTTTTA GGAAAATACT TCCCGTTGTT GTAGAAGCAT 180

TAATTTGAGC CATTGATTCT TCCAGTACAC GTCTAAAATG TAATTGTTGA TTGCCGCGAT 240

CTTTCTTTTC ACGAACAACT TCAATATCTG TTAAACGGCT GTTAATACTA CCTAAATTAG 300

TTTTCACTTG CCCTTCAACA CCTAAGTCAT TTGGCAAGGC CAATTTGATA TTCCCATTTG 360

CAGAGCTTGC TTCAACACGG CGAAcGTTTT TTCTTTAGCT GTAATGCGGA TATCTCCATT 420

AATCAGAGAG ACACTTAGAC TTTCTGGTGC CGCGGAAATA GACACATCAC CATTGACTGT 480

TTCAATAATG TTATCTAAAA TCGTTCCTTC TAGGACTTTA ATTTCACCAT TCACACCTTC 540

AATTTCTAAC ATAGTTGCAT CAATTTTnTT AAACGTAATC GTCCCATTCG TTGATTTTGT 600

GTAAACATCT TTCGCTGTTA ACTCTTCTAC TAAGACATTT CCGTTTAATA ATTTAACAGA 660

TACATGATCG TAAGTGCGTT TTGGTAAATA GAACGTTAAA TCTGCTTTCA CCCGTTTGTT 720

TGGCACTGGG AAAGAAATCG TTCAC 745

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

TGGGTACggG CCCCCCCTCG AGTTTTTTTT TTTTTTTTTT TCTTTTAAAG CATTTATTTA 60

GAAAAATAAC CGTTCCCTGC CCGCCTTGCT CTGTGCCATG GGACTTGAGC ATCTTTCTTA 120

ATACTCTTCT GCATTGGGCC TGCAACCCAC AGTGGTGGGG TCCAGCACAC GCCCCTCGAA 180

ACGCTGCGGC ACTGCTGGGA GGCCTCACGC CCTTCCAGTC GTGACAGTTC CCGTGTTCAC 240

TCCTTGTCCA GGCCTCTGTC TCCGGGTCTC CAGGTGGACA GGGGCCTCTG CGGGATGGGC 300

GCAgcTCTGC CACAGTCTGT GTGCCCCTCC CGArGCTCTG CTCTCCCCGC ATCsGAAGCT 360

CArGGCTGGA ArCGCGGGGA rCTGACATGA rGTTGGTGGA ATGCsTkGGC gCTGTaCACC 420

ACCTCsGGGG GCGAgGCTTC TTGCn 445

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

TGATGTATGT TTCGTATATT CCGCAAATTT ATGGAAATTT ACATGGGGAA AAAGGCAATC 60

CGACGCAACC ATTAGTGGCA ATGATTAATT GTATTTTTTG GACGATTCAT GGGTTATATG 120

GAGACGATGG AGAAACACGA GATAAGTCCA TTATTTTTGC TAATGTGCCC GGAATTATTT 180

TTGGyTTTyT TGCGTTTATT ACAGCATTAT AGTTTCCGAC GAATTGGAAA GTATTCCAAT 240

TCTGTACATA AAAAAGAGCG GGGGAAATTT CCCACGCTTG AAGAATTAAA TCTTTTTCAA 300

TTGTTTGTAA TTAATAACAA TCACACCATT GCTGTGCACC ATTAAGTGAT TGTTTTTTTg 360

CGtTTCGTCA ATTTCGACGA CAGCGGCATT TTTTAATTGT TTCGTAACAc GCCTGTTTGT 420

GGCTGTCCGT GAACAAGAAA AGTAACAkGG GkGyCAaCGG CGAAATCCTT ACCAGCATCC 480

GATGGAACAA CAGGAGTAAC CATACCATTA AAATTTGACA TACAAAAAAC CATCCTTTCT 540

TGATATCTCT ATTATACCAC ATTTTCAGAA AAAAGTTTGT AAAGTCGCTA TTTGGCTTAT 600

TTTAAAGAGA TTTTGCATAA ATAAATAACA AACAGACTTT ACAAATAAAG TAGAAAGTCC 660

TATAATAGAT TTGTTTCAGG CCAGCTTAGC TCAGTTGGTA GAGCAACGCA CTCGTAACGC 720

GTAGGTCGTA GGTTCGAACC CTATAGCTGG CATAGATTGA AAAGACAGAT ACACCAAGCC 780

GTAAAGGTAA TAGGTATATC TGTCTTTTTT GTGTTTTGAA AGTTTTCGCT GCCTAAAATT 840

GCCTACTTAT TAAAAATTAG TATTTAAAAC ATGTTATTTT ATAGCTCGAA AATATCATAA 900

TTATCAAATT TATCGCTCAT TGATTTTTGA GAATTAGGGT ATAAATGACC ATAAGTATCA 960

ATTGTTGTAG TAATTGAAGA ATGACCTAAT CGTTCTTTTA TAGTAGTATT CTTTTCGTTA 1020

TTGTGAATAA GAAGAGCTAC GTGTGAATGT CTAAAGTCGT GTAATCTTAT AGGTTTAAGG 1080

TTCAAGTTGT TTTTTACAAT TATTTTTTTT ATTTGTTTAG AGTAATAATC GCTCGAAGGG 1140

TGTTTTTCAC TGTATTGAAA AACAAGTAAT TTGTCACTAT CAATATTTTG AAAATTATCT 1200

ATTAGTAATT TTGGTTGTAT TTCTTGCCAT TTTTTTAACA TGGCGGTAAT TTTTGAGTTG 1260

ATAGTAATAT ATCTGTTGCT GCTTTCCGTT TTTGGTGTGG TAGTTACGTA ATTACCATTA 1320

ATTAGTTTAG CACTTTTATT TATACGGACT GTTTGATTAT AAAAATCAAT GTCGCnCCAC 1380

GTTAAAGCAA TCATGnCTCC TGGCACGCAG TCCTGGAAAA A 1421

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

AACATGTAAA CAAATCGTAC AGATAACACG CAAGTTGCGT GTCGAGAGAG AGGCGGTTTC 60

TATTCTTATA GAAACTGCTT CTATTTTTTT ACGAAAAAAT GAAAACTATA GAGGTGATTA 120

AATGGAACAA AAnAACGTAC GATTATTCCC TGCCGTTTTA GCGACAGGAA TTATGTCTTT 180

TGCTGGCGTA TTAATTGAAA CAGCAATGAA TGTAACCTTT CCGACATTAA CAAAGGAATT 240

TGGTGTTTCC ACCGGTACCG TGCAGTGGGT GACAACGATT TATTTATTAG TTATTTCTAT 300

CATGGTGCCC TTATCCAATT ATTTATTAAA AACCTATTCG TTAAGACGCT TATTTATTGT 360

TGCGAATCTT TTCTTTTTGA TTGGTTTAGC GATTGATGTC TATTCGCCAT CTTTCAGTAT 420

CTTGTTATTA GGCCGACTCT TCCAAGGGGC TAGCACTGGG ATTGCTTTGC CACTGATGTT 480

TCATATTATT TTGAACTTTA CCCCGCTGGA AAAACGAGGA ACGATGATGG GGGTAGGCAC 540

ATTGACCACT TCAATTGCTC CAGCCATTGG TCCAACGTAT GGTGGAATCT TAACATCTTC 600

CCTGTCTTGG CACGCCATCT TTTTATyCTn AATnCCtATT TaCTGCTTyC TTkGTTwAtG 660

GGcTtAtCTG CTATcCAGAA aTACCTGTnA AAAAAACCAC CACTCTgrAT TgGtaGTTaA 720

TgGgAtgCCC yGTaATaGtG GtTGtgAgGT TTAAGnAAAT GGCCATGTTG GCGGCTTCAC 780

TCTGCAG 787

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 901 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TTTTACCTGC ACCATTCGGA CCAACTAATC CATAAATTTT CCCTACTTCT AAATCTAATT 60

GATCAACCTT TAAATTGAAT GTATCACTTA CTTTTTTATA TAAATTATTT ATATTTATTG 120

TTTGCATTTT GCAATTCAGT CCCTTCTTGA CAATGAAATA AGTGAAAGTA ATGTAGTTAA 180

CACGAACCAA AAACAAACTA CAATAATATT AGAAACATTA ACAGTATTCT GTTCATAAAA 240

CAGTGATCTT ATCAAATTAC TCGATGGAAC AAATGGTAAA AATTCAAAAA AGTTCACTAA 300

AGCAGAAGGC AATCTATCTG TTGGATAAGT AATAGGCGAG AATAAAAGTC CACCTATCAT 360

AATTATCTGA GTTGgCTAAT CCTACTACAT TAGGTGTTAA CCAATATGCC AAAGcAAAAC 420

CTATAGAGAT CmTACATAAT TGAATTAGAC TAAGAATAGC yAGGGCCTTC ATtGAGAATC 480

yAATTTGGAC ATCGAATCTT AAATATGCCG CTAAAAATGA CATAAACACC CCAGGTAGTG 540

AGGCCATTCC CCAAATTATA AAGTCGGAAA TTAATATGTT CAACCGAGAA ACTGGCAATG 600

TCCTTTGATA GTCCACAATG CCCTCCTGTT TTGCTGTACT TACTATTTGA GCAGCAAGAA 660

CGCACCCTAC CGCAATAATC CCAAGAGTAG TTGCTCCAGA TGACAGATAG ATAGCTGTCT 720

GATTATTCAC ATCTGGTATT AGAAGTGCTA ACCCGTAGAC AATTGCTAAT GATAGAAATA 780

CTTGAGTTAA TGTAAAAACA GGCAATAAGT ATTTAATGTC TTAATAAACT CCACCCTACT 840

AAAGGCAATA ATCCTTAnTC CATGATnGCT CTATAATTTG nATCATTTCC ACnATTAACT 900

C 901

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

GAATACGAAT GATACTGACA CTTnATGAGA TCAAAGAACG TGTGAAACCT GTAGCTGAAA 60

AACACAATGT TCCAGTAATC TACATTTTTG GTTCCTATGC TAGAAGCGAA GCAAAAGAAA 120

CAAGCGATAT TGATTTTGCT GTAGACATAA CTGGAGAAGC TGATGAAGAA GAaGCTTACT 180

GGAATyTATA TGGAGATTTT TTTGaAGAGT TGAAAGAAGC GGTAGGACAT GATATTGATT 240

TAGTCGAATT AGAGACATTA TTTGATTCAC AAGATAAACC AGAAAGAAAA GCTTTGCTTG 300

AAAATATTTT GAAGGAGCGT GTAAAAGTAT TTGAAAGATA GTACAGAAAA AGATTTGCGT 360

GTTCTAAAAG GGACGTTAAT CTATATAGAA GATATTGAGG AAACACTCAA TCGTTGTGGA 420

AGACAGTATG AGGTCTTTTA TCACGATAGG GTGTTTTTTA ATGCCATAGG AATGGCTTTA 480

ATGCAAGTTG GAGAACTAGG AACAGGAAGC AATGGATTAT CGGTAGAATT TAAAGAGAAA 540

AATTCAGATA AAGTAGACTG GAATAAATTA AAGAAATTAA GAAATATGTT TGCACATTCG 600

TATGATTCAA TGAATGAGCG ATTTATTTTC CGCATGGCAA CAATGTTTAT TCCGGTGTAC 660

AAAGAATTTT GTATACAAGC AATAGCAGAA TTGCAAAAGA GACGAGGTAA ATAAATGTTA 720

AAAAAATTAT TTAGATATAG AGGAAGGCGT ATTCGTTATT CTTCAAGAAA CCTGTTGGCA 780

CTCTATCGAG TGTTATTTTT TATGCCAATT TTAGCTTGTT TAGGGTATTT TGTTGGCTAT 840

AAATGGATTT ATCCTTTATA TCTTTCAAAT CCGCCTGATT GGAAAATATA CATTGTGCCA 900

GCGTTGATAA TTGTAGGTAT TTCTATAGGT GCAATTGTGC TAATTACATT GCTTATTAAA 960

GCTTCAATTA TTAATTCGGG GTATTTTTCT AAAGTGGaAC AACGTCAAGT ATTAGCaCAT 1020

ATGATTATTG ACAACGGGTA TTACACaAAA AAACAAGTGA AAAGTwsTGA yGGyAAAACA 1080

ArAGAAAAAA TCAAGTTTCC AAAAATTTAT TATAAGTCTG CAAAAAATAG TATTTTyGTT 1140

TCATTTGAAA CAGCrGGTAA TAAATTTCAG GAAAAATTTG AAACCATTGG TGGCTTTTTG 1200

GAAACAGCGT TTCATGCGGA CAATTTAAAT AAGATTGATG AAAAAGGCTT TATAACCTAT 1260

GAATTAGCTT CTGACGTTTA CAATAAGCGT ATTTGGATAA AGGATATGCA AGCGGACAAA 1320

GGAAAGGTTC AATTAATGAA AGGGTTATAT TGGTATTTTG ATAAAGACCC ACATTTATTA 1380

TTAGGTGGCG GAACTGGTGG AGGTAAAACC TTTACCATTT TATCTCTAAT TTATGCGCTT 1440

TGCCGTGTGG GTGAAATGGA AATTTGCGAT CCTAAAAATT CTGACTTGAT GGCACTAGGT 1500

AAGTTACCAA TGTTTGCAGG AAAAGTGCAT ACAGGAAAAA CAGATATTGT TAATTGCTTG 1560

AAAAATGCAG TTGAATTAAT GAATGCACGT TTTGAAATGA TGAATAATAG CCCTGATTAC 1620

AAAATGGGGA AAAATTATGC GTACTATGGT TTAAAGCCTA AGTTTATTGT TATTGATGAA 1680

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TTTGCAGCAT TTAAAGCAGA ATTAGCCAAT GACTATTCAA CAGATGGAGA AGTTGATGAG     1740

TATTTAACGC AATTGATTTT AAAAGCTCGT CAGTGCGGTA TTTTTCTAAT TGTCGCTATG     1800

CAAAGACCAG ATGGTGAATT TATTAAAACG GCTTTACGTG ATAATTTTAT GTTTCGAATG     1860

AGTGTTGGCC GTCTATCTGA AACAGGrATC CTTATGATTT TTGGTGATGA AAACAAAAAT     1920

AAAAATTTCA AATATGTAGA GAAAATCGAT GGACAAAAAG TATACGGTCG TGGGTACGTT     1980

GCACAAGGCG GTTCTGTCGC AAGGGAATTT TACAGTCCAC AAGTACCAAC AGATTTTGAT     2040

TTCATTGAAG AATTTATCAA AATTTCTAAA GAATTAGGTT ATGAAGATGT GTCAAAAGAA     2100

GTGCAAGAAG AAGTATCTCA AAAAATAGCT AAGCATGTAG ATAAAGAAGC CCTTGCGGAA     2160

ATTGATGAAG AGTTAGAAAA AGGTCAAGCA AAGTTAGCTA AGTTAAGTGA AAAATTTGAG     2220

TAATGAGGAA GGAGATTTTT ATTGGATTCT AGCGAAATAA TCAAACGTGT TAGAGAACGA     2280

GTGTATGTTG AAGTCAAGAA ACGATATAAA AAGCCTGATT TAGATATACG TATTCGTGAC     2340

ATTCTGTATG AACAATCAGA AAGCTATGCA AAATTAGTGA GGTTTTCTAA CGGAAAGCGA     2400

ATAAAGAAAT TAGCTGACCC TGTAGAGTTT GAAAAATTTA TGGAAAATAG GGGGGCTAAA     2460

ATTGTTGATG AAGTGATTGT TGGTTTAAAT GAAAAAGGAG AAGTATAAAT GGAATTTAAA     2520

AATAGTAATC AACTTATGGA ATATTGGGAA ACAAAAGTAA AGGAATTTGA AAAAGAACTT     2580

AATAGTGGAA TTTCCCAATT GTCAAAAGAA GAGAGACAAG AaTCATGTGT TGTTGaAGCa     2640

AAAAwATATT TAGAAGaAAA aAGAAAATAT GCGAATAATC TTCATGCGTT ATTTTATGTT     2700

GAAGGTAGTT ATCAGAATTC TAATGAAGTA GATAGGAAAT TTGATAGAGA ATTCTATCCA     2760

GCGTTTTATT CGTTTTTAAG TGAAATTGAT ATTTTAGCTC mTTAATAGrA AGGaATAGTG     2820

ATTGGTATGA ACGGtAAATT GACTCTTGAA GAGTTTTATA AAAAAATGTC TTCGGAAATT     2880

TATAGAAAAG TGAAATTAAA ATACAAGAAA AAAGATTTAG ATGATAGGTT TAGTCAGGTA     2940

TTGCATAATT CGTCTTTTCG TTTTATTTAT AGAAAATATC AGAATCGTCC TGATAGTTTA     3000

CTTACTTATC AGGAAAGTGA AATGGAATTG GATAAAAATT TAGATGGTCT TGTCGATGAA     3060

GTATTAAAAG GATTAACAAA TGTTCGTCAA ATTGATTTTT CGGAATATCT GGAAACTGTC     3120

AAACGTGCAA CATTTAAACG CTGTTCTGAA AAAACAACAA AGTATTTTTC TAGTCAAGAT     3180

TTTAATTCTA TTTTTAGAGA AGAATGTTTT GACTTTGTGA AGAGTGCTTT TAAAAGAGAT     3240

TCAGACGGAG AAAGTGTTAT TTGCTGTGAT GATTTAGATA TTTTAATGGA AATAGTAGTG     3300

AAGGATTGTG TTGAAAAAGT TATGCGTGTA ATTAATAAGT AATGCAGGGG GAGCAGGTGA     3360

GTGAATATGT TCTCATTTGA AGAAGTGCTT TTTGAATTAG ATAATGCTAT TTCTTTGAAA     3420

ACGTTGAAAA ATTGGGCAAA TAAAATTGAA AAATTAACAG ATGTTCGATT TGTTCGCCAA     3480

TACGCTAAAA ATAAACAGGG TAGAAACTAC TCGTATAAAG TTTTTAGTGT AGAACAGGTT     3540

GAACAGTTAA AGCAATTGGT TCAATTAAGG AAGCAAAATG TCCCGCTAGA TCAGGCAATG     3600

ATTGAAGTGT TTATGTCTGC AGAAGAAAAA GAAAGGCAGC AAGTAATTAC TATTGCAAAA     3660
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ATAGATTTTG AAGAAAATAA AGCAACGGTG AAAGAATTAA TTGACTTAGT AAAAGATGTC 3720

TTGTCGGATA ATGCAGAGAT AAAAAAGCGA CTGAAAGTTC TAGAAATGAA GCAAGGAATG 3780

ACAAGAGAGT AGACTAGTAG TTGCTAGGGA TTGTTGCGTG ATTTGTAGGT GGTGTAGGGG 3840

TGGCGCCCTA AGGCGCCCGC CCCTACACCA CCgTACGCAA AATTAGCAAC GTATATCCCA 3900

AATACTTCTA GTCGTGAGGT GGGCTTGTCC CACCTCAAAA GTTTCTACCC CCGTTTTATA 3960

ACATGGGGGT AGAATTTAAC ATACCATATA AAAAAGTTAC TTAAACGCTA TGTCCCACAA 4020

GGGATTGAGC GATTTTGTTT TTGTCACATT TTTTGACTAA AGTTGTCACA TTTTTTTGGA 4080

AGTAGGTTTA AAGCAGTGAG AGGTGTTGAT TTAAAGCGAT ATAGAAAAGA GCTAAAATTA 4140

AAACAGCAAG AATTGGCAAG TAAATTAGGA ATTGAGCGTT CGTTAATTTC AAAAATAGAA 4200

TCTGGAAAAC GTGTTATTTC TAAAGAGTTA GAACAAAAG 4239

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GCATATTAAT GTAGTCCATT TCTCGCTTCC TTTCATGGTG TATGCATCTA TAGTATCCGT 60

TTAAACAAAT TAAATCAAGA TAATGATAAT TAACACCTTC TTAATGTTTA GGACGTTTCG 120

ATTAAAGTGG TTATCAGAGC TTTCCGATAG TAGCGGTTAT AGGAACGTTC CTATAACGTT 180

GGCAAGCAAT GAnCCGGAAT ATCCTTTTGG GATATTCCGG GTnGCTTGTT GGGGTTTCCC 240

CAAGCCCCAG GCCGTCCGCC TGCGCGTCCG GCnGAACACG CCTTTCGGCG TGGCTTTGCG 300

CTCCCTGCGG TCGCTTCCTC CTGCACATCC GCGCAGGAGA GGGCGGCGCA AAATGCGCTG 360

TCAGGAGGTT TACGAGATTG ACAGAAAACT TTATTTCTCT GAATCGTTCC CTGTTTCGTT 420

CTTTGTGATG GTAAGCTGCC CTTGCTGGCA TTTCACAGTG ATTTTGTCGC CGACAGAAAA 480

TCCGGCCTGT TCCAGCCATT TTCCTTGTAA AACAATCTGC GTCGGAGCCT GCTTGTAATT 540

GCCATGCCCG TAACATACGG TCAGTTTGCG GTTATCCATC CGTCCCCCTT TCCCGCAACC 600

TGCCGGCATA CGATTTCAAA TACATTCCCA TCCTCAGTCC TGACAGTGAG CAGCCCGTTC 660

CGCTCGTCTG TGTCCAGGTC GGCAATCCCC ATCCCCTCGC TGTCATTCAG TAAATCAAAA 720

AGCCTGTCCT TGAAATAGTT CAGTTCCATT TTTCAGTTCC CCTTTCGTAT TTTATTGTTG 780

CTTATTAGCG AATACTTAAA AACAAATCCT GCCGCCAGTC TGCCGGTTAA GCAAAACGGA 840

TGCTGCAAAA AATCAGTGCC GTCCCGGTTG GAAAGGGGCG GCGCTTTTGC GTCACCGTTC 900

CGGTTTGGTC TGTTCTTTTT CCTGCGCCTG CTCCGGCGGT TCCAATCCTA AAATCTTATC 960

CATGTTGCGG AGTGCGGTTt GATAAGTAAT CATATCCTGC CGCAAgTCTT GTACTGTtCA 1020

TACTGTTCCC GTTTTcTTCa GCAGCGCGGC ATATTCCGCT GAAAGTGCGC TACTTTGGGA 1080

ATAGCCTTGC CATTCAGGGC ATCAA 1105

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

CGCCAATTGA AGCCCCACGA ACAAAAGGTT CATTTTGTAA GGCTTTGAAA TTTTTGGTTT 60

GTCCGGTGAG CATGACTCCC CAAATAGGTA ATTTTTCGAC TTTTTTATTT yTaTyTkGTT 120

GGATAAmCTT TTGGCCTyCT TGATTGTCAG CaAACAACGG GGATTTTTCT AAGGTTTCAA 180

AAAAGTGTTG CTTGTCGTTT TCAGGATCAA ATATTTCGTT TTGATCGTCC ATGCTTAATT 240

GAAAACCATA AGGCAGCGTA CCAGAAGGAC CTTCTGCTTC ATTAACCGTT TCGGAGTAAA 300

CATAGAGCCA AACTAAGTTG ACATTGCTCG GTAACATTTt GCGGACTTCT TCATATGGAT 360

AAGGTTTATC AAAAGAAATC GCCACTTCCG CTACTTGGTT TTCCATTTTA TCTAATTCAC 420

TTAATTCGTT TTTGATACCA CCATAGTAAT TGGTAATCGC TGGGTTATAA AAAGATGCTA 480

CTTTCTGCTT GGTTTGTCGG TTGTATTCAT AAAAATTCTT AGAAGAATAA TAGCTACCAG 540

GATAGACTTC ATTCCAGTCA ATCGAATTTC TGAAAAAGCT ATATCTGCTA CGTAAATTAC 600

TCCaCTCCAC CGTGTAACCA TCAATATTTT TTGAACGATT GGTCACAACT TCGCCCCCAA 660

AAGGCGAACT ATTAGCAATT ACTTGGGAAT CTAATTGAGT GTTTGGTGAA GCAATCATTT 720

CTTGATCATT AATTACTTCT AGTAGGGTAT GATAGTTTTT CGTCGAAAGT TTATCCATTC 780

CCACAAAAAA ACCGACAAAC AATACGGCAA AACTAACAAC GGTTATGGCA CCAATCACGA 840

TAAATTGTTT TCTTTTCGCT TTACGAATAC TTTTTTTTAA ATCCACTTCT ATTCCTCCAG 900

TTCTTTTTTT AATTTTTGAC GTGTGCGATA CAATTTTTTG CGAACATTTy CAaCmGATAA 960

TTCyAAAATC mACGcAaTCT CGGcATACGA TAATTGaTAA TAATATTTCA AAAGTACTAG 1020

TTCTTGTTCC TCATCTTTTA AGGaATCGAT CAATAATAAT AACTCTTGCC CTTCCATTTT 1080

TTCTATTGAT TGCAC 1095

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

TGTCGGGGAG ATGGAGTTTC CTTCCTCAGA GCTTTTCTAT TACCAGCAAC AACAATTTGC 60

TTTTCCGATT GATACTTCAA TGAATGTAGA AATTGTCACC AATAAAAAGG CATTAGCTAT 120

CGTTCGCAAC AAGAAAAAGG AATTAAAAGA TTTAGACAAC CACGCTTACC AATCTGACAA 180

TGAAACGAAT TCCAATGTTT TGGATGCTTT GGATTCCGTT GATGAATTGG AGACCACCTT 240

GGATCAGTCA AAAGAATGAT GAGGAAAAAT AGACTAGTCA AAACAATGCC TACAATCCGT 300

AAAATTTTCC TTTTCATCTC CTTCACTCCA TTCTCTcTTG aACCGGTGGG CGAGTATCAA 360

AGGCATGGAA GAGTTCTTCA AAGACCGGGT GAACCTGAAC CACACCTACC CGACCATACA 420

AATCCTGCAT CAAGCATTGG CCGTTTTCCA AATCTCGTAG GCGTTTTTGA TTACTTTCAT 480

CTTCTTGATC CAACCCAAAA AATTCCAAAG TCTTCTTGAT TTCATGAATA TCGGTACTAC 540

GAAAAGCAAA TTTCAATCCG ATATTATTCT TCAAGCGTTC ATCCAGTAAA TCGTCACTAT 600

TTTGCGTGAC AAAGTAAACA CCGGCATTCA TGGCCCGACC AGCACGAACG AGCTTATTTG 660

AAAGGGTCTT tCCTTGAGCC ACTTGAAGAA AACTCCAAGC CTcATCCAGG TcCACAATcT 720

TGAAGATTtC TCGATTACTA TGGATAAAAT CCAAGGCAAA CGTGGaAATG ACGATTAGCA 780

TAGAGACACT TAGCAACTCC ATCGTGGTAT ATTCTTCAAA AGTGGTTTCT GCATCTGGTA 840

AAACCAAATC CGCTACTTGA ATGATATTCA ACTGCTTATC TAAACTAATT GATTGGGTAA 900

TCGAACCATC TGAGAAAAGC AAATGGGCAA AATCATAATC GGTAAAGGAC TCGATATGAT 960

CGGCGATATT TTCCGCGACT GGAGAGTTCT CCTTTCGAAG CTCATTAATG ACTTGCAGCA 1020

ATCCTCGTTG ATCACTTTGG GTAACCGTCC GAATGGCTTT GCGCAATACT GGAAACTTCT 1080

CCCCATCCCG ACTGGAAATT CCTGTTAAAA AAGTCAGGAT ATCAATTGCT AAACTTTCTG 1140

AATCTTTCTT TTTCTTCATA ATCACATAAG GATCAAGTAA GCCTTGATTT TCTGGTTTAC 1200

TAGTCAAGTT GAGAATATTG ATTTCATCCG CAATTTCTGG CAAGTTTTCT TTCCAACCAC 1260

CTCGTTCTCC TTTTGGATCG ACAATCACAG CTTGGCCACC AAAAAGAACA GCATAGTAGA 1320

CCAAGAGATT GTTACTAAAG GATTTTCCGC CACCAAGAGA ACCAAGAAAA GCCGCAGCTA 1380

ATGCATTGGT TACTGAGCCC TTTACTCCTT GTGAGGCTAA TGCGGGTTTC AGGTAAACAT 1440

TACGCCCCGT ATCCGCATTG TAGCCAAAGT AAATCCCTTC CAACTCTCCT AACATTTGAG 1500

TGGCGCCAAA GCCAAGTCCT GCTAAAAAGT CAGATGTTAC ATACTGGATA TAGTCATTCA 1560

TATACCGTTT ACTAGCTGGT AGGAATTCTT CATGTAGCCC CATCGTATCG CCAAAGGGCC 1620

GGACTAGTTT CACATTGGTA TCATCATAAA AATCGAACAC TTCATCACAA CGGCGTTTTA 1680

GTTCATCCAC TGATTCTGCT CTCACCCGGA CCACATAGCT CAATTTGTAC ATGGATTCTT 1740

TTGACTGATC CAAGGTGGTC TCCAATTCAT CAACGGAATC CAAAGCATCC AAAACATTGG 1800

AATTCGTTTC ATTGTCAGAT TGGTAAGCGT GGTTGTCTAA ATCTTTTAAT TCCTTTTTCT 1860

TGTTGCGAAC GATAGCTAAT GCCTTTTTAT TGGTGACAAT TTCTACATTC ATTGAAGTAT 1920

CAATCGGAAA AGCAAATTGT TGTTGCTGGT AATAGAAAAG CTCTGAGGAA GGAAACTCCA 1980

TCTCCCCGAC AATGGTATTA ATTGTCAAAT AGGTTACATA AGACTCATGA TTCTCATGTT 2040

CAATCCTTAA GTAACGAGGT TTCTCTTCAA TCAAACAACG ACTGGGACGT AATAAGTCAT 2100

AGCGTTTCAC CAAaGTTTCT GATTTCAATT TTTTCTTTGG TAACTGAAAG GCGTATTCTT 2160

CAAACGGTGT ACCTTTTTCG CCATAAATAT GTTCAATCAA GTAAGTAAGA TCACTGGGAT 2220

TCACTCGTCT GACTTTGAAT CTCCGCGCTA ATTTACTTTC CATCAGTTTT TCAAGCTTGG 2280

TATATCGGCG AATTTCTTCA TTTGATAATG AAACAAAATC GCCCATCAAA TGATGATTGA 2340

CCTCATAGAT AAACTCTTGA AAGCCGGAAA AGAAGGATTT TTTGAGACTT TTCAAATTCA 2400

CTTCTTCATC TGTAGCAATC AGTTTGAAAC CAATAAAAAA GCGATAATCA ATCTGACTAT 2460

CGCCAATCAT GGATACTAAT GCGTCTGTCT GTAAATCAAT CCGTTGTAAT GCTATTTCTT 2520

TGAGTCTACC TATAACTTCC TTTTTAGATC GTTCCTGAGT GGCACGAATA CTACTTTCTG 2580

TCGCAATTTG TAGCGCATGA ATCTTACCTT CTCGATTTTG GGCAATCAAT TGGCGGAAAT 2640

TATCATGCAA TTGATATTTT TGTTCAGGAG ATAAGAAGGA ATAGTTATAA GGTATTAACT 2700

CATAATAAGC AAAACACTCT CCTTCTTGAT TAAAAACAAG ATTATTTTCG ATATACTTAA 2760

TCGGGTACAT AGTTCACACT CCTCACTAAG GTAATGGGTT CATCCCATCG TTTTTTCTGT 2820

TCTTTAACTT TTTTTCCTGC AAAAGTGACC TTAAATCGTA AATGATAACT GATAAAGGAT 2880

CGTAAAAATC CCAATGGTTT CTTGCCATCA AAAGTCTTTT GCGACATAAA CCAAGTAATC 2940

GCCACCGGGA TGCCAAAGTA TTTTAAAAAT GCCCCCTCTA TCACAGATAG TGGAGGCACA 3000

TGGGCAAATA CAATGACAAA CAGCAAGGAT AAAACAAACC AAGCCATTTG GTTAAAAGTT 3060

ACAGGAAAAG GCAGCTGAAA GTCATTGATT GCGTAAATGa CTTTTTCAAC TGCCCAGATA 3120

CTGGTGTAGC TTTTTATTTT TTTCATTAAC TCATCTCCAA ATATATTGTT TTTTAAATTA 3180

AATATTCTGT TATAATTAAA ATTAATTAGG GGGTAGATAA GTTTGAAACA AGAAGAGCTT 3240

AATCTTAAAT TATATGAGTT GCTATTGAAA ATCCAAAATG AATCTGACAC ACTAACAAAT 3300

GCTGACATTT CAGAATCAGA CGCAGATTTT TATGGATATC TTATCTCTAA AGAATTAGTT 3360

TATAATTTAA AAATAGAACA CTATTACAGC GGTCCAAATA TAGATGCTAG CCAAGCAATA 3420

ATCACAGATA AAGGATATGC ATTTATTAAT CAAATTGGTG AAGCAGATAA ACCTATTAAA 3480

ATGAATCGTG AGAATCGATA CAAACAACTT CAGATATTTC TCAAACGATT AGATGACCAT 3540

GACGCTGATT TAAGAACTCC AAATTATCGT GTTCAAGAAA TTGACTACTA CGACTTAATT 3600

AAATATGCTA TTGATTCAAA TCTCGTTAAG GGAATTGCTA TTCGATATGC TAGCAATAAA 3660

CCCCATCTTT TTTTATCTCA ATTTGCAAGG GTTACTACAG AGGGATATGA TGTATTAGAT 3720

ACTCCCTATC CAAAAAAATAA TACACCCGGA GCAACCATCA GTAATACATA CAATATCTAT 3780

GGTGGAGATC AAAAGGGTGC GAGTTTTGGC AGTAACAACA CAACCAATAA TAATTAAAAG 3840

GAGAGATTAG TATTGGACTA TCGAACCAAA GAAAAGAAGT TAAAGCAGCT CTTAAACTTC 3900

ATTTATGATG GAATTACAGT TACGTCAGAC TTATTGGAGT TATCTCAACA AGAATTCGCA 3960

TCATTACTGG AAAGCGCAAC AAAATCTGGc TACATCCgAG GTGCATCCAT AACAAAAACC 4020

AAAATGTACC CCATAATTTG GACTGACGAT GATATGTCAA ATGGACGTAA AGATAAGTGA 4080

TTTTTTTCGG CACCAGTAAG AGGTGCCGTT TTTGATTTAT TGGATAGTCC CGACAAATTT 4140

GTAGTAGATG GTAATGCGCT TTTCCTTACC CTTGCGGCAG CGCCCCATAC CCGGCGTTTC 4200

GTAAATCGTG ATCCGGTCAA TCAGTTCGTG CAGCATGAAG CGGTCGAGTT TTTCAAAGCT 4260

GGTGTATTTT TGGATAAGGG CGGCGAAGCG GTCAATATCA GCCTTTGCAT CCCGAACCTT 4320

TTCCAGTGCT TTTTCCAGTT CTGCAACTTT TGCTTTCAGT GkTTCCCGTT CCGTATCATA 4380

GTCCGCGATA AACATCGCAA AGATATGGTC GGGCAGTTTG CCGCTCATGT TGTCCTCGTA 4440

GGTGCGTtTC AGTTtCACAT CCAGGTCAGC CAGCCGTTTT TTTGCTGATG CAAGGTCACG 4500

CTTCATTGCT GCGGTCTGTT TCTGCTGGTC GGCGCATTTC AGTTCCATTA GCTTTTGCGC 4560

GGCTTTCTCG GTGTCCTCGC TGAACAGCCT GGCGTTGCGC CGAATGTCCT CAAGCACAGC 4620

CTGATGAAAG GTGTCACGGT TGATGTAGTG GGCGGAGCAG GCTAAATTCC CAATCGCATG 4680

cTGCGCCCGC AGGTATAATA GAAGTATTTC TGCTGGCTGA CTTTCGGAAC CATTGAAGTG 4740

CCGCAGkTTC GCAGAAGAAC AGTCCGGCAA ATAAATCGGG TTCGTCTTTG GCTTTGATGG 4800

TCTTTTTCCG CGCCCCCATA CGTTTCTGCG CTTCGTCAAA CAGTTCCCGT GATACAATAG 4860

GTTCGTGCAT ATTGGGAACA ACGATCCAGT CCTTTTTGGG TATCGGTTCC CGCTTTTTGC 4920

TGCGGTAAGA GGGTGTGTAC TGCCTGCCCT GCACCATGCT TCCTACATAG ATTTCGTTTT 4980

TCAGCATGAA CTGCACATAA GTCCGTGTCC AGAAACTGCG GCGCTCAAAT TCGCCGTCAC 5040

GTTCCGGGTT GTGCTTGCGG AAACGGGTGT ACTCTGTTGG AGACAAAATC CCCTCCCTGT 5100

TCAATGTCGT TGCAATGCTC TTTGACCCTA TCCCGGCCGC ACACATTTCA AACATCCGCC 5160

GGACAACCGG CGCGGTTTCT TCGTTGATAA TCAGTTTGTG CTTATCGTCA GGATGCCGCA 5220

GgTAGCCGTA GGGgTCGAGT GCGCCAAGAT ACTCGCCGCG CTTTGCTTTG GTATGAAGCG 5280

TAGACTTGAT TTTCGTGGAA ATATCTTTGG CGTACATATC GTTCAGGATG TGCTTGAACG 5340

GCGTAATATC CATGCTGCTG GTCTGGTTCA GGGTGTCAAC GCCATCGTTC AGGGCAATAT 5400

AGCGCACATG ACGCTCAGGG AAGTAAATCT CGGTGTACTG CCCGCACATG ATGTAGTTAC 5460

GGCCCAGACG TGAGAGGTCT TTGGTAATGA CCAGATTGAT GCGCCCTTTT TCAATATCGG 5520

CAATCATCCG CTGAAAGCCG GGACGGTCGA AATTTGTACC TGAGAATCCG TCGTCGATAT 5580

AGGTGTCAAC AATCTCCCAG CCTTGTTTCT GCACATACTC GGCCAGCAAT GCCCTCTGGT 5640

TCCCAATGCT CATGGATTCA TGGTCGGCTC CATCTTCGGA AGAAAGCCGG CAATAGATAG 5700

CGGCTCGGTA ATTCTGTTGT yCyCTCATAA AACTGCtCCT wATCAGTCCG aGaAACAACA 5760

GGGTTTACGC TCGTCTGTCA TCTATAnTAT ACCACATTAA AGCGTTAAGA GTCAAGCTGA 5820

CAGCCnTn 5828

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1246 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

GCACTTGACT TGCTGGGCTG CCACTTACAG TGAACAAGCA CTTAATAAGG tACTTAGAcG 60

AGTAAGCtCA TTAAAATGTA GGGTTTCCTC ATATAAAGTC CTCACTTTGG TTAATTGACT 120

ATGTAAAAAA CAAATTGCTT GTATCTATAT TAAAAAGAGT GCTACAAGCA ATATTTTAAT 180

CGTAGTTCTA GTAAATAGCA ATACTTTTAT CAAAATTCAT GTTTGGAAAT ATAATTTGAA 240

AAATATTTTT AACTAGCAGA AAAACATTTC TAACAAAAAG TATTGGCTCA AAGTAAAGAG 300

ATCGTTTTGT TAGAAATGAG AAATGGCAAC ATAAAAGTTT TCTATTTTTC TGCAATTAAG 360

ACAGTTTCAA AAGTGAATTC ACTAGGAATA TGATTCGCAA TTGAGTATTC AAAAATATGC 420

CCATTGCCTA GGTAAGCAAT TTGTTCTGCA CGCATCAGGA AATCATTATC GGTTAAGTTT 480

AAATATTTTT TTTCCAACGG AGAAGGACGA ATCCCAGAAA TGCTGACCCG CGCACTTTGA 540

ATTTTTTGAT GCAATTGTTC CGAAATATAT TGATAAATGG AGACTTTCAA TTCTTTCATT 600

GTCAAGTTCG GAATTAAAGC AACGGGCATC CAAGTGTATT CAATAATTGA GGGCACATCT 660

TCGATAATCC GTAAGCGAAT AATTTTGTAG ACTAACTCTT CTTCTGTAAT ACTTAATTTT 720

TCAGTCACCC AAGGCTCAGG TACTTCTGTT GCAAAGCCTA AAACCACGGA TTCAACTTTT 780

CCATCGTAGG TTGAGTAAGT GCCGGTTAAC GGAGAAAATT TAGTAATGGT TCGATTTTGA 840

AAGTCTTGAA CAAAGCTGCC CGAGCCACGT CGTCTGACAA CATAACCTTC TTGCACAAGC 900

AAATGTAAGG CTTTTGTAAT GGTTAGTTCG CTGACCTGAT ATTTTTCTGC AAGAAGACGA 960

CCTTGGGGTA ACTTTTGGTT AATTGGATAA ACACCTGCTT CAATATCCTG TTTTATAGCT 1020

GCATAAATTT CTTTATAACG TGTATTTGTC CGCATCAGAG TCcTCCTTTA TCACCAGTAT 1080

TTCTCTCATT ATACCATGAA TTTAACGTGT TAAAACTATA TATTTATTTT TAACGTAACC 1140

ACTTAATAAT CAAGTACTTA AATAAAAGTA GTTGACTTAT TCTTTTTAAA ACTATATAGT 1200

TTTAAAAGTA AACAGAAGAA CTTATTGATC TGATTGGTAC TTTTTG 1246

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

CAGTTTAGGT TGGTCAAGAG TnATTGGACA CCAGTTATTT GAAAATTGGT GGAATAAATT 60

TCTTCCCTGC TTCGTCATTA TCTACAGCCA AAACAAGtTG GACTTTTTCC GtTGTTAGTT 120

TCGACTTTTC TAATTGTTCA AGAACGGTTG GCTTTTCTTC CTCTTTGACA TAAGAGCCAA 180

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TTTCATTGGC AATAAGCGTA GATACTGCGC CCTTTTTAAG TCCATTCGCA CAAAATAATA     240
CCGCATCTCC AATCGTCTCT TTTTTTAATT CGTAATAACT CATGAGATCT ATAGGCGCTT     300
CAAAAACAAT GATTTTGATT GGCTTTTCTG ACGTAGCTTC TGCAATTTTT GGTGGATACC     360
CTACACGAAC AGTCAACCCA TAATAGCCAT TTCCCCAGAC ACGCTTTAAC CGTCCTCGTT     420
CGCCATGTAG CTTCTTATTT TCCCAAATAC CTTGTAAGGC AACGCCTTTA ATTTTTTCTT     480
CAAGACCAAC GTGCTTGAAG ACTATTACTG GTTCACTTTG TCCGGTCTCT TTATCTGTAT     540
ACGTGGATTG TGCCATGAGG TTTTGTTCAA AAAAGAAATC AATCGTTTCT CTTGATAACT     600
TACGTTCCTG AAGCAAGTAA TCAATGGTGG CATTTTGTTG TGTATGTTCT TTCATATAAT     660
AATGAAAGTT CGTCGGAGTA GGTTCTTTCA ACGTTTCAAT AGCCCCTGCT TCTACGGTCT     720
GTAAATACTG CAATGCTTCA GCGTGTGTAC ACTCTTTTAT CACTTGAACA AGCTTAATAC     780
TCCCACCACC AACTTGGCGA GAGTTCCAAT AAAAAGAATT CTTCTTAGGG GTTAAAACAA     840
AACTATCGTG CTCTGACCAG GTATAACTTT GTCCCTGTCG TACAAGTGTT ATTCCTAAAC     900
TTTCTGCGAC ATCCACAATA CTTTTTCGTT CAATTcTcTA ACACTTTTTG TCGTtGTGCA     960
TGTGTCATtG GCATTTtCTG TtCCTCCTTT TTCTATTTTC TGAAATAAAA AACGCACGTC    1020
TTTTTAAACG TGTGTTTCTT CTTtCAGTTC ACTTGTAATT TCTCCATGGT CAATAATATC    1080
kGTTGCCGAG ATTTTATCCA AAATAGCTTC TTCATCAGTC ATATATCGGC GCCACGTATA    1140
CCACTTATCA TCAGTCGGTC CTGTTGCTAG TTCATCTGCT CGGTCATGCT GAAAAGCATA    1200
GAATTTTTTA TCTTTAAAAA CATGCTCTTT TGATATAAAA ACCAGACACT CGTCTCCTCC    1260
AATAAGCGCA ACTTCACTCC TGTCAATCAA ATCGCGCCCG TATTTATCTC GATTTTCGGA    1320
TCCTCCACCT TGATTTCCTT TATTCATGCT ATGTTTCCGA ATAGATAATG TTTGTTTCCC    1380
TGCACGCGCA GACAGATACT TGGTGGTTTC TTCTTCGTCT CCACCAAGGT ATAGTAAACA    1440
CGCACAGCCA TTTAAAATGT TTTGCCACCC ATTCCGATAA AGCGTTTGTA ATTGGTTCAA    1500
GGACTGTAAA ACAATGGTAA ACGACATTTC TCGCTTACGA AACGTGGTCA ACATTTTCTC    1560
AAAGTGAGGA ATTCGGCCAA TATTGGCAAA TTCGTCAATT AAGAAGCGGA CATGTAGGAG    1620
TTCTTTTCCT TCTTCTAGTA CTCGTTTTCC TAAACGTACT TGGTCTGATT TATTTCGCAA    1680
CACTTCTCCG ACTGTCGCAA ACATCAACGC TGCAATAAAA TTAAACGACG TATTAGTTTC    1740
AGGTATCGCA ATAAACACCG CTGTTTTTTC TTCATTCCAG GAGTCAATAT CCATCGTGTC    1800
TGTACGAATC ATATTGACCA CTTCTTCATG GTCAAAAACA GAGTAACGTG CAGCAGCTAT    1860
CCCTAGAACG CTTGCTCTCG TTTCACTCTC ATACAAATTG TTAAACAAGG TCCATTGTCG    1920
GTAAGCGTAG TTGTCAGGAA TGGCCTCATT TAACTCCTCA AACCATTCTT CCACTGGGcT    1980
AGGTACATTT TyATCTTTTC GTTTTAGGTG ACGTAACATG TCCGCAATCA TTCCTAAATG    2040
TGGCGTATAA TCATTTCTGC GACCGTCAAA CCATAAATAC GCAATAAGAG AGCGAACCAA    2100
TAAGCCTTCG GCTTTTATCC AAAAATCTTC CCCGGTCGTT TTTTCCCCTT CTTTTGTTGG    2160
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CTTCGGTGAC AGCTTCTAAA AACTCGGTCC ACGTCTAAAT CnGAGTGCAT A 2211

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

TACCGATTGA ATTCATTGCT TCCGTTTGCG GAGAATGTGT CAACACATAT GATAAAACCG 60

TTTGTAAAAT AACTGATGCT ACAGCGAAAA CTTTTAAAAA ATCGCTGATA TTCAGATTTA 120

TTGGTTGTTC TTTACTCATG TACGTCCTCT TTCTTTCAAT AATTTAGCGT GTAAGTAAGC 180

GCTCGGATTA AGAACTTACT CACACGCTAT TCACGCTTCT TTGATTTACA TTGCTAGCGA 240

TTCATAATTG GCTAACAAGA TGCCGCGTTC TTCAATCGCT TCTTTGACTT CTTGAGACGT 300

TAATATTTCC ACTTCACGAA TTCGAGGCAT ACAATACCCT GATTGATTTT GTAAAATAGT 360

ATCGATAAAC GCAGGATGAC AATTGATTTC AAAGACCTCT CCTTCACTAC AAACAACCAT 420

ATCAAGCAAT TGCAAGATGG TTTCAGTTGA AATCGCCTTG TCATAAAATT GGTACAACAT 480

TTCATCTGGC GTGCGAACAT CCTGATATAA CTCTAAATAG TCTTkTGTTT CAATACTTCT 540

TGAGGCGTTA CGTAAAGGTA ATTGATATTT GCGAGCAAGT GCCAAAGcTA CGCCCAATAA 600

CTTTTTATTT TTTCCGTGAA CATTATGATG AGAATCAATA TGATCAGGGC GTCTGCCACT 660

TTTCATAAAT GAAATAATTT GAGCATCCCA TTCGTTATAA ACCTCTTCTA AATTGACTTT 720

TTCTTCaAAA ATCGATTGAT GCCAArAATA ACCAGCkTCA TCTACTAAGG AAGGGACCAT 780

TTCTCGAGGT AAAATAGGTT TTGCTTGGTn CAATGTCAAT GTTAAA 826

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

TAAGCTAGAT GCGATAGAGT TATATTTAAC AACAGAGTTG TCCTATCAAG AAGTAGCTAA 60

TCTTCTAAAG ATTCGCAATC CATCATTGAT TGCGAATTGG CTTAGAACGT ATCAGAAGTT 120

TGGTATAGAG GGACTCTCTA AACAGAAAGG ACGTCCACCT ACCATGTCTA AAAAGAAACG 180

AAATGAACCC CAACCACTAC CAAGTGAACG ATCTCAAGTA GAGAAAyTAG AAAAAGAAAA 240

TAGAATGTTA AAAAkTGAGA ATGCCTATTT AAAAGAGTTG AGCAGACyGC GTTTAGAGGA 300

CGAATAAAAA ATGGACGAAT CAAACGAATT ATTCATAGTT TCCAAGGACA ATTTCGATTA 360

AAAGTTATTC TGGAAACCTT AAGGTTTCCA AATATCACTT ACATGTACTG ACAAAAACGT 420

CTCGACAGAA CAGCTCTAAC ACAAATAATC GAAGAAGAAA TTCAAGTGAT TCGTAAAAAA 480

AACATAGGCA TTGTACAAGA ATTTGGATAA ATCTACCTTC CAACAAATTC TTAACACTAA 540

CTTAGTCACG AGTTAGTGAA AAGAGTATCA ATCTTAACAA AGTTATTCTT GAAAAGAACG 600

GGTATCTTAG TTGGTACCTG TTCTTTTTAT ATGATAGATA TTGAAATTTA AGGATAAAAT 660

CTTTAAAATA TGGATATCTT TTAAAGATTT TATAATTGAC CTTCTTATGA GAGATATCTT 720

GTTCAAAAGA AGGGAGCTCC TATCTTTTTC CAAGTTTTAA GTAGGAGTTT TTATATGTAA 780

TACTTTGCTT AGTTTAAAGC TATCGTATTA TATGAAGAAA ATACTTATTA AGGTATCaTC 840

aATTATGAAT GTAAAAAAGA AAACTATTTT TATAAATnAT TTATATAAAA AGTATTGCAT 900

TAAAAAATAG GTTGTTTTAA AATAAAGTTG TCATCATAGT ATGACTCTTT TCGATAGAAT 960

CTCCTATTGG AAACGATATG GATTCTTTAT TGAAAAAGAA TGTTGGAGTA ATGATTAGTC 1020

AAGTCCAGAC TCCTGTGTAA AATGCTATAC AATGTTTTTA CCATTTCTAC TTATCAAAAT 1080

TGATGTATTT TCTTGAAGAA TAAATCCATT CATCATGTAG GTCCATAAGA ACGGCTCCAA 1140

TTAAGCGATT GGCTGATGTT TGATTGGGGA AGATGCGAAT AATCTTTTCT CTTCTGCGTA 1200

CTTCTTGATT CAGTCGTTCA ATTAGATTGG TACTCTTTAG TCGATTGTGG GAATTTCCTT 1260

GTACGGTATA TTGAAAGGCG TCTTCGAATC CATCATCCAA TGATGCGCAA nTTTTGAATA 1320

TTTTGGTTGA TC 1332

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

CTATATAATT AAAGTATTTT AGATCTTAAC TAGGATCTAA AAACTGTATA TAAAAAACCA 60

TCTATACTTT ACAAAAATAA TATTTTTGGA GTTATAAATA ATGAATGAAT TTTAATAGTA 120

AATTAAATTT TGTTATACTT CAAGTTCTGG GTTGCATGTG CAGAATGTGC AGGTGGCTCC 180

AGCAAATTAT wATwCmCCmC AmCAAaTCGT GATTGGTGGT GAGGTTGCTG CTGTTGATCA 240

AGCGATGACA CTTCTCAAAG AAGCTGGTGT GAAGCGAATG ATTCCGTTAA ATGTGAGTGG 300

CCCTTTCCaT ACGGCGCTGT TACAACCaGC ATCaAAAAAA TTGGCTCAGG ATTTAGCAAA 360

ATTGAACTTT CAAACGATGC AAATTCCTGT CATTAGTAAT ACGACTGCCG AAATTATGCC 420

CCAAGAGGCA ATTCAAGCGT TATTGGAAAA GCAAGTCATG TCTGCGGTAC GTTTTGAAGA 480

CAGTATCGAA ACGATGAAGG CTATGAACGT AGGAACGATG ATTGAAGTTG GTCCAGGGAA 540

AACATTAACT GGTTTTGTTA AAAAAATTGA CAAAACAATT GAAATGCACC GTGTGGAAGA 600

TGTTGCAACA TTAACAGAAA CGTTAACAGC GCTTACTGGG AGGTAAAAAA TGGAATTAAC 660

AGGAAAAAAC GTATTTATTA CTGGAAGCAC TCGTGGGATT GGTAAAGCAG TTGCGTTAgC 720

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TTTTGCGAAA GAGGGCGCCA ATATTGTCTT AAACGGTCGG AGTGAGATTA CGCCAGAACA     780
ACGACAAGAA ATTGAAGCCT TTGGGGTAAA ATGTATTGGC CTTTCTGGAG ATATTTCCGA     840
TTTTGATGCG GCAGGTGAGA TGATTCAAGC AACAGTTGAC CAATTAGGCT CGATTGATAT     900
TCTGGTGAAT AACGCTGGGA TTACGAATGA CAAATTATTA TTACGAATGA CAAAAGAGGA     960
TTTTAATGCC TGTTTAGATA TTAACTTGGT AGGAACTTTT AACATGACCC AGCAAGCGGT    1020
TAAACGTATG ATGAAACAAC GAAGTGGTCG GATTATTAAT ATGGCTAGCG TTTCTGGTTT    1080
AATGGGAAAT GTTGGTCAAG CAAACTACGC TGCGAGTAAA GCCGGTGTCG TTGGTTTTAC    1140
TAAATCGGTG GCACGAGAAG TTGCGCCGCG CGGTATTACC TGCAATGCGA TTGCACCAGG    1200
GTTTATCCAA ACAGAAATGA CGGATGTTTT ATCGGAAAAA GTTAAAACAC AAATGAATGC    1260
GCAAATTCCC TTACAAACGT TTGGGCAAGT CGAAGATGTC GCAGCTACAG CGATTTTCTT    1320
AGCTAAAAGT CCCTATATTA CTGGGCAAGT CGTGAATGTC GATGGCGGCT TAGTCATGCA    1380
CGGATAAACG AAAGGAGTCA AAAGGATGAA TCGAGTAGTT ATTACCGGTT ACGGTGTCAC    1440
CTCGCCGATT GGCAATGAAC CTGAGACTTT TTTAGAAAGT TTGAAAACAG GGAAAAATGG    1500
TATCGGACCG ATTAGTAAAT TTGATGTTAG TGAAACAGGT GTCACCTTAG CAGCTGAAGT    1560
GAAAGACTTT CCAATGGAAA AATATTTTGT TAAAAAAGAT GGCAAACGCA TGGATAAGTT    1620
TTCGTTATTT GGCATTTATG CGGCCTTAGA AGCAATGGCT ATGAGTGGCT TGGATACCAG    1680
TCAACTAGAT GTGGATCGGT TTGGCGTTAT GGTGGGTTCC GGAATTGGTG GTTTGGAAAC    1740
AATTCAAAAT CAAGTAATTC GGATGCACGA CAAAGGACCT GAACGTGTGG CACCGTTATT    1800
TATTCCAATG GCGATTGGAA ACATGGTGGC GGGAAATATT GCTTTACGTG TTGGTGCCAA    1860
AGGAATTTGT ACTTCAACAG TGACAGCTTG TGCTAGTGCA ACTCATTCAA TTGGGGAAgC    1920
GTTCCGCAAT ATCAAACATG GCTACTCCGA TGTCATTATT GCTGGTGGAG CAGAAGCGCC    1980
TATTACAGAA ATCGGTATTT CAGGATTTGC TTCCTTGACC GCTTTAACAA AGGCGACTGA    2040
TCCaGAAAAA GCCTCAATTC CCTTTGATAA AGAACGTAGT GGATTTGTGA TGGGAGAAGG    2100
AGCGGGTGTC TTTATTTTAG AATCATTAGA TCATGCTCTA GAACGAGGCG CAACTATTTT    2160
AGGTGAAGTG GTTGGCTATG GTGCTAATTG CGATGCCTAT CATATGACAT CACCAACACC    2220
AGATGGGAGC GGCGCAGCGA AAGCCATGGT ACTAGCAATG GAAGAAGCGG GGATTTCTCC    2280
AGAAAAAATT GGCTATATTA ACGCCCATGG AACAAGCACA CAAGCCAATG ACAGTGCAGA    2340
ATCTAAAGCA ATTGAATTGG CTTTAGGTGA TGCCGCAAAA ACGGCGTATG TAAGTAGTAC    2400
AAAGAGTATG ACGGGACATC TCTTAGGCGC CGCTGGTGGA ATTGAAGGAA TTGCTACCCT    2460
AAATGCTTTA CAACATCAAT TTATTCCGCC AACCATTAAT GTGGAAAATC AAGATGAAGC    2520
AATTACGGTG AACGTTGTTT TAAACGAAAG CAAAGAGCAT AAATTTGaTT ATGCTTTAAG    2580
TAACTCGCTA GGCTTTGGTG GCCaCAATGC AGTTATTTGC TTAAAACGCT GGGAGGATTA    2640
ACATGCAGTT AGAAGAAGTA AAAGCACTAT TAACACAATT TGATCAATCA ACTTTAACCG    2700
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AATTTGATTT ACGAGAAGGC TCGTTTGAAT TATATATGAA TAAAAATACA GTTTCTGGGC 2760

GAAGTGCCGT AGAACCAGTG GCGCAACCAC AAGAAACACC AGTAGCCGCT AGTGGTGTGT 2820

CAGTGCCTGT TGAAACAGTT TCTGTCGTTG AAGAAACGCC AACTAATACA CCGACAGCCA 2880

ATGAAAAGAC AGAAGAAATT ACGTCACCTA TTGTAGGAAT CGTTTATTTA CAACCAGCAC 2940

CAGATAAAGA GAACTTTGTC AAAGTAGGAG ACACTGTTAA AACGGGTGAC GTTGTGTGTA 3000

TCGTTGAAGC GATGAAaTTA ATGAATGAAA TTACGGCGAC AGTTGACGGT GTGATTACTG 3060

AAATATTAGT CAACAATGAA GATGTGGTTG AATTTGGTCA GCCGCTATTC CGAGTTGCTA 3120

AAGGAGAATA AAACATGAAA TTAACaATTA CAGAAATTCA AGAAATTTTA CCACATCGCT 3180

ATCCCTTTTT ATTATTAGAT AGTGTTGAAG AAGTCATTCC CGGGGAACGC GTTGTAGCGA 3240

AAAAGAATGT AACGGTTAAT GAGCAAGTTT TTCAAGGTCA TTTTCCTGGG AATCCTGTTT 3300

TGCCAGGAGT TTTAATTATT GAATCGTTGG CTCAAGCAGG CGCCGTGGCA TTACTTTCAA 3360

TGCCTGAATT CAAAGGGAAA ACGGCATACT TTGGTGGATT AGATAAAGCA AAATTTAGAC 3420

ArAAGGTAAC ACCAGGCGAC ACATTAATTT TAGAGGTTGA ACTTTTAAAA GTCCGCGCTT 3480

CTGCTGGAAT GGGTAAAGGT GTGGCAAAAG TTAATGGAAA AAAAGTTGCC GAGGCTGAAT 3540

TAACCTTTAT GATTGGATAG GTGAAAAATG TTTTCGAAAG TATTAATCGC AAACCGCGGA 3600

GAAATCGCTG TTCGTATTAT TCGTGCCTGT CGCGAATTAG GCGTTCAAAC AGTTGCTGTT 3660

TACTCTGAAG CGGATCAAGA AGCGTTACAC ACACAGTTAG CAGATGAAGC CATTTGTATT 3720

GGACCGGCGA AAGCAACTGA TTCTTATTTA AATGTTCAAG CTGTTTTAAG TGCAGCGATT 3780

GTTACCAATG CTGAAGCGAT TCATCCAGGG TTTGGTTTCT TATCTGAAAA TAGTCAATTT 3840

GCTTCAATGT GCGAAGAATG TAACATTACT TTTATCGGTC CTAAAGCAGA AACGATTGAT 3900

GCAATGGGCA ATAAAATAAA CGCACGTCAA CTGATGCAAA AAGCCAAGGT ACCTGTTATT 3960

CCTGGGAGTG ATGGCGTCAT TGATTCTGTC GAAGAAGCGT TGACGATTGC TGAAGAAATT 4020

GGTTACCCAG TGATGTTAAA GGCAGCTGCT GGTGGTGGCG GAAAAGGAAT CCGAAAAGTT 4080

CTTTCAAAAG AAGAGTTACC GAAACACTTT ACTTCAGCGC AgcAAGAAGC CAAAGCCGCA 4140

TTTGGTAATG ATGATATGTA TTTAGAAAAA ATTATTTATC CAGCACGTCA TATCGAAGTG 4200

CAAATTTTAG GTGATCAATA TGGGCATGTG ATTCACTTAG GGGAACGTGA TTGCTCACTA 4260

CAAAGAAATA ATCAAAAAGT GTTAGAAGAA TCACCATCGA TTGCTATTTC TGAAGAAAAG 4320

CGTCAGATGT TAGGCGAAAC GGCCGTTCGA GCGGCACAAG CTGTGCATTA TGAAAATGCC 4380

GGAACCATTG AATTTTTGAT GGATCCAGCT GGCGACTTTT ATTTCATGGA AATGAATACC 4440

CGCATCCAAG TCGAACATCC AGTTACGGAA ATGGTAACAG GGATTGATTT AGTCAAAGCA 4500

CAATTAGAAA TTGCTTCAGG TGAACCTTTA GGCTATACCC AAGAGGATGT TATCATGAGT 4560

GGGCATGCGA TTGAGTGCCG AATTAACGCT GAAAATCCTG CCTTTAATTT TGCTCCTTCA 4620

CCAGGTAAAA TTCAAAATCT CTTGTTGCCT AGTGGTGGAA TGGGCTTGCG TGTAGACAGC 4680

GCTATGTATT CAGGGTATTC AATTCCGCCT TATTATGATT CAATGATTGC AAAAGTCATC 4740

GTACATGGTG AAAATCGTTT TGATGCCTTG ATGAAAATGC AAAGGGCTTT AAATGAAATT 4800

GTAACAGAAG GTATTATTAC GAATGCCGAA TTCCAATTAG ATTTAATTAC ACATGACAAT 4860

GTTTTGACAG GTGACTATGA CACAAGCTTT TTACAAGAAA CATTTCTACC AAATTGGGAG 4920

CCAGAAAGCA ATCATTAAAG AAAGAACGCC GCAAGAGCTG TGCTCTTGCC GCTAAAATAC 4980

GAGGAGTAAG CAAATGGCAT TATTTAAAAA GAAAAATTAC ATTCGCATTA ATCCAAATCG 5040

TGCTCATGCA AATGATGCAT CAAAGAAGCC TTCTGTTCCA GATAATATGT GGGCAAAATG 5100

CCCTTCTTGT AAGCGAACAC TGTATACAAA AGAAATGGGT GCAGAAAAAA TCTGTCCGCA 5160

TTGTGGCTAT AGTTTTCGGA TTGGTGCATG GGAACGATTA GCGATAACCG TTGATGAAAA 5220

AAGTTTCCAC AATTGGGACA GTGAATTAGT GACAAAAGAT CCACTAAATT TTCCTGGTTA 5280

TCTTGAAAAA ATTGAAAAAA TGCAAGAAAA AACTGGGCTA GATGAAGCTG TCTTAACGGG 5340

AGAAGCAACA ATTGAAGGAC AAGCTGTTGC AATTGGAATC ATGGACGCTA ATTTTATCAT 5400

GGGCAGTATG GGAACGATTG TTGGTGAAAA AATCACACGC TTGTTTGAGC GGGCGACAGA 5460

AAAgCATTTA CCAGTAGTGA TTTTCACTGC ATCTGGTGGT GCCCGTATGC AAGAAGGAAT 5520

TTTTTCATTG ATGCAAATGG CGAAAATTTC GGCCGCTTTG CAACGGCATA ACAAAGCAGG 5580

CTTGCTGTAT CTTACGGTAT TGACTGATCC AACGACTGGC GGTGTTACCG CAAGTTTTGC 5640

GATGGATGGC GATATTATTT TGGCAGAGCC TCAGAGTTTA ATCGGTTTTG CTGGCCGCCG 5700

TGTAATTGAA CAAACGATTC GTCAAGAGTT GCCAGATGAT TTTCAAAAGG CCGAGTTTCT 5760

TTTAGAACAT GGTTTTGTAG ATCAGATTGT GCCAAGAAAT CTTTTGCGTC AACGATTGAG 5820

CGACTTGTTA CGTTTACATT CTTTGGAAGG GTGGCGCTAA CATGGAAAAG AAAACAGCCA 5880

ATGATGTTGT TACCTTGGCA AGAGCCCAAG ATCGTTTGAC AACTTTAGAA TATATAGAAG 5940

CAATTTTTGA GGACTTTTTA GAATTTCATG GGGATCGTTA CTTTGCCGAT GATTTAGCTG 6000

TAGTCGGTGG TGTTGCTACT T 6021

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

TTTTTTAAAC CGAACAATTT TGGCAAAAAA CGAAAAAAGA ATTAACAGAG GGGACACGAT 60

TTATCGCAAT TGGTTATGGG CCCAATATTG GTACGGCGAA AGAGTTTGAG ACGAAGTTTA 120

CAGAAACAGT TCGCTTACCT TCCCAAGGAT TtGAAGTCGA AGCCTATATG CATGGGCCTT 180

ATCTTGAAGC GGATAATACA CATCTTTTGT TTTTTATTGA AAATCAAAGT CCTATTCAAG 240

CACGTAGCCA AGCCTTGAAA AATTATCTAG CCAGTTATGT TGGCCAATGT TACACAATTA 300

CAACGCGTTC AACGAGAGCA TCAAATACGT TAGATTTAGC AAGTGATGTC GAAGAAAAAA 360

TTAGTCCTTT ATTGTTAGTT ATTCCATTTC AATACTTGGC GCATCAAGTA GCTACAAGTA 420

AAGGAATTGA TTTATCTCAA CGGATTTTTG ATGATTTTGA TTGTGTCCTA AAAAGTAAAA 480

TAGCAAAGAA AGAGGGAAAT CAGCCATGTT AAAATTTAAT GAAGAACAAC AAATCAAAGA 540

CATACGAGGT GCCTTAGCCT TGCGTTCAGA TGTTGaAAAA GTTGTTGaTC AAGTTTGGAC 600

GAAAGGATTT GATGCGGTTT ATTATATAGG AATCGGCGGT ACTTATGCTT CaGCCcATGc 660

AAGCaGTTaC TTATGCGaAT GGAAAAAGTA ATTTACCAAT CTATGTTCAA CATGCTGCTG 720

AGTATTACAC AACAGGCAAT AAACGTTTAA CAGAAAAATC ATTCGTCATC TTGTCTTCCG 780

TTACTGGGAC AACACAAGAA GTGGTGCAAG CCGTTCAAGA AATCAAAAAG GTCGGCGCAA 840

CGCTATTTGG TTTTATTGAT GCAAAAGATA GTCTTTTAGC AGATTTATGT GATTATGTGG 900

TGACTTATCC AGCTCCAGGA ACTGAGCAAA TCAAGTTCTT TATGGTAGCT GATCGTTTAA 960

TGCAAAAAAA CAACGAATTT ACAGATTACG AAAATTATTA CCAAGAATTG GAAGAATATT 1020

TGCCTACAGG TTTAGCTGAA GCCGAAAAAA GTGCCGATGC GTTTGGCTTA GCTTTTGCGG 1080

AAAAACATCG TCATGATAGC ATTCACTATT TTATTGGCGC AGGGAACCAA TGGGGAGCGG 1140

TTTATTCTTA TGCAATGTGC TATTGGGAAG AGCAAAGTTG GCTTCGTTCA AAATCAATTC 1200

ATGcAGcAGA GTTCTTACAT GGaACGCTAG AAATTGTAGA TGAAACTACG CCAGTAACGT 1260

TGTTTATtGG AGAAGACGAG CAGCGTCCGT TGGcAGAACG AGTAGCaAAA TTATTGCCGA 1320

AAATCTGTGC CAATTATACA ATTATTGATT CGAAAGcGTA TGAACTTCCA GGrAtTAGTG 1380

AAAAATATCG TGGCCGAGTT GTTTCCATTT CTCCCTAATG CATGCGGTAA CGCAACGCAT 1440

TGATGCGCAT GTAGAAAAAT TAAATTGTCA CCCATTAGAG ATTCGTCGTT ATTATCGTCA 1500

ATTTGATTAC TAAGACAAAA TAGCCTCTTT TTCCAGCAAG CCTGTGGTAG ACTGAAGAGA 1560

GAATACTTCA GAAAGTAGGA AAACCAATGA CAAAACCGAA AATCTATACA ATGACCTTTG 1620

CCAGTGTTTA CCCGCTATAC ATCCAAAAAG CAGAACGTAA AAATCGAACG CAAGCGGAGG 1680

TTGACGAAAT TATTTACTGG TTAACTGGTT ATGATGAAAA AGGCTTGCAA CAACAATTGG 1740

CTCAAAAAGT AACGATGGAA ACATTTTTTG AAGAAGCACC CAATTTTAAT GAAAACGCCC 1800

AATTGATCAA AGGCGTAATT TGTGGcTATC GCGTGGAAGA AATTGAAGAT CCTTTAATGC 1860

AArAAATCCG TTACCTAGAT AAATTAATCG ACGAATTGGC CAAGGGAAAA GCGATGGAAA 1920

AAATTTTAAG AACAkGAAAA cAGGGTCtCa AkGAGACCCt GTTTTCaTGc yCcCtTGTAC 1980

ACGGAATTTA ACTATTTCCT GTATTAATGA AAGAGGTAAC TCTTGCGTGT AGGGAAATTG 2040

AATGGCACCT TTTGAGGTTT TAAAAGGGCG TAATTCTTTG CTGAAACGTT GGATGGCTGA 2100

TGGCGTAGGA TAGAAACCTA AATGTTGCTT AGCCGCCGCA AAATGCACTA AATTGCCATT 2160

TAAGTAAAAG GTCGGCATTC CATAAGCGAT TTTTTCAGTA GTCTCCTGAG GAACAACTGC 2220

TAAAATTGCT TGGTAGATTT CTGTTAACTG TGTTTGATGT TGGGGTTGCT GGCGAATATA 2280

GTTTGCAATG ATGGTCATAT AAAAACACCT CCGTTTGTTT CAGTATACTA TGTAAAAAAT 2340

AAAAGGCGAA GGAGATACAA AAAAACCGTC TAGTATkTTT TCTTTACTAA ACGGCTTTTA 2400

GCTTAAATAA CTACCTAAAG GGTCTTGCAT GGAAATGTTT GTCACkCCTT AGTTTAATTG 2460

TTTTAAGTGT GCAATTGCTT CTTCAATTGT GTGACCAGTT GCTGTTTTAC TTTCATTTTT 2520

kGCATCAAAA ACAATGAAAA TATTTTTGTC TGTGTCTAAT TGAATACGGT ATTGAATGTT 2580

TTTTACTTTG TAAGTCATAG TTATTCTCCT TTCATAAAGT ACTCTAAAAA GGCGACGATA 2640

ACTGATAACG AAATTCCATT GTTACTATAC CACTGGAAAA TTATTTTTGC AACAAATAAC 2700

ATTTTTTCTT TACCATTCCT TAGACTTCTT TGCTAGCTAC TTCTTTACAT TCTTTTTCAA 2760

GAAGCATAAA ATAAATACAT TACTAGTTTT TGAATAGGAG ATCGATGTGA AAA 2813

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

CACTTCTTCC TGTTGAATGA GTCGCTTAAG CGCCAATGTa GGTCACGCCm CTACTATAaG 60

CAtTACATTA GGTAAGACAC GATACGAAAT CGTTTGATCa TTGATGACAT TGCTTTCAGA 120

AATAATGATT CCATCAGAAG TGACCGCTTC AACAAAAGCA ACATGTCCAT ATTGATTATC 180

TGCGCCAGCA ACTCCTGGTT GGAAACTAAT CGCACGACCA GCTTTAGGCA ATGAACTAAC 240

TTGATAGCCT AATGCACGTC CTTTTCTTCC CCAGTCACTG CCATTTCCCA TAAATTCATC 300

CACAGAAGTG CCCAACTGTT TGAAACGATT ATAGACATAC CACGTACATT GGCCCaCGGG 360

ATAGCTACCA CTTCGATTAT AATTGATCCC ATCATAGACT GGAAAATGCa TTTGTTGcTG 420

tTCCGCTTCC GACAGyTTAT TTTTAGATTG GATAATCAAA CCGTCCACTG TTTTTGGTAA 480

ATCAAATTGG GTTAAGTTAT AAACCGCAAT TAACGAATTT AATTTATTAT CGTATTGCTT 540

gTCTGTTGCA TATTTACCTG TTAAAAAACG CGTTGCTTGA AGGTAGTTTT TGGCTTCCGA 600

ACGCCACGCT GGTTTATAAA AATCTTGATT TCCGTCAATC CCTTGTCGGA GTAATTGAAC 660

ATAATCTTGC AGTGAGTCAT TATAGCCACC GTAATCGCGA AACCCAGCGG AAATTGTATA 720

AAGTTGGCCC CTCTGgATCA GCCTCTTTTG TTGAAAAGCT AACACTATTC CTGGAACGAA 780

CCTTTCACGC CAAAGAGATa TAATAAGGTT CTTTGGCTAG TTGACTTTCG CCAGAGCCAC 840

TTTCTAAAAT AGCCTGAGCT ATCATTACTG ATGCAAAAAC ATCGTATTTT TCGCCAAGTT 900

CTCTGGCTGT CTCACCAATT TTTTTAATAA ACGCTGTGGT TTGTTCTGAC TTCTGCATTT 960

CAAATGACGC ACCATATGTT GCTAAAACTT CTTTGCCATA CTCCGTTAAT ATGAACTCCT 1020

TAAAAGGATT AGTCACTACC AAGCGTTTTT CCTCTTTTGA GTCTGGTTGT TGTTTGGCAG 1080

TATAGATATT CTCTAACTGA GCGATTACTT CTGGTTTCTC TTTAGAATCC GATTCCGCTG 1140

CGGCAATTAA ATATTTTCCT TGGCCArGAT AAACACCATT TTGAAGCGTT TTTCCTTCAG 1200

CTGTTTGCCA AAAAATCAGA TCACCAGGTT CTGCCTCCTC TATAGAACGA ACTTTACCAA 1260

ATGTCATTTG TTCTTGCGGC GTACTGCCAA TGTCTATTTT AAATAATTGT TGGTAAATTT 1320

TTTGGGCAAG GAAACTACTG GTCAATGCTT GCTCCGTCAA ATTAAATTCT TTTTTTGTTT 1380

TCCCAACGTG TCTTAATGCT TCAGCGACCA CGACTGCCCG TTTCTTTTCG CCAAAAGACG 1440

ACAACAGTGG AAGTTCGTAG CCTTTTAAAT TTGAAGAAGC TATTTCATCT ACTTTGAgGG 1500

ACGGATTTAA CGATACAGCC TGATTTTCTT CAACAAAGTT ATTGTTGGCT TCAGGAACTT 1560

GgAATAGGTT CTTCGGGTTC TTGCTTGGtC ACAGGAACTT GTGGtGGtTG CGATTGTTcA 1620

ACAGGCTGCG TGaTTTCTGa TGATACCGTT GGcTCTGTAG GTTCTTTTTT TGTTTCAGAA 1680

CTAGTAwTTG TGGTTGTCGT TTCTGTCGTT gACTGACTCG TTGATTCGGT AGTCGTATCG 1740

GTAGAACTAC TTGATTCAGA TGACGAACTA CTAGTGGACG TTGTCGATGT AGCAACAGTT 1800

GTTTCGGTTG TTTCGGTTAC TTTTTCTTCC GAAGTAATTG TCGTTTCCGA GGACAGAGCT 1860

GTTTGTAGCG AGCTACTTGG TAATTCTGCA GCCAACGTAA CAACTGGAGC GACTTCCAAA 1920

CTCAGAAGAA CGAGAATACT TGTTAAAACA AGTAGTTGAT TCTTGATTTT CTTTCTTTTC 1980

ATTCGTAAAA ATCCTCTCCT ATTACTTACT TGCGCATTTG CACACTGTTT TTGTACAAAT 2040

GCGCCTTGTA AGTTAATGAT ACGCTAATTT TGCTCTTTTT TATTTTTGAA GAATAATTTT 2100

CCTAAACCAA TACTTACTAT CAATAGAAAA CCACTGATTG ACCAGATTGG CGAAACAACT 2160

TCATTTGCTT TTGGCAAAGT ACCAGAAGTG GTGGTTTTCG TTGTCGTTCC ACCTGTTGCT 2220

GTGCCCTTTC CTTGGCTGGT TACACCACCA GTACCGCTAA CCGTGCTATG ATTTCCATTG 2280

TTGCCTGTAG AGTTGCTACT GATTGGCTCT TCTGCCATTG CTTCAATGGC TTGTGATAAA 2340

ATACTTAAAC ATTTGTCCAC AGCTTCTTGC GTCGCATTTG GGTCCTCAAC AAGTGCTTTT 2400

GCTTGTTTAA TTGCTTCAGC TAAAGCTTCT TGCGATGCTT TTGTAAATTG TTTTCCTGCT 2460

TTAGGTTTCA AGGTTTCTGC TTTTTGAAGC AGTTCTTTCA ACTTTGTTTT ATCCGTTTGA 2520

AGGACTTGTT CCTCTAAACT ATCCAAAGCA GTTTTTACAT TTTTTTCAGC AATATCAATT 2580

TGTTCTTGCC GAGCATTTTT ATCAGCTAAA ATCCCTTCCG CTTGGTCAAT TGCTTCAGTT 2640

AAGCGCGCTT TAGACTCGCT GGTAAATTCT TTTCCGGCAG ATGGTTTGAT TGCTTTTGCT 2700

TTGGCTATCA TTGCCTCTAA GGCTTTTTTA TCTGTAACTA ACACTtCTTC TTGTAACCCA 2760

TCGATGGCAC TAGTTAATTC AGCAACCGCT TCATCAATCA TTTTTgATTA GCTGCTGG 2818

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

ATATTCTTAT GGTCACTTCT GCCACAGCGG AATATTGTAA TAGTTAGAGC GCATTGCACT 60

CACCAAATTA GTTTACCACA GACAAAATAA GCTGTAAAGA GAATTTTCTT GAAAGTTCCC 120

TTATTTTTGC TCTTCTTGTT TAATTTCCTC TAATAACTTC AACATTTCAG GCGTCATTTC 180

TACTGATTCC AACATGTCAG GTCGACGTAA AAAGGTCCGT CGTAATGATT CTTTTAGTTG 240

CCATTCTGCA ATTAATTTAT GGTTACCAnT CGTTAGCACG GCAGGGACTT CCATATCGTT 300

GAAAATAGCA GGTCTGGtAT ATtGTGGATG CTCTAATAGG CCAGTGGaAk GkGAATCCgT 360

TTGTGcAGAA AgATkGTtAC CTAAgrCaTC aGGTAATAAA cgGACTGTCG CATCAATCAT 420

GACCATTGCG CCTAATTCGC CCCCTGTTAA AACGTAATCC CCCAATGAAA CTTCATCTGT 480

GACCATCGTG CGAATTCGCT CATCATAGCC TTCATAATGT CCACAAATAA AAACTAAATG 540

TTCTTCTTGT GAAAATTCCT CGGCCATTTT CTGATTAAAC GGTTTTCCTG CTGGATCTAA 600

TAAGATGACC CGTTTTGGTT GCTGGTTTGT CTCTTCTTCA ATTGCCTTTA GGTTATCATA 660

GATCGGTTGT ACTTTTAAAA GCATCCCCGC GCCACCGCCA TACGGATAAT CATCGACCGT 720

TTGGTGTTTG TTATCTGAAA AATCGCGAAA ATTAGAGACA TTCAATTCTA ATAACTGCTT 780

TTCCCGAGCT TTCCCAATAA TTGATTCCCC CATTGGtCCT TCAAACATTC TAGGAAAAAG 840

AGTTAATACA TCAATTCTCA TCGTCAATCA ATCCTTCTGG AATGTCCACA TCAATCCGTT 900

GATTTTCGAC GTCGACTTTT GtAACAACGC CTTCAATATA CGGkAAAAGT AAATCtTTTT 960

TCyTTGGyCG TTGGACGACC CACACATCAT TCGCACCAGG AGATAAAATT TCTTTAATTT 1020

TTCCCAGTTC ACTGCCGGTT TCATCGTAAA CAGTAGCACC AATGATTTGG TGATAATAAA 1080

ATTCGTCCTC TGCCAATTCA GCGAGATTGT CTTTTGCAAC TTTTAAAATA CCGTCACGAT 1140

ATTTTTCAAC ATCATTGATA TTTGGATGTC CTTCAAAGCT TAAAATGTCA AAATTCTTAT 1200

GCTTGCGGTG GGACTTCACG ACCAATTCAA TTGGTGCTTT TTTCTCTTGA AATAGTAGTA 1260

ACATAGCCCC TTTTTGATAA CGTTCTTCTG GAAAATCCGT TTTCGAAATG ACTCGAACTT 1320

CTCCTG 1326

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

CAGAGAAATT ATTTTTCTAA TTACTGGAAA AATAGTTTTT CTTTTTTTGT GTAATCAAAG 60

AATCAACCAA TTAATTCATT GACACAAATT TTAAATGGAA CGATTTCTTG TACATCTAAA 120

GTAGTTTTAG AAAGCATTGT AAAAAGCAGT TAAAAGCAAA CTTATGAGCT CACTCTTACC 180

TGCTTCAATT TATTTCTATA GATTAGTAGT TGCTCTTACA ATTCTTCATC AATGAGTTTA 240

GTCTTGTTAT TCTCCATCAC CTTAAAAAAT GGATAGTAAA TAGCAGCACT AATTAGGATT 300

AATACAAAGC AAAAAACAAT ATTTCGCCAG TCCATACTTG AGAGATATGC TTGTGCAAAA 360

AATGGTGTGA AAGATGGGTC GATGATAAAT CCAACGCTAA TCAGTCCAAC ACTCTGCGCA 420

ATATACGTCA ACAACAATGA AACAATTGGT GTAAGCAAAA ATGGAATAGC TAAAATGGGA 480

TTGAAAACAA TCGGAAGCCC AAATATGACC GGTTCATTGA TTGAGCATAT CCCGGGAATA 540

AGGGAAAGCT TTCCGATTGT TCGATATTCT GAAACTTTGC TACGTATCAT TAAGAGTACT 600

AAACCAAGAG TTCCACCCGC ACCACCTAAA ACCGATATAC GGAACATTTG TAGATTCATC 660

AGATGAGTCA TTGCTTCTTT ATTTGCCATC TGTTCTGCAT TCAAACCTGT TTGTGCCATT 720

CCTAAAGTGA AGACGATTGG GaAAATGATA GATGAACCAT TGATACCGAA TAACCATAGA 780

ATGTTTCCCA AAGTGACAAT CAATAAGAAT CCACCAAGGC TACCAGCAAT ATTTGTAGCA 840

GGCGTTAAAA CCTGCATCAC TGTTTCTGGG AAAATCTTTT TCGTTGTCGC TAAGAAAATC 900

AGATTGATGC CATAAAAAAG AATGATGTTT GTCAACAGTG GAACTAAAGT ATTGATGAAA 960

GTAGCTACCA TAGGAGGGAC AGTATCTGGT AATTTTAACT TGATGTTTTT CACTTCAAAC 1020

ACTCGATTGA CTTCAACAAC TAATAACCCG ATGATGATAG CTACGAAAAG GCCATTAGTT 1080

CCCAAATAAT TTAAGTTtAT TGTTCCTTTT GTCACCGGGG TACATACCAT CAGGTAAATG 1140

ACAGAAGCGA CCATACCATT CATAGATGGG TTGGTTTTGT ATTCATTTGC AAGAGAGAAC 1200

GCAATACCGA AGACACTGAT TAATCCGATG ATCCCCATTG TCAAGTTGTA TGGCGCAGTA 1260

ATCAAGTCAT AATTAGCGAC TGCAAAATCC TTCCATCCAG CCATAATTTT CATAAAGAAA 1320

TTAGCGGTCT CTGGATTATA ATGATCAATA TTTATTGGTG GATTTGCAAA AATCAGAAAA 1380

AAAGAACCAA TAACAATAAA CGGTAATCCA AACATCATTC CACTAGAAAT GGCTTTAAGA 1440

TGTCGCTGAT TTCCGATTTT TTCAGCAATC GGGCTAAGTA TCTCATTCAA TTTTGTGATA 1500

ATCTTAGAAT TTCCCATAAG TATTCCCCCT TATACTTGCC AAGGATTAAA AACAAACGTA 1560

CTTGGTACGA CATGATTCGG ATCATATTTC TTAATAATTT CTTCATATTG TTCTTTGTAA 1620

TCATTCTCTA CTTTTGCTTG CGGGATAACT TTACTTGCTT CATGTAAGAA ATGCTCTGAT 1680

CCTCGTCCCA TCTCCTGACC TCGTGTCGTG TGTTTATCAA GAGCGATATC TGGAATTTCA 1740

GGGACATATC CCATAGCAAA GCTTTTAATT ACAATATTTT TTAAAAGATC TGAGGAACGA 1800

TCTTTCTCTG ATCCGCATAA GTAGCGAATG GCATGAAAGA AAAACATCGC ACGATCTGAT 1860

TCATTATATT GAAATTCCTT ACGCATCATA TTCAAGTTAT TGATCATCAA TGCTGCTATA 1920

GGATTTCCCA TACCGATATC CTCAACACTG ATTGCCAACA AACGTCTCCA AAGCTTTTCT 1980

TCAAACTGTG GTGAAGTAAT ATACATCTCG TAAGCAAATT CGCAAGCGTC TTTTTCTTTT 2040

CCTCTACGGA TAGATTTTTG TAATGCAGAA ATGACTTCGT CACCAGCTAA ACCGTTTCGC 2100

GTAGTCATCT TTGCCCAAGG ATCTTGAATA AATTTTTTTT CTGTCATGTT ATAATACTCC 2160

TAACTAAAGA ATTTGAGGTG GACCTTATGG ATACTGAAAT GCTAATCGAT AAATATCAGT 2220

TGAATGATTC AGAAGCTGCT GTTTTACGGT TTATGGATAA AAACCGTGAC TGCTTGAAAA 2280

GTCTTGGAAT TCGAGAAGTA GCAAAGGCTT CTTATGTCTC AACTACTGCA ATCATCAATA 2340

TGGCAAAAAA AATCGGTTAT TCTGGTTATA GTGAGCTGGT CTTTGCCTAT GGAAACAAAC 2400

ATTCATCAAT TAGCTTTCCT GAGAATTTCT CAAACGAAGA AAAAGATGAA TTTATCCGAT 2460

TATTATCTCG CTATCGAGAA AAACGGATTA TGGTTCTAGG CTCGGGTTTT TCACAAAATA 2520

TTGCAAACCA TTTTTCTGAA ATGCTTAACC TTTATGGATT TCGTGCAACT GCCAACAGTC 2580

ATTTAGAATT CCTACGAGAA AATGTTGAAA AAGATGTCCT GATTTTTATT GTTTCCAACT 2640

CTGGTGATAC TCTTCGGTTA GCAGAACTTG TTAAATTAGC AAAAAATCaT CATATTGATC 2700

TCaTkGCTTT CgTTGGtGaA AAGAAATCCA AAATTGGACA ACTTGCTACA CTAACTATAA 2760

GCaCgGAAAC mtwTaAtCCy CaGGkAGtTT CAGAATATCA ACCAAACCTG TTCTTTGGGA 2820

CTGCnTTGAA TCAATTCGnA CTATT 2845

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

ACGACCACAC CAATTAATGA AATGGCAATC ACTGTAGCTA CACCTGCACT TGTTCCAAAt 60

CCaTATTAGT ATTtGGCAAT ACTTTTGGTT TTTCTTGTGG AGTTGTAACA TTCACTTTGT 120

TAGAATCTGT CGGTTCATCA TTAATCACCA ATTGTGCCAC GTTTGGAATC ATAATATTCC 180

CTTTATCATC GACATATTGC GAAAAGTCTG CGTCTTTCAA TTTCCCTTTA ATGTACACAA 240

ACAATTGTTT TTCTTTTAAT TTGTTTGGTT CATTAGCATT CCAAGAAACT TTTTGTGTTT 300

TTTCATCAAC ACTAATTTTT CCTTGATCCG TAATGTCTGT CCCATCTGAA AGAGTGACTT 360

TTACTTCTTT ATTCGCTTCC AATACATCTT CTAAATCATC TTGaATGACT AAAGACGTCA 420

TATCTTTGGT ATTTGGTACT TGCACATCTA ATTTGAACGT CACTTCATCG CCCACTTTGG 480

CACTGGTCAA ATCCACTTCT TTATCGCCtT CGAGGATTTT CTTAGCGATA GACGGGTCTT 540

TTGGTGTGAC AGTGGTTGTT GTTTCATCAG TTGGGACTTC TTTGTTGTTT TGGATAATTT 600

TTGCTTTATT TGGAATTTGT AACTTGCCAT CAATAAGGTA CTTATCTAAG CTGGCACCTT 660

CACGAATTTT TGTTTGGAAA TTGAATTTGT ATTCGTGATT ATAGAAATCC GCTGTTTTTA 720

ATACGTCAGC CTTTGCAACC ATACGTACTA AATTGCCTTC ATGctTCGCT TCAAATTTAT 780

TGGTAACGTC CTTTCCTGCT TCGTCCGTGA CTTTCACATC AGACACACGT TCCAATTCAG 840

GAATCAGTTC GTCTTGCATT TCATAGTTGC TATAATAAAA TTCTTTCATT TCATCAGGAA 900

CTTTATGTGT GATCGTATAG CTATATACTt CGCCTAATCC TTCTAACGTA TTTTTATCAA 960

CATTTGTTTC ATCACTATCT GTCACCGTTT TAGTAGGAAT CATCGGCGCT GTCCGAACTG 1020

GTTTTTTGGC ACTATAGCCA AAATAACTAT ACTGGTTATT ATTTTTTGAC GGTAATGGAT 1080

TCCCTGAATT TTTTTCGCGT GTAGCGAAAT CTTCACTATA CGTGAAATCG AATCGAGAAC 1140

GATTAGAATA CAAGAACGTA AAATCACCAC GATTATCACC ATCATCTAAA GGAATATCAT 1200

CAGAATCGTA AAAAGTTTTT CCACCATCTT TTTCTTCTTT GTATTTAATG ATTGTATCTT 1260

TCGTTGGAAC GTACAATTTA TCGATTGCTT TATACGAATC TTTGTCAATC GTCATTCCTT 1320

GTAAATTATC AATATCAATC CATGAATAGT AGCCTGAAAC TGGCTTTTCT TTGTCTGTGC 1380

CATGTTCTAG GTACGTCCAT GTTTGTTTCA CCCATGAGAA ACCACCTTGG TAGGTTGCAA 1440

TTGCGGATAC ATTGTTAAAA GCAACAATAT TATTTGACAC CATATTTTGT GCATTTTTAT 1500

ATTGTTCCCA ATCTTGAATG GTAATTTTTA AATCAATTGG TGTCCCATCA TCAGCTGTAC 1560

CTACATTGTT GTAACGAATC CACGATTGCC CTTTCTTCGT TTTCGTTACA TCAAGACCGA 1620

TTTTCCCGTC CCATTTTTGT GGAGGCATAT TAACGTAAAC ATCATTCGTC CACCCATCAC 1680

CACCTGTTTC AACCGTAGTG ACACCTTTAA TAAATTTTGC AATAAAGCTA TACTTTGAAC 1740

CAGCTTCATC ATCTGGTGGT CACTACAGAA GCATTCGGCG CATTAATGAT tGAATTAGCG 1800

CTTGCACGTT GGAAAAAATC TGCTTTCACT GTTTGTGGTA CTTGTCCGCT TTCTtGTGCT 1860

TGAACCATCA TTGGCATTTC CATGCCTGCT AAAATTGTTA CAGTTGCTAA TCCTTGAATA 1920

ATCGTTGTTT TCTTCAAAAT ATTTCCTCTT TTCATTATTA ATTTTTTGTA GTTCTATTTC 1980

ATTTCTCCTA GATTTTGCAT AAAAAATAGG AGAGCCACGA ATCTTCTTCA TTGGTTCACC 2040

TTTCCACAGT TATTCACTTA AAAAGTTATT TGTATAAACT ATATAGCGTA ATACAGGAGC 2100

TTCTTGATTC TTTTTATTCT GGAATTCTTC TTTAAAATTT ACATTTTCAT ATACATACTC 2160

CTCAACAACT ATACAACTTT TCTTTGCTAT ACTAGCATTA AAAATCAACT CATTTTCTAA 2220

AGAAATTTCT GAAAGAACAA AACCTTCTTT CATTGAATCT GCATGCtTCA AACTATCTCC 2280

CTTTAAATAG AGTTTCTTTT CATAAAAAAG TAATCTATCC CTTACTCTAT CAACAACTAC 2340

AGGAnACAAT TCTTCTAACT CTCGAnCATC TCT 2373

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11036 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

CGATGATGAC CTTAAGCGAC CGAAATGAAG CGATTGATGT GGTAACAATC AAAGATCGCC 60

TAGAACAAGA GAATTTGTTA GAAGATGTTG GTGGACTAAG TTATCTGTCA GATTTAGCTT 120

TAGCTGTGCC GACAGCTGCC AATGTCATTT ATTATGCAAA AATTGTTGAA CAAAAATCGT 180

TGCTGCGCAA CTTAATCCAA ACCGCTACAG AGATTGTAAC TAAAGGCTTT GAGCAAGGTG 240
AAGATGTTGA ATCTATTTTG GATGATGCAG AACGAAGCAT TTTAGAAGTC TCCGAAAAGC 300
GGaATCGTAG TGGCTTTTTA TCAATTTCAG ATGTtCTAAA TACaACTATT GCGAATATTG 360
ACCAATTATA CCAAAATGAT GAAGAGATTA CTGGTTTACC TACAGGCTAT CAAGCATTGG 420
ATAAAATGAC TGCTGGCTTG CaAGCGGAaG AGCTAATTAT tCTAGCGGCC CGTCCAGCGG 480
TAGGGAAAAC CGCTTTTGCA TTAAATATTG CCCAAAATGT CGGCACCAAG ACAGATAAAg 540
CTGTCGCTAT TTTTAGTTTA GAAATGGGGG CAGAATCATT AGTGAACCGG ATGCTTTGTG 600
CAGAAGGATC CATTGAGGCC AGCCATTTAA GAACAGGGCA ATTATCTGAA GAAGAATGGC 660
AAAACTTAAT TATTGCGATG GGTAGTTTGT CCCGTGCGAA TATCTATATT GATGACACAC 720
CAGGGATTAA AATTACCGAA ATTCGTGCGA AATGTCGTAA ATTAGCACAA GAAAAAGGCA 780
ACTTAGGTCT AATTTTGATC GACTACCTAC AATTGATTGA AGGAACTGGA AAAGAGAACC 840
GCCAACAGGA GGTTTCTGAT ATTTCACGTC AATTAAAAAA ATTAGCGAAA GAATTAAAAG 900
TCCCGGTTAT CGCTTTGTCA CAGCTTTCTC GTGGCGTGGA ACAACGTCAA GATAAACGTC 960
CTGTGTTAAG TGATATTCGT GAATCAGGTT CCATTGAGCA AGATGCCGAT ATCGTTGCCT 1020
TTCTTTATCG TGATGATTAC TACGATCGTG GTGAAGGAGA AGACGGTGAT CATGAGCCAC 1080
CAGAAGTTGA CAATGTTGTA GAAGTCATCA TTGAGAAAAA CCGTAGTGGT GCGCGTGGAA 1140
CGGTCGAATT ACTTTTCATT AAAGAATATA ATAAATTTTC TTCGCTTTCG CCGAGGACAG 1200
AATTTTAAAA AACGAACTCA TTTTTTGAGT TCGTTTTTTT GCTTATTAAG GGATTAAAAT 1260
CAGAGAGTAA AACACGAACA ATATTCGTAT ATTTTATTAT TTTACAAAAA CATAACTAAA 1320
AATGTTCGTA TTTTTGACAG AAACGCTTTT GATTGTGAAA GAATATTCGA TTTTTACCCT 1380
TGAAAGGGAC TGGTTTTACT GGTACAATGA TTCAGGACAA AAAAATTATG AACGAGGTGT 1440
TCGAATGTCA TCAGTAGTAG TTGTTGGAAC GCAATGGGGC GATGAAGGTA AAGGAAAAAT 1500
TACAGACTTT CTAAGTGAAA ACGCAGAAGT GATCGCTCGT TACCAAGGCG GAGATAACGC 1560
CGGACATACC ATTAAATTCG ACGGCGTAAC GTATAAATTA CATTTAATTC CTTCAGGGAT 1620
TTTCTATAAA GAAAAAATTA GTGTAATTGG TAACGGCGTA GTTGTGAATC CAAAATCTTT 1680
AGTAAAAGAA TTAGCTTATT TAAAAGAAAA TAATGTTGCC ACTGATAATT TACGTATTTC 1740
AGATCGTGCC CATGTCATCT TGCCGTATCA TATTAAATTG GATCAATTGC AAGAAGATGC 1800
GAAAGGTGAA AACAAGATTG GGACAACGAT TAAAGGAATT GGCCCAGCCT ACATGGATAA 1860
AGCAGCACGG GTGGGAATCC GTATCGCTGA TTTATTGGAT AAAGAAATTT TTGCGGAACG 1920
TTTGCAAATT AACTTAGAAG AAAAAAATCG TCAATTCGTT AAAATGTTTG ATAGCGAaCC 1980
ATTGAATTTG ATGATATTTT TGAAGAATAC TATGAATACG GACAACAAAT TAAACAATAT 2040
GTTACAGATA CTTCGGTTAT TTTAAACGAT GCATTAGATG CTGGAAAACG GGTTTTATTT 2100
GAAGGGGCAC AAGGTGTCAT GTTGGATATC GATCAAGGAA CCTATCCATT TGTTACTTCC 2160

TCTAATCCAG TAGCTGGTGG CGTAACTATC GGTAGTGGCG TTGGTCCATC AAAAATTAAT 2220

AAAGTGGTTG GTGTCTGCAA AGCGTACACT TCACGTGTCG GTGACGGCCC ATTCCCAACA 2280

GAATTATTTG ATGAAACAGG AGAAACCATT CGTCGTGTCG GTAAAGAATA CGGAACAACA 2340

ACAGGACGTC CGCGTCGTGT CGGTTGGTTT GATTCAGTAG TCATGCGTCA TTCAAAACGT 2400

GTATCAGGGA TTACAAACTT GTCATTAAAC TCGATTGACG TGTTAAGTGG TTTAGAAACG 2460

GTGAAAATTT GTACAGCTTA TGAACTTGAT GGTGAATTAA TTTATCATTA TCCAGCAAGC 2520

TTGAAAGAAT TAAGCCGCTG TAAACCAGTT TATGAAGAAT TACCAGGTTG GTCTGAAGAT 2580

ATCACTGGTT GCAAAACTTT AGCCGATTTA CCAGCTAATG CTCGTAACTA TGTGCATCGG 2640

ATTTCAGAAT TAGTTGGTGT GCGCATTTCA ACATTCTCTG TAGGTCCAGA CCGTAACCAA 2700

ACGAACGTTT TAGAAAGCGT TTGGGCACAA ATTTAAGCAG ATTTTTAAGG GAACGTAAAG 2760

GATGGCTTAT GCCAGTTCAG CCTTTACGTT CTTTTTTAAT TTTATATAAA AATGAAAAAC 2820

TATGGTAAAA TAAAAGAAAA CATGAAGGGG GCAATTGTCC GTGAATTATC AATTAGTGAC 2880

AGATTCTTGT TGTGACTTGC CGTATACATA CTTAAAAGAA AACCAAGTAC CTTTTATTAG 2940

CATGAATATT CAAATTGACG GGAAAGAATA TCGCGATGAT TTAGGTGAAA CGTTTGATTA 3000

TCAGAACTTC TTAACGGCTA TTAAAAATGG AAGTATGCCC ACTACCTCTC AAGTTAATGT 3060

AGGACGCTAC AATGAATTTT TCCGTCCTTT TGTGGAGCAA GGGTTACCGG TGATTTATTT 3120

AGCTTTTTCA TCTGGGTTAA GTGGCTCTTA TCAAAGTGCG TTGCAATCAG TAGAGATGTT 3180

AAAAGAAGAG TATGATAATG TAGAAATTCA TATTATTGAC ACAAAAGCAG CTAGCTTAGG 3240

TCAAGGGATG TTAGTCCGAG AAGCCATTCG ATTACAAACA GATGGTCATT CATTAGGAGA 3300

AGTTGTTGCC TATCTTGAAG AGCAAAAAAT GAAACTTCAC TCGTGGGTAA CGGTAGATGA 3360

TTTAAAACAT TTAGAACGTG GCGGACGGAT TTCTAAAACA GCGGCTGCAC TTGGTGGCTT 3420

AATGAACATT AAACCAATTA TTCGCGTGGA TGCGGCAGGC AAACTAGCAT CCGTTGGTAA 3480

AACTCGTGGA CGAAACAAGT CCTTGCAAAA GATTGCGCAA GAAACGATTC AAGGCATTGT 3540

AGAGCCAATG AAACAAACAC TATTGATTGC ATATGCGGGA ACGAAAGATG ACGCGGAAAA 3600

AGTCAAAGAA TTAATTGAAA AAGAAATAGA GGTTAATGAG ATACTGATTT ATCCTCTAGG 3660

ACCCACCATT ACTAGTCATA CCGGAATAGG TTGTATTGCT GTGTTTTCTT TTGGTGAAAA 3720

AAGAAAATAA AAAATAGAGA AGTCATTTTT TAATGACTTC TCTATTTTTT TAATAATCTG 3780

AACTGAATAA AACGTCCATT TGTTTTTGAA TTTCTGGGTT TTCCAAGAAT TCATCATAGG 3840

TTGTTTCTGC CCGATCAATG ACCCCTTTAT CAGAAACAGC AATAATTCGG TTCGCTAATG 3900

TTTGGATAAA TTGGTGGTCA TGTGAAGCAA AAAGAATTGA ACCAGTGAAA GCCATCAACC 3960

CATCATTTAA TGCAGTGATT GATTCTAAGT CTAAGTGGTT CGTTGGATCA TCTAAAACTA 4020

AGACATTGGC TTTGGAAAGC ATTAATTTTG AAAGCATGAC ACGCACTTTT TCGCCTCCGG 4080

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TACGTAAGAA CGTATTGTCA TCTTCTTCTT TACCAGCAAA TTGACGTAAC CAATCTAAAA 4200

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ACGTAGTCGT TGTAATATCT GAGTCAGCGA TGAATGCCAC TTTATCATCT TTTGTTAAGT 4380

TGAACGAGAT ATTATCTAAG ATTTTTTTGC CATCAATCGT TACAGAGACA TTTTCAACTT 4440

GTAATAAGTC ATTGCCGATT TCACGTTCTG GTGTAAAACC AACGAATGGA TAACGACGAG 4500

AGGAAGGTTG AATGTCATCT AAGGTAATTT TATCTAACAT TTTTTTACGA GACGTTGCTT 4560

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GTTCTTCTTT TTTGGCATTA GATTGTGCTT GCAATTTTGT CGCTAGTTGG CTTGATTCCA 4680

ACCAGAAATC ATAGTTACCA ACGTAAAGTT TGATTTTACT AAAGTCTAAA TCTGCCATGT 4740

GAGTGCAGAC TTTGTTTAGG AAATGACGGT CATGGGAAAC CACGATAACG GTATTTTCAA 4800

AGTTGATTAA AAATTCTTCT AACCAATTGA TTGAGCGGGT GTCTAAACCA TTTGTCGGCT 4860

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TTTGACCAGC TGTTAATTCG CTCATTTTTT GATCATGTAA TTCTTCTGGA ATGTTTAGCC 4980

CTTGGAGTAA AACAGCTGCT TCAGGTTCTG CTTCCCAACC GTCAAGTTCA GCAAATTCGC 5040

CTTCTAGTTC TGCGGCACGA ATCCCATCTT CATCTGAAAA ATCTTCTTTC ATATAGATAG 5100

CATCTTTTTC TTTCATTACT TCGTAAAGAC GTTTATGTCC CATAATTACA GTTTCTAAAA 5160

CAGTGTAGTC TTCGTAGTCA AAGTGATTTT GTTTCAGCGT TGCTAGTCGC TCATTAGGAC 5220

CCATTGAAAC CACGCCAGTT GTCGGTTGAA TCTCACCTGA TAAAATTTTA AGAAACGTTG 5280

ATTTTCCTGC ACCGTTTGCG CCGATTAAGC CGTAACAGTT GCCAGGAGTA AATTTAATAT 5340

TCACTTCTTC AAAAAGTTTA CGATCTGGAA ATTGTAAACT TACATCATTA ACAGTAATCA 5400

ATTGTTTTCC TCGCTTTTAA TATATTCTTG AACCTCTCTG CATTATATCG GCTACAGAAC 5460

CTTTTTTCAA GGAGTTTCAA TCTTTTTACA GAAACGAATA AAAAGGTGGG TTTTTTATAG 5520

AAAAAAGGCG CTTTTTTAAA ATGTTTCATG TGAAACAGAA ATTTTTTTCA TGAAAGGGTT 5580

TTTAGTGTAT TTTTTTAATG ATACACTGTA TCATGTAAAT TAATTAGTGT ATCGATTAAA 5640

GGAGCCATCA AAAATGAAGC GGATTGAAAA AATCTATCAA TATGTTAAAG AGCAAACGAA 5700

GAATTTAACG CCAATGACCT TAACAAGTGA TGCGGGAGTC ACGACACAAG AAATTTCAGA 5760

ACGTTTAAAC ATTCAGCGGA CCAATGCTAG TAAAGATTTG AATCAACTGG TTCGTGAAGG 5820

GCGCTTGAAA AAATTATCTG GTCGACCAGT AAAATATGTC GCGCAGGTGG CGTTTCAGCA 5880

TCGACCATTA ACCAAGCCAG TTAAAAGTTA TCGGGAAAAA TCAATGGATC ACTCCACAAA 5940

AACTTTTATC GAACCATTGG TTGAACCAGT AGTCACGACA AGTAAAACCC CAGAAGTTGA 6000

AGATATTTTC AAAAAAATTA TCGGTTCAGC TGGAAGCATG AAAACGCCGG TGGAACAAGC 6060

CAAAGCAGCG ATTTTATATC CGCCAAAAGG CTTGAATTGT TTAATTACTG GACCAACAGG 6120

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TTCTGGGAAA ACTTATTTTG CTCATGCCAT GTTTCAATTT GCGAAgCTGa ACCAAATTGT   6180
GGCCAAAGAA AAAGAGTTTG TGGTGTTTAA CTGTGCAGAC TATGCGCATA ATCCAGAACT   6240
TTTGATGTCG CATTTATTTG GGTATGTAGA AGGGGCCTTC ACAGGCGCTA CGAAAGCGAA   6300
AGAAGGGATT ATTGATGAAG CAGATGGCAG CATTCTGTTT TTAGATGAAG TACATCGGTT   6360
ACCACCCGAA GGACAAGAAA TGATTTTTTA TTTTATGGAT CACGGCGTGT ACGCGCGTTT   6420
AGGTGAAACA GTGAAATCAC ATCATGCGGA TGTTCGGATT ATTTGTGCTA CGACGGAGAA   6480
TCCTACTTCT TCTTTATTGA ATACTTTTGT GCGACGCATT CCGATTATCA TTCAATTACC   6540
GAACTTTAGT GACCGTCCTG CGAAAGAAAA AATTGACCTC CTAAAAGTGA TGGTTTCAAT   6600
GGAAGCAGCG CGGATTCAAC GGCGAATCTC TTTGTCAGAA GATGTGGTCA AAGCGTTAAT   6660
TGGAAGTGTT TCTTATGGAA ATGTCGGTCA GCTAAAATCG AATGTGCAAC TTGTGACTGC   6720
GCGAGGGTTC CTTAATCAGA TGGAACAAGA GGAATTAATG ATTACGATGG ACGAATTAAC   6780
GGACAATATC AAAGAAGGCA TTATGCAACT TGCCAGTAAT CGAGAAGTAT TGTCGGAGTT   6840
ATCGAAATAT CTGGAACCGC AATTAGTGGT ATCACCAAAT GAATCTTTAG TAGCTATTCA   6900
GTCAGATGCC TATGAATTGC CTTACAATCT ATATGAGATT ATTGGAGATA AAGCGGCTCT   6960
CTTAAAAGCA GACGGCTTGG ACCAAGAACT AATTAATAAT TTTATTACAA CGGATATCAA   7020
TGTTCATTTA AAATCTTTCT ACAAAGATTA TGGGTTCACC TTTGATACAG AAAATAAATT   7080
GGCTGAAATT GTTGACCAAC GAATTATTGA TGTCACTAAG AAAATTTATA ATTTTGCAGC   7140
GAAgCGGTTA TCGTATTCGT TTCAACCCAA CTTTATTTAT GCAATGAGTT TACACATTAG   7200
TTCTTTCTTG AAACGCATCC AATTAGGCAA AGATCCTAAG CATCCTTTAA ATGAAAGTAT   7260
TCGAAATATG GTTTTAGATT ATCCAACAGA GTTTGAAACA GCAAAAGAAA TTAAAAATAT   7320
TATTGAAAGT AGTTATCAGA TGGAGATTCC TGAATCTGAA AGTTACTATT TAGCTGTTTT   7380
GCTCATTTCT TTAAGAGAAA ATCCTGAGGC TGGCCGGATT GGCATTGTCG TGGcTGCGCA   7440
CGGAAATAGT ACCGCTAGCA GTATGGTACA AGTGGTTTCT CAATTGTTAA ATGTTGATAA   7500
TTTGAAGGCT GTGGATATGC CGTTAGATAT GCCACCGAAA GAAGCTTTGC GTAAAATCGT   7560
TGAAGCAGTT GGTGAAGTGA ATGAAGAGAA TGGCGTACTA TTATTGGTGG ATATGGGTTC   7620
ATTAAGTACT TTTTCAGAAG AAATTGTACG CCAGACAGGC ATTGATGTGC GGACAGTAGA   7680
CATGGTGACC ACGCCAATTG TTCTTGAAGC GGCCCGCAAA ACCGCATTAA TTGATACGCA   7740
ATTGGAAACA CTTCACGAGT CTTTAAAAAA CTTTCATGGC TATGCCGATA TTCGCCAAAG   7800
TGAAACGAAA CAAATCATTG AAAATTGGAA AACAAGAGCA ATTATTGCTA TCTGCGCTTC   7860
TGGAGAAGGA ACTGCGCGCC GAATGAAAGA GCTTATTGAG GAAGCTGTCT TGCCACAAAT   7920
AGACTGGCAT TTAGAAGTGA TTCCTTTGTC CATTGTAAAT ATGAAAGAAG TCTTGCCTAA   7980
AATTCAAGAA GACTATGAAA TTATTGCGAC AACTGGGATT ACCAATCCCA AAATTGGTGT   8040
TCCTTATATT TCCATGGAAA ATTTCTTTTC CGGTGAAGCA GAAAAAATTA TTCAGCAATT   8100
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ACTAGCAGAG CGGAAAGAAG AAGTAATGAA TAAGCCGTTG GACGAAGCGG CAGCAAAAGA 8160

AATTTGTCTA AAATATATGG AGCAAAGTTT CACTTTCATT AATGGAAAAA AAATCATTGA 8220

TCTGTTGTGG TCATTCGCTA AAAATATCCA AACCCAATTA GCGATGCCAG AAGAGTACAC 8280

ATTTTACATC AATTTGATTA TGCACACATC GGGCATGTTG GAGCGTATTT TACGGAATGA 8340

TACACTGACG GTTTCAGAAA AGGAACTTGG TCGATTGGTT CAAGAACCAA TTTATCCAGT 8400

GATTGTGTCC TCAATTGAGA CTATGGAAGA AGCTCTTAAT ATGGATGTTC CAGCAGAAGA 8460

AGTTTATTTT ATCGCACAGT TAGTCAAAAA TGCTCAGTGT ATCGAAGATA AAATCACCGA 8520

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CGATTTAAAA GCATTTCTGT TTTTAAATGA ACAAGGTATT GAATTGGAAA TTCGAAAAGT 9180

CGCAGCAGAC AGCCAAGTGA ATTTGATGGA TTTACTGAAA AAAGAGCGTA gCAAAGAAAA 9240

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GACCAACATC ATTGCTTCAT GAACTGTATT GATAAAGGCA AGTGCTGATG TTGAAAAAAA 9360

TCAAGAACTA TTGAAATTTT TTCATTTATT TTTGTCAGAA TCTGATTTAT CTGATTTTTT 9420

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TATTGAAGCA TATGCTTCTC GTTTCTCTAT GGAATCAGCA CAAGAAATTG CGACACACAT 9840

TCTTGAAACA GCAAAAGATG GTGTCAAAGT TAAACCAGAA GAGTTACAAC CAGCAGAAGC 9900

ACCAAAAGCT GCTGCGACAG AAGATGCACA GCCAAAAGGT TCGTTACCAC CAGGTACAGT 9960

TGTTGGCGAT GGCAAAATTA AATTTGTGCT AGCACGTATT GATTCACGTT TATTACATGG 10020

TCAAGTAGCA ACAGCTTGGA CAAAAGCAAC ACAACCAAAC AGAATTATTG TTGTTTCTGA 10080

TGCCGTTGCA AAAGaTGACT TACGTAAGAA ATTAATCGAa CAAGCAGCTC CTCCAGGAGT 10140

AAAAGCCAAT GTTATTCCAA TCAGTAAAAT GATTGAAGTA GCGAAAGATC CACGTTTTGG 10200

CAATACAAAA GCATTATTAT TATTTGAAAA TCCTGAAGAC GTCTTAAAAG TGGTTGAAGG 10260

CGGCGTAGAA ATCCCAGAAG TAAACGTTGG TTCAATGGCT CACTCTGTTG GAAAAGTCGT 10320

TGTAAGCAAA GTATTATCAA TGGGTCAAGA AGACGTTGAT ACGTTTGATG AATTAAAAGC 10380

CAAAGGCATC AAATTTGATG TGCGTAAAGT GCCAAATGAT TCAAAAGCGA ATATGGACGA 10440

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ATAGGAGGCT TATCATGTCT GTTATATCAA TTATTTTAGT TTTACTCGTT GCCTTTCTAG 10560

CTGGTATGGA AGGGATTTTG GATGAGTTCC AATTCCACCA ACCGTTAGTA GCATGTACAT 10620

TAATCGGATT AGTTACTGGT AATTTAGAAG CCGGAATTGT TTTAGGTGGT ACTTTACAAA 10680

TGATCGCGTT AGGTTGGGCG AACATCGGGG CTGCCGTTGC ACCGGATGCC GCTTTAGCAT 10740

CTGTTGCCTC AGCAATTATT TTAGTTTTAG GTGGCCAAGG TGTTAAAGGT GTTCCTTCAG 10800

CGATTGCCAT CGCAGTTCCT TTAGCGGTTG CAGGTTTGTT CTTAACAATG ATCGTTCGGA 10860

CAGTTGCGGT TCCAATCGTT CACATGATGG ATGCGGCTGC TGAAAAAGGC AACATTAAAC 10920

AAGTTGAAtG TaCACATTTT CGCTGTATGT TTACAAGGTA TTCGTATTGC GATTCCAGCA 10980

GGTGCGTTAC TATTCATTCC TGCTGACACT GTTCGTAATT TCTTAGAATC AATGCC 11036

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

AACGGTGATG CAGGAAAAAG AATCCTCTTC GGCAATCGCC GAAAGCAGTA GCGGAAATGC 60

GGTTGCAGTA ACTACTGAAA CCACAAATGA GATACAAAAT AGTGATACAG ATGGaAAAGC 120

TGTTTCTGCr GAGAGTGTTT TTTCAGAAGC AGaTTATAAA CAAGCAACTG CACTGGAGTT 180

AGCAACTTTA GTAAGAGAAA AAAAGGTGAC GAGCGAAGAA TTAGTAAAAA TTGCGTTGGC 240

CATCACTAAA CGTGAAAATC CTACATTAAA TGCGGTCATT ACTTTACGAG AAGAAGCGGC 300

TTTGACAGAA GCAAAAGCTT TACAAGATAC AGGTCAACCA TTTCTAGGTG TGCCGCTCTT 360

ACTAAAAGGG TTAGGACAAT CCTTGAAAGG TGAAAGCAAC ACGAACGGTT TTGGTTTTCT 420

CCAAGATCAA GTAGCTGGTG GGACATCGAC CTTTGTCAAA GCACTACAAA ATGCCGGATT 480

CATAATCATT GGTCAAACGA ATTATCCAGA ATTAGGTTGG AAGAATATTT CAGATTCAAA 540

GTTATATGGC GTTTCCGTCA ATCCATGGAA TCCTAACCAT TATTCAGGTG GTTCTTCAGG 600

CGGACnGGGT GCTAGTGTCG CCGCGGCATT TGTTCCCATT GCTTCTGGAA GTGATGCTGG 660

TGGCTCTATC CGCATCCCTG CTTcTTGGAC AGGCACCGTA GCTTGAAACC TTCTAGAGGA 720

GTAATCATTG GTAATTCTAA TAGTGCAAAA GGTCAAACTG TTCACTTTGG TTTAAGTCGA 780

ACCGTGGCGG ATACAAATGC ATTATTTGAA ACCTTATTAA CCAAAAAAGA TCTTCCTGCG 840

GGACATTTAA GTCAAGCGCA ACCCATTGCT TATACAACAG AATCCCCTGC CGGAACGCCT 900

ATAAGTGCCG AAGCAAAAGA GGCGGTCGCT GAAGCTGTTG CTTTTTTAAA AGACCAAGGG 960

TACACATTGG TTGAAGTGAA GCACCCTGTT GATGGGGAAC GTCTAATGAA AAATTATTAT 1020

ACTGTAGCTG CTGGCTCAGC AGGAATTGCC GATTTTATGG CGCGGCAGAA ATTGAAAAGA 1080

CCGCTTGAAC GAAATGATGT AGAACTGTTA ACATGGGCGC TTTTTCAAAC AGGAAAAAAT 1140

ATAACGAGTG AAGAGACAAC TGCGGCTTGG ACAGATATTG CTTTACAAGC ACAAGCGATG 1200

GACGAATTTT ATCmACAGTA TCtATCyTAt TAmCACCAAC GACGGCTGCa CGGCACCTAg 1260

TAaTTGATAA TCCGTTACTA AAACCAGAAC ATGCcAGCAC AGATtGGAAA AAAaTTGATC 1320

mATTGTCACC cAGCcAGAaC aAAaACmATT GgtTTaTGaC CaTgGCTGAC GGCGTTCACa 1380

TTACmcCgtT TACCCCACCA AGCCAAATTT TAnTTGGGGC CATCCCGCCA TTAAGGGGGT 1440

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

TGCACTGAAT CATCCTAACC TAGAAGTTCG CTTAATAACG ACGGTTGCAG GGAATGTAGA 60

TGTAGAAAAA ACAACAAATA ATGCCTTGAA ACTTGTCGAT TTTTTGGGA AAAAGGTTCC 120

TGTAGCCAAG GGGTGTAATT GTCCGTTACT TATTCAATTA GAAGATTCTG CTGAGATTCA 180

TGGGGAGACT GGTATGGATG GCTTTGAGTT TCCGCAACCT ATCTCTACGT GTTTAGATAT 240

TCATGCAGTG GAAGCTATGC GAAAAGAAAT TCTGTCTAGT GATGTTCCTT TGACCATTGT 300

TCCAATTGCT GCATTAACGA ATATTGCTTT GTTACTGACC CTCTATCCAG AAGTCAAAGA 360

AAATATTGCA GAAATCGTCA TGATGGGTGG CTCATTAGCA AGGGGAAATA CAAATACAAG 420

TGCCGAATTT AATACGTATG TCGATCCACA CGCTGCACAA ATTGTTTTCC AATCAGGTGT 480

CCCGCTAACA ATGGTAGGAT TAGATGTTAC AAGTCAAGCT GTGTTAACGA ATCATGAAGT 540

AACAGCCATC AGAGCGCTTG GTAGAGTTGG GGAAATGTTT TATGGTCTTT TCCGTCATTA 600

TAGAGGCGGC AGTCTAACTA CAGGTTTGAA AATGCATGAT GTCTGTGCGA TTGCCTATTT 660

AACTTCACCA GAATTATTTG AGACAACTGA AACGTTCATT GAAGTTGcTT TGGAAGGTCC 720

AGCTGCGGGA GcTACTGTTG CGGATTTAAA AATGAAGTAT CATAAAAACA CGAATGCCGT 780

TGCCTGTAtA GATGTAAATG TTGAAGCTTT TCAAAAATGG G 821

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

CTTAGGGATG GTGACTACTA GTGACGGTCG AAGCTTCGCT GCAGCAGATT TGCCAGGCTT 60

AATTGAAGGA GCTTCTCAAG GTGTCGGCTT AGGAACACAG TTCTTACGCC ACATTGAACG 120

GACGCGTGTT ATTTTACATG TCATTGATAT GAGTGGCATG GAArGACGCG ATCCTTATGA 180

AGATTATTTG GCAATCAATA AAGAATTGGC TTCACACAAT TTACGTTTGA TGGAGCGACC 240

TCAAATTATT GTTGCCAATA AAATGGACAT GCCTGAAGCA GAAGAGAATT TAGCGAAATT 300

TAAAGAGCAA CTTGCGAAGG AACGCACCGA TGAGTATGCT GATGAGCTAC CTATTTTCCC 360

AATCTCTGGG GTTACTCGCA AAGGTATTGA ACCTTTATTA AATGCAACAG CTGACTTGTT 420

GGAAGTAACG CCTGAATTCC CATTATATGA AGATGAAGTG GTAGAGGAAG AAACCGTTCG 480

TTATGGCTTC CAACCAGAAG GTCCAGAATT TACGATTGAT CGTGAACCAG ATGCTTCATG 540

GGTTTTATCT GGTGAAAAAT TAGAAAAATT ATTTGAAATG ACGAATTTCG ATCATGATGA 600

AACAGTAATG CGTTTTGCAC GTCAATTACG TGGTATGGGT GTCGATGAGG CATTACGAGC 660

ACGTGGCGCG AAAGATGGCG ACATTGTTCG GATTGGTAAT TTTGAATTTG AATTTGTCGA 720

ATAAGCATAA AACCAGTTCA CTCAGTGAAC TGGTTTTTTA TTTTAAAATT AGTATTAAAT 780

TAGCGAATAG ATTGAAATAA TAtTTTTAAT AGCtTATAAT TTTaAATGtw ACaAAATAAC 840

AAACGAAAGG AGCGAAATTG AAATGGAAAA CAATCAAGCA ATGGTTCCTA AGTTTTCAGT 900

TAAAAGTGCC GGTTTTCTTT TTAGTATGGG GCTCTTATGT GGTGTCCTGT TGCCGAGTGT 960

TTTATTATGG ACTTTCAGcT GCCGTTTAAT ATTGGTGCCA TGATTTTTTT GCCTGTTGGG 1020

ATTGCTTTTG CGTTAGCGTA TAGTCATTAT TTATTGAAAC GAAAACAGGT TTTTGTAAGC 1080

GTTTTATnTG GTTGTTTTTA ATTTCTCTTA TTTTATAGAG CTTATCTCTT ATTTATGGCT 1140

GATTAAAGGA GTTATTTTTT AAGAGAAAAA CAGAGGAGAG TGTTATTTAT GTTAGATAAA 1200

CTGACTGTTT GGATTGAAAA TCATCTAGCT GGACCAATGG CTAAAATTGC CAATCAGCGC 1260

CATTTACGTG CGGTGCGGGA TGGGATTATT GCGACATTAC CTTTAATTAT TGTCGGTTCT 1320

TTTTTTCTAA TTATTGCGTT TCCGCCGTTA CCAGAATCTT GGGGCATTAC TCAATTTTTA 1380

ACAAGTAATG CTGCTACAAT CTTATTGCCT TACCAATGAC 1420

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

GGTATATCCA tGTATwACAG tATAgCCmTT aCAtAAtCAT GTAACTaTCA ACAATCaTCA 60

AAGgTTTCCw AAtCTTTATG GATTGCTGgT ATCCTATCGA TGGTGTGTCA CCATATCCCA 120

TTGTATGCTT ATTTCCCAAG CATGGATGGT ATTGGCATTT GGCAATTCAC ATCCGCTTAT 180

ATTGCAGGTG GTTTAGATGG TAACGTAGAT TTAACAGGAA TTACGGATAG TGGTTATACA 240

GATACAaATA AACCAGAAAC GGATACGCCA GCAACAGATG CAGGCGAAGA AATTGAAAAA 300

ATACCTAATT CTGATGTTAA AGTTGGCGAT ACCGTCAAAG TGAAATTTAG TGTTGATGCT 360

TGGGCAACTG GCGAAGCTAT TCCAGATTGG GTTAAAGGAA ACAGTTATAA AGTGCAAGAA 420

GCAACTGGAA GCAGAGTATT GCTAGAAGGC ATTTTGTCAT GGATTAGCAA AGGTGATATT 480

GAACTATTAC CAGATGCAAC AGTTGTCCCT GATAAGCAAC CAGAAACAAC ACATATAGTT 540

CAACATGGCG AAACATTATC AAGCATTGCT TACCAATACG GTACCGATTA TCAAACTTTA 600

GCTTCGTTAA ATGGATTGGC TAATCCAAAC CTTATTTACC CTGGACAAGT TTTGAAAGTA 660

AATGGATCAG CAACAAGTAA TGTTTACACA GTCCAGTTGG GTGATAATTT ATCAAGTATA 720

GCGGCTAAAC TTGGCACGAC TTATCAAACA TTGGCAGCTT TAAACGAATT AGCAAATCCT 780

AACTTGATTT ATCCGGGTCA AACGTTGAAC TATTAAGAAA TAAGTAAAAG GCCTACTTCT 840

CTTTGTGAGA GGTAGGTCTT TTTTCATTTA TACTAATATA TACATATCAT TGAATGCTAA 900

AAAATTAAAA TTTGTCTTAA GTAAATTTTC AAGTTATGGT ATACTTTGCT GGTGAATATG 960

GGAAGGAGCA TAAAATTTGA AGAAACATTC TAGGAAAATA AAAAATAATA AAGAACTAAC 1020

TTTACTGATT ATAGGAATTT GGGTTGTTTT TTTTCTTTTT AATATGTATA TGCCGACAGT 1080

GAGAGCTGAT GACTTAGTTT ACGTAAATAG ATTAGATAAA TTAGGATATT TGGGTGCTTC 1140

AATAGAACAT TATAAAACAT GGAGTTCAAG AGTTATTATT GAATTATTCT TGATGTTTTT 1200

TTCTAAACAC CTTATGTTAT GGAAATTATT AAATTCAACG ATAATGACAG GTTCTATAGT 1260

ATTGCTTTGC AAATATGTTT TCAACAAGTT ATATTCTAAA AATTTGCTAC TAGTTTTTTC 1320

TATATTTTGT CTAATTCCTT TAACAATAAT GGGGGAAACT GGTTGGATCG CTACTACGTT 1380

AAATTACCAA TGGCCAGTAG CTTTTGGTTT GCTAGCTTTT TACCCTTTTT TTCAAGTGTT 1440

AAGCGGTAAA GAAATAAGCA AAAAAATATA TTGTATAAGT ATTCCTTTAT TAATATTCTC 1500

TGCTAACCAA GAGCAAGTTA ACGTATGCTT TTTTGTTTTA ACTAGTCTAG TAAGTTTGTA 1560

TTTATTATTT AGAAGAAATT ATAATTATAA GTTATCGGCG CTTTCCATAA TAAGTTTAGT 1620

GGAATTATTT TTTTCTTTGA CGGCCCCAGG GAACACATTG CGGGCTGCTC ATGAAATTAA 1680

TAAATGGTTT CCTGAATACA AAAAATTTAA CTTTGTGAAT AAATTAGACC TTGGTATATC 1740

ATCAGAGAGT GTAAAATATT TTGTGTAAAT GAAAAAATCC ATACAAAAAA GGAAGTCGCT 1800

TCTGTAGAAT AAAGTTAACG ACAACCAATT CACAGAAAAG AGGACTTCCC TATGAATGAT 1860

TTTACTACAG AAATTGTGCA AACTCTAGTC ACTAAAGGCG ATTTAAATGA ATTATTCCGT 1920

TCGCACTTAG AAAAAGCGAT AAACACACTC CTACGGACTG AATTAACGGC TTTTTAGAT 1980

TACGAAAAAT ATGATCGCAC TGGTTTTAAT TCAGGTAATT CGAGAAACGG TTCTTACTTT 2040

CGATCAATCA AAACCGAATA TGGTGaATTA ACATTGGgAA tACCTAGAGA TCGTAATGGT 2100

GAGTTTAAAC mACmAACTTT ACCAGCCTAC mAAAgGAmCA cGrTACaTTG GaaCCmCTAT 2160

TATCCnTTTA TCCGAAAAG 2179

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

TTTATATAAA TAAAATAGTA ATTGGAATGG CAATCAGCAC AaTCtGtGTA AAgCCaTGAa 60

TAGTGAaTTG GCTGTgATTT GGTCATCATC GAAAaGAGnC CAaTCGCAAC GGTGTAATTT 120

TCAACTTTAT CACCCATAAT AACTTTTGCG AAAATAAAAT CCATCCAAGG GCCCATGAAG 180

GCGGTTAAAG AAGTATAGAC AATAATTGGT TTCGACAATG GCAACGTAAT TTTTGTGAAA 240

ATTTGCCACT TGTTGGCACC GTCAATCATA GCCGATTCGT CTAAAGCCAT CGGAATGGTG 300

TCGAAGAAAC CTTTGGCGAT GTAAAAACCT AGCGCCGAGC CTGCAGAGTA AACCAGAATT 360

AAAGCGAATA AACTTtCAGT TAAATTTAAG GCTTTTAAAA TATAGTAAAC GGCAATCATA 420

CTCATAAAAC CAGGGAACAT ATTTAAAACG AGCGCCACTT TTAAAAATGG TTTTCTTAAG 480

CGGAAACGCA ACCGTGACAG CGCATAAGCC ATTGCGATTG TAATGAAAGT TGATAACAGA 540

CAGCTTGCGA TGGAAACGAA CAAGGTGTTC AAAAACCAAC GGACAAAGGG GAAGTTGCCA 600

GTCTGATTTG TTAATAATAC TTTATAATTT TCTAAAGTGA ATGTTTTGGG AATGATATAG 660

GGAACAAATG CACCGCCTTC GCCACGAAAA CTTGTTAAGA TAATCCACAC AATGGGGAAC 720

ATCCAAAAAA CTGCTAAAAT GGTTAGAATG ATGTAAACGC TGGTAAGTGC AGTGCGTTGT 780

TTTTTCTGGT AACTTTTTGC TTTAGCCATA AGTTACGCCT CCTTAAATGA ATTCGTACGT 840

GTATAGGCAA TTAAACTGAA GACTGCGGAG AGAATGAAGA TTAAAATACC AATCACAGAG 900

GCTAAATTGT AATCCATTGT ATCGACAGTC AATTTGTATA GCCAGGTAAC TAAAAGGTCA 960

GTTGAGCCTG CACCGTAGAA GTTAGAATTG GCTGGCCCAC CACCTGTTAA TAGATAAATG 1020

ACATTGAAGT TATTGATGTT GCCAATAAAC TGTTGAATCA GCGCTGGGGT CATCACAAAT 1080

AGAATTTGTG GAAACGTAAT ACTTTTAAAA ATTTGCCATT TATTGGCACC GTCAATTCTA 1140

GCTGCTTCGA TTTGATCTTC AGGAAGGTTT TGGATAATCC CTGTAGAGAT TAACATCGTA 1200

GCAGGAATAC CAATCCACAT ATTGACAACA ATAATGGTTA ATTTTGCCCA ATTCGGATCT 1260

GTTAAGAAGG GGATAGAAGA ATCGATTAAG CCCCAATTTA ACAACAGAGC ATTGATAGGT 1320

CCAGAACCAT TTAAGAGGTT TCGCATAATT AAAAGTGAAA CAAACGGAGG TACGGCCATC 1380

GTGATAACAA AAATAGTCCG CCAAAATGCT TTATATTTTA AGCCTTTTGT ATTGATAAGC 1440

AAGGCTAAAA TGATTCCAAA AAAGAAACAA GTTGCGGTTG CGAAAACAGC CCAAATCAAG 1500

GTCCAGCCAA GTACTGGAAA GAACGTTGAA GCCATATCGC CTGTGATTAC ATTACCTAGA 1560

TTTGCCAATC CAACCCAAGT AAAAAGGTTT TTCGGTGGCA GATGGTTATG GTCGTAGTTG 1620

GTAAAGGCAA TTGAAATCaT ATACAACAAC GGCAAGATGG TAAAGAAAAG AACGCCTAGT 1680

AAGGGGATCG TCATTAAAGT TGCATGGAAA CGTTCGTTTA ACAAGCTACG TAAATCATCC 1740

ATAGTTGTTG GAATTTTTTT GCCGGCTGTC TTTAATTCAT ATAGGTGACG GGCGCTTTTT 1800

AAATTGATTA CATATAAAAT GATTAGCGAT AAACAGACTA AAATTGCTGC AATTCCGAAT 1860

AATAATAAGA GCATTGAATT ATCGCCTTCT TTTAGAACTT CAATCCCTAA AGAATCATCA 1920

TAtACTAATC CTTGCTGTTG GGTCCCTAGT GTTCCTAGCA TCATTAATGC GTGGAAACCA 1980

TTACGGATTA ACCAATAGAT AAAGC 2005

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

GGTCCACCAA TATATTTAGG ACGAGAATAT AATGCTGTAA CATGGGCCGC ACCTAACGTT 60

CGAATGCTCA AGCGAAGAGG AACTTGCACA TGTTTTACAT GCATACCGAT AGATGTGTCG 120

CCAATGTCAA TCCCTGCTTG AGCAACAATA TGTTCAACTT CCACAGGTTC ATCAAATTTT 180

TCAAAGGCAG CCACTGAACA AGAACCGCCA GCATGTAATT GTGGTACTAC CGAGACAATT 240

TCAAAGCCTT TTTCTTCAGC CACACGACGT TCCATCGmTA AAGCACGATT AATATGTTCG 300

CATCCTTGGA CAGCCAAAGA GATGCCTTTT TTATCTAATT GTTCAATTAA GGTTGAGACA 360

ATCCATTGTC CTACTTCGGC ACTGGAATTT TTACCAATGA CGCCACCTAC TACCTCACTG 420

GTGGTACAAC CCAAAACGAA TAGGTCCCCT TTTTTTAAAT TTCCTGCTGT AATGACTTCT 480

TCTGTAATTG TCACTAACTG TTCTTnTAAC ATTTTnTCAT CGATAGTCA 529

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

AAGTTTTAGT CGTATCCACT TGATTATCTG GAATAATACT TTCTACTGTA AaCCCCATTT 60

TTTCTTCTGT TGAAGTAyTC TCTGCTTGAA CAACTGAAGG AAAGAAAATA GATAATAGTA 120

AAAACGCTAT AAACCCCATA AAAAATTTTT CTCGTTGTTT CACCTACATC CTCCTAAAAA 180

AGGAGAGGAT GCATGATCCT CTCCCAAAAA ATTTACCGAT TAGATCGTAT CATTCAATGA 240

CCAAGTCAAT GTCCCACTGT ATTGTTGATT AATCTTCGCT GCATTCGCAG GAACTTCTAG 300

TTTAACATTT GACATCTCCA TAGCTGTTGA TCCTawGAAG cTAGCGCCGC CAGTTCCAGC 360

ATCTTTCATA ACAGGCACTG CAGCAgCTCC AGCAGTCACT GATTGTGAAG AAGCATTAAC 420

GGTTGCCGTA cGTGCTCCTT TATCAACAAT T 451

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

TTCCTTGATG CAATACGCTT TCTGCATCAA TACGTCCTTT AyAGTTyTCG ACTAATTGTT 60

TyGCAATCGA TAGACCTmAG CCATTACCAC CTTTATTTCT TGCACGGGCT TTATCTACTC 120

GATAGAATCG ATCAAATATT TTCTCCAAGT CTTCTTCAGT GATTCCTTCA CCAAAATCTT 180

GCACAGCTAT TTCAAATTCA TTCATCGTTC GAGAAATGGA AATATGCACT TCTTTTCGAT 240

CGGTTGAATA TTTAATCGCA TTATCTAATA GAATAATTAG CAATTGTTCA AAGTGATTAC 300

GATAGATTTT CAGCTCAACT TCGGTTGGTA AATCGTCATC TAATGTGATA TGAAACTCAG 360

GATAAACCAA TTGGAAGTTA TTAAATACTT GGTAGACTAC TTGTTTAGCA TCTGTTCGTT 420

CATTTGCATA TTGGGTGTCC ACTTGTTCAG CGCGTGAAAG GTCAAGCATT TCTTGGACCA 480

AACTCTTCAT ACGACTAATT TCTTGTAAAC TGGCCTTTAA TGATTcATCT AAAATTTCAG 540

GATCGTCTTT CCCCCAACGA TTTAAAAGGT TTAAATGGCC TTCCATAATC GCAACGGGCG 600

TTCTTAATTC ATGGGAAACA TCTTCAACAA ACTGCTCTTG TTGTTCGATA TAGCGTCTCA 660

TACGATCTAA CATTTCATTA AAGATTTCCG AGATATCTGC TAACTCATCT CTCGTATTAA 720

TCTCCGGCAT GTGGACATCT GATTGCGGGT CTTTGCGGAT TGTATCCATC GTGTCTCTCA 780

ATACTTTTAA TGGTTTTAAG AAATAAGAAG AGAGGATAAA GCCTAAGACA CTACTTACAA 840

TCAGAGAAAT CACTTCTAAA ACTACAAGTG TTAATAATAA ATGATTACGA ATTTCATAAA 900

AAGAAGAAAG TTCATAAAAC GCTTGAATAT AGCCAATCTT TTCTCGTGTT TCTTTTGAAA 960

AAATAGGTTC CACGGAATAA AAACCGGTTT TATCAAAAAC GGTTCGAACA ACAGGTAATT 1020

GTCGATCCAA TTGTAATAAC TTATCATATT CATTTTGTGT TTTAAAAACT AGCTTTTGGT 1080

TTGTGTCATA CACAGATAAA TAAAGTTCTG GTTGTCCTAG TTCAGATATG AAACTGTCCA 1140

TTTCCATAAA CGAACCTTCT ACTGCTGTAT GCTTATTATA GTAGTTTTCA TCTCTTTCAC 1200

TCGGCGTTTT TAAATAGTCA AAAACGTCTG TTACCGTTAA ATTTTCATTG GCATTAGCTA 1260

ATCGATTTGT TACTTCTGCA ATCGTTGCTT CGACATTTTC CTTTTCTTTG GcAACAATAA 1320

GACTGACAGA AGACTTATAG GtAATCACCG CAAAAATGGt AAAAACTACA AATATAAAGA 1380

AAGAACTTGC GAAAGCCCAC TTTATAGTTA AAgATGGGcC TTCCAGTTCT TTTTTAATCG 1440

TtCTTTTCAT nAATTAGTTC TCACGAAcGC ATAAcGTAGC CAGTTCCAcG GACAGTTTGG 1500

ATGTAGCTTT CTtCTCCAGG TACGTCAATT TTATTTCGTA gTAGCGGATA G 1551

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

TTCGTGAATT TTTGTAGCTy TCAATTTTTC CtAAACGTCG TAGCCtATAT TGCTACCTTA 60

AGTATCTCCC TGACCATCGG ATTGAATCTA CTGGTACCTT TTTACTTAAT TTATACAAAA 120

TCATCGCAAT TCAACCCCAA AGGCTACTTT ATCAATTTAA TGACTTTTAC CTTTTGCCAA 180

TTTCTCCCAA TTAAAATGAC TTTTATCCAA CAATCTAAAG CATTTTTAGC CGGATTACTT 240

CTTTTTTTAA TCGCAGTGAA ATTCTATAGC TTTGTTTCTC AATATTATGC AAAAAGAACA 300

TCTGAAAAAA ATGAGTTTAG CTTTTTCGCT GATTTATTGA ATTCATATGG TAACGAACAA 360

GAATATCAAG CTAACTTAAA CAAATTAGCC AAATTGACTC AACAATTGTA TTTCCAAGcA 420

TATCTTTCTT CTAGTTCTAA AAACAAAATT ACTCCTAAAA CTCGTATTGC ATTCAACTAT 480

GCCTTTTTAT CCCAACGTGC TCTATATTTT TTTACAAGTA TTGATAAATT GGTAAAGCCA 540

GATTCAATTA TTGAAAAATG GATGACAAGA ATTTCTGATT TTTTTGAAAA GTCCAGTCAG 600

TTTACTACGA TGTCAGTTAT yGAAAAAAAT GAGTTGAGAA TACAAGGGAA AATACTTATA 660

ACTTCTTTAG AACACTCCGA TGAAGTAGCA CTGATACTTT TAAGAAACCT GCTTATTCAC 720

AGTTTATTTA TATTACGTTT ATTGGATAAT GATCCAGAAA TAAGCAATAA TCATTGGTCA 780

ACGCCTCTCC mTCaCCrGAC CAAATATCTT TyCCAACACA AaTTTAGaAT tGATTCaTTT 840

GaATTAcGTG TTcGCaCtAC GTTTCaGTAT CGTTCTGGCT TTCTGTTTTT CTTTATGCAC 900

ATTGACTCAT ATTACTCGTG GAACTTGGTT ACCGATGAAT GCTTTCTTAC TGCTTCAACC 960

AATGAATGAA GAGACTACTT ATCGCTTAAA GACTCGTTTT TTAGGAACCA TCTTTGGATG 1020

TTTGATAAGT ATCTACACTG TGCAGCTCTT TAGCAACAAC TTACTCCATC TAATTTTGGC 1080

TAGCTTATTA GGGATCTGTG CCTTTACGAT AATTCCAGGA ACTACATTTC AAGCAACTTT 1140

ATCAACTATT TTCGCATTGT TCCTATCATC ATTAGTTATG TCTAATTTAA TGGCCGCTGG 1200

ATTGCGCTTT GTTTATGTTT TATTAGCTTG TTCATTAGTT TTTCTCGTCA ATCAATTCAT 1260

TCTTCCAACA GGCATAAAAA ATCAATTTCG ATTTAATTTA CAAGAACTTT TTCATATTCA 1320

TCAGACTAGT TTAATATTCC TTCAAAATTC ATTTCATCAC AAGATTGATT ATGGcACAAT 1380
CGCTGACTTA CAAATGaATT ATCACTTACT CCATGGTGAA ATTAAGAATT ATTTCGGCAA 1440
AAGCGATAAA TTGAAACAGA TATCCTACAA AGAATTTTTA TCTATATCTT GGCAAATGAT 1500
TACTATAGTT GAACAACTTT TACTACTTAT TGACAGTAAA AAAATTACAG AAAATGATAT 1560
TACAGTTATT GAAAATACAA TTGACTCTCT ATGTTACGTA TTGTCTCTAA TCCAAAACTT 1620
GTTAGACTGC AATTTAAAAA CATTAAAAAT ACCTGAAGTA CTTTTTAAAC GTGaTTTAGC 1680
AATTGaTCCT GAAATAGCGT ATCTGckATT TCaATACTCT aAAAAATTaT CAGCmATGtA 1740
TCGCCTCGTA CTTTGnATTG TCATTCAATT AAATTTCGAA AATrTTCGAT AATCTACTAT 1800
CTAAGGGAAT TATAAAGGGT ATTCTTATTA AAGAATGAAG AATACCCTTT AATTTACCTT 1860
TTCAAAATCT ATCCTTTACT CTTTTATCTG TAGTGCTAAT ATAAATGATT GTAGAGATAG 1920
TTTGTATATA AGGATATTTT TGTTCAGCTT AAAGGAGTTT TTACTCTATT TAATGATTAC 1980
TACATACAAT TATAGAAGTA CAAGTGATAA CaATAAGTCT ATACGCATAG GrAATAGyCA 2040
TyCATTAGCa AkGmCTTCCC ATTTTTTTGC TTTTTGTAAT ATTAAAACGT ATTGAAATTT 2100
TGATGTAATC TTAGATGTAG GATCAAkaTA TTTAACTAAA ATATTTGTCT TTATTGCTTG 2160
TCCTTTTTTC TGATAATTGA TACTGCTAAT TTCAACAAAC TTTAGATTCT TATAAATTGg 2220
CTCCAACACA TCTTTTTTTA CATAAtATCC tAGTTCTTCT TTAGAAGCkG TTGGATATAA 2280
TTTAAATAGA ACCTCTAAAA ATTCTTCAAT TTCTTCTTwG TkCTTTTCTT TAATCATCGA 2340
ATCATCTGTA AACTGCTTAG TTTTATAATT TGCTTTAACA GGTTTACTAA TCATTGTTGG 2400
CAAAGAAGTC ACAATACAAT TTCCAAGTCT ATCTTCAAAA ACAGAAATTC GGTATGCTGT 2460
TTTTTCTTGT AAAGCTTTTT TTTCCTCTAC TATTTCTTGA TCCACCAAAA ATGATACGAC 2520
GAACCATTTT GACTTTTTCT CAACATTTAG AATTTTCACT GAGTTCACCT TAGAACTTGT 2580
TGGTATATCT GCTCTAACCA TATCTTGACT TAAATCTAGT ACATCTTTTG TAAGATAATG 2640
CCCTAGAGAA CGTATTCTTT TTTCAATTGC TACTCTATCA TTTTTCCAAG AGAAATATTC 2700
TTTGGgCAAA tCTACAGTAA AATTTTCTAC ACCTGAGGgT ATTCACAATT TtTTCCTTCA 2760
CAACCACTTT CTCATGAGTT GTATGTTGAT CAATAGCGGT GAAATTTTTG TAGATTCCAA 2820
AGGATAAACT ACTAAGAAGT AATAACCAAA GGACAAGCAC CATTTTTCGA TGCTTCCCCA 2880
TTGAAACAAC TTGTTCTTTT TTCTTTCCCG AAATCTTCTT TTTATTTCGT TCTATTTTTA 2940
TCTTCATCAT CTGTCCCCTT TTCTATTTTT ATACCGACCA GCACCAATGA TATGTTGCTG 3000
CCAATAAGTT TCGGTAAGAT TAGTCCATCC AACGGGATCA CCTGCATGGA ACATCCGATT 3060
GTCTCCAGCA TAGATACCTA CATGTGTCAC ATAAGTTCCT GCATCATACG TTGAGTGAAA 3120
GAAAATTAAA TCTCCTGGCT TAGCATCTTT CAACTCGATA TGAGACATAG CATCATACTG 3180
ATCCTGCGCG ACTCTGGGAA GTTGCAAACC AACTTTGGCA TAACACCACT GCGTTAATCC 3240
GCTACAATCA AAACCTGTTG CTGGACTTGA ACCTCCGAAC ACATATGCCG TCCCTTCATA 3300

CTTAAAAGCT TCATCAAAAA TTCCTTGAAC GGTTTTATCA TCAAAtTCGT TGTAGTAAGA 3360

TATTGTTTCA CTAACATTAC ATAAAACATA TTTCCATAGT TATAACGCCA ACCACCATTC 3420

TCCTTAATAG CGATTGGATT CGAATAGGTC ACTTTTTCCC CATCTGATTT TTCTTTTGAA 3480

AAAGATTCCG CTAAGGCAAA GCTGTACTTC TTTCCATTTT TTCCAACATA GTCTAAATAT 3540

CCACCACCAT AGTTATACGA TTGAATGATG CTCTCTTGaT CACAACCGAT ATCCTTTGCT 3600

CGATTGACTA AGGAAGCAAA ATAAATGCAC CCTTGCTTGa TTGAAGCTTC GGTGCTTAAC 3660

GAGTTAgGTG GGgAATCCCG CTGGATTCnG AACTTTGGCA yCACATCTTC CaTCGTACCG 3720

CCaGACTCTA CCTGaATAaT gcTAGAAGaA TCGGaACATA CTCTAAAtAT CCGaTkCTTT 3780

AGCaTACTTC TcTACAAGTG GaCGATGCTT TAAAACTTCT AAGrAAACAT TACTCCCTCC 3840

AgAGGACAAT CCAGTACTGC TATTTCCTTC ACTATCGTCA CCAAATAATA GACCGACACA 3900

AATCAAAATT CCCATAAACA AAACCGTTAA AAGAACTAAT AGAACGGTAC TTAACTTTTT 3960

GATTGTCATG CCATATCACC TGTCTTTACC TTCTCCCGGT TTATAGAATT CTTTTGATAT 4020

TGCTTCTTTC CATTTTTCGT TAGAGTGGAT TGATTTTTCA TTTTTTTGAT ACTCATCATC 4080

TTCGGTGCAA TCTTAGGATA AATGGTTTGT AGGGAATCCT 4120

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

AGAAAGAAAA CACAATTGTC TGAAnCGTTT TACGCACAGA CGACACAGTT GTTTTGGAGa 60

AAATGAaCAC AACAACTGAT GGATTAAGTG CACAGGAGGC TCAAAAGCGT TTAGAAACGT 120

ACGGGGAAAA TGTGCTAGAT GAAGGGAAGA AAAAATCACT TGCCGTGAAA TTCTTTGAGC 180

AATTCAAAGA TTTTATGATT ATTGTTTTAT TAGCGGCAGC GGTCATTTCA GCCGTCTTTT 240

CCCATGATGT GGTAGACTCG ATTATCATCT TAGTGGTTGT TATCTTGAAT GCCATCTTTG 300

GGGTCATCCA AGAAGCCAAA GCGGAACAAG CCATTGAAGC ATTAAAAGAA ATGTCTTCAC 360

CAAATGCTAA TGTTCGCCGT GATGGACACG TCATTACTGT TAAAAGCGAT GAATTAGTGC 420

CAGGTGACAT TGTTTTATTA GAAGCAGGGG ATGTCGTTCC AGCCGATTTA CGTTTATTGG 480

AAGCGAATAG CTTAAAAATT GAAGAAGCAG CGTTAACCGG TGAATCTGTT CCAGTTGAAA 540

AAGAAGTAAC CATCTTAGAG GGAACCGATA TTGGTATCGG TGACCGAATC AATATGGCTT 600

ATTCCAATAG TAATGTGACG TATGGACGTG GTCTTGGCGT TGTGGTTGGC ACAGGAATGA 660

ATACAGAAGT CGGTAAAATT GCTGGCATGC TAGCAAGCGA ACAAGAAACG GAAACGCCTT 720

TAAAACAAAA CTTAAACCAA TTGGGTAAAA TGTTAACAAT TGCCATTTTA GTCATTGCAG 780

CGGTGATGTT TGTGGTAGGA ATGATGArTG GTCGTCATGG ATTGACATGT 830

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

TTGTTCATTT TTTTTGAAAG TTTTGAGAAT ACTATAGATA GGAGTTTTTT TATGGAGGAA 60

GATATTGTAA GGnTGTTTTA TAAAGGATCT GAAATTATTT TAATTGGGAC CAGTCATATC 120

TCAGCTGAAA GTGCTGATTT GGTCAGAAAA ACAATTCAGG AAGAAAATCC TGACACTATT 180

TGTATTGAAT GGGATCAAAA AAGATACAAA AAAAACATAC ATCCAGACGA ATGGGATGAT 240

ACTGATATAG TTAAAATAAT AAAGAATAAG CAATTTCCAG TTTTTATTTT TGGTGTAATT 300

TACAAATTAT TTCaAAAAAA AGTTTCTCAA GATATGAATA GCCTTGTAGG AAAAGAATTT 360

GTAGTGGCTG TTGATGAGTC AAAAAAATTA AACATAAAGT TTTATCTAAT TGATAGAGAT 420

TCTTCTCTTA CTTTTAAAAG AGCATGGAGG ATGTTAAATT TTCGTGAAAA AGTGAAATTA 480

CCATATGCTT TTGGAAAAAT ATTTGAGGGT GCGGAAGAAA CTGAAGAAGr GGTTCAAAAT 540

CTGCTAGAAT CkGAAAATTT TGAACCTGTT TTTGAAGAAT TGAAGGAGTC CTATCCTAAT 600

TTGTGGGAAG TTTTCGTAAC TGAAAGAGAC GATTATTTAG CAACAAAAAT TCAAAATACA 660

GCGAATGGAA AGACTGTTGC TGTTTTAGGG AAAGCTCATT TAAAAGGGGT TTCTGACAGA 720

TTAAAGAATA ATCAAAAATC CGATTTACAA AAATTAGAGA TTATTCCACC CAAAAAATTT 780

GGAAGTAAGT TGCTTGAATG GATTATACCA GGTATATTAC TTATTCTTCT AGGAGTATCC 840

TTTTACCAAG GGACACAAGT GGGAATAGAG CAATTGTTAC GTTGGCTTTT ATGGAATGGT 900

GGATTAGCTG CATTGTTTAC AGTATTTGCT TTAGGACACC CTTTAACTGT TCTAACGTCC 960

TTAATATTTG CTCCTTTAGC TACTTTACTT CCAATGGTTT CTGTTGGAGT ATTTTCAGCA 1020

ATAGTGGAAG CTACTGTTAG AAAACCAAAA GTAAAAGATT TTCAAACGAT GGATTTAGAT 1080

CTTCAATCTA TTAAAACAAT ATACAAAAAT CGTGTTTTAA GAGTGTTTTT AGTATTTTTC 1140

TTATCAAGTC TTGGAGGGCT TTTAGGTAAT ATTATTGGTG GGTTAGGAAT AGTTAAAAAT 1200

TTAnTTTAAA GGAGTGAGT 1219

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

ATATTTTTGA AACGTTTGTT TAGTTACAAC ACGTGTTGCT ACCACCAAGC CTTGGTAAAT 60

TAAATAGTAT TTGATTTTTT TCTGACAAGG TAACCACATC AGTTGCCAAT CTCGTTGGTT 120

AGCTTGACTA ATTCGTTGAT TTTGGTTTGC AAAGCGCGTC AGAAAGAGCC AATCTTCCTT 180

GAGTTTTGCC GCTTTTTCGA AGGCTTGTTT TTCAGCAGCC TCTTGCATTT GTTGAGCAAT 240

TCGTTTGATT GGTTCTCGTC CTTGATTATG GAAAAAGTCG AACAATTCTT GTTGAAATAG 300

TTCGGTCGGA ATGGCACTCT CTTTTTGAAA GGTTTGATGC CAGTAGTTGG TTGGGACGAG 360

ATCGTAGATA CTATCCAAAA TTATTTTTAA ACGGTTTAAT TTTCGGCGAA TCGAATAAGG 420

ACCAAAAACAG TTCTCTTTAG TGGGAATATT TAAGAGTTTA ATCTCTAATT GCCGCTCATT 480

AACGGCTACC GATACATAAG AATATTGTTC ATAAGCATTC ATTTGGCGAT TGTAGCGCGG 540

CCGATACTGT TGAATCAGTT GACATTCTAG GAGGAGTGCA TCCAATTCTG TGTCAGTATG 600

GAGAACATCG AAGTCTATAA TTTGTTTGAC TAAACGCATC GTCTTTCGAG AATGTTGATT 660

ACTATTAATA AAATAGCTCG ACACGCGATT TTTTAATTTT TTGGCTTTAC CCACATAAAT 720

AATTGTGTCG GTTGCGTCTT TCATTAAATA AACACCCGGT GTTAACGGTA AtTGATGGGc 780

TTTTTCCTTT AAATATTCTT TCATAAGTtT CCTCTTTtCt TAAAAGGATC GGCTTCAAGT 840

aTACAAAGTT TTCTGAAATA GTCAAGTAAc AGAAATAGnC ATAGGTAATT TCACTGAAAA 900

ATAGTTTTCA TTTTTTTTAA AATATGGATA ATTCnAGGGA ATT 943

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

ATAGATGTCT TTTCTGTCTC TTTTTTTGTA TAATAAACTT ATCAAATGAT GTGTATCTTA 60

CAACTTTGTT CGTTTGCAGA AAGAACAAAC GATGTTTTTT ATTGATAAAA AGTTATATAC 120

TAAAAGTACG ATGAGTATAA CTAAAGGAGA TGAGAAATGT GAGTGTTACC CTATCTAGAA 180

AAATTGTTAA TATTATTTCC ATTTTGGGCA TTGTTGCAAC CATAATTGCA ACCATCTATT 240

TTATCCGATT AGGTGTCTTC AAGGACATCA ATGCACTAAG AGGACTAGTA GGGCAATCTG 300

TCATTCTCGG TCCGATTATT TTCATGTTAA TTCAGATTAT TCAAGTGGTT ATTCCGATTA 360

TTCCTGGTGG TGTTAGCTGT GCTGCAGGGg TcTTGATTTT CGGGCCAACA ATGGGCTTCG 420

TCtAtAATTA CGTTGGTATt GCACTTGGCT CTATTATCAT TTTCTTATTA GGTCGTAATT 480

ATGGGAAACC ATTCATTATG AGCCTTGTCA GTGATAAAAC ATATAACAAG TATATCGGTT 540

GGTTAGACAA TGAAAAACGT TTTGAACGAT TGTTTGCTTT AnCAATTTTC TTCCCGATTG 600

CACCGGATGA TGCGCTTTGT TTAATGGCCG GTTTAACAAA AATGTCTGTG AAAAAATTTA 660

CTCTGATTAT TTTATTAGCA AAACCTGCTT CTATCTATTT ATATAGTCTT GCGTTAATTT 720

ATGGCGGTAC ATTTTTAACT AGCTTACTGG GAATGTAAAA TAAATAAAAA AGCGAACGGA 780

CTAAATCAAA ACTCTGCCTG TGtCAGTTTg ATTTAGTCCy TTTAwTAtGG AATTTTGGtA 840

GAAcTGGGGG rctTTTGawG kTTAgtTAtt TTAAAAAtAG tATTGkGaAa CgCCCAGATT 900

TTCCTTAA 908

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

CGAACGAGAT TTAAAAAAAT nACGTAGCCT TTTTACAAGA ACAAGGCCTG CATTCTTGGG 60

ACGAAGTTGA CCGTTACATG ATTACAGAAT TTTTGCAATC CCTTCACGAA GAACAGCAAG 120

CTTCAGCaAG TGTGATTCGG ATGATTTCTA GTTTGAGAGG ATTTCATCAA TTTTTACGTC 180

AAGAACgCTT AAGCGAACAT AATCCGATGC AACATATTGA CTCCCCCAAG AAAGTTCAAA 240

AATTGCCAAG TACATTATCT GTTGACGAAt GACTCGATTA ATTGAAACGC CTGATACAAG 300

TAAACCACTA GGTATGCGGA ATCGTGCTAT TTTAGAAGTG ATGTATGCAA CGGGCCTGCG 360

AGTTAGTGAA CTAATTGAAA TAAAATTAGG GGATCTGCAT TTATCCATTG GTTTATTGCA 420

AACAATCGGA AAAGGGGACA AAGAACGAAT TATTCCTTTA GGCGATTATG CGATTCAATG 480

GATTGAGCGC TATATGAACG AaGCCAGACC TCAATtGATT AAAAACCATC CGAATGAAAC 540

ACACCTGTTC GTTAATCATC AkGGCGAACC GTTATCTaGA CaGGGCATTT GGAAAAATTT 600

AAAAC 605

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 955 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

TGGCGTCGTT CTTACGATAC TCTTCCTCCA TTAATGGAAG CAACAGATGA AGGTTCTGCA 60

GCAAACGACC GTCGTTATGC AATGTTAGAC CAACGCGATA TTCCTGGTGG CGAAAACTTG 120

AAAGTTACTT TGGAACGTGC ATTACCATTC TGGCAAGATG AAATTGCGCC AGCTTTAAAA 180

GACAACAAAA CTGTTTTAGT AGCGGCTCAT GGTAATTCAT TACGTGCTTT AGCTAAACAC 240

ATCGAAGGCA TTTCTGATGA AGATATTATG GATCTTGAAA TCCCAACAGG TAAACCATTA 300

GTTTATGAAT TAAACGATGA TTTAACTGTG AAAGAAAAAT ACTACTTATA AGAACTTGTT 360

TCTTATTAAC AAAAGCGGTT TGCCAAGGCA AACCGCTTTT TTATGGgATT AAATAAATtG 420

ACTTTtCGGkT AAACmATCTT TATAAAyCGC TACTAwAtCC GCTGCATCCA ATGGTACATA 480

AGCCTTTTCG GCAATTGCAC TATGGTCCAC AGCTTGTTGT GCCATTTCTT CAAATTTATC 540

TGCTTCGATG CCAACTTCTG GTAATGTCAT TGGAATGCCA CAAGCCACAA AGTAATCATA 600

CAATGCTTGA ATACCTTTTT TCGCTGCTAC TTCCTCCTCT TGTTCGACTA TTCCCCAAAC 660

ATTTCGAGCA AACTGTGCAA ATTTGCCTAC GGTTTGTTCA GACAAAACGT AATTCATCCA 720

ACGAGGCGTT AAAATTGCTA AGCCAATCCC ATGCGTAATG TCATAAAACG CACTTAATTC 780

ATGTTCCATT GGGTGACAAG ACCAAACACC TTGTTTGcCG CGCCCTGTTA AACCATTtAA 840

GGsTAAACTA mTTGsCCACA TTAAATTAGC ACGTGCATCA TAATCnTCyG GGATTTCyaA 900

AGgCAaTAGG rCAATTTTga TAACsGTcGs ATtAAGCCTt CTGACACnAA ATCTT 955

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

TTGGCTTTTA TCTGTGTTAT ATTTTTTTTA GTTACTTTTA CTATTGTGTC ACTACCATTA 60

ATCACTGCTC TTAAGACACA AGGATTTTCT TCTGAAGAAT TAATTGAATT AGCTAATTTT 120

GATTTAAATG TTGATATCCC TTTTTCTGAA CTAAACGTCT CAATTATTTy AATTAGTTTT 180

TCTGGTGCCG TTATTGACGG AAGTATGGCT ATTTGTAGTy CTACTTACGA AATATATACG 240

AAGAACCCAG ATTTAACTTT TAAAGAACTA TTTAATTCTA GTTTTAACGT AGTAATTGAG 300

GTATTAAATT CGACTATATA CACTCTCTTA TTTGCTTTTA TAGCATCTAA TTTTGCATTA 360

GTAATTTACT TACAGGATTT AAACTATTCA TTTTTAGAAT TAATTAATTC TAAAATTTTT 420

GTAGGGGAAC TATTAGTAAG TATTTTAACT GGTTGTGCAG GAATTTTAAT TTTACCTTTG 480

TCCTGTTTAC TAGGTAGCTG GATATTAAAA AAAAGATTCC ACACTTTGTA TTGAAACCCa 540

AAAGCTAGGC CGAATACCTT TTATAGAAAT ATATTTGGTA TTTTTATACA ATTAACCGTT 600

CACTTATATT GAACAAAATT GCAGCCAAGT TTCGTTTTGA TTTATTGGTG ATTGAAATAA 660

TTAAATCCAT TTGTTATGTA AGTCTTGATT AGTGTGAAAA AACACCCTCT AATCCAGTCC 720

GCTCTTTTCC AAATACTTAA ATAAAAGAAT CCACAACTAA TTTATCTGTT ATTCTATGTA 780

ATATACTCAA CAAAATTCAC AGTAACTTAA CTATGACTTT TCAGTAAAAA TCAATTGTGC 840

ATACTGATAC AGTAAGTTTA AACTTTTATT GTAATAGTAT AATTCTTAAT TTATATTTTT 900

TACTTCTATT CCTAATTGAT TTATTCAAAA TTATCACAAA ATCGTAAAAG TTAAAATTGC 960

ATATTCTAAC ACAAGAAAAT CAAAAAAAGA TTTTCTTGTG TTAATATTTT TGAATATACT 1020

AAAGTTCGGA TAAGTAGAAA ACACCCTACT GATTTATATA ATAGTAGGGT GTTTTGTTAA 1080

TATAATTTAC TTAAATTCTA TAACTCACAG TCTATAATCA CCTTTTATTC ATTTAAATTT 1140

AATCCGATAA CATACTTAAC TCTACGTCAA AGTATAATTT TACCACACGA ATCACCATAT 1200

ATAGTTGTAT AACTATTTAA GATGACTTCA TTAACTTGTT CAGGTTTAGT AAAAACAACT 1260

ATGACAGATG GATCTTTTCC TGCTTGTTTA ATTTGATCAA AATCAACTTC GGCTAATAAT 1320

GTTTCGGTAG TAACTTTCTC TCCTGCATTA ACAAAAATTG AAAAAGGTTT ACCCTCCAAT 1380

TCAACTGTGT CTATACCAAT ATGAATTAAA TACTCAATAT CTGCATCGCT TTTTATACTA 1440

ATTGCATGCT TTGTTGGAAA AACAGCTTCA ATTCGTCCAG TCAAAGGAGC ATATATTTTG 1500

TTACCTTCGG GAACAACTGC AAATCCTTCT CCAAGTACTT TTTTTGAAAA TATTGGATCA 1560

TTTACTTCTG AAATAGGAAT AATCCTCCCT GAACAAGGAG CAGTAATGGA AATTCCTTCT 1620

TGTTTTTTAT TTTTAAATAG ATTAAACATA AGATATCTCC TAATTCTCAA TTTCTAAAAT 1680

TTGATTAATT TCTTGACTAA GTAAATCAGC TTTACCGCCA AAAACTGCCT GAATACCACC 1740

ATTCACTTCA AAAACAGCAG TAGCACCTAG TTGTTTAATA GTTTCTTTGT CAACCATTCG 1800

GCCATCTACA ACAGCTAAAC GTAAACGAGT AGCACAAGCT TCAACGGgAT TCAATATTGG 1860

TTTTACTACC AAGAGCTTTA ATGATTATTT GAGCTTCATC ATTTAATGAT GTTTTTTTAT 1920

TTAATTTATT TTCAGTAGTC GTTGGCAACT CTTCTCCCAT TCCAGGAATA GCTACTTTAA 1980

ATTTCTTAAT GAAGAAAGTA AATACGCAGA AATAAACAAT TGCCCAAGCA ATTCCGAAAG 2040

GAATTAATTT CAGCCAATTT GTCTTATCGT TTCCTTGGAG TACACCAAAT AATAAGAAAT 2100

CAATTAATCC ACCAGAAAAT GAATTTCCTA CTCGGATATT TAAAATATCA GCAAAATAAA 2160

AAGATAGACC ATCTAAGAAT GCATGAATTA TATATAACCA TGGGGCTACA AATAAAAACA 2220

TATATTCAAC TGGTTCAGTA ATCCCTGTTA AAAATGAAGT CAAGCCACCA CTAAAATAAA 2280

GTCCACCATT CTTTTTACGA TTTTGTTTaG GTATAGCACG ATACATAGCA TAACAAGCTG 2340

CTGGTAAACC AAACATCATT GTCGCGAATC TACCTGCAAA GAAACGAGTA CCATAAGTAA 2400

ATAGTCCTGT ATGGTTTGGA TCAGCTAGTT GCGCAAAGAA AATATTTTGT GcACCAGAAA 2460

CAGTAACTCC AGCTACACTT TCTGtaCCTC CTAAAGACGT wTACCAAAAA AGTGGATAAA 2520

TAGTATGATG TAATCCTACT GCGCCAGTCA AACGAAGTaA AAATCCATAC AAAAAAGTAC 2580

CTAGACTTCC CATTTGTGCA ATATGTTCTC CAACTACTGC TAATCCATTT TGAATTGGTG 2640

GCCAAATTAA ATAAAAGAAA GAACCGATAA TAATTGCCGC TAAACTAGAA ATGATTGGAA 2700

TAAAACGCGA TCCGCCAAAA AAGCCCAAAA ATTGCGGTAG TTCAATTTTC CGATATCGAT 2760

TGTGTAGAAA TGCAACAGTT CCGCCAATTA CAATAGATCC AACAACACCA GTATCAAGAG 2820

TTGCATCTTT AGCAGAAAAT AACGCAAGAA AGCCGCTGAT CGTTGCTGTA TACACTAAGT 2880

AAGATACTCC ACCGGCTAGA CCTGCTGTTC CTTTATCCCC ATTTGCTAAC CCTACAGCAA 2940

TACCTATAGC AAAAATCAAT GCTAAATTAG TAAAGACAGC ATTTCCTGCA TAACTCATAA 3000

TACTTAATAC TGTATGGATC CATGGCTGTT CTAAAATTGG ATACGCATTC ATTGCACTTT 3060

CATTTGTTAA AGCACCACCA AGGCCTAAAA GTAAACCTGC TACTGGTAAG ATTGCAATCG 3120

GTAACATAAA TGCGCGACCT AATTGTGAAA ACTTCTTAAA CATCTTTTTC CTCCTTATTC 3180

AATGCATCGA CAAATCTTTT AGCAATTTCT TGTGGTCGTG TAATTGCACC ACCAACGACA 3240

ATTCCTGCAA CACCCAGCTT TTTAATTTGT CTTGCTTGTT CAGGTGTATG AATTTTCCCT 3300

TCAGCAATAA CACAAATATT TTCTTGTACT AATTGTTTAA TTAATTTCAT ATCTGGGCCA 3360

TTTTGTTTTT TGCTCTCCTT TGTATAGCCA CTTAAGGTTG TACCAACAAA ATCCACACCA 3420

GCTTGATAAG CATTCTTTCC TTCCTCAAAA GTAGAAATAT CAGCCATTAA TAATTGTTGA 3480

GGATACTTTT cTTTACTTTT TCTATAAArG TATTAATAGA TAATCCGTCA kGACGTTaCG 3540

TAAAGTACAG tCCAAAGCaA TTACCTCCaC AcCAATTGcA cTAATTCAcT ACTCCCCCAT 3600

AGTG 3604

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 646 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

GCGCATGGTT ATATGGGTTC GGCAGAAACG ATGTCTGTCT TTGCGAAAAT GTATCATGAT 60

TGGGGCTACA ATGTGTTAGC GCCAGATGCG CGTGGTCACG GGAAAAGTCA AGGAGATTAT 120

ATTGGGTTCG GCTGGCCCgA TCGTAAAGAT TaTGTCCAAT GGATTGAGAA AGTTTTAACC 180

GAAAATGGTC AGCAAGAACA AATCACTTTA TACGGTGTCA GTATGGGTGC TGCTACAGTC 240

ATGATGACGA GCGGGGAAAA ATTACCAGAT AACGTGAAAG CCATTGTGGA AGATTGTGGC 300

TATTCTACAG TCAATCAGGA GTTGCAATAT CAATTGAAAG AGCTTTTCAA TTTACCAAGT 360

TTCCCATTAG TTAATGTTAC TAGCGGGATT ACGAAACTTA GAGCTGGCTA TTTCTTTGGG 420

GAAGCAAGCG CTGTTAAACA ATTACAAAAG AATCATTTAC CAATGCTCTT TATTCATGGT 480

GAAAATGATA CGTTTGTGCC GTTTAGTATG TTAGACGAAk TTTATAATGC AACCCAAGGa 540

CCTAAAGAAA AATATGTCGT GcCTGGaGGC AGAGCATGGC GAAAGCTTTA TAATAAAAAC 600

CCAGAAAAAT ATAAGGGAAC AGTAnGCGGC TTTTCnAGAT AAATAT 646

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

AAAGAAGAAT TAATATTATT ACTGAATGAT AAAGATTGTG CCTATGATGT ACGGATTCAA 60

ATTCAACAAT TTCTTGAAGA AAGGTGAGTA AAGACAAGAT GTTCAGAAAC AAATGGAAAA 120

ACAGTTCACT AATTAAAAAT GTGTAAAAAG GGTCTGATGA AAAAAGGAGA CATAATAGTT 180

ATTATCTTTT TAATAGCTAT CTCTTTTTCT CCATATTTTA TTTTTTTTCA CAATAATCCA 240

TTTAACTCCA AAAGTTTTGA CGACACTAAA TATGCTGTGG TCAAGATAGA TGGGAAAGAG 300

ATTGAGCGTA TAAATTTAGA TGATTCAAAA GAATTTATCA AAACATATTA TCCATCAAAA 360

GGGCAATATA ATACTATAGA AGTTAAAAAT GGGCACGTTC GTGTAAAAAA AGATAATAGT 420

CCAGATCAAA TTGCGGTGAA AACAGGATGG ATATCAGAAC CAGGGCmAAC TAGTATCTGT 480

ATTCCTCACA GATTCATTTT AGAAATTGTT CAACAATATT CTAAGGATtA TTaTATTtAC 540

TAAAATCATT TTTTGGCATA CATGCTAAAA AATGATTTTT TGTAAATATT TTATTGCATT 600

AATATCAATA TAGTTTAGTT TTATTTGGAA GAATGTAATA ACAAATATGA GATGGGATTG 660

TCCTTATTAA ATAACATTTA TAAATGTTAT ATTTTAAGTG AAAGTAATGA TTTACAGTTA 720

ATTAAATGGA GGTTTTATGA ATAACCTATT TATTTTtGTT TGCTTTTGTT TTATGTGGTT 780

AATGATTTTT GGAGTAATTT TATACTATGT TGGTCTAGTT AATCACAGAT ATATACATCA 840

TACTTTAATT TTGGGTTTAG TAACTATTAT TTCTGGTACT CTATGTTGGT TATTTGTAGG 900

ATACTCATTA AGTTTTTTTG GAAATATTCA ATATAGTATC kTTTATAGCC CCTTAGCTTC 960

TAGTGAAATT GTTTCTATAC TGATACAATT ACTTTTTTGC TTATATTCTG TAATTATGAT 1020

AATTGGTTCA GTATTAGAAA GAGGTAATTG GAAATATATT GTGTTGTTTG TTCCTTTGTG 1080

GATTGTATTT GTTTATGCAC CTATTTGCwT TTCGTTATGG GGACATGGAA ATTGGCTAGG 1140

GAAAATGGGA GTACTGGATT ATTCAGGCGG ACTAGTAGTC CATACTACCG CTGGAATAGG 1200

AAGTCTTGTT TTAGCAATAA CATCACCAAT ACGTTTAAAG AATTCATTGA TATTTAAATC 1260

ACAAGAAATG aTAGCTTTTG TAGGAATGCT GTTTATTACC TTAGGaTGGt TCGGaTTTAA 1320

TA 1322

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

GACCTGGTTT GGATCGGATT AATGCGTTAT TAGAAAAAAT TGATCATCCA GAAAACAAAG 60

TGCCAACGAT TCATATCGCA GGAACCAATG GTAAAGGCTC AACCGTGACA TATTTACGCT 120

GTCTATTAGA AGAAATGGGC TTGAAAGTCG GAACCTTTAC CTCTCCTTAT ATTGAATCAT 180

TTAATGAAAG AATTGCGATA AATGGTCAAC CAATTTCAGA CGAACAATTG ATTACCTATG 240

TGGAAAAGTA TCAACCAATC ATTAAAGAAT TAGACCAGAT CACTGAAGTG GCTGGAATTA 300

CAGAATTCGA AACATTGACA GGAATGGCCT TGGACTATTT CGTGAATGAA CAAGTGGATA 360

TCGCCGTTGT TGAAGTTGGC TTAGGTGGAT TACTTGATAG CACCAATGTC GTGAAGCCAT 420

TATTGACGGG AATTACGACA ATTGGGAAGG ATCACACAGA AATTTTAGGT GAAACAATTG 480

CTGAAATTGC CTATCAAAAA GCGGGTATTA TTAAAGAAAA AGTCCCAGTA GTAACAGGCA 540

ACATTTGTGC TGATGCGCTA gcAGTCATTG AAAAAGTCGC ACAAGAAAAA CAGAGTCCAA 600

TTTTTCGTTT TGGCAAAGAG TATCAAGTGG AATATCTACA TCCTGATACA CAATGGGGGG 660

AAGTATTTAA TTTCTATGGA GAAATGGGCA AACTGACAAA AATTAAAGTT CCCTTGTTGG 720

GGCGTCACCA AGTAGAAAAT GCGGCGGTAG CTATTCAATT ATTTGACAAG TATTGCCAAC 780

TACAACATTT GCCATTTAAA GAACGAGACA TTACTCAAGG GTTGGCTAAA GCGCAATGGC 840

CAGCTCGAAT GGAACGTCTT AGTGATGAAC CGTTGATTGT TTTAGATGGT GCCCACAATG 900

ATCATGCAGT AAAACGCTTA GTTGAAAACT TGCGCAAAGA GTTTCCACAA CACACGATTC 960

ATATTTTATT TTCAGCTTTA GCAACTAAAG ATGTGGATGA GATGATTCAG GACTTAAAGC 1020

AAGTACCGAA TGCGCATCTT TACTTAACTA GCTTCGATTA TCCTAAAGCT ATTGCACTTA 1080

CAGAAATGGA AAAATATGAA GACGATTTAA CAGAAATTGT GTCTTTATGG CAATTTGGCT 1140

TAGGCGAAAT TTTAGAAAAA ATGTCGACAG ATGATTTATT ATTAGTAACA GGTTCATTAT 1200

ATTTtGTTTC TCAAGTAAGA GAATTACTTT TAACTATAGG AGGAAATGAT GAAGAAATTT 1260

GATGGCGT 1268

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

nAAGCAATAA TTGAACCGTA AATTGCaCCA ACCCCtTTGT TCGTACCaAT CATGATTAAA 60

GGCGCAACTG CTTGAATGGC ACAACCTAAA ACGACTGGCA AGCCAATCCC AAAAAACTTA 120

TTCACCGTTA ATTGTAAAAG TGTCGCAACG CCGCACATAA AAATATCGAT TGAAATCAAA 180

TACGTCATTT GTTGCGAATC AAAATTCAAG CCGGTTCCGA TTAATAAAGG TACGGCAACT 240

GCTCCAGCAT ACATCGCTAA TAAATGTTGC AATCCTAAAA CGGCGGCTTT CCCATTTGGT 300

GTTTCCGTCT GTTGTGGTGT ATTCAATTGT TTTGTTTCCA AGATTATGCA TCCTCCTCTA 360

AAAACGTCAC CGTTCCTTCA CTTAATGAAG CAATACGTGC TAAAGAGACT ACATTTaAGC 420

CCATGTCTTC TAATAACTGa CGACCATCTT GGaATGaTTT TTCaATTACG aTACCAATTC 480

CTTCAACCTT TGCACCAGCC TGTTGGCATA ATTCTACCAA TCCTTTGGCA GCTTGTCCGT 540

TAGCTAAAAA GTCATCAATA ATCAACACTT TATCAGCATC AGATAAAAAT TTTCTTGAAA 600

TGGAAATTTG ACTTGTCACT TGTTTTGTAA ATGAATAAAC TGAAGCCGTT AAAAGCTCTT 660

CATCCATGGT TAAACTTTTT GCCTTACGAG CGAAGATCAT TGGCACGCCT AATTTTTGCG 720

CTGCGTATAA GGCAGGAGCG ATTCCTGATG CTTCAATTGT AATTACTTTG GTAATGCCTG 780

CTTCTGCGAA AACCTCAGCA AAACGATTAC CCATAGCCTC CATTAATTCT GGATCCACTT 840

GGTGCGTAAT AAAACTATCT ACTTTTAAAA CACCTTCACC TAATACACGG CCATCATTTT 900

TAATACGTTC GACTAATTCC TTCACAATAT GAACTCCTTT ACTTATTTTT CGATAGATGC 960

TTTGTTCTCA TCCTGAGGAA AGGACGGTTC GTTAAAAACG AACGAAATAA AACAAAGTGC 1020

TATTTATATT CGTGTTCTAA CAAAAGAArA AAGCCCATTT TGCCAAAGCA AAAAAGGGCT 1080

ATCCGCTCTT CTTCACTTAT AGACCAGCAT TTACGGTGCT GGGTAGAGAn GGTCAACCGT 1140

ATTTTGACCT TATACAAGCT TCTATGTGTC TCTAnGGATA GTACAAAAAT CTCTAACTnT 1200

CCAATGGGTA ACAACTT 1217

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

AACCATCCCC TAAGGATTGA TTCAACTAAC GCTTTACGGT CGATTGAGTA AGAAATTGCT 60

TTACGTAAGT TCGCATTTCT AAATGGTGAT TTTTCATCAC GTTGATTTAG TTCCATATAT 120

TGTGTTGATG CTTCTTTTTG ACTAACAAAA GCTGGGTCAT TGGCCATTTG TTGGGCTAAT 180

TCACCAGAAA GAACGACATC GTCTGTTTGT CCATCTTGGA ACAAGTTCAA CGCGGTTGGT 240

GATTCTTTCA CGACATTCAC ATCTACTGAG TCCAGTTTCA CAGTATCTTT ATCCCAATAT 300

TGATCGTTTT TCTTGAATGA CCATTTTGTA TCTGTACCAG GACCATCAAA GCCGTCTAAG 360

ACGAATGGAC CATTGTAGAC AGCACTTTCG CTGTTTGATG CATAATTTTT ACCATATTTT 420

TCCACAATGT CTTGACGTTG CGGGAAGAAT GATGGGAAAG CTAATAAGTA ATCAAAGTAT 480

GGTGTTGCTT TTTCTAAAGT GATTTCTAAT TCTGTATCAC TGACTGCTTT AATTCCTAAT 540

TCTGATTTAT CTTTTTCCCC TTTAGCAATG GCATCACCAT TTTTTACAGA GGCATACAGA 600

TAAGCATATT CAGAAGCTGT CGCTGGATCA ACTGTTCGTT GCCATCCGTA AACATAGTCA 660

TTAGCAGTCA CTGGTTTACC GTCTGACCAT TTTGCATCTT TATTTAATTT AATTTTGTAT 720

GTTAGTCCAT CTTCAGAAAC TTCTGCTTTT TCCGCTGCAC CTGCAGGTTG GACTTTGTTA 780

TCTTTGTCTA AACGATAAAT TCCTTCATAT ACATTATTTA ATGCAATAAA ACTAATTCTG 840

kCTGTTGCTA GTGATAAATC AGCTGTTGGC ATTTCTTGTT GTTCTGTGAC ACGTAAAACT 900

TGTTCGCCAC TTGCCTTACC GCCACCAGAC GCGCTTGAGC TATcTGACGT TCCGCCGCCT 960

CCACAAGCCG CTAAAGTTGT TACGCTAAAT AATGTAATCA CACCGAATGT TAATGACTTT 1020

TTCAATTTCA TAGTGTTGCC TCCTAAAATA ATGCAATCTG TATTTTCTGA AAAATCaGaA 1080 kTTAATAATT ATTaTkGCTA TGGaATATaT CTtACATTTt TCATATTAAA AtgCAAGTCA 1140

AAtGkTAACT TTTtTTAATT tTccTCcCTA TCAGAAACCA CTCTTTTTCT TCCTGTCTTT 1200

TATTGCAATT CTTTTGTCAG TTTTCTAAAC ATTATGGTAA ATTAGGAAGT AAAGGAGTGA 1260

CAAAATATGA AAAATTCTAC GTTTTTAAAG GATTTGTTTG CTATTGATAA AGCAAATGAC 1320

GAaTTATTTC GGTTaGTTGG TGTCGCAATT TGTATGGCAA TTCCATTATT AATTGGTTAT 1380

TTTTCCAATA ATTTACTCAT TGGGACCTTT GGCtCGATGG GCATTTATAC GTTTATTTAT 1440

TATCAGCCGC TTCCTTTGCC TCAATTATTG CGCAGACTGA ATATTGTTGG CTTTTTTATT 1500

GTTCTGGGCA ACAGCTTAGG AATGCTAAGT CACCATGTAC CTTGGTTGAT TCCCATtACA 1560

ATTGCCATCG TCGCTTTTCT TGCACGCTTA CTTTTTAGAT TGTATGGCAT TGAGAAGCCT 1620

GGTGCTTTGT TAGTTATCAT GTCAACCGCA ATGGGAACAA GCAACAATTT TCCTTTACAT 1680

AAGATTCCCA TCATGGCCAG TTTTGTTCTT TTAGGAGTAG TGACCGGCAT TATCATGGGC 1740

ATTGTGCTTC ATTTCATCGA CAAGCGCCCC TACGTTTTTC AAAAACGGAT GTCTCTTCAA 1800

GAACGACTTT ATATCGATCC CGCTTCTTTA TTAGATGCTT TGCATTATGC GGCCATTTTA 1860

TTTTTAGCGG CTTATTTAAG CCAATCGCTT CATTTAGTCA ACGCCTATTG GATGACGTTT 1920

ACTTGCGCA 1929

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3893 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

TTGGTGATTA CGACTGCATT CAGTATTTCT ACGATGTTTT TCAATATTTC GGCTACCTAT 60

CCCTTCTTTA TGGTAGCTTT TCTACAAATT GTGACCTTTG CCGGTATCTA TTTCAAATTG 120

GGTGACATTA TGAGTATGTT CAACCTTCAG AGTAATGACA GTCAGTCAAT GGGCAGACGG 180

GTCATGCGAA GACCGCAAAT GTTGATGAAC CGTAAATTGC GGCAACTCAA TCGAAATGTG 240

GGCCGAACTC TGGCTTTTGG CGGTGCTGCA GCAGTTGGGA ATAAGTTGGC AAAGGAACAA 300

TCAAAACCCA AATTTAAGCC AGCAGGTTCT TCTCTACGAA AGAATTCACG ATTACCTAAC 360

GATCGCGAGG TATCCTCAGA CTCGGCTAAG GAGAATCCAA TTTCAAATAA TAAGAAACAA 420

TCCCGAATGA ATTTGACTGG GAGAAAAATA GGCAAAGTTC TGGATACCCA GGCTTTGGTG 480

AAAGATAAGG CAAAACAAGT AAAGGATCaG GTACGGAATA CGCCGACCAA CTTGAAATAC 540

ATCCTCCATA AAGGTCTGGA AAAGACGAAA AAAGCACCGA AAGAATTTAA GCGAGGGCTT 600

GTTCAAGAAA AAGCAGATCG AGAGAAGCTG CGAGACAAAC AACGACAACG CAGAGATGAG 660

AAAATGGATG AAAAGCGAAA AAACTTGGGC GAAGTAACAG ACCGTCATGG AAAAAGAAGA 720

AGTAATGTTT CGATAAAAGA GGATCCAAAA CCTCAGAAGG ATAGGATACT GAAAAATGAA 780

CTTCCAAAAC GGATTGTGAT GGTAAAACCG AATTCTGAGG TAAGGAGAAG ACTTGTTAAA 840

CAGAATTTGG TTGCGAGAGA GAATAACCAA CTATTAAGTA AGAAAAATTC TTTCCAGCAA 900

GTTAAGCAAC GATCTACTCT TCCGAAGAGA GCCAATCAAA AAGTACAAAG AATAATGAAG 960

GCTCGTCCaA AACCAAAGTC GGGTGATAAA AAATGAATTT AAAAGAATTG AGTGTCATTT 1020

CGTTAACCAT GTTGATGCTC TCTTTTATGG GCATCTTGAT GTGTGTAAGC TTATTGTTTG 1080

GGGAAGATAG TGAGGGGAGT GGTACTTCTG GTATTTCTCC TGGTGGCAAT AGTGTCTCAG 1140

AAGAAGTCTT GAAACATCGC TCAATGGTTG AAAAATATGC TAAAGAATCG GACATATTAG 1200

ACTATGTACC AATTCTTTTG GCAATCATCC AAGTTGAATC TGGTGGCACA ATGGAGGACG 1260

TCATGCAAAG TTCTGAGTCT GCGGGTTTAC CACCAAATTC ATTAAGTACC GAAGCATCTA 1320

TCAAGCAGGG ATGTATTTAT TTTGCTTCCT TGGTTAAGAG CTCCAAAGAA CTAGGGTGTG 1380

ATCAAGATAG TATTATTCAA GCCTATAACT ATGGTGGCGG CTATTTGAAT TATGTCGCAA 1440

AAAACGGGAA GAAGCATAGT TTTACTTTAG CCGAATCATT TTCAAAGGAA AAATCGGGTG 1500

GTCAAAAAGT AGACTACCCC AACCCAATAG CGATTAAAGA AAATGGCGGG TGGCGCTATA 1560

ACTATGGCAA TATGTTTTAT TGCCTATTAG TGAAGCAATA CCTGACCACG ACACAGTTTG 1620

ATGATAAAAC AGTCCAAGGG ATTTTTGACG AGGCTTTTAA GTATGAAGGT ACTGCCTACG 1680

TATTTGGCGG TTCGAGTCCC GCAACGGGTT TTGATTGTAG TGGATTGACC CAGTGGTGTT 1740

ATGCCAAAGT TGGTCTGAAA CTTCCCCGGG TGGCTCAAGA TCAGTATGAT GTCATGACTC 1800

ATATTGACTT AAAAGATGCC AAACCTGGTG ATTTAATTTT CTTTCACTCA ACCTATGATG 1860

CCGGTACTTA TGTGACTCAT GTAGGTATTT ATGCAGGAGA GAATCGCATG TTTCACGCAG 1920

GAAATCCAGT GGGTTGGACG AATCTTACAG AAAGCTATTG GCAGCAGCAT CTGATTGGAG 1980

CCGGCCGATA CAATTAAGAG AAAAGAGGAA AAATAATGAA GATAAAAATT GAACGGATTC 2040

AAAAGGAAAA GATGTCAAAA AAGAAAAAAG AGCGGACAAT TTCAGTGGGC AAGCATCGAA 2100

AAATGGTGCT TGCCCTTTGG CTTTTACTGT CaTGTAGTCT TGCtTTTGGg TATCTACAAA 2160

TATTTCACCG CCATTGaTCA GCATACaCTC ACGTAAAAAT GGTTGTAAAn GAAAArGTAA 2220

TAAaTACTTC TGGAGTTGAA AGTTTTACAA AGAATTTTGT GAAAGAATAC TTTTCATGGA 2280

AGAATAACAA GGAAGTAATT GAAAAGAGAA TGAGTAATCT TGGACAGTAC CTTACAGAAG 2340

AAGGCCTTGC TTTGAGTCAA GATATGGTTC GAGTAGATAT TCCCACTAGT TCAGAAGTAA 2400

ACTCAGTAAA AATTCTAGAT GTTGAAAAAC GTTCGAAAGA TTTTGTCGTT TCATTTTTAG 2460

TAGACCAAAA GATTACAGAA GGGAAAAAGT CAGAACAAAT TTCTTCTGCG TATCGAGTGA 2520

AGATATTTGA AGATGAAAAA GAAAATCATA TAGTGACGAG TTTACCAACT ATGATTAGTA 2580

AGCCAGGTAA GGCAAAATAT GAAGTAAAAC AAGTAGAAAG TGATTCTGAC ATTGATGCAA 2640

AAACAACGCA AGAAATTACT GAGTTTCTAG AGACATTTTT CAAACTTTAT CCAACTGCTT 2700

CTGAAAAAGA GCTAGAGTAT TATAGTGAAA ATGAATCTAT GAGCCAAGTT AGTAGCGATC 2760

TTAGATTTGT AGAAATAACC AATCCTATTT ATCTTGAAAA GGACGGTTCG GTACAAGTAA 2820

AAATCGTAGT AAAATACCTA AATGAAATTG AAAAGGTGAC AAATAGTTTT CAATACAATC 2880

TATTGTTAAA CAAAGAAGAA AATTGGAAAA TTATTAATGG AGAATAATTT TTTAAGGAGA 2940

ATATAAAAAA CAAGGAAAGA ATGAATCATT GTAAACTTGT GGGAGCGTCA ATAATTTTGT 3000

GTAAATGATT CTTCCCTACT GCAGATTGTT TCTAATTCTC AATCAGTTGG CTTAGCATTT 3060

GTTCAAGTTC GCCTTCGGCC TGTTGAAAGC CTTTATGACT GCGACCTAGG AATTTTTGGT 3120

TGTAAGTATC AAAAGACGAG ACTAAGAAAC GTTCCATCGA CTCTTCGTTT TGGAACTGTT 3180

CCTTGCGGTG GCTGTATTTC TTGATTTGCT TATTAAAGGA TTCAATCAAG TTCGTAGAAT 3240

AAATACTCTT GCGTATGGCC AAGGGGAAAT CATAGAAAGT GAGCAAGTGA TCGTTCGAAA 3300

GAATCGATTC AACCACTTTT GGATAGCTGG TTTTCCATTT TTCCGCAAAA GCACCACGTG 3360

CTTCCAACGC CACCTTTTTA GATGAGGTTT GATACACCAT TTTAAAATCA TCACAGACTT 3420

CCTTACGATC ATCGACACGC ACTTTGTGAC TGATATTACG GGAAACGTGT ACACAACAAT 3480

GTTGAAAACG AGCTTTGGGA TAGAACCGAC TAATCGCTCC TACCATCCCC TTTAAGCCAT 3540

CCGTGATGAA CAGGAGGACA TTTTTCAAAC CGCGCTCTTG AAGGTCCAAT AAAATTTCCT 3600

CCCAAATCGT GATGGATTCA GTCGGTGCAA yCGCATAGCT CAATACTTCC TTTGATCCGT 3660

CCGGGCGAAT GCCAACTGCG ATATGAATGG CTTCCTTGGC GACGGTTTTC CGCTTTAACG 3720

GAATATACGT TGCGTCCATA TAAATAGCGG CATAACGGTC ATGAAGCTCC CGCCCTTTAA 3780

ACGCCGTTAC CTCTTCTGTA AATGATTTkG TTATATTGGA CATGGTTTGG GgCGTGTAGT 3840

GaTGCCCATA CATTTTCTCA ATCAAGCTGC GATTTCGACA TGGTAATACC TTG 3893

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

CTCGTTCATC TTATCCAGCA CCGCCCGCTG TGCAGGGGTA AGGACACGGG GCGGGGTGAT 60

GCGTACCCAT TTTTTCGGCA GTTCAAAGGA AAGCCCGCCA TATCCATTAT CCCCGGTCTG 120

CCGTACCTGT TCGGGGTAAG TGCCGCACAG TTCGGAAAGC TGCCTGCAAA GACTGGTATT 180

GTGGGTGTAG ATGCTGGCGG CGGTTTCTGC TTCGTTATAC AGCACGATAG TTTCCCTCTC 240

GGTTCCGGAC AGCTTCATCG CTCCACCTCC TGTCCGCGCG GGGGGTTCTC CGGCGCGTCA 300

CGGCCTTTGG CGGCATCTTC CCGGCACTGG TTCAGGGCAT CCAGCACCGA GGGTTTGGGC 360

GGCTCGTTAT TGATGATCCC GTCAATCTGG TTATAGTTGC CCTCCACGCT CATTTCAGCG 420

GCGGCAAGGT AATTTTCGGG GATtACTTCC TGAAAgGCGC GGACGTTCCC GTCCCCCGCC 480

AGTACCGGCA CATAGAGCCG CCCGGTCTGt AAATACATCC CGTCCAGGCC AGCCCCGCcT 540

TTGTAGCGTC cTGCGtGTCA CGCTCACACT CCAAAAGGGC AATCCCGTTT GCCAGAAGAT 600

A 601

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

ACTCTTCTGC TAATTCTAAA AATACTTGAT CAACCACTTC ATCACCAATC GAATGGCAAT 60

CAAAATGTTC AGGATAATGT CCAGTTAGTT CCTTAAAGCG CGTCAATTGC GCAATCGTTT 120

CAAGTCGTAC TTCTTCATAT ACGAAGGTTA CTTGCTTTTG TTGACGATAA TAAGAAGAGC 180

GATGAAAATT GCCTTGTTCA TCTACCAGTG AAGGAATCAT ACATGGGTCC GCACAAGGTT 240

TCCCTAATAA AAAATTCGTA TGCTGACCTA CAAATAATCC TGGATAATTT TTTGCTAACG 300

CAACGGCGTG TtCTGCTGTT GGTAAATTGG GCATCAAAAG TGTCGACGTT GTTAAACCAT 360

CGACATAACT TTTGATAATG CCATGATTAA TCGCTTCTGA CATCCCAAAA TCATCAGCAT 420

CAACAATTAC TTTAACCAAC AGCTCCCCCT CTTTTCTTTA CGTATTTTTG aTGACAATTC 480

CGACAATAAT ATTAACAGCT GATTCACAAT CATTAATCGT GCGCTCAAGC TGaTCATAAA 540

CATCTTTCCA CTTGATAACT TTCAATAAAT CTTTTTCGTT AGTCATCAAA TCTTTCATGG 600

CGCTACTGTA TAATTTATCG CCTTGAGATT CAATCGTATT CACTTCATCA ATCAATGAAA 660

CTAACGTTTT GGAATTCTTA AATTTTGCAA ATTCCTTCGT TGCTGATTTA ACGCCTTCTG 720

TCGCTTTAAC AATATAAGCA GTTAATTCTA GCGCGGGCGC AATCATTTCT TCGACAACTA 780

AATGATCAAG TAAATAAGAC AAACTATTAA TGCTATCAAT AATGTTATCT AAGTGATCCG 840

TAATATCGAC AATATCTTCT CGATCAATCG GCGTAATAAA GGAAATATAG AGTTCATTTA 900

AAATTTTGCG AACAATTTCA TCATTCTCTT TTTCCAATTG ATGAATCGCT TCTGATTTTT 960

TTACTAAGTT TTCTAATGAA TAATTGTCTA CAATTTCTTG CAAAACCTTT GCCGCTTCAT 1020

AAGCATTTGT TGCTAACTGG TTTAATTCTC CAAAATAATC AAATTGTTTT TTACGTGCCA 1080

TGTTTTTCTC TCCTTAAAAA ATTGCAATAA ATAATTTTGA CATCACATAA GCGATCrGCC 1140

CACATCCTGG GAAAGTTAAA ATCCATGmwA TCAGCATTTC TTTCACGATA CGCCAGTCAA 1200

CACTTGAGAT TCGCTTAGAA GCACCTACTC CCATAATCGC TGTTGTTTTT GTATGAGTAG 1260

TTGAAACTGG AATCCCAAAA GcCGaTGsTw AAAATAAACA AaTAGCCGTG CTTAAATCTG 1320

CAGTGAAGCC TTGATAGCGT TCAAGTTTTA CCATATCCAT CCCGACTGAT TTAATGATTC 1380

TCATGCCGCC CACAGAAGTT CCAATGCCCA TTGTAaTGGA aCACrGAaCC ATAcCCATAA 1440

CGGAtCACAA AACCGCCACt GTTTTTTCGA CTAAATTATT ATAAAAAAGC ACTAACATGA 1500

ACACGCCCaT AAATTTTTGC CCATCTTGCG CACCATGTAA AAAGCATTAG CTCCTGCACC 1560

AAgGCTTGTC CAACTGTAAA AAATTTGTTG GCTTTTCTTC TAGGCACAGC CGAGAAAGCT 1620

TTCACAACAA GTTTGGCAAT TAAATAACCG CCGCCAAAGC CCATAACGGT AGAAACAACT 1680

AGACCAACAA GCACTTTGAT CCATTCCGAG CCATTGACTG CACCCAAACC ACCTAATGCC 1740

ATTGCCGAAC CAGTCAAGCC GGCAATTAAC GCATGGCTTT CACTTGTGGG AATACCAAAA 1800

TACCACGCAG CAACTGCCCA AACCACAATT GAAAAAAGCG AAGCAGCCAA AGCCACCTGT 1860

GAAGCGTTTC CATTTGCGTC AAAACTAACA ATGTTACTAA TCGTTTCAGC TACTtGGGCA 1920

TTAAAAAAGG TCATGACTAA TGCACCTAAA AAGTTCATCA CAACAGCCAT CCAAATTGCG 1980

ACATTCGGTT TTAACACCCG AGTCGAGACA GCGGTTGCAA TTGCGTTCGG CGCATCCGTC 2040

CAACCGTTAA CAAAAATTAC ACCCATTACC AAAGTAATCG TTACCAATAA TGCAATACTC 2100

ACAAAGACA 2109

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7712 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

GTAAATTCAC TTCAATTGCC CCTTCCTTCT CCTGTTCTAT TTTACGTTAT CTTGCTGGCA 60

GTGTCACGAA AAGAAGAAAA GAATCTGGAA TAATTGCCGT TTGACAGTTT ATCCAGATTC 120

TTCTTACACC ATTTCTAACG AtACGTAATC CCTAATGTAA CATCCTTACG AATTAAAACT 180

GGCGTTTTTT CCAGTGTTAA ATCGGCGCCA TCGACTTGAA TGGCGACGTT ATTTGAGGCG 240

CCTAGAATCA GTGTTGCATT GGCGGCATTC GCAGGTAAAG CTGTTGTTTG GGTCTCTCCT 300

GCTTGCAGGG TGTGTTGGTA CGTATAGTTG CCATCGACCA TCACGCCAAT CCAGCAAGAG 360

CCTTCAGTCC CTTTAAAGGT AATGTTGATT GGACTATTCG CATCTTTAAC CGTTGCAGTC 420

ACTTGATTGT TAGCATCACT CACCACAGCC ACAGCTGTTT TCTTCTCTGG TTCGCTTGAA 480

GAAGACGGCG GTGTACTACT TTGTGTGCTA CTTTCTGGGG CTTGACTTGA TTCTTTGGGC 540

TTTTCCACAC TGGCACTAGT TGCCGGTGTT TGAATAATCG GTTCGGCTTT TTGATCTTGC 600

CACATAATGT ACAGCACCAC GACCGCAATG GCTAAACCAA TTAACGAAAA GGCAATGGCC 660

GGTAAGTTCC GCAGTAACCA ACTGGATTGC TTTTCTTCGT CATGCAATTG CTTACGTGAT 720

CCTTCAAGCT CTTCATACAC TGGCTTGGGT TCTTCGACAA TTGCTGGTTC TTTGCCATCA 780

TAGATATCTA CCAATTGATT GCCATCTAAG CCGACCGCAC TTGCATATTG GCGGATAAAC 840

GCCCGCACAT AAAAGGTGCC TGGTAAGGAC TCAAAATCGT TTTGTTCAAT AATTTCTAAA 900

TATCTTTTTT GAATTTTTGT CATTTGTTGC AGTTCATCAA TTGAGATGTT CTTCTGCAAT 960

CTTGCTTCTT TTAGTGTTTC TCCAATATTT ACGCTGGCCA CTCGTCCATC TTCTCCAGTC 1020

TATTTTGTTA ATTTATCGAT TGTCTCATCA GTCTTTTTCA ATTGCCAAGG AAAACATTCC 1080

CGTCCTTTAA GAATACCACA AAAGAAGCCA ACTGAGGATA ACAAAATTGA AAGATTTCAA 1140

AGATTTTTCT TTTTCTTAAA CAGTkGGTTT ATTGCTCGGT TTCTCCTTTA GGATACATGT 1200

AGAAACGGCT CAATCCTTCT TCACGAATAA AGGTCTCTGC TACTTGGCGG ACGTCGGCTA 1260

ATTGAATACT TTCAATGACT TCAATCTTAT CAAACAGCGT GGTTTCCCCA AACAATGATT 1320

GTGAAAATTG GTTGGCGATA TACTCTAAAG AGTTTAAGGA TTGGAAATAT TTACCAATCA 1380

TTTTTTTCTT CAATAAGGAC AAATTTTCTT CCGTTAATTC TGGACTTGTT GTGGCAGATA 1440

ATAAAATAGC TTCAATTCGT TCTGCTAAGA CTTCTGGTTG CTCACTATCG CCGCCAATAT 1500

CCGCAAAATG GAAACTGCGA TCTAAATTAA AGTCATAACT AAAACTATCA TCTAACAAGC 1560

CTTCATCATA AAGAGCCAAA TAGTTTTGAG AGGTATTACC AAACAATAAT TGTAACAACA 1620

AGTTCACGGT GACTTGATAT TTCATTAAGT CACGACCCGT TGTTGGCACT TCATCTAAGC 1680

CTTTCAAACC AACAAGCACT TTTGCCCGTG TGACTGTCAT TTCAATGGCG CTCTCTTTGA 1740

CAATGTCAGC AGCTGTTTCT TCAGGAAAAT GCCGACGAAT AGGTTGGGCG GCAGGAAACT 1800

CTTTCGCCGC TTGGTTTTCA CGAATGAAGG CCATTAACGC TTCAGGGTCC ATTTTCCCTA 1860

CCACGAATAA GGTCATATTA CTTGGATGAT AAAACGTATT GTAACATGTA TACAAATCTT 1920

CTGCGGTAAT CTCCGCAATA CTTGCCACTG TGCCGGCAAT ATCAATATGC AATGGATGCT 1980

TCGGATAAAG ATTGCCTAAA ATCCCAAAGA ACAAGCGCCA GTTAGGATCA TCTAAATACA 2040

TTTGAATTTC TTGTCCGATG ATGCCTTTTT CTTTTTCGAC CGTTTCCTTC GTGAAATACG 2100

GCGATTGCAC AAAATCAAGC AACGTTTCTA GATTTTGTGT CACTTGATCC GTCGTTGAAA 2160

ACAAATAACT CGTTTTCGTA AAACTGGTAA AGGCATTCGC TGAAGCCCCT TGTTGCCCAA 2220

ATTTTTGGAA GACATCGCCA TCTTCTTTTT CAAACATTTT ATGTTCTAAA AAGTGGGCGA 2280

TTCCGTCAGG CACTTCAATC ATTTCCTCTT GACCAATTGG CACGAACGTA TTGTCAATGG 2340

AACCATAATC GGTCGTAAAC AAGCCATACG TTTTTTGGAA ATCATTTTTC GGTAATAGGT 2400

AAACCTTTAA ACCATTTTCC AGTGTTTCTG TATACAATGT TTCTTTAATT TGTGCATAGT 2460

CTTTTTTAAT CATTTTCCGT TTCTCCTTCC AAAAAGAAGA TCGCTTGAAG TTCCAAGCGT 2520

TTGGCTACTT CTTGGATTTC TGGAATAGTC ACGGCATTGA TCCGCGCAAT CCATTCCTCC 2580

GCCGTCAGCA TCGTCTGCGG CATTAATTCG TTCAAGTATT CTTTTTCCAG CCACGCGCCT 2640

GCATTATCTA ACGCTAAGAT ATACTGATTT TTTAACATTG CTTTCGTTTG TTCAATTTCT 2700

AATTCCCTAA TCTTACCTAA GCGAATATTT TCCAATTCTG TCGAAATCAA ACGCAAGACC 2760

TGATTCCGAT TTTTGCCATC GATCCCTGTT TGAACCGTCA TGAAGCCaCG GAAGGTGTCG 2820

ATACTACTAG AAGCATAATA CGCTAAATGC TCTTTTTCAC GGACATTCAT AAATAATTTA 2880

GAATGCGGGA AACCGCCAAA AATCCCATTA AACACTTGCA ACGCAAAATA ATAGCTATCG 2940

CCATAATAAA TATCTGTGTT GTAAGCCAAG TTTAATTTCG ATTGGGCTAA CACCTCACGC 3000

TCGGTCCGCT CTTCAATCAC GTTGCGAATT GGTTGATTGT AGAAAATCGC GGCTTTGCCT 3060

TCTTCACGAG GTGTAAACGG TAATTGCTTG AACAATGGCA CTAACTCCGC CTCATTGACA 3120

TCACCTAAAA CAAAAATATC CACTTGATCT TCCGCCAGCA TTTTTTGATA ATACGCTGCT 3180

AATGACGCCG CTGTTTCCTC AGctAACGCC GCAACAGTCC CGAAACTAGG GATTTTTTGA 3240

TCCTCCGATT GATTAAAATA GACACTTTGA AGCGCCAAAG AGGCATAGGT TTGCTTATCC 3300

TCCACAATAC TTTCCAAGTA CGCTTTCAAG TTCTCTTTTT CCCGTTGGAA GGTTTCCGCC 3360

TCAAATTGGC CCGCTTGAAT ATTGGGGGCA AAAATAATTT CCTTCAAAAA GTCCACCGCT 3420

TCGGCGAGAA CCTGACTATC CTGTAAATAA TGATCATTGA CAATGTTCAT AGAAATATTA 3480

AACCAATGTT GATTGCCTTT TTTGGAAACG CCAATCCCAA AGcTGGCGCC GTAAAGcTCC 3540

GCCAAACGCT CACTTAACTT GACTTGATTC GGGTAATTCA AGCTGTTGGT TTCCATCAAA 3600

CTGGACAACA GCGTTCTTTT TGTAATAGTT TCATGATTTA ATCGTGTGTT AAAGCGGACT 3660

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AATTGAACAG ACATTGCCGC ATCGCTCCTT CATTTGCTTC ATCTTACCTA AAGAATGCTG 3780

TGAAATATAT GTATCGCGTA AATTCTAAAG CATTTTTTAA TGTTTTTTCC AATAGCTCCA 3840

TTATAACACA GCTTCAGGTG CTTTCTGAAT GATAAGAGTT TTTCAGTTCA AATTTTCAAG 3900

AAGATTCGGT ATACTGTTTT TAAAGTGAGG AGGGAAAAAA GAATGATTAA AGAATTTAAA 3960

GAGTTTATCA TGCGCGGGAG TGTCTTAGAC CTAGCCGTTG GTGTTGTCAT TGGTAGTGCG 4020

TTTACAGCGA TTGTGACACA AGTGGTGGAA GGCTTGATTA CCCCGTTAAT TAGTCTGATT 4080

TTTGTCTTGA CGACTGGGAA AAAGAGCGCC GACGATGCAT TGGGTGCCCT TGTCTATAAA 4140

GTCGAAGGCG TTGAATTCAA TATTGGTAGC GTGATTAGTG CACTTATTAC ATTTTTAATT 4200

ACGGCCTTCG TCCTCTTCTT GATTGTCAAA GCGGCCAACA AAATGAAAAA CCGCGGCAAA 4260

AAAGAAGAAG CGGCAGAAGA AGAAGTGGTA CCAACGAGCG AAGATTACTT AAAAGAAATT 4320

CGCGACTTAT TAGCGGCGCA AACACCGCCT GCTGAAACTG TCAAAACAGA CAGCACTTTC 4380

ACAGAGAAAT AAGCAAAAAG TCATCCTAAG GGGATGACTT TTTTGTTTGG ACTTACACAG 4440

ATGGTCCTGC GACGAGGTTC CACGTGATAC TGCCTGTGTA GGCCCCTGCT TTAATATTGT 4500

TGGCTGGTGT TGTGATGTTT AAAGCTGTAT TAAACAGTGA AAATTGCCAT AATCCTTGGC 4560

CTTGACCAGC TGCTGCGTTA gcCATTAATT GGGCTTCCCC GCCTAAATCA AGGGTCCAAT 4620

TTTGCGGAgC AGCCAGTTGT GGTCTGACTT CTGGTGTAGA GACTGCTGTC GTCAGAGCTA 4680

CATAACTATT GCTTGTTGCC TCGTATTCTA AATCAAGTTG AGTAATCAGC GCCACTTTAA 4740

TGTTGCCTTG TAAGCTTTCA GTGCCTAATT TTAGGCCATT AGATTGGGCC GTTAAATGCC 4800

AGCCTTCTTT GCCGCCGCGT ACGTCACCGA CACCAATCAT TTCTGTATGG CCGTTGGTGG 4860

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CAAAATTAAA TTCTCGAGGA ATAAACAGTA AATCAAAGTT ACTGTTTGAG CCACTCGGGT 4980

CTGGATCAAC GGTATTGGCA TCGCCGTTGC CATCTGGCAA CGTGCCGCCT TCAAATGCTG 5040

CTGTGACTGG CGTATTCCCT GTCGTAGTCG CCTGTGCCGA AAGCGGGGCT AAACTTGCGC 5100

CAACCACTGC GCTACCAACT AATAAACTTG CCATCATTTT CTTTTTCATT TGTGTTCTTC 5160

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GTCCTCTGTT CTTTTGTTGC TTGTGCTTAA ATTGATGGTC CTGCGACTAG GTTCCAAGTG 5280

ATATTGCCTG TGTAGGCACC TGCTTTGATA TTGTAAGCTG GTGTCGTAAT ATTTAAATAT 5340

GGTCTAAATG AAAATTGCCA TAATCCTTGC CCTTTTCCTG CTGTAGCATT CGCAAGAAGC 5400

ACTGCATCTC CGCCTAAAGC AATTGAAAAA GCTGTTGTAT CAACAGTTTC CGGTTTGGTA 5460

ACTGGGTCGG CAAGATCAGC ACTTTGATAA TCATACGTTT TAGTTTCCTC ATTATAAATT 5520

AATGGATACA AAAACATTGC TCCTGTTGTA ATACTGCCTT CCAAACTTTC CTCGCCGAGC 5580

TTCATACCAG TCGATTGAGC AGTCACATGC CAGCCTTCTT TGCTCCCTCG TATATCTCCT 5640

ACACCAACAG ATTCCACATT TCCAGCACGT CCTTCATCTG TTTTATTAGG AATTGGTTTA 5700

GTTAAATCAT CAGAAATAGA TAATTTCCCA AAATCATATT CTCTTGGAAT AAAAAGTAAA 5760

TCAAAGTTAC TATTTGGCTT CGTCGGGTCT GGATCGACTG TATTTGGAAC GCCATTACCA 5820

TCTGGCAACG TGCCGCCTGC AAATTCTGCT GTGACTGGTG TATTCCCAGT GGTCACCGCT 5880

TGTGCTGAAA GAGGTGCTAA ACTTGCGCCT ACCACTGCGC TACCAACTAA TAAACTTGCC 5940

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GAATAGCTGA GGTTCTGCCC TCTGTTTTCG TTGCTTGTGC TTAAATTGAT GGTCCTGCGA 6060

CGAGGTTCCA TGTGATGTTG CCTGTGTAGG CACCTGCTTT GATTTGTTGG TATGGAGTAG 6120

TAACTTCAAG ATTCATGGTA CGAATACCTG AATACCATAT GCCTTGTCCT TTTCCTGAAC 6180

TTGCTGTCGC AATTGCAATA GCATCACCGC TTAACGGAAT ATTCGTTCCC GAAAAATCAG 6240

GTGTAGTTGG ATCAGCTTCA TAATTAGCTA AACTCTCAGC ATCAGTTAAA TAAACATATA 6300

TTTGTTTTGT TGCATCAAAT TTTGAATAAT ATCCGATTTG ACTAAAATTA AGGTTTCCAG 6360

CTAAGGCTTC ACTCCCATTA GCCAAAGTTG CTGAAGCTGT GACATGCCAC CCTTCTTTCG 6420

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GACTATCGCT AATTTTTGTG GTGTTAAATG TAACTGCTTT TGGTATCTTT ACTAAGTCGA 6540

AATTAGTGTT AGGTACTGTC GGGTCTGGTG CTGTGTTATC TCCAGCATTT CCTGTCTCGT 6600

TATCTAATGT TCCTCCACCA AACTCCACCT GCACTGGCGT ATTCCCTGTC GTTACAGCCT 6660

GTGCCGAAAG TGGTGCTAAA CTAGCGGCAA CGACTGCGCT ACCAACTAAT AAACTTGCCA 6720

TCATTTTCTT TTTCATCATA ATATGTACGT CTCCTTTAAC TGTTCTGAAT TTCCAGAGCG 6780

CGCGGTTCTT TTTTCTGCGC TTCCGAAGCT ATAGCCTTAT TATACAAGAA TCTGCCCTCT 6840

TCGTAATTTT AAATATTTAA CAGCCATTCA TGAAAATTGA TGATTCCTTT AAAACCAAGC 6900

ATTTCTCTTG ATTTCAAGCT TTAATTTCAG CACTTTTTGA TATTCACAAA TGTTATTTAA 6960

TGATTTTTTC GTCAAATTCG TTTTCTCCTA AAATCTTATA CATTTACCGG CGGTTCTTGC 7020

GAAAAAAACCG TCAATTTTCA TTTAATGACA GCCGTTTTTG TATTTGTTCG TCACTAAGAC 7080

TTACAATTTA CGGCGACGGG CGAATTCCAC AAACTTAAAT TTGTTTAAGC GGTGACGGGA 7140

TTCCGTATAG CCAAAACAAC GGGTATCTTC CAAGTTCATG ATACTACGAA CCACGACGAC 7200

ATGATTGCCT TCGACTTCAC CAATCAGCTG CTTGTCCATC TCTGTGAGCG GTTCCACGGT 7260

AATTTCTTTC TGGGCATAAC TAATCGCCAA GCCAAGGTCG TTTTCCAGAT AATCGAAAAT 7320

CGAATCTTCG GCACGGTGCT TCGGCAGTTC TGGGACAATC TCTTTAATCA AGTAATCAAT 7380

ATCTAAAATA TCGACTTCCC CTTCAATCTC CCGTTGCCGA ACTAAGCGCC ACACAGGGGC 7440

CCCTTCCGTC CAACCAGTCA ACTGAGCCAA GTTGCGCTCC ACAGGAATTT CTTCTAAGGA 7500

AACCACATGA GTATGACTTT CAATATGTTG CGTTTGTTGT AACTCCTTGT AACTGGTCAC 7560

CCCTGAAATA GGAAAATTAA ACTTTTTAAA GTTGAGCACA ATCGAGCCTT TGCCTTGTTT 7620

TTTCTGAATG TAGCCAGCGT TAATCAGTAA ATTCAAGGCT TTCCGAATTG TTtCaCGGGA 7680

AACATTGTAA GTTTCCACTA ATTTGATTTT CA 7712

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

CGAACTTTGT GTTTTTCGCC AGCCATGTCA AAATAACTGA CGGTAATTTT GTTATGGCGA 60

ACGACATACC CAGGTACATC CCGATCGACA GATAAACAGC CTTCCCCTTC ACCTAAACAT 120

ACATCTTGCA CAGAATGGCT CAAAATTTTA GGGTTGTACA TCACCGTACT TAATGAAGGC 180

GTTTCGTTTT CTGGGTCGTT ACTAGGAACA TGGACAGCAA TAATTCGTTT AGAAATATCT 240

AATTGTGGTG CAGCTAAACC AACGCCACCA CGTAATTGTA ATTCTTCGGC TTTGACTGGA 300

TCTTGACTAT TTTTTAAGAA AGTCAACATG TCCTCACCTA ATTGTCGGTC TTCCTCAGTG 360

ATAGGGACAG GCACTTCTTC TGCCACAGCA CGAAtGTGGG GATTCCCTTC ACGAATAATA 420

TCTTTCATTG TAATCATTCA ATGGTTCCTC CTTTGAAACA TAAAAAAATT CTTCTTTTAT 480

TTATTCaTGC GCTGrAATAA TCAGTTGtTT ACCACCyTTT AGtGkAnCmC aAAAyCmCCA 540

AAAAAGGGGs tAgAwTGgTT TAAAAAACn 569

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

GnTTTACAAC TTATAATCGT ATCTGGCGTT TACCCACGTC TCTGCATCGC CATTAAGTCT 60

GGAATAAATC GCCTGCATTT TGCGAACGAA AAAGTTGCAG TAAAAAGAGA AATTCATCAT 120

CTTTCAACCA ATTTTTTGGT AATGATCAAA TAGTAAGTTT GAGATTGTTG TTTCACCAGC 180

TTCTAAATAT TCACGAATTG ATAACATTGT TGTTGTCCAC TTCCCCTTGC TTGTTTCaCT 240

TATTGCACTT GATAAACATC AAAATAAATA GCTTTCATAT AATCAATTAA ATAACTAGGA 300

TTCAATTCTT CTCCCgTTGC ATCATAAATT AATTGATTTG GTTTACGTGA AGCGCCGTAC 360

TGATGAATAT GTTGTGTTAA CCaTTTACGG ATATCAGAAT AATCCTCCGA AGCTAAAATT 420

TCATCAACAG ATAATTCTTG TTTCATTGCG TGAAATAGTT GCGCGGCGTA CATATAACCC 480

AAGGCATAAG ATGGGAAATA ACCAAAGCTA CCTCCAGACC AATGAACATC TTGAAGGGCA 540

CCTTCTAAAT CATTTTCAGG TGATACGCCT AAGTACTCTT GGTATTTTTC GTTCCATACT 600

TTTGGCAAAT CAGCGACTTC CAAAGAACCA TTAAACAACA TTTTTTCAAT TTCATAACGA 660

ATAATGATAT GCAAAGGATA GGTGAGACTA TCGGAATCAA TCCGTATCAA ACTTGCTTTC 720

GTTTCTTTTA AAGAAGCATA GAAATCTTCA AAAGCAATAT CATCAAAAGT GCCTTCTGCG 780

CATTCTTGGA AAAACGGGTA TTGTTTTTGC CAAAAAGCTC GGTTGCTACC AATGATAATT 840

TCATTAAAGA GCGATTGTGA TTCGTGAATC CCCATAGAGG CGCCTTCGCT TAGTGGTGTA 900

AAGTCAAATT TAGGATCAAA ATTTTGTTCA TACATCCCAT GACCCGCTTC ATGAATCACA 960

CCAAATGTTG CCATTGAGAA ATTATTTTCT TCCCAGCGnG TAGTAATCCG CGCATCATTT 1020

CGATTTAGAG CTGTCATAAA TGGATGAACT GTATCATCGA ATCGGnCTTT TGAAAAAnCA 1080

TAGCCTAATT GTTCAACCAC ACCAATCACA AAACGGnGGT GGTGG 1125

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

GAAATtAcaA CAACATTGTC TAGTGCTGCT CCAATTCCTC CTAaCATTAA GCTGGCAAGA 60

AAaACAGTTC GATAAGGTCT AGTTAAAAAT TGCATTTCTT CATAGCGCAG TCCTTGATCG 120

TTTAATAATT TCATAGTAAT TGTGGTAATA AAATAaGrTa GAAAaaCACT AaATATTGTT 180

GCTAAAACCT TCCTTAAATC AATTTTTTTT AGTCCGTAGA GAGTACCAGT TGATATAATA 240

ATaGCAATTA TTGTATAGAT TGATATTAGC AATAGTAAGT TTATGGATCT GTTTCGCTGA 300

TTTATCCAAA GCAAGAAAAA AAGAAAGATT ATATTGAATA AAATACCAAC TAAAGAAAAA 360

AATCCTTTTT TTCCAGCGAT ACCTAAGACT AATGAAACAA AACTAACTAC TAAAATAAAA 420

GTATAGCCAT CTCTTTTTAG AGAAATAAAT TCCCACTTTT TAGTGGAATT ATCTAATAAT 480

ATTTGATTAT TTTTATTAAA TACTGGaTTG GTACTTTCAT TTCCATTAAA TTTTACTTTT 540

ACAACAACAG TTTTTTTTGt ATTATTTACT AGTTTAACTG TTAGTAATTG TTCGCTGkCa 600

ATTATTTTTA CtGaTTTTAC aATACCmACC nGGGGAnGTA TAAAAGGTAA C 651

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

GATGGTTCAA CTAATTTCTA TTATTTTTGC GTTTTTGATT ATACACACTT TATTTAAAAC 60

AAGAGAAACA AGTAATtCTT CAAGAAAATT AAGAATGTTA GTGTACACTT TTTTGGGGAT 120

AATTTTTCTA TTAGGCTTAG TAAGTGTCGT ATTAGGAACC TATGGGCTGT TGAATTCTTA 180

TAACATTAGT GGAAATTGGC GTATAAATAT GTCCTCTATT TTAGTTGTGT TGGCTGGAAT 240

TTTACTAGTT GTACTTTCTT ATGTTGGTAT TTCAAAATTT AAAATGAATT GTTAGGTGAA 300

TTAAATGAAG AAAGTTATCT CTACCATTTT ACTAGTAATC CTTTTTGTGG GATCAGGTTA 360

TGTGGTAAAC GCTGCTCCTG AAATGAAGAG TTTGACTAAT TTCGAAACGA ATGATCAACA 420

TTATGATTTA CAAGGGATAG AACATTCCTT TTGCTAAAGT GTTAAACTTT AAAACAAGTA 480

GAAAAGATAT TACAGCAAAA ACGATATTAA AATTTGTATA TCTAAAAAAG ACAGACAATG 540

AATTGAATAA TGCTTCTGCA TCTATTAAAG ATTGTATTCG CTATGCCACT TCTATTGGGG 600

TAAATATGGA ATAGCTTGAT GCAATGAAGA ATGAACTTGA TTTCAACCAA GTGAAGAGTG 660

AGATTGATAA GGATCATCCA GTATTACTAT GTTATAAACC AAACAAAACC GATTTAATGG 720

AACCTTATTT ATTAGCTGTA GCGCATGGAT ACGTATACGT TGCTCCAGAT GGTCAAAATA 780

CTAAAGAACC ATTTATGAGT ACAAGTATCT GGATGTCGAA CTATATATAT CCTTCTATCC 840

TGACTACGTT GGCGAATAAA AATAAGTAAC AGTTACATAT TTTTCAGTGA ATAATGCGCC 900

ACAAAAAGAT TATACATTTA TTGGTATGAT TATTTTTAAG TAAGAAAGGT TGTAAGGAAA 960

TTGAAAAAAT ACATTTTGTG TTTGAACACA TTTGATTGAA GAACATCAAC GCGACTATCT 1020

CTATGGTAAT TAGGGGCACG TACTAAGTGC CTTTTTGAAT GTAGAGTCAT TTATTATGCT 1080

TAAGAAAAAA ACTTACACAA AACTCTATAC AGATCCGATT TCACTGTAAC TGCTTTTAAA 1140

GAAAAGACGA TATAAAGATA GTATAAAGAA ATAAACTTAA GTTTCACACT ATCTTTAGGT 1200

CTTTTTTTTT ATGCTTACAG AGTAAAGAAA ATTAGTTAGT TTATTTAACT GGTTGTTTTG 1260

AAAAGGAGTG AAGTGAAATG ACGATTATTT TAGGAATTAT TGGACTCTTA TTAATGATCT 1320

ATCTTTTCTG GTTTTTATTT AAGGGGGAAG AATTATGAAT AGCTTGATTT ATCAAGGATT 1380

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ATTTTTCCTA TTCATATTAT TGTTATTGGC AGTGCCGTTA GGcTGGTACA TTAAAGAAAT    1440
CATGCAGGGG GAAATCCCTA AAGGAGTATC CTTCTTACAG CCAGTAGAAC GTTTATTTTA    1500
TAAAGCGATT GGACCTATCA GCAAAAAAGA AATGTCAGCG AAACGCTATG CACTGAATGT    1560
GCTGCTGTTA AGTTTCTTCT CAATCGTACT TTTGATTGCT ATTTTAATGA CACAGCACTT    1620
TTTACCGGGA GGTTCCTCAG TAAAAAATCT AACGCTGCCG TTAGCGATAA ATACGGCCGT    1680
CAGTTATGTT ACGAATACCA ACTGGCAAGC ATATGTAGGT GAAACGACTT TATCAAATAC    1740
ATCGCAAATG TTTGGTTTGA CAGCTCAAAA TTTTGTTTCA GCAGGTGTGG GACTTTCTGT    1800
TTTGGTAGCA TTGCTTCGAG GACTTTCACA AGTCAAAAAG AAAGCTTTAG GAAATTTTTG    1860
GCAAGATTTA ACTCGTAGTT TAGTTTACAT TCTGTTACCG ATATCAATCA TTCTTGCTGT    1920
TTTATTAATT TCACAAGGAA CCGTTCAGTC TTTCCAATCC GGAGTCGCTT ATCAAGGTTT    1980
GGAAGGGAAA AGTCTTTGGT TGCATTTAGG TCCGGTAGCT AGTCAGGTGG CAATCAAACA    2040
ACTTGGTACA AATGGCGGTG GTTTCTTTGG TGCTAACTCA GCATACCCAT TCGAAAACCC    2100
AACACTATTC TCAAACTTTT TAGAGAATAT TGCGATCTTG TTGCTCCCAG CGGCATTGAT    2160
CTTTGCTTTT GGCTTTTGGG TCAAGGATTG GAGACAAGGA CGAACGATAA TGATAGTATC    2220
CTTGTTTTTC TTACTATTAG CTTTCGTCGG CGTTGCTTTT AGCGAGTATT ACGGGCCTGA    2280
ATTTACGCAT GTTCTTGGAT CTACCAATTT GGAAGGAAAA GAAATTCGCT TCGGCATTGG    2340
CTGGTCTAGC TTATGGTCCG TCGGTACGAC CGCCGCTTCG AATGGTTCGG TGAACGCGGT    2400
GTTGGATAGT TTTACACCGC TTGGTGGCGC CATTCCAATG TTCTTAATGC AGCTTGGCGA    2460
GATAATTTTT GGTGGTGTTG GGAGCGGACT GTATGGAATG TTGGCATTTC TATTGCTAGC    2520
AGTTTTTATA GCAGGTCTTT TAGTTGGGCG GACACCTGAA TATTTAGGTA AAAAAATCGA    2580
AGCTTTTGAT ATCAAAATGG CTAGCCTAGT TATCTTAACA CCATTGATGT TGACGCTTTT    2640
CGGGGCAATG GCTCTAGTCC TACATCCAGA GGTAATGTCT TGGTTAACGA ACCAGGGTCC    2700
CCATGCTTTC ACTGAATTGC TTTATGGGGC AACTTCATTA GCCAACAACA ACGGAAGTGC    2760
TTTTGGTGGG TTGCTAGCTA ATACGACATT CTTAAACCTT TTAGCTAGTT TAATGATGGC    2820
TGTTTCAAGA TACTTGCCGA TCATCGCCAT CTTACTTTTA GCGGAAAATA TGGGAAGTAA    2880
AAAGAAAGCA GCTTTAAGTT CAGGAACATT ATCCACGGTT AGTCCAACAT TTGTTTCTAT    2940
GTTGATTATT GTTATTTTGG TAATTGGAGC TTTAAGTTTC TTACCATCAT TGGCACTAGG    3000
TCCGATTGCG GAATTCTTTA CGATGAAATA GATGGAGTGA GTAAAAATGA AAAAAATCTA    3060
TCAATGGGCA GTGGGACAAT CCTTTAAAAA ATTGGATCCA CGCCAACAAG TTAAAAATCC    3120
CGTGATGTTT GTCGTTTATT TAGGTGCGCT CATCACTACA ATATTATGCT TCTACCCAAT    3180
GGGTATACCG TTATGGTTTA ACATTTCAAT AACCATTTTT CTTTGGTTGA CTTTGCTTTT    3240
TGCGAATTTT GCTGAAGCTG TTGCAGAAGG ACGAGGAAAA GCACAGGCCG ATAGTTTGAA    3300
ACAAGCAAAA AAGGAAGTCA TGACTTATAA AATTAACAGT TTAGAAGATA TCAAAGAAGA    3360
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GAATTTCATT GAATTACAGT CTTCTGATTT AAAGCGAAAC GATTTGGTCT ATGTACGTGC 3420

AGGAGAGCAA ATCCCAGCTG ATGGTGATGT AATCGArGGG GCTGCaTCAG TAGATGaAAg 3480

TGCCATTACT GGcGAATCCA G 3501

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1856 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

ATTCATCAAC GACAGCGTTG ACAATCGCTC CTAAAATAAT AATCGTGGCA GCAAAATTCA 60

ACCATAACAT CAAGATGATA AAACTCCCGA TGATTTGATA ACTTGCGATT CTAGAACTAA 120

AATATTTTAC GTACAAaCCA AAAaTTTGTG ATAATAGCAT CCAACCGACT GTCGAAAAAA 180

TAGCCCCTGG CAAAATAGAA CGTAACGATA ATTTCCGATT AGGAACGACC GCATAAATCA 240

AACACATAAT CACTAATAAA ACAACGGTCG TTAACGGCCA TTTTAACGCT TGGAAAGTAT 300

CGATCACAGA TGTTGAGTAA TGGAAAATTG GTTGCAGTAA TTCAATAATG TACTGACCCA 360

GACCTAAAAT TACTACTACA CCAACAATCG CTACCATAAA TAACAAAATA ACTAAAAATG 420

AGACCACTCT TACGAGAATA AAATTTTTCC TTTGTTCGAC ACCAAAAGCT TTATTCATCG 480

CATTTTGTAG TGCATTAATA CTTTGACTGG CACTCCAAAA TGCTGCTAAA GCGGAAACAG 540

AAAGCAACCC GCCTGAACGT TGAGTCAGTA GTGAACGAAT CGCTGGTTCT AAGTTCTTAT 600

AAACATCTTT CGGAATCGCC TCTGCAATAT AAGGCAACAC AGAATTAGGG TCGATTCTTA 660

AATAAGGTAA GACATTACCT ACCGCAATCA GTAATGGAAA CAGCGAGAGT AATAAATAAT 720

AGGCAACAAC CACTGAGCTG TTGCCTATTT CGGCTGTGAC CATGTGACTT TGCGTTGTCT 780

cAATAAAACG CATCAAAGAT TGATTCTTTT TGATGTTGTC GAGAAACTTC ATCACACACT 840

CTCCTTATTA ATAAGTCAAT TCTTCGCCTT GTGACGTTAA GATTCTTGGA CCTTCTTTCG 900

TAATCGCTAA TGAATGTTCA TATTGACAAC TTAGACCGCC ATCTTCAGTA TAAGCAGTCC 960

AACCATTTGG GTCCATTTTC ATGCGCCAAG TTCCTGTGTT AACCATTGGC TCAATGGTAA 1020

TAACCATTCC CTCTTTTAAA CGTAGTCCTT TACCTGCTTC ACCATAGTGA GGAATCATTG 1080

GACTTTCATG GATAGTTGGG CCAATGCCAT GACCTACAAA GTCGCGAACT ACCCCGTAGC 1140

CTTCTCCTTC TACATACGTT TGAATTGCAT GACCAATGTC GCCAATTCTA TTTCCTACTT 1200

GTGCTTGTTC AATCCCAAGA TATAGCGCTT TTTTGGTTAC TTCCATCAAG CGATCAATTT 1260

CAGGTGTTGA TTCACCCACG ACATAAGACC AGCATGAATC AGAAATTGCG CCCTTTAAGT 1320

CGACACACAT ATCTACTTTG ATTAGGTCGC CATCTTTTAA TACTTTTTTA CGAGGAAATC 1380

CGTGGCAAAT TTCGTCGTTG ATACTACAAC AGGTAGCATA TTTGTAACCT TCATAGCCAA 1440

TTTGAGCCGC CACGCCACCA TGACTTTCAA TAAAGTCTCT CACAAATACT TCAATATCCC 1500

AGcTTGTAAT GCCAGGTTTA ATAAACGTCC GTAAATGACG GTGAACATCC GCTAATAATT 1560

CCCCTGATTC ATCCATCATT TCAATTTCTC GTGGTGATTT TAATGTAATC ATACTATCTC 1620

TCCTAAACTT GTTTCATTCA AATTATTTTA TCACATTTTT TGCAAAAAAG ATTGTTCAAA 1680

CACCAATTTT CAAAAAGTCC CTTAATAAAA GCACTCGCTA GTCTTTTATA AGAAATGCGC 1740

ATCTGCTATA ATAAGTGACA GAATTGTATG AGGGGGAAGA AAGTTTATGA CGTTAGCTAA 1800

AATTGTGTAT GCAAGCATGA CTGGGAATAC AGAAGAAATT GCCGACATTG TTGCAG 1856

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

ATATGGTTAA GGAATTTGGA AATCGTGTAG TAATGCCTTT TGTAGATCAA GTAAATGTTT 60

ACTTATCTGA TATTGCAACA GATATGGGAT ATGATGAGGA GAGAAAATAT ATGATACATG 120

TAAGTGGTGG ACAAGCTCAG GTAAATATTT CCAACGATAA CAGCACCATA AATGCTAACC 180

AAAATGTTCA AATCAATCAA TCTAAAGTTG ATGATTTAAT TTCTGATTTG AAAAGTAATA 240

TTGAAAAGGA ATTAGTGGAT AATGAACCTA TTAAAGATGT TTTGTTATCT CAATTGGCTC 300

TGATTGAGTC ACAACAGACT GAGAGTGAAC CTCAAAAAAA TGTTTTGAAG ACGGCATTTG 360

AGACAATGCA ATCTTTACTT AAGACTGCCC CATTAGCAGT AACTGCTGTT GAAAGTTGTA 420

ATAGATTGTA TGAACTGATG TCACCTTTAT TTAATTAGGA GCAAAAATTA AAATAGTTTT 480

AGAAGCCAAG AGCAAAAAaT GTtCTTGGCT TTttACTTTG CAaTGAaTGA GGTtATTTAT 540

GACATTTTtA GATTtATTtG CCGGGaTtGG TGGTTTcGTT tAGGTATGGA ACAAGCCGGC 600

CACCACTGTA TCGGCTTTTG TGAAATTGAT GATTTTGCCA GACGGAGTTA TAAGGCAATT 660

TATGATACAA GTGAGGAGGT GGAAATGTAT GACATCACAA GTGTATCAGA TGAGTTTATT 720

CAATCCCTCG GACCAGTGGA TATCCTTTGC GGCGGATTTC CGTGCCAAGC TTTTTCAATT 780

GCGGGAAAAC GGCAAGGATT TTCCGATACT CGAGGTACTT TATTCTTTGA AATCGCTCGG 840

TTCGCCGCTC TTCTCCAACC TAAGTTTTTA TTCCTTGAGA ACGTCCGGGG ATTACTCAAT 900

CACGAAGGAG GGGCTACGTT CGAGACAATC CTCCGAACGT TGGATGGATT GGGGTATGAT 960

GTGGAATGGC AAGTGCTTAA CTCAAAGGCC TACGTTCCCC AAAGCCGCGA GCGGGTTTTC 1020

CTTATCGGAC ATTCTCGAGA CATATGTACC GAACAAGTAT TTCCTATCAT TGAATCGTCT 1080

GCAACATCTG ATCAAAACCT CAGAAACTTG TTAAATACCA ATCCTTCCAA CCGAGGAATG 1140

AGTGAACAAG TCTATGGTTC AGATGAGTTT GCCCCAACCG TAACAGGCGA TGAAGGAATT 1200

AAAATCGCAC TACCAGTAAA TGATGGAATT TCTGTAGTGG GTATGTTGCC GGGAAATTTT 1260

GAACAAGGTA ATCGGATTTA CGAGGTAACT GGAACAGCTC CCACCTTGTC AACGAAGCAA 1320

GGGGGAACGA AGATTATGAT TCGAAAAAAT AAAATAGAAT ATCAAGAGGT TAAGCCAGAG 1380

GGCAGTGTGA ATCTGGCTTT TCCTCATTCC AAAAGTCGCC GAGGTCGTCT TGAAAAGCAA 1440

AGCGTCCATA CGTTACTAAC AGGAGATCAA CAAGCAGTCA TTACAGACCA GTATCAAATT 1500

CGGAAGCTTA CACCAAGAGA ATGTTGGCGT CTTCAGGGTT TTCCCGATTG GACTTTTGAT 1560

CGAGCCTCTC AAGTCAATTC AGATAGTCAG TTGTATAAGC AGGCCGGAAA CTCTGTAACA 1620

GTTCCGGTCA TTTTTGATAT TGCCAAGAGA TTAAAGGAGG TGAAAACGGA TGATTTATGA 1680

TGAATTGATT GGAGAAATCT AATGGGTGAT TGGCAAGATT CACTCAGATC CGGAACTGAA 1740

AGAAGAATTA CGTCAGCTTA ATTTTGATAT TCGCAAAAAT GTTGTGAAAG TCACTGGTGA 1800

TTCGTATGTA ATGGACGAGG GAACAGATAC TCGAATTGAG CTGAATCAAG TCATCAAAGA 1860

ATTAGAACGG ATTGCGTACC TTGCGAAAGA ATCGGATATC CGTCAATACT TGTTTGAGAT 1920

AAAAGCAGAA CTGGAAGTAG GTGGCATTAC TGAAGGGTAG CAGCCGAATA AACTAACTGA 1980

TGGGCGCCGA CCGCGGGGGA TTTGCGAAGC AGAAATCCTC TGTGGTGCTG TGCCTGTTCA 2040

TGGACGGCGT CAGCCGGCCA TGATGTCTCA CCCCCCCGTA TCTAACAGGG GGGTACAAAA 2100

ACACAAAAAA TGAGCAAGTA ATCATTAAGA ATTATTGGTG TAGCAAGGAT ATTAAGTAAT 2160

TTGCATAGGT GTTAACTCAT TAAAAAAAGT TAACACCTTG AATTTGGAGG TGAGAACTTG 2220

GCACAACGGA ATTTAGATTA TCGATTATTA AAAGACCGAC GTAATGAATA TGGTGTTTCA 2280

CAAAATAAAT TAGCTATCGC TTGTGGGCTT AGTCGGACCT ATTTAAATCT GATAGAAAAC 2340

GGTGGCGTAA CTGCCTCTAC AAAAACCATG AGAAAAATTT TTGACCAACT GGAAAGTTTT 2400

AATCCCGATT TACCTTTAAC GTTACTGTTT GACTATGTAA GGATTCGTTT TTCCaCAACG 2460

GATGTGCGGA AGATTATTCA AGAGCTTCTC CATCTGAAAT TTGAGTATAT GCTTCATGAA 2520

GATTACGCCT TTTACTCCTA TCAGGAACAA TATGTCATGG GAGATATTGT AGTGATGTTG 2580

TCTCATGAAG AAGATAAAGG TGTTCTTTTG GAATTAAAGG GTCGTGGTTG CCGGCAGTTT 2640

GAAACTTTTT TACTCGCTCA AAAGCGTAgC TGGTACGACT TTTTCGAAGA TTGTCTAAAA 2700

ACCGGTGGTG TGATGAAACG CTTGGACTTG GCAATCAATG ATCGAGTGGG GCTACTGGAT 2760

ATTTCTGATT TAACGAAAAA ATGTCAGAAG GAAGAATGTA TCTCCTTGTT TCGTACCTTT 2820

AAAAGTTATC GTTCCGGGGA ACTTTTAAAA GCTGATGAAA AGGATGGCAT GGGAAATACC 2880

TTATATATCG GCAGTCTCAA GAGTGAGGTT TATTTCTGCT TGTACGAAAA AGATTATGAG 2940

CAATATATCA AGTTAGGGAT TCCATTAGAC CAGACTGAGA CGAAAAATCG TTTTGAGATT 3000

CGACTGAAAA ATGACCGTGC TTATCATGCG ATTCAAGATT TGTTAAAAGG TCGTAGCATT 3060

GAGAGCACCA CGTTTTCTAT TATCAATCGT TACTTGCGAT TTGCGGATAA GGTGGAAGGC 3120

AAACGGCGAA CCAACTGGCC CTTGAATGAA CAATGGGGTC GCTTTATTGG ACGGAATCGG 3180

AAGGAAATTC AATTAACTTC TGAACCGAAA CCTTATACCA TTGAACGAAC CTTGAATTGG 3240

CTTGGACGTC AAGTCGCCCC TACGTGGAAG ATGGCAAAGG AATTGGATCG GCTGAATCAG 3300

ACAACGTATA TACAGGATAT GGTACGGAAT GCACGGTTAT CAGACCAGCA TAAAAAAATT 3360

TTGGAACAAC AAAGTATGGC AATCGAAAAT TTGATTGTAT GAAAAGAGGA ATTTTGATGG 3420

GAATTGTAAA AGATATTTTA TTGGTATTTG GTGGCAGTAT GCTTGGTGTT ACTGTGATGT 3480

GCTTGATGCA TGCAAGTACA GCAGCAGACC GAGTAATGGA AAAGAAAGGA AAGTGACGAG 3540

ATGAATTTTG GACAAAATTT ATATCAATGG TTTTTGACCA ATGCTCAATC CTTAGTCTTA 3600

CTAGCGATTG TAGTCATTGG TTTATTTTTA GGATTTAAGC GGGAGTTTTC TAAATTAATT 3660

GGCTTTTTGG TGATTGCCTT GATTGCGGTA GGTTTGGTCT TTAATGCTTC TGGTGTGAAG 3720

GATGTCTTAC TCAATTTATT TAACCGAATT GTTGGTGCAT AAGGGGGAAT CACGATGGAG 3780

CAGATGCGTG TTTATATTGC GAACCTTGGA AAATACAATG AAGGAGAGTT GGTGGGGGCG 3840

TGGTTTACTC CACCTGTCGA TTTTGATGAA GTCAAAGAAC GAATTGGGTT AAATGATGAT 3900

TATGAAGAAT ATGCGATTCA TGATTATGAA CTACCCTTTG AGATTGATGA GTATACATCA 3960

ATTGAGGAAA TTAATCGATT GTGTGGCTTA GCGGAGGAAT TAGAAGGAAC GCCAATTGGT 4020

GAGGTTGCTT CAGAGATTCA GCACGCTTTC TTTAATTCTT TCGAGGAAAT GGTGGAGCAT 4080

GTGGATGATA TTGTGTATTA TCCAGATTGT AATGATATGG AAGATTTAGC TTATCAAATG 4140

GTAAATGAGG GGTATTTAGG AGATGCTCCA GAAAATTTTG TAAGGTATTT CAATTATTCC 4200

TCTTTTGCTC GCGACTTGGA GATTGAGGGA AACTATTTAG TTACTAATCG AGGTATTTTT 4260

GAATATCCAA TCTAAATATA AGCCATTCAA CTTGAATGGC TTATATCTCA ATTTATTAGT 4320

GGAAGTTTAT CAGTGTTAGA AAGCGCCCAA ACAATTGCAT TACCTGCTAA AGTAACAATT 4380

TTAGGATGTT TTTCGAGAAA ATCAGAAAAT CTTTCTAAAA CGTTAGGTTT AAAATCTTTA 4440

GTTTCTACGA TATTGATAAG CTCTTTGCCA ACTTGTTGCT CTTCAGGTGG TAAAGCATCA 4500

ATATATTCTT TTAATTCATC AAGAGAATTA TTCCAATTGT TTGTAACGGT ATTATTGTTT 4560

CCGAATGTCG CTCCTCTATA GTCACCTGAA GAGTTAAAAT TAAAGGTATT TGTCGTCTGA 4620

ATCGATTGAC TATTTTTTTC TGAAGGATGA ATTTTCTCTG CCCCCTCTTC TGTTAGTTCG 4680

ACATCATCTG ACGAAAAGAC GAATAGACGT AGAGGAAAAT GCCGAGAAAA ACAGGGGAAA 4740

TGCCCGATTA TCTGTCAAAA CTCCGACAAA AAATGCAGAA AAGATGGCCT ACCTCTGGCA 4800

CACACCACAA AAAAACAGAA TATCGAAACC ACAAGCCGTG CAGTAACTGA CAAACAATCA 4860

GCTACTGCAC GGCTTTTTTT GTTATAGATC GCTTTGCCCC GACGACACAG ATCGCCGGGG 4920

CTTTTTTCAT TTAGACAGGA GGCTTTGAAA ATGCCGGAAA CATTGAATCT GAATTACTAC 4980

TACGGGAATG AAGCCGACCA GTACAGCTTT TACCGTATCC CCAAAACCCT GCTGACCGAC 5040

CGCCGCTATA AGGGCGTGTC ACTGGAAGCA AAGGTACTGT ATGGCTTACT GCTTGACCGC 5100

ATGGGGCTGT CGGCCCGGAA CGGCTGGCTG GACAATAATG GGCGGGTATT CCTCTACTTC 5160

ACGCAGGAGG AAGCCATGAC CATGCTGGGC TGCGGCAAAG ACAAGGTGAC AAAACTGTTC 5220

CGCGAATTAG AGGGGATTGG CCTGATGGAA CGGAAAAAAC AGGGGCAGGG ACATCCCGCC 5280

CGGATATACG TTAAAAATTT TATCTTGGAA CCGGAACCCA CCGCGCCGGT TCAGACTGCG 5340

GAAAATCAGC AGTCAAGACC GCTTCCCAGT GCCGCCGTCA AGACTGCTGA AAAACCGCAG 5400

TCTGCACCAC GGAAAACCAG CGGTCAAGAG TGCGGAATTT CCGCCCCTAA TAATACTGAT 5460

ATAAATAAAA CTGAAAAAAG CGATACTGAT CTATCCATCC TACCCCCTAC CCCCTCGGCA 5520

GTTTCTTCTC CTGCTGGTAA AnrCGCTCCG CGCAGGATGG GATTGGATGA GATGGAAAGC 5580

TACCGTGAGC TGATCATGGA GAATATTGAC TACGACATTC TCTTAGAACG TTATCCCTAC 5640

GAAAAGGACT TGCTGGACGG CTATGTGGAG TTAATGCTGG AGGTCTGCTG CTCCACACGG 5700

GAATCTGTCC GTATCTGCGG GCAGGAAGTA CCCACCGAAG TTATCAAAAG CCGGTTCCTG 5760

AAGCTGAACA GCGAACATAT CGGCTATGTC ATGGACAGCC TGAAAAGCAA TACTGCCAAA 5820

ATCGGCAACA TCAAGGCATA TACGCTGGCG GCACTTTACA ATGCCCCTGT CACGATGGGG 5880

CAATATTACA CATCCCTTGT CAGCCACGAT ATGGCGCATG GGCTGCTGAG TGGTTAAACC 5940

ACCCAGGGCT TTGCGATACA TCAATCAAAC CAAAGGAGGA CATTTGCATG GAACATGAAA 6000

TCAACATTCT GGTGGTGGAA CCGGGCAGAC CGCCCAGGCC GGCACGGGTG GACTACTCGC 6060

TGGAAACTTT TTCACAGCTT GTCGGCGGGG ATCTGGCAAT GGGCTGTTTC CTTCCCCAGC 6120

GGGTCATGCT GCTTTATAAC GAGGAGGCCA ACCGCCAGGG ACTGCCGCCC AACCGCTGCA 6180

ATCCCTTTGT GAACGAGTGC ATCAGCGGTA CATTCCTGCT GTGCGGGCTT TCAGATGGGG 6240

AGGGCTTCTG CTCCCTTTCT CCTGCCCAGC AAGCCGAGTT TCAGCGCCTT TTCGCCAGCC 6300

CCGGCGAGTT TATGATGCTG GGGGCAAACC ACATCTGCAC TTCGCCTGCC GAGTTTGCCG 6360

AAACTGTCAG CAGGCTTTGG GGCGGTATGG CAAGCGGTGA GTCTGTGGTG CTGACCAAGT 6420

GGGGCGGCAC GGAAAGCGGG GCCTGAACAT GACAAAACAA AATAGCAATA CCGACCGCCG 6480

CAGTTTGCAG GACTGCGGCG TTTTTTCATC GGCAGAATAC CATTCAGTCG GGTTAAGCGG 6540

CGGCAAGGAT TCCTCGGCGC TACTGCTCCT GATGCTAGAA AAAGGGATGC CGATTGACAG 6600

CGTGATATTT GCCGATACCG GCATGGATTT CCCGGAAATG GCGGC 6645

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1075 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

GGAACACAAG TnAGTACACA AGATACTGTT GAGGTTGATG GTGTACCAAT TTATCAAGAA 60

GaATATGGTT ATTaTTTATT CTATAAACCA AGAGGGGTTA TTTCTGCGGT GTCTGACGAT 120

AAAGGCCGTA AAGTAGTAAC GGATTATTTT ACAGATGTTA CTGAGCGAAT TTATCCAGTC 180

GGTCGTCTGG ATTATGATAC TTCTGGGTTG TTACTTTTAA CGAATGATGG AAGTTTTTCA 240

CAAAAATTAA CCCATCCTAA ACATGAAGTA GATAAAGTCT ACGTAGCAAA AATTAAAGGT 300

GTTCCAACTA AACGGGATCT ATTGCCATTA GCCAAAGGCA TTCGCATTGA TGGCAAACGC 360

ACAGCACCAG CCAATTTTCA AATTCTTTCA GCGGACATTA AAACAGGTAG CAGTGTCGTG 420

GAATTAACGA TTCATGAAGG ACGTAATCAT CAAGTGAAGA AAATGTTTCA AGCTGTTGGT 480

TTCCCTGTTC AAAAATTAAA ACGTGAACGT TACGGTGAGT TGACCTTACA AGGTTTGCGA 540

CCAGGGCAAT ATCGTGATTT AACTAAAAAA GAAATCAGTC AATTATTAAA TCAAGCTAAA 600

TAAGATAAAA CGACTCGATC TCTTCGCGCT TATGGCGAAG GGATTGTTTT TTTTGAGAAA 660

CGAAGCAATC AATGAAATTT AATAAAAAAG CTTAGTTAGT TGCATTCATT GTTCAAATCG 720

GTTACACTAA GTAAGTAAAA AAATATAATA CAAGGTTCGT CTTCAGGGGC AGGGTGTAAT 780

TCCCGACCGG TGGTTATAGT CCACGACTCG TTTTTAACGA TTGAATTGGT GTAATTCCAA 840

TACCGACAGT ATAGTCTGGA TAAAGAAGAT AGGGCTTATT TGAGACGCTT TTTCATCAGA 900

TAATCCTACT CTATTTTTCC CTGCAGAAAA ATAGGGTTTT TTTGTATGAC AAAGAAGCGA 960

ATCAAAAAGT TCGTTGAAGa TGGGTCCTTA ATTGGAGGAT TtCAGATGAA CAACAAGGTA 1020

CAAAAAATGG TCAGCATTGC AATGTTGGCC GCAATnGGTA CAGTATTACA ATTTG 1075

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

TACCACATCC CACCACTTTC TACCACTATA AATCTAAAAA CTTCTATTTT TTAACTGTTA 60

TTTAAAATTT CTGTAATATT TAnAGGGTTT TATGTAACAA GCATCACCCA ACAAAAAATG 120

TTATTATAAC AAGGTTTTTA CTATGTTTTT TATAAAATAA CCCCACAAAT AACAAAAAAA 180

CCCCACGGAG gaAGtTGTGG GGGACATTTT CCCACAGCGT ATTTCCCCTA TTGTCTCCAC 240

GCTTTATTAC AGTAGATAAT GACTGATATT TAGCAAGATA AGCAACACAT ACAACACAAA 300

CGTTAGTAAA AACGTCAACC GCCAAAACAT CTTGAAATAT CGTCTATATA AAATCTCTCC 360

ATAATAATAA GCTTGAAACA GGGCAACAGC GACTCCTAAT AACAAAATAG AAATCACAAA 420

ATACGGCATA ATCGATTCAT CATAACTATC TTTGGATAAC TCATGGATCC CTATGAATAA 480

AAACGGAATG GCCAAATCCG GTGCTTTTAT TTTCCAACGT TCCGTTAGGG AAAAAGTGGA 540

CACGAGaAAA TTGCACGCAA AGAGCACAAT TACCGGAAAA ATATACCAAA ATAACATTAT 600

TGCCGAAAAC GACACCATTC TCTCAACAAA TCCTTTCATT CCACCTGCTA TAACTATACT 660

TCATCAACGT TACACAGATG TTTCATTTCG TTTAAATATA TGTGCTAAAA GCCCTTTTTG 720

CTTGCTTTTT CATATAAAAA ACGGATTACT TATCAAACCA TTTTCAAAAC GAGGCCTCAC 780

CTATCGCGGC CACTTATTTT TGAATGTTTT TTATAAGCTT TTCTTCTCGT ATTGTGTCAT 840

ACTTCTATTA TAATGGATTT AGAACAAAAA ATGTTGATTC GGGGTGAATC TTTTGATTAA 900

TTATTTATTA TTGAAAAATG ACTATTTTGA ACCTTGTTCA CCAGACGATG AAGCCCTAAG 960

TTGGATTTCG GTAGAATCTC CTACAGAAGA AGAAATCGAG CGTCTCGTCA ATCAATACCA 1020

CTTACCAACA GATTATCTTA CCGGCGTTTT AGATGATGAA GAAAATGCTC GAGTGGAAGG 1080

CTTCCGCCAC GAAAAATTAC AAACGCCTAC GTTACTTTTA TTTCGTTATC CCAAAGCTAG 1140

TATCAGTCCT AGTGGCTATC TGCAAGTAGA AACGGTGCCG ATTGCTTTAA TCGCAACCAT 1200

CGATAACAAA CTAATTACTG TTAGCAACGG GCCTAACGAC ATCGTTCATG GGATTCAAAA 1260

AGAGGCGTTC ACCCATCAAG ATCTTTCTAT TGAGAAGGCC TTAATTTTAG CCCTTTCATG 1320

GAAGATGGCC CTTTCCTTCA ATAAAAACTT ACAAGCACTT ATCCAACAAA CCAACAAACT 1380

TGAAGGAGAG CTCCAAGTAG CCACAGAAAA TAGTCAATTG TATCAGATTA TGGACATTCA 1440

AAAAAGTCTA GTTTATTTCG AAGCAGCTTT AACGGATAAT TTAAAAGTAT TAAAACGTTT 1500

ATATAGCGCT GAAATTTTTA ATCATCCAGA AAAACATTTG CCATTTTTAA GGGATATTCT 1560

GATTGAACTA GAmCAAGGAC TGAATACGAC TAAAATACAa CTAAAATTAG TTGATAcATT 1620

AGTAATCCTT TTTCAGCAAC CGTTCCAATA CTTAAATAAT GCATGAAATT TACAnCTTAC 1680

AATGGCCTG 1689

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

ATATnATTTG ATTAnnAGTT CATCAAATTA CCCTGCATTA CAACAATCTA TATCAGGTAT 60

TTACTCAATT TCAAATAAAT TATTTTTTGG CTCATTAATA TTTGCAGGAG TTGTAGTTTC 120

ATTATTATTA TTCTTATGGA TGAATGCTAG AAAGAAAGAA ATAGCAGTAT TACTATCATT 180

AGGTATATCA AAATTAGAAA TTTTTGGTCA ATTCCTAATT GAGATGGTAT TTATATCAAT 240

CCCCGCATTC GTTGGTTCCT ATTTCTTAGC TCAATATACA GCTGACAAGC TTGGGAATAA 300

TATATTGAAT AAGGTTACTG GTGATATAGC TAAACAAATA GCTAAACAAT CTGCATCTAG 360

CCAATTAGGT GGTGGGGCAG AAGCTGAAGG ATTTAACAAG ACATTATCAA GTTTAGATAT 420

CAATGTATTA CCTAAATTCA TGATTTATGT AGTTATATTT ATGAGTTTAG TACTTCTTGT 480

ATCATTGATT ATTTCTTCAT TCAATATATT AAGAAGGAAT CCArAAGAAT TATTAATTGA 540

CAATAATTAA AATTTTCGGT GCTTTTTAGC ACCAAAAATG AGAGTGTAGT ATAAAGGCTC 600

TTtGTCAAAT GATGTTGGTA AAGAGAAATC TTAGAATAAT TTGGACAGAA CAGArAGAAG 660

AAACCCTCTT CCtGTTCTGk TTATyTGGTT AAAAATGtTT TGCCATGACG AATCATGATC 720

CGTAGTTTGA AATTGTAmAA GCTGCGAAAG CCGTACGCAT TGCGTTTTAA TACTTTGATG 780

TGGTTGTTTA AACATTCCAA TGGTCCATTT GAATAGCTGT AGTGAAGCGC ATTTTGGATC 840

TGTGGCAGAA ACTTTTTAAA CGTTCGTAAA GTGGTTGTAT AGGTTTCAGG AAGACCGCTG 900

ACTTCTCTGT TTAAACAGTC CTCAAATAAT GACTGATCTC TTTTCTTTAC CGCATAAAGA 960

ATGTCTTGGT ATAACTGATA GCCTTGGCGC AGGTTGGGAC AAGCAGATAA CAGTCGATCG 1020

ACAATCTCAC TTTCAGTCAA ATAATCTTTA AAACTGGCAC GCCAAACCCT TTTTTCGTAG 1080

TTTAACTTTG CTTCTTCTTT TTGTAGGAGT TTCCAATAGC GTTTCAATTT TTTCCCTAAC 1140

CCTCGTTGAG AGTGGGAAGT TCCTTTAAGC CGTGCCGTGG TTTCTTTCAC TCGATGATTC 1200

AAGAAGGTTC TGCCAATATG TTGGACGATg TGGAAACGGT CGATGATCAA CTGAGCATTC 1260

GGGAAAAGCT TTTTCACCAA TGAAACATAA GGCGCATACA TATCAATAAC AATCCATTGA 1320

ACGGCTTCAC GAGTCGCTAA TGAAAACCGA GAAAATAGCG 1360

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

TTTTTTATCG GnCTCGCCAT GCCCGTTTCC AACTTGGACG GGAAGnTTGA AGCTTACTGC 60

GAAAAGGAAG TTGGCTGCTT nCAGGAAAAG TTGGAATTCG CAACCACTTT AAACCAATGA 120

GgGAAtTACm AGkTGrAGCT TCTTCmATGn ATAwTAArGT CTCTGAGtTA aAAGarAAAA 180

TGGCGGATaA TGaAGAATTA TTGGCTCAAA TTTCGACAGA CAAACAGAAA GAGCAACAAC 240

GCTTAGTCAG CGAAAAAGCA GCAGCTGAGG CACAGAAAAA ACGTGCGGCA GAAACTGCCA 300

AAGCAGAAGC AGCGAAGAAA CAAGCAGCTG CCGACAAACA AGCGCAAGCA GATGCGGCGG 360

CTAAACTAGA AGCCGAAGCT GCTGAAGAGT CAAGCAGTCA AGCATCAAGC TCTTCTACAA 420

GTATGGAAAG CAGTAGCACT GAATCTTCAA GTTCAGCTAG TTCATCCGAA TCGTCATCAA 480

CGCCAGAATC ATCGACAGGC GAATCATCAA CACCAGGAAC TGGyTCTGGT CGTGTGCTTC 540

AGATGGAATC AACTGCTTAT TCTTGGCGCG AAGCTGGTGC AAGTAATCTA AGTGCTaCTG 600

GTATTGACTT AAGTAAAGAA AGCAATGTAG TTGCAGTCGA TCCAAGTGTA ATTCCTCTAG 660

GTTCATTAGT GAAAGTCTCT GGTTATGGCT TTGCTATTGC TGGGGATAcA GGTGGCGCTA 720

TTCAAGGCAA TATTATTGAT GTTCATTTTG ATTCAGTAGA CCAATGCCGT CTTTGGGGAC 780

GACGTCAGGT TACAGTAGAA ATTCAATAAT AAATTTGTTA TACTAAAGAT AAGATAAAGG 840

GAATTGGCTA AGTCAGTAAT GATAGTAGCC AGTTCTTTTT TAGTTAAATG TAAAGGAGAA 900

TTACAATGAT TCGCTCAGCA ACAAAAGAAG ACGGTCAAGC GATTGCTCGG CTGGTCTTAG 960

TTATTTTAAA AGATATGGAG TTACCAATTT TAGAAGAAGT CTCAGAAGAA CAAATGATTG 1020

ACCTGTTAGC AGAGGCAACG GCGTATCCAA CCTATCGCTA TGGCTATCAA CGAATTTTAG 1080

TTTATGAACA TGCAGGTGAA GTTGCAGGGA TTGCTGTCGG CTATCCTGCA GAAGATGAAA 1140

AGATTATTGA TGAACCTTTA AGAGAAGTCT TTAAAAAACA TGGCTTAGCA GAAGATGTTC 1200

GGCTATTTAT TGAAGAAGAA ACCTTGCCTA ATGAATGGTA TTTAGACACG ATCTCTGTGG 1260

ATGAACGTTT CCGTGGAATG GGAATTGGTT CTAAGTTATT AGATGCTTTA CCTGAAGTAG 1320

CCAAAGCTAG CGGGAAGCAA GCCTTGGGTC TAAATGTTGA TTTTGACAAT CCAGGGGCGA 1380

GAAAGTTATA CGCAAGCAAA GGCTTTAAAG ATGTCACAAC AATGACTATT AGTGGTCACT 1440

TGTACAATCA TATGCAAAAA GAAGTGTAAA AATAACGAAG CTAAAGTCAA TCACTTTAGC 1500

TTCGTTATTT TTCATTAATC CGTTAAAGGA TCAAAATCTA ATCCAAAATC ATCGGAAGTT 1560

TTTTGTTTTT TCTTATTATA TAACCAGTAG TCAAGGACAG CTGCTATGCA GATGCACAAC 1620

GGTGCGTCCT CATCATTGGC AACAGTTAAA ACAAAA 1656

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

TTACTTGGAC TGCTTCTGCT TCAGTACTTT CTTTCATTTT TTCAGTTCGT TGATCTGGTT 60

GGCACCCCAT TAAAACAATC ATTGAACAAA ATAACCCGAC AACTATCTTT TTAGTTTTCA 120

TTTTCCCTCC TTTTAAAACT CATTGAATTA CCATTTAATT TTAATATAAG TAGAATGAAA 180

AGTATAGCTA AGCAATCGTT TTTTCTTCAT ACGGCGATAA ACTTAACTGT CCAGATAAAT 240

ACTCACCTAA ATAGATTTCC TGTAATCTTT GAAATCCTTG TTCTTGGATT TGCGTTAATA 300

GCCAGTGCTC ATCTTTTTTG ATTAACTCTA GGACATCCAT GTTGGCTTGA CCGTCCACAA 360

TAATCGGATA ACGAATACTT TCATCGCCAT ATTCGACGAT TGTTAATTGA CCATTTTGTT 420

CTAAAACCGC CCGTTTAACA AGCTGGACTT CATAAATACC ATTTGCTCGT AATTTAAACA 480

TTAGATCATT TGCAGAAATA CCATTTTTCA AACATTCCTT CACCACAACC TGTCCATCCT 540

TGATTAAAGT AATGGGTTTA CCATCCACAA TTTGCTTCAC ATAGCGATTG TGTTCTTTTG 600

CAAATTTTAA AATTAAGACT AATAATGTCC ACAAAATTAA CACTAATACA AATTGGAGCA 660

CCGTAATTGA ATCATTATAA ATAACACCAC CAATAATGCC CCCCAATACA TAGTTTTGCA 720

CTTGGTCCAT AGCCGATGTG GGCGCCAAAT TCCCTTTTCC CATCAAATTA ATTTGGACAA 780

TTAAACAAAT AATACCTAAA GCAAATTTAA TAATAATTGG ACTATAAAAC TGCATTAATT 840

TTCCCTCACT TTACTTTATG ATTTCAATCG TTGGTGTTAA TAAATACGTT TCTTGTAACG 900

TATAAGACTG CTGATCCGTA CTTAAACTCA TTTTGTAAAA CACTTCGTCA ATTTTAACTA 960

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TGGTTCCGTC AGCCAATTGT GTACCATTGA CATAAACTTT TTCTGGAGAA ACTTTTTTTT     1020

CCTGTGCCAC TTGTTCGACA AAATGTACCA TTTGTGAAGA TTGTGAATGC TGATTTTGGT     1080

TCAGTTGATA ATTGGAATAT TGAACCCCTA AAACAAATAA TAATGATAAA AAAATAATAA     1140

TACTTAATTC ACGATATTTC GTTTGAATTT GATGTCGCAC ATAAAAACTA rACACAATGA     1200

CTAGCCCGAT TAACAAAGcA AAAATAAAAA AATACTTTAA GTAATCATTT AAATTAGaTT     1260

GGCTTTTTAA ATACTCGATG CCATAAAAAT TCATGTTCTT GTCCACTCCT TGATAGGTTC     1320

GTTATAGTAA GTATTCTATC TCAAAAAAAA CAATCACCCC TACTTTAATA CCTTATrACA     1380

AGAAAAAGCT CAGCGCAATC ATCTTGAGAA TGACTGCGCC GAGCTTCAAT CTTCTAAAGA     1440

TTCAGCTACT GATTGATTAC AAATTAATTT TACATCAAAC TTTTCAGTTC AACATCTGGA     1500

TATTTATCCG CAAACCAGcG TTCCGCAAAT TGGTTTTCAA ATAAGAACAA AGGTTGATCG     1560

AAACGGTCCC GTGCCAAAAT GTTTCGGCTA GAGCTCATGC GTTCATCTAA ATCTTCTGGA     1620

TTAATCCAGC GGGCAATTTT AGAACCCATT GGCGTCATTA CCACTTCAGC ATTGTATTCA     1680

TTAGACATTC GGTATTGGAA AACTTCAAAC TGCAATTGAC cTACGGCGCC AATGATATAT     1740

TCTTCCGTTA AATATGTTTT GTATAATTGA ATGGCTCCTT CTTGAACCAG TTGGTAAATT     1800

CCTTTATGGA AAGATTTTTG TTTCATTACG TTTTTGGCAG TCACTTTCAT GAATAATTCA     1860

GGGGTAAATG ACGGCAACTC TTCGTATTGA ACATTCATTT TCCCTTCATA CAAAGTATCG     1920

CCAATTTGGT AATTTCCTGT GTCATACACG CCGATAATAT CGCCTGCAAC AGCTTCTGTG     1980

ACGTTTTCGC GGGCATCCGC CATAAATTGC GTCACGTTAC TTAATTTGAC TTTTTTGCCT     2040

GTTCTACCTA AGGTCACGTC CATGCCTCTT TCAAAAACAC CTGAACAAAT TCGAACAAAA     2100

GCAATTCGAT CACGATGGGC GGGGTTCATA TTCGCTTGAA TTTTAAAGAC AAAGCCTGAA     2160

AATTCTTTTT CATAAGGACT TACTTCGCCA CCCTCTTCTG TTTTATGCGC ATGTGGCGCA     2220

GGCGCAAATT GTAAGAAGGT TTCTAAAAAT GTTTGAACCC CAAAGTTTGT CAAAGCAGAA     2280

CCGAAGAAGA CTGGCGTTTG ATCACCACGA GCGATTTTTT CCTCGCTAAA TTCATCGCCT     2340

GCTTCTACCA ATAACTCAAC ATCTTCCAAC ACTTGTTGAT AAACGCTGTT ATTGTGCAAT     2400

GGTAAATCGC TTGGTATATC GCCATCTTTT AAmGGAATAA AACGCTCCCC GCCATTATTT     2460

TCTGGACGAT ATAATTCCAC GCGTTCATTA TAAATATCGT ATAGACCTTC TAGGCCTTTT     2520

CCCATACCAA TTGGCCAGTT CATTGGATAA GATTCAATAT CCAATAGTTC TTCCAATTCT     2580

TCTAAAAGTT CCAATGGTTC CCGTCCGTCA CGGTCCAATT TGTTAATAAA AGTAAAAATT     2640

GGAATACCAC GTTTTTTAAC AACTTGGAAA AGTTTTTTCG TTTGTGCTTC AATCCCTTTG     2700

GCACTGTCAA TAACCATCAC AGCACTATCC ACGGCCATTA AGGTCCGATA CGTATCCTCT     2760

GAGAAATCCT CATGCCCTGG GGTGTCCAAG ATATTAATCC GTTTGTCTTG ATAGTCAAAT     2820

TGCATCACAG AACTCGTTAC CGAAATTCCC CGTTGTTTTT CAATTTCCAT CCAGTCAGAT     2880

TTGGCAAAGT TCCCTGTTTT TTTCCCTTTG ACTGTTCCAG CTTGGCGGAT GGCGCCCCCA     2940
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AATAATAATA ATTGTTCAGT AATCGTTGTT TTCCCGGCAT CCGGATGGGA AATAATCGCA 3000

AACGTACGGC GACTATCGAC TGCTTCTTTT TGaTTGATCG TCATAAAAAT CTCCTTATCA 3060

CTTnGTGATG TyaTyTATTT ATTTyCTTCA GCtAATTTTg ATTAACCTTT GCTAGTATAT 3120

CATGTCAAGC CTTGAGAATA AAGAGCTGCT GTTGGCTGTT TTTTAAAAGG AAAACCTGCG 3180

ACATTAGTCA AAACGACTGA TGTCACAGGT TATTTTTAAC GTCTTGGTTC GTCATCTTCC 3240

ATTTCTTTaC GGAAAAAACG ACGATTTTCT TCTGGTTCTT CATCGACAGT TTCTTCATCG 3300

TAGAAATGAA CGCGTAAGAC TAGCAAACGT GTGCCTTCCA TTTCTTCAGC AGTTAACTTA 3360

ATATTGCCCA CTTCAAAAGA AGGTTTTTCC CCTTCATCAG GAATGGTTCC TAATGCTGTA 3420

ATTAAGTAAC CCGCCATTGT ATCAACATCG CTCATGTGTA AATCTGTTTC AAATACTTCA 3480

TTAAATTCGT CAATTAACAT GCGTCCTTGA ACCAnnTATT CA 3522

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

TTGTACTAGn AGATaACTTC CtGATcTAGT GCCtTTTTCA GAAGCAATCT CTTGGGCAAT 60

AATTGAAGAA TAACTGcTGa TGAAGACAAA TAACAAAATT GTTATCCCCA TTGCTAACGC 120

CATTTGAATC CCTGTGTTAT CTTCTCCTGT TTTTATTTTG CCATTTTCAT CAAAACTAAT 180

TTTGGCTTTT TTAAATGTTG CTTGTTGATT CAACATGGCA ACTTGCTCAG CTGTTAGGTT 240

TAAACGATTG GCATTCGCCA TTGTTTGTAA TTGGTTTAAC ATTTGAGGAA TTAGCATCTC 300

GGTTGCATTT CCTAAAGAGC GTTCAGAGTA AAGCTGACCA GAAATCTGAT TATCTGTAGT 360

GTCCAAAAGT AAATAGGCAT CAATTTTCTC GTCTTTTAAT TGTTCTTGGG CCTTTTTCTC 420

AGAAGAAACA GCTTTGAAAG AAAAGTCCTC TGTTTTATTC TTTGTCAACT CTTTAACGAG 480

CGCTTGATTT TCCGAAACCA GACCAATGGT AGTATCTCCT GAAAAACCGc TAGCTAGAGA 540

GCCCGCTAAG TAAACAATTC CTACAAGAAG AAATGGCGCT AAAATCATGA TTAAGAAAGA 600

CAGCGACTTC ACATTTTTCT TATAGACATC AGTCGCAATA ATCCAAAATT TACTCATCTT 660

GCCCACCTAC TTTCATTTTG AAAATTTCTT CCAATGTTGG TGGTTGTTGA TTAAACATTG 720

GAATGTAGCC GTTGGCTGTC GCTTTATCAA ACAACACTTT GCCCACTTCA GCGTTTTCtA 780

ATGTCGCTTC TAAGACGCCa TCTTGtCGCA AGTGTGCTTC TTTCACAmCT GcTGTAGCAG 840

CAACTTCCTC AACAGATAAC GGTGATTCTA AGAATAATTT TGTTCGACCA AATTGTTGTC 900

GAATTTCATG AACCTGACCA TCTAAAACCA TGCGTCCATT TTTTAACATG ACTAAATGGT 960

CACAGATTTT CTCCACATTG TCCATATTAT GACTGGAAAA AATGACACAA GAACCTTGAT 1020

TTTTCAATTC AATAATGCCG TCTTTTAATA ATTCTGCATT AACTGGATCC AAGCCACTGA 1080

ATGGTTCGTC TAAAATAATT AACTTCGGTT CATGAATAAG TGTCGCAATC AATTGAACTT 1140

TTTGTTGATT GCCTTTTGAT AAAGATTTAA CTTTATCTGT TTTTTTGCCT TTAACTTGAA 1200

ATTTTTCCAT CCAAAAGTCA ATTTTAGGTT CAATTTCTTT TTTAGTTTTT CCCCGCAACG 1260

AAGCGAAATA AATTAGTTGG TCTTCAATCG TAATTTTAGG ATATAAACCC CGTTCTTCTG 1320

GTAAATAACC AATAATATTG TACTCTTTTT CATTTAATGG TTGACCATTC CATAAAACCG 1380

ACCCGCTATC TTGTGTTAAA AAATTTAAAA TCAAGCGAAA TGTAGTTGTT TTCCCGGCAC 1440

CATTTTGGCC AATTaATCCT AAAATTTTCC CGTCCGGTAT CGTAAAGGAT ACATGATCAA 1500

CTGCTTTAAA ATCCCCAAAG GTTTTGACTA ACTCTTTTAC CTCTAACACA TAAACGCCCC 1560

CTTCACTTTT TcTAAACCGC TGTTTAGTTA CyCATATCGT ATCTTTCCTG TGTTGGGCTT 1620

GTCAATGACA ATTGTnATGG AAAGATGTTG CACTTTAATC AGACGCTTnA TTTTCCGCCn 1680

AACGAAAAAG GCC 1693

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

nAAAnCTCGG TGGTGAAAAA ATGACAGACA AAAAGACAAC CGAAAAAAnA GAnACAGAAA 60

CTGCTGCAAC CTTTACAGAA GAACTAACAG CAGTTCTTGA AGAAATAAAA GAAGAACCTG 120

TAAAAGAAAA GAAAAAAGGG GAAATTGTCA CCATTGTGAA TGAAACAGAT ATTCAAATTG 180

GTGAAAGAGA GTACCGAATT GTTAAAAATC ATCGTGATGC CTTTGATCCT GAACGCTTAG 240

GTGAACGGTT TAGTGAAGTA TTAGCTCGTT ATGATTATAT CGTAGGAGAC TGGGGCTATG 300

AACAGTTACG CTTGCGTGGC TTTTTTGATA CTTCTAATCG TCGGGCAGCG CCGGATCAAC 360

GCATTGATAC ACTAGAAGAC TATTTGTATG AATATTGTAA TTTTGGCTGT GCCTATTTTG 420

TAATTGAACG AACAGGGGAA CGTAAAGAAA AAACAACGCA TCGTCGTCGT CGCCATAAAA 480

AAAATAATCG TTCTAACGCG TTTGTCGAGG AAAAGAGTGC GCCCGCTAAT AAAAATAGCA 540

AGCCAGTGAT TCGTACGAGA AAAGAAGAAA ATAAAAAAAC GACTACACCC AAACAGCCTA 600

GTCCCAAAAA ATCTGGCAAA GGCTTTACGA TTCGTCAACG TGAGGAGTAA ACAGAGTGAA 660

AAAAGACTAT CAAGGATATT TAATTGATTT AGATGGAACG ATTTATTTAG GAAAAGAACC 720

AATTCCAGCC GGAAAACGTT TTGTCGAGCG GTTACAGGAA AAAGATTTGC CTTTTTTATT 780

TGTAACGAAT AATACCACTA AATCTCCTGA AACAGTGGCA CAACGTTTAG CAAATGAATT 840

TGATATTCAT GTCCCAGCAT CCCTTGTTTA TACAGCGACT TTAGCGACGA TTGATTACAT 900

GAAAGAAGCC AATCGGGGCA AGAAAGTCTT TGTCATCGGC GAGGCTGGTT TAATTGACTT 960

AATTTTAGAA GCAGGTTTTG AATGGGATGA AACAAATCCT GATTATGTTG TCGTGGGACT 1020

TGATACAGAA TTATCTTACG AAAAAGTGGT TTTAGCTACC TTAGCCaTTC AAAAAGGGGC 1080

GTTGTTTATT GGGACCAATC CAGATAAGAA CATTCCGACA GAAAGAGGCT TATTACCTGG 1140

TGCAGGTTCA GTTGTGACGT TTGTGGAGAC AGCTACTCAA ACAAAACCAG TTTATATTGG 1200

CAAACCAAAA GCGATTATCA TGGAACGAGC CATTGCGCAT TTAGGCGTGG AAAAAGAGCA 1260

AGTGATTATG GTTGGAGATA ATTATGAAAC CGATATTCAA TCAGGGATTC AAAATGGTAT 1320

TGATAGCTTG TTAGTTACAT CAGGTTTTAC CCCTAAGTCA GCTGTTCCAA CTTTGCCAAC 1380

GCCACCAACC TATGTTGTTG ATTCCTTAGA TGAATGGACT TTTTGAGTAT GATGAGGTCG 1440

AAATTGCGTT TAAGGGAAAC ACTTGGACTC ATTTGTTTGT TTTTAACGAT TGTGG 1495

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

GAGGAGTGGA AATGAGCATT GCATTACCAA AACAAAAACA TTTAAGAGGT CCGTTACTTG 60

ATTACCTGAG AATTGCAGAG GATAATGGCG ATTTGTTTGC ATGGAGAAAG GCGTGCGAAA 120

TTGGGCGAGA AATATTCTCA GGTGATTTTT CAGACAATGC TAAACCATTA ATTGTTATAT 180

ACAAAGATGG ATCTTCAGAA GTATTTAACA CAAGAGCTGA TGTAATTTCA GCGTGTCGAA 240

TCGGAAATGA AACTTTGCGA AAATGTTTGG AGACTGGCAA ACAAGATAGA TTGGGTCGCT 300

GTTATGACTA TGCCATTTTA GAGTAGCAAA TTGTAATAGC TAATCGTATC TTTTGGCTCA 360

AGAGGTTAGT CATTATGAAT TTTAAAATTA TGAGTTTGGA GGGGGAGCAA TGGGAAAAAA 420

TTTACTCAGA GAGAAGAAGC GATTGATACG ACAAAAAATT CTTTTTCTGA CGGGTGAAAA 480

CGAAtCTTGG gATGAAGAAT CCAGAAATCG TGAAAGAAGT CCAGAGGCTC TCTAAGCAAC 540

TAGAGTCaGA TCTTATAGCa GATaAGCgAC CATTGCCCAG TTTAGATCCT GATAAATTAA 600

CAAAAGAGAA GTATCAACAT TTCTTAGATT TAGGTTATCA AGTAGGAG 648

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

CACTGTTTTC GGATCTACTT TGGCAAGTTC TGTCGTATCC CCTGTCACAA TGTATTGTAA 60

AGAATCGCCT CGTTTCACAT TTAAATCATT GATATTTTTC TGrCCATCAG TGACtTCTTT 120

ATTCGGmACA AGAACAGGAA CCACATTGGC TTTGTATCGA TTGAATTCAA TCGTTGCTTT 180

TTCTGGTTGC TTTGGACGTC CTTTTTCTTG ATAAGGCGTA ATTGATTTTG CTTTTAAATC 240

CGTATTAAAT GCGAACCACA TCGAATTTCC GTCATACCCT GGATTGTTAA CAATTTCATT 300

CCCGAAAGTG AATTTAATTC TATTTGGTGT TGAAATAACA GTTGCGCCAA TATATTCTTT 360

GCCTTGAACT GCTTCCCAGT CACTTATTGA AATCCCATTC GTCCCTACAT CAATATCCGT 420

TTTAGAATAA ACTTTATTTC CATGACGAGC TACTTTTGAT CCATTAATTT CATGAACAGT 480

ATCCGTGTTT CCTACTTTTA CGAACTCATA CGTAATGTTT TCACCACGTG AATTTAATGA 540

AGCACCTGAA AATACAAATG GATTCTCTTT CGTTGGCAAG ATTTCTTTGC CATCTTCTCC 600

AAAGAAGCGA ACGAGCATTT CAATCTCAGC ACCAGCCTTC TTTGTACGAG GGTCAATGTT 660

AATTCCATAG ACAATTGTGG CCACTGGATC ATCATGTAAG AAAGCATTCA ATCGACCTTT 720

TGAATCAGGT GTGGCCTTCA CTGTATATTG GAATTCAGCA CTAGCAATTT TTTTACCCAA 780

ATAACTAGCA TTCAAATTGC CATAGGTAAT AGTTACTGGT TGATTTTTGT GAAGAACAAC 840

CAATGTTCCT CCTGCACCGT TATTATAATA AAAATGTGCT TTTTTCGAGT CTTTAGTTGT 900

TaACCCGCTT GAATCTACAC TAAGCATACT GATAAGTAAT TTTTTATCTT TATGTTTATC 960

AGTTAGTTTT TTAGCGtCTA TATATTCTGC AGCTTTTACA GAAACAACTT TGGAATTTTT 1020

TGTTGCTTCA CGAkCGAAAA TTAGCGTTTT aTTTACTGGT TTTGCkACAT AGCCATTTTC 1080

ATTTTTATGT TTGTTGTATT CCGCGACTTC TTTCTCGTAG CGTTCTTTTT CCGCTTTGTt 1140

TTTTGgCCGC AATTTCTGGC ATTTTCTTTG nGCAATTTTT TCAGTTTTGG GCTTTAATTC 1200

AGCTGCTTGT TGCGCAAACT TTTTCGCTTG nTCTTTTTGT AAT 1243

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

ACAAACTGGT ATTTAAATCT TGTCTTAGCG AAAAAACAGC TGCTAAACAG GCAATCATAG 60

GTGAGCCACG ATGGAAAAAT TGAAATAAAA GnATACACAG CATGACAGCA ATTGCTGTTT 120

TTAACGTTCG CATGCCTAAA CGAAATCGAC CCACTATCAT AAATATTCGC TCCTAAATAA 180

CTTTTCTCTT TAATGATAAC CGAAATAGAG GTAAAATTAC TAGAGAAAAG TGAAGAATTA 240

TTATTTTTTA AGGGGAGTAT GCATGAAAAT TGGTTTACGA ACAGTCAAGA CAGCCATTAG 300

CGCTGCATTA GCAATGATTA TTGCGGAAAA ACTGGGATTA CTTTATGCCC CTTCGGCAGG 360

GATTATTTCA GTTTTAAGTG TTACTAGCAC GAAAAAAACA TCTGTCATGA CAGGAATTTA 420

TCGTTTGTTA TCCTTAGCTT TAGCAACTAT TTTAGCGTAT ATTTGTTTTA CTTTTTTAGG 480

TTTTACAGCG ATTGCTTTTG GTATTTTTTT ATTATTATTT ATTCCAGCAG CCGTGTATTT 540

TCAATTATCT GATGGGATTG TTGTGAGTTC CGTTTTGGTA ACTCATTATT TAGTCGAAAA 600

AAATCTTTCT TGGGCGATTA TTGGAAATGA GTTTTTATTA ATGAGTATTG GTGTGGGACT 660

AGCGTTATTA GCTAATTCTT ATATGCCTGA TACAGAAAAA CGTTTAAGAG AAGACCAAGA 720

AGTCATTGAA ACAAgTTTCG TAAAATTTTA AGGGAAAtGG CGCTACATTT AAACAACGCT 780

GCAGGAGAGC GAAATTTGGT CATGCATTGT GCAGATTTAA AAACCTTTAT TCGTACAGGT 840

GAGACGTGGG CCAAAAATCA TGGCCGAGAA TCCAATTGCn GGTCTACCCC AATACGkACt 900

ATTTAGAGtA CTTTGCgATG AGAaAAATGC aAAGTAATAT TCtAAAAAmC ATGTTGGAAT 960

TATTAGaAGA TATTmCyGTT GATGCGCAAC AAGTTCGCTA TATTCAACAA 1010

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 789 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

GATAAACTCT TCGATTCTTT CGCCGTTGAT CCATTAAAGA AAGAAGTACC TCTTGAAGAA 60

CTGGCAAAAC AACGACAAGA AGTAAAAAAA GAAGAAGCAA AAAAACAAGC AAAAGAGTAA 120

TTTTGCTTGT TTTTTTCTAT AGAAATTTTT CAATTGCTGT CCAAGCTGCT TCTTTTCCTT 180

CTTTTGTTTC AGAAGAGAAA ATAATAAAGT CATCTTGTTT ATCAAAATTC AAGGCTTTTT 240

TGATGACACT CTCGTGTTTG TTCCATTTGC CCCGCGGAAT TTTGTCTGCC TTAGTTGCTA 300

CAATAATAAC TGGCAAATCA TAGTATTTCA AAAATTCATA CATTTGGATA TCATCTTGGG 360

TCGGCGGATG ACGTAAATCA ATTAAAGAAA CGACTGCACG TAATTGCTCA CGTTGCGTGA 420

TATACGTTTC AATCATTTTT CCCCACTTCG CACGTTCTGT TTTAGAAACT TTGGCATAAC 480

CATAGCCAGG AACATCCACA AAGTGTAAGG CATCCTCAAT TAAATAAAAA TTTAGCGTTT 540

GCGTTTTACC AGGTTTGCCT GAAGTTCTTG CTAAATTTTT ACGATTAATC AAGGTATTAA 600

TAAAaGATGA TTTCCCAACG TTCGAACGTC CAGCTAAAGC AATCTCCGGT AATTGAGATT 660

CAGGaTATTG kTTaGGGGga TACCGcACTA ATCACGAwTT nCyGCATtAt GTACGkTCAt 720

kGTTTTcCyC CGkTCyTCyA tTCAgTCTTT CATGCAAAAG CTTAACAnAA ACAGCTCTnT 780

CGGAGATCC 789

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

GGGAGTGAAA CGCCCTATTT GGTAATGGAT GAGCGAGGAA TGGCCATGTC GACAACAGAA 60

TTGGCTGAAA ATCTAGCAAC ACTCTATGAA TCGCCAAATA ATGTTTTATT GGTGGCATTA 120

GCGGGAGAAG CGATCATTGG GACCGCTTCT GTGTCTGCTT CTTCTAAAAA GCGGATGGAG 180

CATATTGGTG AAATTGGCAT TAGTATTTTA AAAGAGTACT GGGGCTATGG ACTGGGCAGT 240

ATCCTGATGG AAGAACTTAT TCGCTGGGCG CATGAAAGTC ATGTTATTCG TCGCTTGGAA 300

TTAACGGTAC AGGATCGTAA TCAACGAGCG ATTCATGTCT ATAAAAAATT AGGTTTTGAA 360

ACAGAGGCAA TTATGCCTCG GGGCGCCAAA ACAGACCAAG GTGAATTTTT AGATGTTCAT 420

TTAATGCGTT TGCTGATTGA TTAATTATTG GTTAATAATT TTAATTTCTT AAATAATCGA 480

ACGATAATTG CATGAAAAAA CAAAATTTTC GCAATTATCG TTTGTTTCAT ATTTATTTTT 540

CTGATATTTT TGTTATAATT ATAGAAGAAT TaACGAAAAA ATGAAAATTT ATTTTGGGAA 600

GGAATGTAAG AAATGGCGAg GCAACGAAAA TGAAGTTAAC TAT 643

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TCTTGCTCAT CTTCATATAC TCCGTTTCTG ATTTTTTCTT TATTTTCAAC GACAATTGTC 60

GACATATTCT GGTGCGAAAC ATTGCTATTA TACAGGGAAA TGCACGAAGA ATCAAAAAAG 120

GCATACTTAG AAACAAGAAA ACTGTCTGAA TCTGCTCGCT AGAATGAGTG ATTCAGACAG 180

TTTAATCTTT TTACGGCTTT AACTACGTAA GCCACGCCCT GTTTCTACAA GGTACCAACA 240

AATGCCATAT AAAACGACAA TAAATAAGAT TAAAATGGTC ATAGAAATAC CAATTGGCAC 300

ATCTTGAACC CCTAGGAAAC CGTAGCGGAA CCCAGAAATC ATGTAAACAA TCGGATTAAC 360

TTTTGAGACA GCTTGCCAAA ATGGCGGCAA CATGGAAATG GCATAGAAAA CCCCACCCAA 420

ATAGGTTAAA GGCTGTAACA CAAAGGTTGG CACAATCGAT ACATCATCAT AGGATTGCGC 480

AAAAATACCA TTTAACAAAC CAGCTAAAGA AAAAAGAATC GCTGTCATCA ATAAAGTCAT 540

GATGACCATC AGCCAAGAAA CAACGTGCAA TGGCACAAAA AATAGAGAAA TGATGGTGAC 600

TAACGCACCG ACCAAAATAC TACGACCAAC GCCCCCAATC ACAAATCCCC AAATAATCAC 660

ATGAGTTGGA ACTGGCGCCA CGAGAATTTC TTCGATATTT TTCTGGAATT TTTGTGAGAA 720

AAAGGAAGAT GAAACATTGG CGTACGAACT TGTAATGGCT GACATCATAA TTAAACCTGG 780

CACGATAAAT TCCATATAAG AAAAACCGCC CATGTCGCCA ATTCGCCCGC CAATCATTTT 840

CCCGAAAATC ACAAAATATA AGGACGTCGT AATTACTGGC GGTACCAGTG TTTGGACCCA 900

AATCCGTAAA TAACGGTTGG TTTCCTTCAC AGCTAAACTT TTTAAAGCAG TAAAATACAG 960

ACTAAACATG TTGATCCTCC CTTTGGTACG TATCCTCGGT AATCTTCAAG AAGAGCTCTT 1020

CCAAACGGTT GGACTTATTC CGCATTGACA ATACTTTGAT TCCTTGTTGA CTTAGCTGTT 1080

CAAACAAGTG ATTGACTCCT TGGTTTCGTT CCACTTCCAC CGCTAACGTT AACTCGTCCT 1140

CAAATACGCT TTGATAGCCT TCAATAACTG GCGCCTGCGT ATAAGGTGCT AAATCAAAAA 1200

TAAACGTTTC AAATTGTAAT TTTGCTAACA AGTGCTTCAT GCTGGTGTTT TCAATCAATT 1260

CACCAGACTG AATAATCCCA ATGTTGCGAC ACAACATCTC AGCTTCTTCT AAGTAATGGG 1320

TCGTCAAAAT AATCGTGGTT CCCTGCGCAT TTAACTCTTG TAAAAAGGCC CACATTTCAC 1380

GGCGCAATTC AATATCGACA CCTGCAGTTG GTTCATCTAA AATCAATAAC TTCGGCTCAT 1440

GCATCAGCGC GCGAGCAATC ATCAAGCGAC GTTTCATTCC GCCAGAAAGC ATTCGCGCCC 1500

GTTCGTTCCG TTTTTCCCAT AAATTGGACT GTTTTAAATA CTTTTCACTC CGTTTCATGG 1560

CTTCTTTACG AGACACCCCA TAATAGCCCG CTTGATTGAC CACAATCTGC TGGACCGTTT 1620

CAAACGGATT GAAGTTAAAC TCCTGCGGAA CTAACCCAAT CTGTTGcTTC GCCCGCACCA 1680

TCTCCGTATC TAAATCATAC CCAAAAATTT TGACTTTCCC CGAAGTCTTA TTAACTAACG 1740

AGGTCACAAT CCCAATCGTC GTTGATTTTC CTGCGCCATT CGGTCCCAAA AGAGCATAAA 1800

AATCGCCTTC TTCGACTGTT AAATCAATCC CCyGCAACGC TTCAACACCT GAAGCGTACA 1860

CTTTGCGTAA ATCTTGTATC ACAAGAGCAT CAGTCATTCG TAACTCTCCT TAATGTATAA 1920

ATATTCATGA ATATTATTGT AACACTTCTC GATAAAAACG GGGGTTATTT TGATTAAATT 1980

TTACAGTTTT GCTTAGCTAT TTTTCAACAA CAAACTAGCC AACGATTAAC GTGTTTATTT 2040

TGATTCAAAA CTGTTTAAAC AGTTTCAAGA GCGTTAAAAC CCTTTCAAAT CAAGGATTTA 2100

GAGTTCTCTT TTTTTGGCAC AGAACTTGCT TTATATAAAA GTGAGGTGAA AAGAATGAAA 2160

AGAAAATTTT TAATTGCTAG TCACGGAAAC TTAGCGAAAG GCTTCCAAAG TTCCTTGGAT 2220

ATTCTCGCAG ACAAAGGAAA AGAGCTGGCG GTCATCAATG CCTATGTGAC TCCTGAGGAC 2280

TACACGCCAA TTATTCAAAC GTTTCTTCAG TCCCTTGGCG CAGAAGAACA AGCTATTATT 2340

TTAACAGATT TATATGGTGG TAGTGTCAAT CAAAAAATTG TTCAAGAAGT CATGACGACA 2400

AAACCAGACA ATGTTTTTAT CATTTCCAAT GCCAACTTAG CCATTGCCTT GTCGCTGATT 2460

TTCTTAAAAG AAGGCGAAAA GCTAACCAAA GAAGATATTC AAGCAGCAAT TGCTGAAGCA 2520

CAAATTCAAT TCGTTGAATT AAACCCATCA AATGAAGAAG AAAACTTTTT TTAGGAGGAA 2580

ATTAAAATGA TTACACAAGT ACGAGTAGAC GACAGATTAA TTCACGGCCA AGTAGCCGTA 2640

GTTTGGACCA AAGAATTGAA TGCCCCCTTA TTAGTTGTAG CGAATGATGA AGCAGCCAAA 2700

AACGAAGTAA TGCAAATGAC GTTAAAAATG GCGGTCCCTA ATGGTATGAA ACTATTAATT 2760

CGCTCAGTCG ATGATGCGAT TGATGTCTTC AATGATCCTC GGGGCAAAGA CAAACGAATT 2820

TTTGTAATTG TGAACAGTGT AGCGGACGCT ACTAAAATTG CGAAAAACGT GACAGATATT 2880

GAAAGTGTGA ATGTTGCCAA CGCTGGCCGC TTTGATAAAT CAGATCCAGC CACCAAAACA 2940

ATGGTTTTCC CAAGTGTCCA ATTAAACCCT GAAGAGTTAG AAGCTGCCAA AGAATTAGCC 3000

AGTTTGACTC ACGTGGAAAG CTATAACCAA GTCCTGCCAA CCAACTCAAA ATTAAGTCTA 3060

AAACAAGCCG TCAATTAAAA GGAGGAAATG AACAATGCTT ATGCATGCAA CAATGGCAGC 3120

CTTAGCTGTA TTTATCTGTT TTGCTGGGAA TTATTTAACT GGTCAAAGTA TGATGGAACG 3180

TCCCTTAGTC GTTGGATTAG TCACAGGAAT TTTAATGGGC GACATGAAAA CAGGGGTCTT 3240

AATGGGGGCC TCTTTGGAAG CAATTTTCTT AGGAAATGTT AATATCGGTG GTGTTATCGC 3300

AGCGGAACCT GTAACTGCGA CTACTTTAGC CACAACGTTT GCAATTATTT CAAATGTCGA 3360

ACAAAAAGCC GCCATGACGT TAGCCGTACC AATTGGGATG TTAGCCGCTT TCGTGGTGAT 3420

GTTTTTAAAA AATGTCTTTA TGAATATCTT TGCTCCTTCT CTTGACAAAG CAGCACGTGA 3480

AGGCAACCAA AAAATGGTTG TGACACTGCA TTACGGAACG TGGATTATTT ATTATTTAAT 3540

CATCGCTTCG ATTTCATTTA TCGGAATTyT AGCAGGAAGC GGGCCAGTAA ATCTGTTTGT 3600

TGAAAGTATT CCACAAAATT TGATGAACGG CTTAAGCGCA GCTGGCGGAC TTTTACCTGC 3660

CGTTGGGTTT GCTATGTTAA TGAAACTGTT ATGGGATAAT AAATTAGCCG TCTTTTACAT 3720

TTTAGGCTTT GTTTTAACCG CGTACCTACA ATTACCAGCC GTTGCGGTAG CGGTCATCGG 3780

GACAGTAATT TGTGTCGTGA GTGCCCAACG GGATGTAGAA TTTCGCGACA TTCTAAAAAG 3840

AAAAcTGCGG CGTCTTCTGC GGTTGAAGGC AGCGCGAAAG AAATCGAAGA GGAGGACTTT 3900

TTCGCATGAA GTTAAAAGAG AATTTATCTA AAGAAGAGAA AAAAATGATG CGCTCTGTTT 3960

TCTGGCGTTC TTGGACGATG AACGCTAGCC GGACAGGAGC TACACAATAC CACGCAGTGG 4020

GTGTCATGTA CACTTTACTC CCAGTTATCA ATCGTTTTTA TAAAACCAAG GAAGAACGGG 4080

CAGAGGCATT GGTGCGTCAC ACCACTTGGT TCAATGCAAC CATGCATATC AATAACTTCA 4140

TCATGGGGCT CGTTGCTTCG ATGGAAAAAC AAAACAGTGA AGACGAAAAT TTTGATGCTA 4200

GCTCTATTAC AGCAGTTAAA GCCTCATTAA TGGGGCCACT TTCAGGCATC GGTGATTCCT 4260

TCTTCTGGGG CATCTTACGT GTTATTGCTG CTGGGATTGG GATTTCATTA GCCAGCACTG 4320

GTTCGCCATT AGGGGCGATT GTCTTCTTAC TTTTATACAA CGTTCCTGCG TTCTTAATTC 4380

ACTATTATGC GTTGTATAGC GGCTATTCAA TCGGTGAAAG TTTTATCCAA AAAATGTACG 4440

AATCAGGCGG AATGAAGATA CTCACAAAAG TATCAAGTAT GCTAGGCTTA ATGATGATGG 4500

GCAGTATGAC TGCTTCAAAT GTAAAATTCA AAACGATTCT TGAAGTTTCC GTTAAAGGAA 4560

GCAAAGACGT AGTTAAAATC CAAGACTATT TGGATCAACT ATTCGTCGGT ATCGTACCAT 4620

TAGCCGTGAC ATTACTTGCT TTCTGGCTAT TACGCAAAAA AGTCAATGTT AACGTGGTGA 4680

TGTTTGGTAT CATGTTCTTA GGCATCTTGC TAGGATTACT AGGCATCTGT TAAAATTGAA 4740

ACAATAAACA TTTAATTATT AAACACTTAG AGCCTGAGAC AAAAATCCAA AGTGATTTTT 4800

ATCTCAGGCT TAAAAGCTGA TAAACGGCGG GAACAGAAGC AACCCCTGTC CCGACCTCTC 4860

TTTTGGAAGG ACGATGAATC ATGCGCTTGG AGACCTACCA ACACTTAGTT GATATTTTAG 4920

AAACCAGCAA CACCCCGATG AGCACACAAG AAATTGCCAC AAAAATTCAA TTAAGCCGCT 4980

CGGTAACCAG CTTATACTTA AATAAATTAT TGGAAAAAGG TGAAGTCCAA CAAACGGGAA 5040

AAAAACCCGT TTATTGGCAA TTAACCCGTG CAACAACCCC CACGACCGAT GTGTTTCGAC 5100

AATACATCGG TAGCCAAGGT AGCGCCAAAA AAGCCATCGA ACAATGCAAA GCCGCTATGT 5160

TGTATCCCCC ATTGGGTATG CCTTTATTAA TCCATGGAGC CAGTGGCGTC GGCAAAAGCT 5220

TTTTGGCAAA ACTGATTTAT GAGTATCTAA AAAACGAACA AATCATCGGC CTGGAAAAAT 5280

TCTATACCTT TAACTGTGCC GATTATGCCA ATAATCCCGA ATTGCTATCA TCTATTCTCT 5340

TCGGCCATAC CAAAGGCGCA TTCACTGGGG CTGAATCAGA AAAACAAGGA CTCTTGGCCC 5400

AAGCTAATAA TTCCGTACTC TTTTTAGATG AAGTACATCG ATTATCCAAC GAAAACCAAG 5460

AAAAACTCTT TCAGTTTATG GATACAGGGA CCTTCCGCCC TATTGGTGAA GAAGGAAAAA 5520

TGGTGCATTC CAAGGTCCGG CTACTATTTG CGACCACCGA AAACCCGAAA AAAGTCTTAT 5580

TACCAACCTT TTATCGCCGA ATTTCCGTAA TCGTCTCACT TCCGAACTTC AAAGAGCGCC 5640

CCATTCGAGA ACGGATTGCG ATTTTGAAAA ACTTATTCCA CCGAGAAGCG AAACGAATGA 5700

CCAAAGACAT CAACGTGGAC GAAGAAATCT TTACGGCATT ATTAGAAAAT GACGAACCTG 5760

GCAACGTGGG GAGTTTATCC AACAAAGTGC AGCTCCTTTG CGCGTCGCAA TTACGAAAAA 5820

CTTTGCCCAA TCAACCTGTC GTCATTGGCG ATGCAACTCA ACCAATGATT GCGATTCCTT 5880

TAGACAAAGA AGTGTTAGAA GAAGACACAC TTTCTTCCGA TATTTTCGCA ACATTTGAAG 5940

CCTTATTTAC AAAAGAAAAA ACACTGGCCC ACTTAAAAAC TGAACTGACA CAATTCATTA 6000

AATATTGTTT AGACGATGAA ATAACCTTGG AAAATGATTA TTTTTTACAA AACCTAGTCA 6060

CGGAAGTCGA TAAAGTCCGT ATAATTGTGT AAAAGTAAAA AGGCCATATA ACAGTCCTTT 6120

TACGGTACAA TGTTTTTAAC GACAAAAACA TACCCAGGAG GACTTTTACA TGaCCCAAGT 6180

ACATTTTaCA CTGrAAAGCG AAGAGATTCA AnGCATTATT GAATATTCTG tAAGGaTGAC 6240

GtTTCTaAAA tATTTaACAc gGtATTTAAT CACTATGGGG AAATCACGGA CCGAATTT 6298

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

CAAATAGCCC TTGATTAAAC GCCAAGACAT CGACGCGTTC TTTTTTCATA AGTGCCTTCT 60

TTCTATCTCA ATTGTAACTG AGTTAACAAG TTTGCTAAAT GTTCTTCTGA AAAGTTGGGA 120

ACATTTGCTT TGATTTTTTC TAAAACAGCG CTACCTTCTG CTAATTGATG TGTTAGCGCA 180

TCTTTCGCGC CAgCAATCCC TAGAAGAGCT GGATACGTAC TTTTATTCAA CGCTTCATCT 240

CGGCCTACTT TTTTACCTAA ATCTGCTTCT GTACTTGTGG CATCTAATAA GTCATCACGA 300

ATTTGaAAAG CCAAGCCATA GTGAgCGCAA ACTGTGTCAG TAAACCaATG ACTTCTTCTG 360

kTTGATTGGg CTAATACGCC CCCAGCAATT AAGGsGrATT CAATTAGCGs TCCGGGTTTC 420

TTTTCATGAA CAGcCGcTAA ATCTTCTnAA GGCAAGCTGA ATTTTTCTCC TTCAAATATC 480

ACCCATTGGC CGGAAACC 498

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

ATTAAAAGTG nACGACAAAA TCAAAGCCGC TTTACCTTAA CCAAAATGAA TACGTTCATC 60

AAAAACTTCC TTGGTAGCTA CATTCTGTTA AGTTTAGAAA TTTTAATTGC TGCTGATATT 120

ATTGAATCCA TTGTCAAACC AACTTTTCAA GATATTTTGA AATTGGCAAC CTTGGTGATC 180

ATCCGTACAG TTATTTCTTA TTTCTTACAT AAAGAAATTG AAGACACTAT GACCGATATG 240

GAACAACAAG AAAAAGAACC AGAGACCCCA AAAAATTAGC GGGTACGCTG GTTCTTTTTT 300

TATTTAATCG CTTTAAAATA ATGAAGTGGT TCGTTAGACA AACGCTGCAT TTTACGTTTT 360

TTATCTTCAA TAATTGCTAA AATCTCGTCT GAAAAATTTT CTAAAATAAC ACGGCCGCCT 420

TTATAGGTGT GTCCTCCCAT TTCAGCAACT TCGCTGGCCG TCAAAATGAC TTTACGATGC 480

GCAATTTTTT TGAAAAATTC TTCAATTAAG TACGTCGGTA AGTAAAAATT ATTTTGAGCA 540

GAAAATGATT CCAAATAAAT AAAATCATCG ATGCTGATGA AACAATCATC CATCGATAAG 600

TATTCAATTG ATCTGTCTAT ATATAATTCA CGCTTTTGTA AAATTTCTTT GACTTTTTTA 660

TTTAATAAAT TCAATGATTC AATTTCTTTA ACCAAATGTT CTAGTTCACG ATAACGTACT 720

TCTTTTCGCT CTTTGTAAGA tGAATGTAAG GCGGCACTTG CTGTGACTAT TAGCGCACCG 780

ACGATTACAC CGACCATTCC GGCGATAAAA ACAAACATAT TTTTCCCCTC GCTCTTTTCT 840

AATTTTCCAT TTTAGTATAA CATAATCCAA AAGTTTCGGA TAAAAAATGA CACAAAATTT 900

TTCAAGCGAC TtCGTTGACC TTTATTGACC AAAGAGGTAT ACTTTTCATA GGCATTCAAA 960

GTGCTTTGTG ATAGAATGAC TTTAAAAGTT TCTTTATATA GGAGGATTTA CTTATGAATT 1020

TAATTCCAAC AGTTATTGAA CAATCATCTC GCGGTGAACG TGCTTATGAC ATTTACTCTC 1080

GTTTATTAAA AGACCGCATC ATTATGCTAA GCGGCCCTAT CGATGATaAC GTGGCAAACT 1140

CAGTGATTGC ACAGTTATTA TTCTTAGATG CCCAAGATTC AGAAAAAGAC ATTTACTTGT 1200

ACATTAACTC TCCTGGTGGC AGCGTTTCTG CAGGCTTAGC GATTTTCGAT ACCATGAATT 1260

TCGTTAAAGC GGATGTCCAA ACGATCGTAT TAGGAATGGC AGCTTCAATG GGTAGCTTCT 1320

TATTAACAGC TGGTCAAAAA GGCAAACGTT TCGCTTTACC AAATGCGGAA ATCATGATTC 1380

ACCAACCACT TGGTGGCGCT CAAGGGCAAG CAACAGAAAT TGAAATTGCT GCTCGTCACA 1440

TTTTAGACAC TCGTCAACGT TTAAATTCAA TTTTAGCTGA ACGAACTGGC CAACCAATTG 1500

AAGTGATTGA ACGTGATACC GATCGTGATA ACTATATGAC TGCTGAACAA GCAAAAGAAT 1560

ATGGTTTAAT CGATGAAGTA ATGGAAAATA GTAGCGCCTT AAATTAAAAA TAAAAAAATG 1620

GAAACAGCGA CAGTCGCTGT TTCCATTTTT TTTaTTTTTC AATGTATCCG CGTAATTCTT 1680

CTTCAGTGAC ACTTTCGTCA AAGATATACT CACCAATGAT GATCGTTGGT ACAAATTGAA 1740

TGTGCGCCGC ATTGGGCTTC AGCAATCACT GGCGGGAnAC AAGCGTTGGC ATCTTTTTGG 1800

TTCTTTTAAG CCCAGATTTT TTTCAGCATA CGTCGGCTAC TTCTTCTAAG GGTAAGTTTC 1860

CCCATTCATC nTGCGTGAAA CCATTTTAGG CAnGCTGACA CGCTGGTTCA GGCGCTGAAT 1920

AGT 1923

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

TTCTCGCTTA ATTTCTGGAA AAGGATATGT GAGTGCCGAT AGTCAAGAAA AAATTCTCAA 60

AGCAATGAAA GAATTAAATT ATACCCCGAA TTATGTGGCG CGGAATTTAC GAGCAGGTGC 120

CACAAAAACC ATTGGCTTTT TAGCCCCTAG CTATTTAGGT TCCTTAGGTA TTTTCTTGAA 180

TCGCTTTATT TCAATTGCCA AAAAATACAA TTATTCCGTA ACCTTATTTT TTACAGATGG 240

CGATCAGCAA AAAGAAATTG ATGCCTTGAA CCAATTAAAA TACAAACAAT TAGATGGCTT 300

GTTTTTATTG ACACGAACAA ATGAATGGTC GGTGATTGAG CCTTACAGCG CGTATGGTCC 360

TTTAGCAACC TGGCATCGTA TCGATTCACC TAATATATAC TCTTCCTACA TTGATCATTA 420

CTCTGGTTAT TATCGTTCCT TAGAATATTT ACAACAACAA GGATACCAAA AAATTGGTCA 480

TGTCCTCGGT AATCCCGAAA ATTTAAACAC GCAcGCACGA AAACGTGCAA TGAAAGATTT 540

TTATGAAAAT ACTCAGGCAC CTTGGCAAAC TGAGTGGCTG ATTAATGATC AGTATACTAA 600

CCATTCTGGT CGCAAAATTG CCCATTACTG GCAACAATTA ACCGACAAGC CAGAAGCTTT 660

GGCCTTTTAT AATGATCACG TAGCAGCTGA GTTTATTTCA GAACTTGAAA ATCTAAATTA 720

TGcCGTTCCT CGCGATGTCG CTGTCATTGG CTTTGATAAT AGTTATGTCA GTGAGTTGAT 780

GCATATTACG ACTGTTGATT ATGCCATTCA GTATCAAGCC GAAAACTCAT TTATTTACCT 840

ATACAACCAA TTAAATCAGA CGAATATTCC TGAAAAAAAA TTAACCGTTC GTCTAGTTGA 900

ACGACGAACG GTGCCTAAAA AAGACCCGGC AGATCAGTCA CTTTGACTGA TTTACCGGGT 960

CCTTTTATAG TTAAACAAGG ATTATTTATG CTTTTGTTCA TTTTTTAAAA TAGAAATTGA 1020

CTGTTTTAAA GATTGAATCA TGCCGCCTTC ACTGTATACA AGAACGTTTG ATTTGTATAA 1080

ACGAGCAGAG AAGATTGTTA AAATAATTCC AAAAACTGCC AAAATCACTA ATGAGACAAT 1140

TGCTTCCATT GTTGATGCCG TTTCGGTCGC CAAGCGTACT GGCATAATGT ATGACGAAAT 1200

CAGCGGAATA AAGGAAGTCA CTTTCACCAC GATATTTTGT GGATCATTCG TCCCAAACGT 1260

AATGCCGATC ATATAACCGA TTAAACCAAT ATACATGATG GGCTGAACTG CTTTTGCTGT 1320

ATCCTCTGGT TTGGAAACAA GAGAACCACA AAGTGCTGCC AAAACAGCAA AAACGAGAAT 1380

ACCAATAATG AAAAAGCCTA ATGTAAAAAT AAAGGTTGAT GAAAAAATAC TTTGTGGTGA 1440

AATACCACTT AATAGACTTT TCATAAAATC AAGATTTTTC AATTGAGAAT AGCCGAGAAC 1500

AAACGCCACT CCGTAAATGA AAATTTGTGT TAAAGCTACT AGmATAAcCC CAGTTAmTTT 1560

GCCATAAAAA TGGGTTgCGC yTTTGTACTA GAGAGAATAA CTtCCATGAT TCT 1613

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ATAAAATTTC ATATTATcTC TATCCTTTCT ATAACTATTA ATGATATGAA CTTTTAAGTG 60

TAAAATAAAA CACCTAAACA ATTAATTTCA TTTCCAAAAG TTAGATAATT ATTTAAAAAA 120

TGTTTCGTAC TAAAACATTT TTTAGTCTAA ATTTAATGTA AATTTAGAAT CAACTGACAT 180

CTGATATTTT TTAGGAGTCG TCCCTGTTAT CTTTTTAAAA ACTTTAGTGA AGTGAGACGT 240

ATCTGAAAAA CCTAATAATA GTGAAATATC ATTAATAGGA TAATTAGATT TTAACATTAC 300

TTTAGCTTCT GAAATTTTTC TTCTTAAAAT ATAATTATGT ATACTAATGT TCATTTCTTT 360

TTTAAAAGCT GTGCGTAACC TAGCTTCACT CATTGAAAAA TATTGAGCAA TCTGTCTTAC 420

TGTAATCTTT GTATACATAT TTAGACCAAT GTACTGAACA ATTGATGATA TCTGAGGAGA 480

AAGATTCCTT ACTTTAGCTT TTCCTATTTC AGAGGTATAA AATACTATAG CAGTATCTCT 540

AACTTTTAAT ACTTCTTTTA AATTTATACA TAGTTCATTT TTCCTTATAA AACTATCTCG 600

ACTCTGATAT GCATTTATTA AGTCCATTCC CATATTTATA GCTGCTTGTG CTAACTTCTC 660

AAATACAACT ATTGAATAAT TCTTTcAGAA CGTACGTTAT CCCCACTAAC CACAGGwACA 720

ACACCATTAC TTAGTTTAAA TATCATATTA CTTAATTCTT GTACATTACC ATTTACAACA 780

TATTCTAAAA TTTTATTTTC ATATAAAAAT AAATAAATTT CTGGATCATA ATTTTGAGAT 840

AATAACATAT CTATCCGTTC TATTTGGATA TCTTCTGAAA ATTTTTTCTC ATAATCATGT 900

AACGGCTTAT GAAATAAGTC TTCAATCTTT CCCGTAAAAA AATAATTTAT AAGGATAAGA 960

ATATCTCTAA TATCCCCTAA TGAAAATAAT GGTAATTCAT TTAATAATTT ATATAAGGAT 1020

TCTTTATCAG AATGCTTTAT ACTTTTATAT TGAACCATAG AAAGTCAAGT CCAGACTCCT 1080

GTGTAAAATG CTATACAATG TTTTTACCAT TTCTACTTAT CAAAATTGAT GTATTTTCTT 1140

GAAGAATAAA TCCATTCATC ATGTAGGTCC ATAAGAACGG CTCCAATTAA GCGATTGGCT 1200

GATGTTTGAT TGGGGAAGAT GCGAATAATC TTTTCTCTTC TGCGTACTTC TTGATTCAGT 1260

CGTTCAATTA GATTGGTACT CTTTAGTCGA TTGTGGGAAT TTCCTTGTAC GGTATATTGA 1320

AAGGCGTCTT CGAATCCATC ATCCAATGAT GCGCAAGCTT TTGAATATTT TGGTTGATCG 1380

ATATAATCAT GAATCAATCG ATTTTTAGCC TCACGCGCTA AGTTAATATC TGTGAACTTA 1440

AAAATTCCTT TAACAGCTCC TCTGAAAGAT TnGAATTTTT TAGGATGGGG nAAGAA 1496

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

GGTACTTTAC AAGAATCACG TAAACGTGAA TTCTACGAAA AACCAAGTGT AAAGCGTAAG 60

AnAAAATCTG AAGCAGCTAG AAAACGTAAA AAATTCTAGT TTTGAATGAA TTGGAGTTGG 120

TGGTATGTCA TTGCTAACCA CATTGAATGA CGACATTAAA ACAGCGATGA AAGCTAAAGA 180

CAAAGAAACT TTAGCCGTAC TTCGTATGTT AAAGACTGCC ATTCAAAATG ATCAGATTAA 240

AGCGGGCCGT GAATTGAACG GAGAAGAAGA ACTCACTGTA TTGTCTCGTG AGATGAAACA 300

GAGAAAAGAT TCTTTATCAG AGTTTGAAAA GGCGGGACGC GACGATCTTG TTGAAAAAGT 360

AAAAGTTGAA ATAGCAATTG TTGAAAAATA TATGCCTCAA CAACTAACGG AGGAAGAAAT 420

TCGTCAACTA GTTCAAGAGG TAATGACGCA AACTGGCGCC ACTTCACCAA AAGATTTTGG 480

TAAAGTGATG GGCGCTATGA TGCCGAAAGT CAAAGGCAAA GCcGATGGcA ACCAAGTTAA 540

CGCaATTGTG aAAGAATTAT TACAAGaAAA CTAAGAGCGT TwTCGAAACT AGGACAGGAT 600

ACTGcCgawT TtTTTTTaTG sCcaaGAgAA AcCGGTAGCC TTTTTTACGG TTTCCCCTTT 660

TTTGGACCTT TCCAAGGTCC AAT 683

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

CGAATAGTAT GAcGTACACG GAATAATTTC CTTCGTCAAC TGTTTTGACT TGAATAAAAA 60

AATAGTTATT TTTAGAATAC GTTTCCACGC TTTCTATCAA TAACTTGCCG ATACCTTTGC 120

GATGATACCG CTTTTTAACT GCCATACAAT GGATTTCTAC TGTATCTTTA CTTGTTTCTG 180

AAAGTGTTAT AAAACCGAGT ATTTTATTCT CTACATCCTT TGCCACCCAC ATAGGTAAAG 240

TGCTAGCTAT ATCGATATAC TTGCGGGTCT CTTTTTCAAG GCCAAACCAT TCTGGAAGAT 300

TAAACAATAC TTCTTGTGCT GCCTGAGTCT TTTTATCTGC ATTTTTTTCC CTTATAATTG 360

TAAATTCTTT CAATTTACAA CCTCCTTTTT GTTTACATAA CAAAATTATT GTATACCCAA 420

TCTTTTTTAT TAAATAATAG CATAGGTAGT TTAAAAATGT AAGTTAGTCA TTTATTCTTT 480

ATTATTTCCT TAAAACGACG CCTTTTCTCG CTAAATCTGC CCTTTCTTTA TTTTTTTCTG 540

TTAAACTAAA CGTATTAAGT CTATGAGGAG CGTGCGTATA TGGATTATCT GAACACTTAT 600

AAGCGGTTGC TAGCATTGGC AGATGCTGGT CTTTTTTACG GGAAAGATGC TTTTGATCAA 660

GAACGTTACC AAGAACTACG AGAACTTACG TkAmAACTTA TtAGCGCAAC CGGACACGAA 720

GCGAcTGTCT GGCCCGACTT AGGAAAAAAC CTTACCTAAA GAAGAnGGTA TCCAACACCG 780

GAAnGTAGAT GTT 793

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

ATAAATGGCG TCGATGATGG GAAAACTTTT CTTGATCATA TCGACGATAA AATAACGTTT 60

CTGCTTCAAT AATAGAGCGA TAACGTTGAG GACTCATTGT ACGATAATCT AAAACAGACA 120

ATTCTTGTTT TAGGTGGATT GGTAAGACTT CAATCTTTTT ATTGGCTTGA TTCAATTGAT 180

AAAAGAACCA ATGATCTAAA TAGTCCAAAG GAAATTCTTC CGAAAATCCT TCCAACCAGC 240

GCAGTGTTTC TGCCGTAATG ACTGTACCAG AATTGATAGC CATCAACGGT TGGTTGGCTA 300

TCCCTGCTGT TGGCTTTGCT CCTTTAAGTC CAACATATTG ATCACTATAA ACTGGCGAAA 360

TTTGTTGTCC ATTTGCTTCT ACAATTGGAA CATAGACTGC CACAGTCGGA TCTAACGGCA 420

TGATGATCAA CGTATCAAAA TAAGAAGCTG GCACTTCTGT GTCTTGGTCA AGGAGCAACA 480

ATAATTCACA TTGATTCGTT TGACTAAAAG CAATCGCTTC ATTATAAGCG GTCGCTAGGC 540

CTGGATTATC AGGATTATGT CGATAAGTAA CATTTTGTTG TAAAAATAAT GCATCTTCTT 600

GAGGAAGTGG GCTGTTGTCA TAAATAAATA AGTGCAATTC GGGGTGATCT ACCACTTCTT 660

TTAATAACAA ATAATTCGGC GTATCAGCCA TTTTCATTTG ATATAAGACG ATGACTACCT 720

CTAATCTTTG ACTCATTAAA AGAACCTCCA GCCCCATTTG TTAAAAAATT TTCCCATTGA 780

TTGCATAAAG ATTTTAAACA ATTTTCGACT TTTATGGGCG CCCTTTTCAT ACATGTGAAC 840

AACCGTTTCA AAAGGCGTAT AGAGAATCCG ATAGCCTGCT TTGCCAAAAC GTAAACATAA 900

ATCGTTGTCT TCaAAGTACA TGaAGAAACG TTcATCGAAC CCACCAATTT CAACGAATTT 960

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TTCACGATCA ATCAACATAA AACAGCCTGA GCCCATTTTA ATATCCGTTG TTTCTGTATC      1020

CGACAAATCG CGACATTCAT AAATACTCAA ACGTTTATCA AAAATTTTCT TTACAAATTG      1080

AAAGGGAATA AAACGTAACA TATAATCGAA AACATCTAAT TTTTGACGAA CTAAATATTG      1140

CGTCGTGCCA TCTTCATTTA GCACTTTAGG GCTAACGACT GCAATGTTCT TATCTATTTT      1200

GATACGGTTT AATAGACGAT CAAGCACGTC TTTAGTAACC AAAACATCGG GATTAAAAAT      1260

AATTGCATAC TTTGTCGAAG CATTGAATAA CACTTGATTA TGACCATGAC CAAACCCTTG      1320

ATTTTCTTCA GCGCGATGGA TAGTAATAAA TGGTTCATAT GTTGTTAATT TTTCAAGATA      1380

CGCTGTTTCA GAATGATTGT CATAGATATG AATATCATAG ATACTATCAG TACCCaGTTC      1440

GGCTTTTAAT TGGTCTAGTA CATTAAAAAT GTAACGACTA TTATAAGTGA CAATCGAGAT      1500

TGTTACCATT TCTTGCATGC TCATTtCTCC TTACTACTGA AACATCGTCT TAAAAAAAAA      1560

GCATATGTTT CACACATATA CTTTTTTAAG TTTAATGGAA TTATATCATA GGTTTACGCT      1620

CTCGCAAAGC AACCTAAAGA TTTCTTTACT TTCTCTTAGA ATGCTTGCCA AGTCGCTTTT      1680

TCATTTGCTC CTGACGATAT TCACGATTCC CTAAAATCCG TAACAAATAC ATCAACGGTT      1740

GATGTCCTTC GCCAACTAGA CCGATTAGTT CAATGAATAG TTCTAAGCCA ATTAAACAAA      1800

AGACAATTAA TAAAATTGAT GCTACTGTAC TTGAATAGCT GAACAATAAA GAGACAAAGG      1860

AAAAAACTAA CGCTAATGCA TAAATAGTCA TGACCGCCCC TTTATGGGTA AAACCTAAAG      1920

ATAACAAGCG GTGATGCAAA TGCATTTTAT CTGCTGAGGA AATGGGCTTC TTGTTCAATA      1980

GCCGTCGAAT AATTGCATAA ACCGTATCCG TAATTGGCAC ACCTAAAATC ACCATTGGCG      2040

TAATTACCGT AATAAACGTA GCATTTTTCA AGCCCTGTAA CGACATTACT GCAATCATAA      2100

ACCCGAGGAA TAACGCCCCG GTATCTCCTA GAAATATTTT AGCCGGATAA AAATTGTATG      2160

GGAAAAATCC CGCAATGCTC GCAACTAAAA TAAAAATAAC AATTGGGATA TAGACCGTTT      2220

TAGCATGTAG GAAAAAATAC CCTGTAATAC CAATCGTGGT TAATCCAATA ATGGATACGC      2280

CTGATGCTAA ACCATCCAAA CCATCAATTA AATTTACTGC ATTCGTAATC GCTAAAATCC      2340

ACAATAAAGT TAGTGGTAAA CTAAACCAGC GCAAATCAAT CATTCCAACA ACTGGCAACG      2400

TCACAAAATC TATCCGAATT CCAGCAACAA AATAAATAAC TAATGCTGCT AACAAAATAC      2460

CGATTGTTTT TTTCATTGGA GTAATTTCTT TAATATCATC AATGAGGCCT GTCAAAACAA      2520

CCATTCCACC AGCCAAAATA ATCGGCCAAA TATAATCTTG TGGGATAATC GAACGAAAAA      2580

TCAATAAACA TGAACTAGCA AAAGCnATGT AGATTGCAAG TCCTCCkGCT GTAGGCATAT      2640

TTTTGGTATT GaTTCGTCGC TCTCCTGGTG cATCATAGGC GCCAATCCGA AACGCTAGAA      2700

GCTTAACAaG TGGTGTTAAT AGCAAAGATA AGATAAATGT CATAAATAAA CGTATCAAAA      2760

CTTCATAAAT AAATAGTGAC ATAGTCGAAC CCACTTTCTT CTCGT                     2805
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(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5101 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

AAAGGTGGCG TCATCGAAGG AAAAGTTTCT TCAGTGGAAC AAATTACTGC GTTGGCAAAA 60

CTACCAAACC GCGAAGGTTT ACTATCTATG CTATTATCTG TATTACAAGC GCCAGTCCGC 120

AACGTGGCTT ACGCTGTCAA AGCAGTGGCA GAGAAAAACG AAGAAGTTGC TTAATTGCAG 180

TCTAATTCAA ACCAATAAAA AACAAACAAT TTTAATTTAA ATGGAGGAAA TTCAAAATGG 240

CATTAAACAT TGAAAACATC GTTGCTGAGT TAGAAACAGC AACTATCTTA GAACTAAGCG 300

AATTAGTTAA AGCTATCGAA GAAAAATTTG ACGTATCAGC AGCAGCTCCT GtAGCAGTAG 360

CTGGACCAGC AGCAGGTGGA GCAGCAGAAG AACAAACTGA ATTCACTGTT GAATTAACAG 420

CAGCTGGCGA TCAAAAAGTT AAAGTTATCA AAGCAGTTCG TGAAGCAACT GGCTTAGGCT 480

TGAAAGAAgC TAAAGCTGTA GTTGATGGCG CTCCTGCACC AGTTAAAGAA GCTGTTTCTA 540

AAGAAGAAGC AGAAGCTTTA AAAGCTGCTT TAGAAGAAGT TGGCGCTTCA GTAACAGTAA 600

AATAATTCAT TCAACTTTTG AATGTTCGAG AACCCTTGTG TTGCAAGGGT TCTTTTTTAT 660

TAAGCTTTTA AATGGTGGTA AAGTTAGTGA ATTGATTGTC AAAATAATCT TcGTTTAATA 720

AAGtgCtTCC TAGCTAAggA AAATCCAGAG GATCTTAACC TCTGGATTTG ATAATTTTCT 780

ATAAATTCTC GTTACCAATA TTATTTGAtA AAAAGCAAAT TATTTAAATA GTGACTGAAT 840

AGTAGGTCTA TTTCTTTTTA TnTTTTATAA TGAATATACT AACTAAAGAT AGTAAGATGA 900

TTCCAATGAT AGTAAATAAA ACTGATTTTT TTTCGCCAGT ACTGGGAAAT ATCCCCTTTT 960

TGTGCTCGGT TGAACTTGAT GTAGTAGCTT TCTTCGAACT GCTCGTAGTT GTTTGTAATG 1020

TAGATTCTGT ATTAGTAGTA TCCGAAGAAA CACTTTCAGC ACTTTGATTA ATTGACGTAT 1080

AATCGTTTGC TTTTATTTTA TCTGCCATTG CTGCTAAACC ATAATCACCA CGGACATCAG 1140

ATGGGTAATT TTGGTTAGCG TAGTCTACCT TGACTTGATT AATTAAATCG ACGAGTGTTT 1200

GATCGCTTAA ATTATTtACA ACATCACTAT TTAAATcATA TACATAAATT AACGAAAGTC 1260

GAATTTGAGG TAAATAATTT TTTAAGTCAT CAATCGTTAA tGTTGaGTAA TCTGTAGAGT 1320

AGGAGTCCTC CGGGATAGGT TTCTCACCAT ATAATTTAGT AATCATTCTC GCTGTTCCAC 1380

TGATGTCTTG GTTTACAAAA TGAAACGAAA CTTTTTTTGC GTAGTCCAGT TCGTCATCAG 1440

ATAAACGATT TATCAAGGTT TCTGTTAAAC CATACATACC TACGTAATTA AGAAGTGTTT 1500

GACGAAGCGA TGGAAGTTCC TCGCTTTCAG CTGTAAGTGC TGTTGAATCA GTTGAAGCAT 1560

TAATTGTTGT TGCTGAAGTT TCTTGAGTTA AAGAAGTAAC TGTTGACTTT TCCACAGAAG 1620

CTTCATTAGC CGAATCTTCT GCCCATACAT TAGAAACTGA TAGTGTGGTA ATCGAAACAA 1680

AACAAAAGAG TCCTAAAAAC ATTTTTTTCA TTTTAATCAT TCCTTTCGTT ACCTATTGTA 1740

ACATTTTTGA AATATTTTTG TAACAATTAA ATATTAAGAA AAGCTTAAGA ATATATACTA 1800

GGTGATAAAA AATATAAATT TTAAACTATT AATCTATCAA AAATACGATC CGTAGAGACT 1860

ATTACATTAG TGTCAAAATA TTTCAAAGGT GTTGGTTAAA GAAGTACTGT ATTTGCTTAA 1920

TGGTAGTTTC GAGTAAATTA GTCATTATAT AAAAGATTGA CAAGTATGCT GCATAGCGAA 1980

AACTTCGTCA ATCTTTTAAA AGGATAAAAA TACAGATTTA AGAATAATGA CAATTTATTT 2040

TAAGTCAAAA ACTGTTGACG ATATTGTCGA GGTGTCATCT CTTTTTTCTG GAAGAAAAAT 2100

TTTGAAAAAT AAGAAGGTGA AGAAAAACCT GTTTCAAAAC TGATTTCCGT GATGGTTAAG 2160

GAACTTTTTC TTAATAGAGA ACAGGCTTTT TGCAATTTTA AGTTTTGTAC ATAAATACTA 2220

GGATTTGTTT GTTCATAACG CTGAAATAGC TTAAATAAAT AGCTACGATC AATGTTATAC 2280

TCAGAAGCTA ATTGACTAAT TGAAAGATTG TTTGAAAAAT TTTCGTGAAT AGCCATTTTT 2340

ATTTGGTTAA ATAATTGTTG GCTTTGATTT TCGTGCTGTG TAACGGAATG ATGCTCTAGA 2400

TAATTCAACA ATTGAAAGCT TTCACTTAAG CTGCCAAAAT GATTATGTTT CTTCGCTTCT 2460

TGGTAAATAT TTTTAAATAA ACTTTCTAAT TTCTTATCAA CAGTTCCTTT TAAAATACAA 2520

TTTTCGGTAG TCAGGCCTAT TTTTTCTAAA TACTGAGACG AAAGATCTCC AACAAAACCG 2580

ACCCAATGAT AGGTCCAAGG ATTTTGCCGA TTAGGATAAT AAATATTGCG ACAATTGGCT 2640

GGGATCATAA ACAAATCGCC AGCGGTAATG TGTTGTTTTT CCATAAAGGG TGTTGAAAAA 2700

TAGCCTTCAC CATCGCTACA ATAATGCAAA ACCCAATAAT TAATGGGGGC AAACTCAGTT 2760

GGTTTTGTCG GACGGCATTT TTCATAGCCA GCTTCATAAA GATGAAATTC TTGGCTAATA 2820

GGTTGATCAT TAATCAGGAT GCTGACATTA TTTGTAAAAA CATTTTGCAT GCTATCACCT 2880

CTTTATAAGA GTATGTAAAG GCTTTCTAAA AGTCAACATC TTTACAAGAA ATAGGCAACA 2940

TTTTTTATTT TTAAAAAACT GTAAGCGTTT TACAATGTGT GAGTACTAAT TAATTTGATA 3000

AAGAGAGGAT GTAGTAAAAT GGCAACACAT TCACGGGAAC GATTAGGTTC TGTCGCATTG 3060

ATGCTCATGA CTTTTTCAGC GGTTTTTGCC TTTCCTAGCA TTGTTAACAA CAGTATTCAG 3120

ATTGGCCTAG CAACTATTCC AGGCTATTTA TTCGGCTCTA TTTTTTACTT TTTACCATTT 3180

ATTCTAATGA TTGCAGAATT TGCTTCTGCT AATTCTGAAA ATGAATCAGG TGTTCACAGT 3240

TGGTTGGAAT CTGTGCTAGG ACCTAAATGG GCATTTTTAG GCGCTTGGTC GTATTTCTTT 3300

GTCAACTTGT TTTTCTTCTG TTCATTGCTA CCGAATACAT TGATTTATGG TTCATACGCT 3360

TTTTTAGGTC AAAACGTTTT TCAAGGAAAC CATAGCACTA AAATAATTGC AGTGATTTCT 3420

ATCCTGTTAT TTTGGTTAAT GACATGGGTT TGTATTAAAG GGGTTTCGTG GATTTCGAAA 3480

GTGACTAGCT TAGCGGGTGG TGCTCGTTTA TTTATGGGCG TAGCTTTTGT GGTTTTAGCC 3540

TTTGTCGTCG TGTTTGGTTT TGGCAATGAG CCAGCACAAG AGTTTACCAC GACGTCAATT 3600

ATGCCAACTT TTAATTGGAC TTTTTTCATG ACGATGGCGT GGATTTTACA AGCTGTTGGC 3660

GGTGGTGAAA GTATCGGTGT ATATATTAAG GATGTTAAAG GCGGCAATAA AACGTTTGTC 3720

CGCACGATAA TTGGTGCAAC GATTGCGGTC GGTATCATGT ATATTCTTGG TGCCGTTGCT 3780

GTAGGTTTGG TAGTGCCaAC GGACGTCTTA AAAGGAAATT TTTCAAATGG TATTTTTGAT 3840

ATTTTTAAAA TTTTAGGTAC GTATTTCCAT ATTCCCGCAG CAATGATGGT GCGCTTAGTA 3900

GGAATTATCT TATTTGTCGG AAGTCTTGGT TCTTTGGCTC TGTGGACGGC AGCACCAGTT 3960

AAAGTATTTT TCTCAGAAAT TCCTGATGGG GTCTTCGGTA AGTGGCTAGT GAAAACGAAC 4020

GAAGAGGGAA ATCCAACCAA TGCTTTGTTA GTTCAAGGAA TTATTGTGAC GATTTTAGTT 4080

GCCATTCCAG CATTAGGAAT TGGAAATATG GATAGCTTTT TAGAAACGTT AATTAATATG 4140

ACAGCTTCTA CGTCATTAGT GCCTGTCTTG TTCTTGTTAA TCGCCTATAT TGGGCTTCGT 4200

TGGAAAAAAG AAACAATGCC GAGAAGTTTC CGCTTTGGTA ATCGAACCTT TGGCTTAATT 4260

GCGGGAATTT TCTTATTAGC CATTTTTATC TTTGTATTCT TTATGTCAAC TGTGCCGGAT 4320

CCAAAATTAA TCATGGAAGA AATCAATTGC ACGTTACCGA AAGGAACCGC TAGTCCACTG 4380

GGCATGTTGG CGTATAACAT CATTGGGTTA ATTGTCTTTA TGGGCTTTGC TTGGATTTGT 4440

TGGAAACGAT ATGAAACAAA AGAAAAAAAT GAAGTTGGTA AAGGAGAAAT GGATTATGAA 4500

GACTTGGGAA AATTATAAAG TAGATAGTAT TAATCGGTTG CCTGGACGAG CACACTTTTC 4560

GAGCTTTCCT TCGAAAGAAA CAGCGTTATT AAATGAAAAT AAATATACAC AAGCATACAA 4620

AAATTTAAAC GGATGCTGGC ATTTTCTCTT TTTAGAAGCG CCAGAATACA GCCCAGAAAA 4680

CTTTTTTGCG ACGGACTTTG ATACAAGCCA AATGGATCAA ATCACTGTTC CTGGAAATTG 4740

GCAAGTCCAA GGATATGGCA AAATGCATTA CTCTGATTTA TGGTACAATT TTCCCATTAA 4800

TCCGCCGTAT GTACCAACGG AAAACCCAAC AGGTATTTAC AAACGGACAT TTGCTATAGA 4860

TGAAACATTT CACGATAAAA AAATCATTTT ACGTTTTTGT GGCGTAGATT CAGCTTATCA 4920

kGTTtGGGTG AACGGCCATG AAGTTGGCTA CAGTAAAGGt GCaCGAAATG AAGCAGAaTT 4980

TGgACATTAC GCCTTACGCT AAAAtTGGgT GaACCAAATG aTTTamCGGg CgAGTCTATC 5040

aATGGtCaGA TGGkACgTAT TTwrGAGGGT CCAAGATATT nTGGnnGGGT TAAGTGGGGA 5100

T 5101

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1084 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

ACAATTAGAT GGTACCCGAA TCGGCTTTAT CCTTAAAGGC ATCGTCGTCG GAATTCTTGT 60

CGGCTTTGTT GTCAGCTTAT TTCGCTTAGG CATTGAAAAA ATTGGCGAAC AAGTCGTTCA 120

TCTGTATCAA ACGTTTCACG AAAAAACCTT TTGGATGATT CCTTGGTTCT TATTTTCTCT 180

CGTGCTTGCT TATTTATTAG GACGACTGAT CAAAAGCGAA CCAGCAATTA AAGGCAGTGG 240

CATTCCCCAA GTGGAAGGAC AACTTCAAGG TCAATTAGAA ATTCACTGGT TTCCAGTGCT 300

TTGGAAAAAA TTTATCGGTG GGATCTTAGC GATTAGTCCT GGGCTATTTT TGGGACGTGA 360

AGGTCCTTCA ATTCAACTAG GTGCAGTGGT TGGACAAGGC TATAGTCAAT GGCGGCAAAG 420

CACCAAGTCT GAAGAAAAAA TTTTAATCAG TAGTGGTGCC AGTGCTGGTT TAGCCGCCGC 480

TTTTAATGCA CCAATCGCAG GACTTTTATT TGTTCTAGAA GAGGTTCACC ATTCCTTTTC 540

ACCTTTAGTT TGGTTAACCT CTTTTTCTGC GGCCATTTCC GCTAACTTTG TTTCTTTGCA 600

TTTCTTCGGA TTGCAGCCAG TTCTTTATAT TGGTCCGGTT AAATCTTTGC CTTTAGAGTA 660

CTATTGGACA TTAGTACTGc TGGGCGTTTT GCTAGGATTA TTAGGTTGGA TATATCAAAA 720

AACATTGTTG TCCTTACCAA AAGTATATGG AAAAATCAAA GGCCTTTCTT CTAATTATTA 780

TGGTTTTGTT TCTTTTATTT TGATTTTACC GATTGGTTAT TTCTTTCCAC ATTTACTTGG 840

CGGTGGGAAT CAAATTGTTT TAGCTTTAGG CAATCAACCG ACTACGATTT GGGCTTTAGT 900

CGGCTTACTG GTTTTACGTT TTGTTTTTTC AATGGTTCTT ACGGTCGAAT CTCCCTGGTG 960

GATTTCTGCC ATTCTAACTT TAGGGCATAT CGGACATGAT GGAGCACTGT CCAAACGAGG 1020

AGGAnCATTT GGAAACTTAA TTTGCAnGCG GATTACGGTG GAAnACGTAC ACGTATTAGA 1080

CAGA 1084

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

CCACCTTCCA ATTTTGGTCC AAGTTGGGGT TAGCGGGArG CACGCAACrG CACAGCTTGA 60

AAAAAGCCGC TGATTATTAT GGCAACGGCA CACGCAATCC CTATCTGCGG ATCAAGAAAA 120

CCCAAGCGAA TTGGAGCTTA ACGGCGCAAC TGTCGCAACC GAAATCAGCG ACAGACAGCT 180

TGCCAACAGC GACCCGCTTA TTATTAGGGG CGGCTCCTGT TTCGAGTTTC TCAAATTACA 240

ACCAACCTAC CGAGTTGAAA AATGCGGTCG GTACTACGAG TGCCATTAGT TTGAATGCCA 300

ACAACACGGC CACTAGGATT ATTGCCAATC AACAATTCAC TGGGAGTAAT ATCTATCAGT 360

TGGACTTCAC CTTCAACAAT GTCAAACTTG AAGTGCCAGC CAACCAAGGG GTCAAGGGGC 420

AACAATACCA AGCCGCAATT ACGTGGAACC TAGTTACAGG TCCTTAAAAT AGTTAAGTTA 480

TCATGAGGAA AGCTCAAAAT GTTAGTATCA AACACTAACA TTTTGaGCTT TTGTTTATGG 540

AAATTAAGGA ATTTGGCTGA AAATCAGAAG CAAAATGGCA GATTCTCTTA ATTTTCGAGT 600

GTTTTTCTAG TGAAAAAGGA CTCTTCTACT TTGGTATAAT AGGAATCGTC GGAAAAGTAG 660

CTTAGCTGTA GCAAAATTTG AAATTTCAGG GCCACCTTTT TTTTGATAGA ATAATGGAGA 720

AAATTAAAAG CTGTACATAT ACCAATGAAC AATAAATCAA TACATAAAAA AGGAGAATAG 780

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CATGAATCAA AAATGGCAAA AGTTACTTCC AACAAGGAAC TCACTAAGAG GTGGTTCAGC     840
ACAAGCTATC ACGACTGACC CTTGCGCCCT GTATGAGGGA ACAAGGGGCA AGCAAATCTT     900
AGCATTCTCA GCATAGCCTT CATCGGCTTG GCGGGAATGG TACATAGAAA GAAGGGACGA     960
CATGAAGAGA ATTAACTGGC AACGCTTAGC AACCATTGGC TTGTGTAGTT CTTTAGTGAT    1020
TAACGCCTTT TTTGGCGTAA CAGCCATTGC GGAAACAGTC ACGAGTGAAA GTAGCCCGAC    1080
AGTGGCAAAT AGTATTAAGG AAGCAACACC AGCAAGTAGC GCAAGGCAAG AAAGTACGGA    1140
AAGCAGTCAA GAAACGACTG AAACGAGTCG GGAAAAAGTA ACACAGGAAA CAGCGAAACA    1200
AGCAGAGACA AAAGCGCCAC TGGAAACACC AGAGATAAAA ACAAACACAA CAGCACAACC    1260
TGCAGAAAAT AGTAGTGAAA ATGACCGACA AACGAGTATT TCGCCACGTT GGGTGCCGAA    1320
TAATCAAGTG ATTTATCCGA GAATAACCTT GGCTTTCACT AATGAATCAG GGCAAGCTTT    1380
TGCTGATGAA AACTTAACGT TATCAGGGAC GTATACTAAA TTTGGATATG AAGACGCAAC    1440
TAGTTTATGG CGACCATATG CGGTTAATTA TCCAATTACT TCTTCTAATG CAGGTGGTGG    1500
TCAATATCGA GTAGCTGTCA ATGCAACGGT TCCTTTACCA TACGATTTTT TCACAGATTT    1560
ACCAGCAAAT TATAGGATGA ATATATACGC GGTTGAACAA TTAAAGATTG ATAACACGCT    1620
AAAGTATGTC GACAGTATTG TTGCTGTGCC CGATTCTACA CTGAGGATGA CCAGATATAG    1680
TGCGCAACAA ACAACTGAGT TACCGCAGTT TGGAAATCAT ATGACTCCtT TTGtATTACG    1740
CACAAGAGAT AGCATATTTT CTAAAAGCAG TGAAAATGTT TTCTCTCTAA ACACGGATGG    1800
TAATGAATTT TTAAGAATCC TGAGTGTCGC CCCCATTGGC ACTCCAGTAG AACCAGTATT    1860
ATACGGATTT GATGGCACTG CAACGTACCG AGAAACACTT AATTACGTAG TCACTCGGAA    1920
ACAAGTCACC GAGAAGTTCG TAGATGCTAA CGGCGTAgcT ATCACGCCGC CAACAGGTTT    1980
TACCCAAAAC AAGAAAACAC CAATGACCAG CAATGACTTC ACCTTCAAAC AAGCTAGTAC    2040
TTTGCCGGAC ACCTATCAAG CAGACGGCAA AACCTACAAA TTCAAAGGCT GGTACAAAGG    2100
CAAAACCAAG CCAAATACCT TGACCACCAC CAAAGCGCCA AGCTATGCGG TGACCTATGA    2160
TGGGAATGAC GATTTGACGG TGGTGTATGA GGCGATTCAA GAAGGAAAAG GAATGTCATC    2220
TGTTCAGGTG ATGAATAAGG CGATTCAGAA TCCAGTGACT TTGCCTGATC GCATGTATCG    2280
TGTCCTATTT ATCAATGAAA CAGGGGGGCT GACATTTGCT GATCGTTATG GCTTTACTGG    2340
AGAATTAGTT GAGGTTGCGG ATGGCAAAGT GACGCCAATT GGCCCAGTCC CGACTAACAA    2400
TAATAGCGCA GTAAAAGAAA TCACTATACC AGGTCGGGTT TTCGATACAG AAAGACCTAC    2460
GCCGTTGCAA TATGGAGTTC GCAATGCAAC CTTTACGTTG CCCAAAATGT ATAAAaCCGT    2520
AACGTATCAA CCTGGCCCAA ATTATACAGG TACAGCCTAC TCTATTCCAG AAACGTATCG    2580
tCTTAGTTTA AGAAGTGGTG TCmAAmGTGA CATCGATACm ACTGGATGGC GAATTGGCTT    2640
GACCCGACAA CAGATCCACA AAAGTTTACG ATGAGCG                             2677
```

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

AGATTGTCCn AATTTTAATT CCCAATCCAG TGCCCAGTAT GGCnGGGATG TTTTCCnTCC 60

TTGTGATTAA AATCCCnAAC CAGTAAATGT GTCCAAATTT GGACCACCCA GTCCAAGTGA 120

CCAAATATGA GGGGTATGTT TTCCTCCATT GTTGGGAATT ACCAAGCCAT TAGATGTAAC 180

TAAGTTTGAT ACATCCCAAA GTGACAGATA TGAGTGATAT GTTTTATGGT TGTAAGGAAT 240

TACAAACATT AGATGTGTCG AATTTTGATA CGAGTCAAGT GATATATATG AGTGACATGT 300

TTGGTGAGTG TAGCGGATTA CAAACATTAG ATGTGTCGAA TTTTGATACG AGTCAAGTGA 360

TATATATGAG TGACATGTTT GGTGAGTGTA GAGGATTACA AACATTAGAT GTGTCGAATT 420

TTGATACGAG TCAAGTGATA AATATGAGTA GTATGTTTGC TGATTGTAGA GGATTACAAA 480

CGTTAGATAT AACTAATTTT GATACGAGTC AAGTGACAAA TATGAGTAGT ATGTTTGCTG 540

ATTGTAGAGG ATTACAAACG TTAGATATAA CTAATTTTGA TACGAGTCAA GTGACAAATA 600

TGAGTAATAT GTTTGATGgT TGTAGAGGAT TACAAACATT AGATGTATCA AAGTTTGATA 660

CAAGTAAAGT AACCGGTATG ATTTATATGT TTAGAGATTG TAGCGGATTA CAAACATTAG 720

ATGTAACTAA GTTTAATACC AGTCAAGTAA CATATATGTG GAATATGTTT TCTGGTTGTA 780

GTGGATTACA AACGTTAGAC TTATCCAATT TTGATACCAG TCAAGTAACA AATACGGATG 840

AGATGTTTGA TAATTGTGAT GCCCTAAAAA AGATAACATT GGGGGCTAAA TCAATATTTG 900

GGACTAAGAC TAATACTAAC TTGCCGTCTA TAGCAGrTAC TTCTTTGTAT ACTGGAAGAT 960

GGATTGGAGT AAACACGAGT AACACTTATA GTGATAGTAA TACATTTATG TCTAATTATG 1020

aCGGATCaGT TCCaGATACG TATGTATGGG aAAAAGCTAG CGTTCTAAAC aGTACTTTaG 1080

AGCCTTCTTC aGTAAGGGtT CATTCaGAAA GTGAAGTAGA ATGGACTTGG AAAATAACTA 1140

ATTCGTCGTC TAAGTCAGCC GAGAATGTTT ACTCAGATAT AACCTTACCT GAGGGTCTTA 1200

AAATTGACAA GAATAGTGTA AAAAAGAACA ATTTGCCTGT GTCGGTAGAT GATATTAATG 1260

GTATGAACAA TTTAGGAACA CTATCTAGTA ACGAAACAGT TACATTTACG TTTAAGACAA 1320

TAGTATCAGG GAAACCAGAT AAAtGGTTGG AATTAATGGG AAAAGTGACT kGGGAAGATA 1380

ATGcmTCCGC ACAGTCAATA GTTCTAATAA AGTGrAAATC ATCGATGAGG AGCAAAAAGA 1440

TAAAGGGAAT CAAACAAATG ATTTAGAGTT ATTATCAGTT CCAGTTGGGT TTCG 1494

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 884 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

TATTTATGCT GATTCGTTAC TGGAACAACG TATTAAAGCA ATTAAACGTA TGGAAAGAAC 60

TATCGCTTAA AAATTAAAAA AATTAGTCTA TTCTTTTGAT AGGCTTTTTT TTTTAACCGA 120

AAGAAAACGC TTACGCATTT TTCTATCTTT TTTTTCAAAT CATATTATTC AATTAAAAAT 180

GATTCTAATT TCAAGATTAT TTTTTTCATT TCTTTTTTTT CGCCGTCAAA TACCGTCAAA 240

CGTTTTAATA AACATCTGTT ATTTCAAGGT AGTATATAGT TTTTCATAGT TTTCAATAAA 300

CTAGGATAAA AAACTTGTTT ATCCATTACA TTTTACCATC AATCTAATCT TTTTTGAAAA 360

AATTGGTATT AACTTCTTAA GTAAGTTTAT ACATATAGTT AGTTATTTTA AAACAAAGAG 420

GAGAGAAAAG AGATGAAAAA AAATTTAGTA GTAGGTTTCG TATCAAGTGT CGCTTTAGTA 480

GGAATTGCTA TCGCAGGAGG GGGTAATGTT CAAGCAACTG TTACTGATAG TGCAAGTACT 540

GATATAGGAA TTGGATTTTC AGGACATGGA CCAGGAACGA CACCGGGACC GTTGGATATT 600

CAATGGGCTC CAATAGGATT AGATTTTAGT AATTCGAACA TGGTAAATAC TACAGCCGTA 660

CAAGCATTTC CTGAAACCAC TGGAACCAAT AAATATGTTG TTGTAAGTGA GAAACGTTCC 720

AATGAGCCAA CTAGAGAATG GAGTTTGACT GCGCAATTAT CAGACTTGAC GAATGCGGGA 780

AGGTCAGAnA CACTTACTGG GGnTGGACTA AAAGTTTGTG CTGCTGTAAA AAGGATACAC 840

TGGAACGAnT ACACCAGAAA GCCCAGGATC AATTGTGAAA nAAG 884

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

GAAACGTACA GAAACAAGAC AATTAGAAGT ACTTAAATAT ATATACGAAC AAGTCGAATT 60

AAAGGGCTAT CCGCCAACCG TTCGCGAAAT TGGGAAGGCT GTTGATTTAT CCTCAACTTC 120

TACCGTTCAC GGAcATTTAG CTCGTCTTGA AAAAAAGGGT CTAATCTTAC GTGACCCAAC 180

AAAACCGCGA GCAATCGAAT TAACACCAGA AGGCTTGGAA AAGATCGGAA TTCAGCCGAC 240

AACTATTCCG ATGTTAGGTG TCGTAACTGC TGGTGAACCA ATTTTAGCGG TGGAAGAAGC 300

ATCAGATTTC TTCCCGTTAC CTCCkGATTt ACGTACAGAA GAAAATGCTT TATTwATGTT 360

GACGATTCGA gGAGAAAGTA TGATTAACGC AGgTATTCtA GATGGCGACC AAGTGATTGT 420

TCGTAAGCAA TCGAATGCCA ATAATGGCGA CATCGTAATC GCaATGACCG aTGAAGATGA 480

AGCAACCTGT AAACGATTCT TCCGAGAAGT AGATCATATC CGCTTGCAGC CTGAAAATGA 540

TGCATTAGCG CCTATTCTTT TAGATAACGT TACAATTTTA GGTAAAGTtG TTGGTTTATA 600

TCGCAATCAT ATTTAATAAA AAAAGGAAGT CACTCCGTTG AGCGGCTTCC TTTTTTGCTT 660

GTTAACAgTG AAtAGCCTTT TGGGCTTCCT CGATAACCTC TTCTTCAGTT TCTACAGAAA 720

GTAGATAATT TAAAGCTTCT AAACTTTGCT CGGGTTCyCT TTTTGcGAGC TGACCTaACG 780

ACCAAGCAGc TGTTCCGCGA ATGACAGGAC GCTGATCATT TAAACAGAGA ATAATTTGTG 840

GGATAGCTTC ACGGCCGCCC AAATTcGtAA CGCAATTAAA GCATTCCGTT GCAAtGGTTT 900

TTTACCACGC CAAGAGCCTG CTAAGTGTCC GAATTGCTGT TTAAACTCTT TATTGGAAAT 960

AGTTAwTAAC GGTGCTAATT TGGGATAAAC TTCTTCAATC TTTGGTTCCA TCTCTTCATG 1020

AAAATGAAAA TCTTTTCCTT TATTATAAGG GCAAACCAGC TGACAAATGT CGCAACCATA 1080

AATGaCGTTA CGCATTTTTT TCCGATAGTC TTCAGGCATC ATGCCTTTTG TTTGCGTTTG 1140

ATAAGACAAA CATTTTTGAG CATTCATTCG ACCGTCCCCT AACAAAGCCC CTGTAGGACA 1200

CCCTGTGATA CAACGAGTAC AATCACCGCA ACCATTTGGA ACAGGTTCAT CTGGTTCAAA 1260

TTGAATATTG GTGGTCACCT CACCTAAAtA TACAAAGGAA CCAAATTCTT CGGTAATCAG 1320

TAGACCATTT TTACCAATGA ATCCTAAACC CGCCCGCTGA GCAACAGCGG TGTCAACATA 1380

TTCGCCAGTA TCTACTTGCG GCCGAAAGCG CCAGTGTyCT TTTTCTGCTT CAGTGGCAGC 1440

TTGCTCTTCA ATAAAAGCAA TTAATTTTTG CAACCGATCC TGCAAAATGT GATGATAATC 1500

AATTCCCCAA GAGGCTCGCG CAAATTGTCC ACGCTTTTCA TCTCTAGGCA TTTTTTCCTG 1560

AGCTTTGGTG GGATAAGCTA AAGCAATGGA GATAATACTT TTAGGATGCT CAAACGTTTT 1620

TTCTGGGTAA ATTCGTTCTT CCACATTTTG ATGTTCAAAT CCCGAGTTAT ATCCTCGCTC 1680

TCGTTGTTCA TGCAGAGAAT CTTCTAATTC AATAAATGGT TCAGCATGAG TAAAGCCGAT 1740

TTTATCGATG CCTAAACGTT GACTCTCTTG AATAATTTTT TCTTTCAATG TCGGCATTGC 1800

TCATGACTCC CTTCATTTTA TTATTTATCG TTTCGATGAT ACGTTTCATA GTCATGTGCA 1860

TAGAGATTTT TCTCGTCCAC GACGCCGGGA ACAGTGGCAA CTTTTTCCCA AACAGACCAG 1920

TCGATTTCTG GAAAGAAGGT GTCGCCTTCA AACGTTTCAT GAATCATCGT CCGATATAAG 1980

ACATCGCATG CGGGAATCAA TTCTTTAAAA ACGACAGAAC CTCCACCAAT AACGGTCACG 2040

CCTTCATACT TGTCAGCATA CGCAAGAATT TCCTCTACGG AATGCATAAC CAAAACGCCT 2100

TCAGCTTGGT AATCCGGATT ACTGGTAAGA ACAATCGTTG TTCGATTTGG TAACGGACGA 2160

CATCCCATAC CTTCGAAAGT TGCACGTCCT AAAACCAATG TATTATGAAT TGTTTTTTCC 2220

TTGAAAAATT TCAAGTCGTT GGGTAAATGC CAAGGCAATT TGCCTTCTTT ACCAATCACT 2280

CCTTGTTCAT CTTGGGCCCA AATGGCTGCT AACATAGCTT CTCTCTCCTT TTTTATACGG 2340

CAATCGGCGC TTTAATCGTT GGATGTGGGT CATAGCCTTC TACTTTAATA TCTTCCATAT 2400

CAAAATCAAA AACAGAAGCC TTGTCTGGAT TCAAAACGAG CGTTGGGaAA GAACGAACTT 2460

CTCGTGATAA TTGGTTCTTG GCATTTGGTT CCACATGGAT TTTTGATATA AGTGGGGGCA 2520

TCTCCTAGCG TGnTGGTACA AACTCCCCCA CTnCTAAAnC TGTTTCATGC GGCAATCAGA 2580

TGT 2583

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 965 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

GATGGTTTTT CGATCAAATT TCTTAnnCnC TGTAGCAGTA TAAATTAGTA ATAACTTACT 60

CAGAGATTTT ATAGAGAAAG ACGTTGTTGT AGCTTCTCTT AATTGCTTTA ACTGCTTTTG 120

CAATTTTAAC GGATTTTTAT CTTTTAATAA TTTAATTTTC GTTAAACGAA AAATGTGTTC 180

CTGATGCTCA AATGAACGTT CAGCATCTGA ATGACTAAAA CGAAGATATT CTGAAAGCAC 240

CTCTTGATTT ACAGCAACTT TTCCTTTTGG TAAAAACCAT TCTTTGCCAT TTTGATCTAT 300

TAGATGCCGC TCACTTTGAT TTGAAATAAC AATTTCTTTA TCGTCTTCAA AAAGATACGA 360

AAAAAGCATT GCTTTTTTTA TAATTATGTA CTCAGTTACT TCATATGAAG ACAATTTTCT 420

TAATTCTTCT ATCAAACTAT TCCATTGATT ATTTTGAACA AATTTACTTA GTTTGTGAAT 480

AGGTGGTACT CGTAAAATGA ACTTCTCATC TTTCTCTATT TTCACGATAT AAAAAGTTGT 540

GTCTAAGTCA TTTTCCCAAA TAAACAAAAT AATCATTTAC TGCCCCCTAG ACTTGTTGTT 600

CCGATACTTA ATAGTCAAAT AAATATATTT AGGAATTTGC ATTAACCGAT CGTATCTCTT 660

CATTGTCAAA CAACGATATA ACCATTCCAA ATTGTGATTT ATATAAAATT CTGGCGCTCT 720

TTTTACTGAT CCAGCTAATA CGTCAAAAGT AmCGCcTACG TCTAAAAATA CATTAGCTGT 780

CAGGTGATCA ATTGTTTGTT CCAAAAAAAT CTCTTGTTtC GGTGAACCTA ATGCTACaAA 840

GACAAACCTT GGkTCAGCTT TGkTAAwTTG kTCCACAATT TCTTGCTGTT TTTTCTTTGT 900

ATAGCCATGT AAAATACCGC TAATAACAAT CCCTGGATAT TGTCGTTGAA TATTTTTAGC 960

TGCTG 965

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

CATnCCGGGG ATACAATTGG TGGATTGGCT TTAAACTATA TTCATTTTGC GACAAGTGAA 60

AGTAAGTTAT ACCGTGCGCT TTATTTAGAA GAATATGGTG GCGGCAAAAA AATGCCAAGA 120

ATTCTCTTAT CACTATTTTA CTGAAGCGGT AAAAGCTGAT CCTGAGTATG CTAATTTAAA 180

CGATGTTCAA ATTGACTCTT TACACATGGG AACATGGGTG GTCGCTACTG GTGTGGCTGC 240

ATTGATGACT TCTGGAATTA TCCATCCTTC AGAAGAACAA ATCATTCATT TAATGAAAGA 300

TAGTATTGAA GCAATTCTTG AACGAGATGA ACCAATTGAT ATTGACCTAT AAAAATTAAA 360

AAAAGTGTAA CCTCATGCTG ATAACTTCTG TGAGGTTACA GCAAAAGACT GTTTCTTAAA 420

AGAACGGTCT TTTTTTGTTA AGTGTATTAA TGGTAGATTA TTCGCAACCA TGCTACAGTA 480

AAGAAGAGAA ATAGAAaGGG GCAAAAAACA TGAACCGAGT GAAAGATAAG CGTTTATGGC 540

TAAGTATTGT AGGAATTACC GGACTAGGGC TCTTGTCGGG CTTATTTTCA GTAAATGCGA 600

GAGAATATTA TCAAGCGTTG AGATTACCAA GTTTTGCTCC GCCAGGCTGG TTATTTGGAC 660

CAGTGTGGTT GGTGTTGTAT ATTTTTATGG GCATTACTTT TTATTTCATC TTAGTTCATC 720

CAAATAAACA ACAGAAAAAA CGGATGATTA CGCTATTTAT TTTACAATTT ATTGCGAACT 780

TTTTCTGGAC ATTTTTCTTT TTTTCTTTAC AAAATAATTT ATTATCTGTG ATTGATATCT 840

CATTGTTATG GCTATTATyA ATAATTCAAC AGTGGGACTA CTTGCGTTAT AAATTAATAA 900

CGCGTGGCTG GTTGATGATT CCTTATATTC TTTGGGTTAC TTTTGCGGCA GCATTAAATT 960

ACAGTATTTT ATTTTtAAAT TAGGAATATC AAAACACCAG AGAAAAATGG GAACTAGCCA 1020

TTTTTTTCTG GTGTTTTTTT TATTTATTTC AACGTAGTTA TTCTGCGGCA GTTGCTAATT 1080

TTTTCGCAAA TTCTTCTAAA CGTTGGAT 1108

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

TTAGTAATTT CCTGTACTTC TCTCCCCATA CAATTCATAA TATCCTCACA TTGTTTCGTT 60

GTACGTACAT CATTCCATAA AATAGCAGGA CGAATTATTT CATTATCCTT GTCTAATAAT 120

ACTAAACTAT GCATTTGTCC AGATATACTA ATCCCTTTCA ATTCTTTTTT CATTTCGGGA 180

AATTCACTCA ATAAATCATT AATTACATTT TCAATTGCTT TAATCCAATC GTGTGGATTT 240

TGTTCACTAT ATCCTGGTCT TGAAGAAAAC AATGGATAAT CTGATGAAGA CGTAGCAATG 300

ACATCCCCTA TTTCAGATAC CAATAATCCT TTTAATGAAC TTGTACCTAA ATCTATACCT 360

AAAACATAAC TCATAATTAT TAAATCCTTT CAAAAAAgCT GAAATACCTA CAAAAGATAT 420

TTCAGCTCAT TTTTCTTAAT ACmGaTaATC aTTTAAAATA TTTTTTACAT ATTCTATATG 480

ACTTGATTCT ATTATTGGTT CATCATTTTT TAGGGCATAA TTAGTTAAAC TTTCTAAATT 540

TTCTTTTCCA GAAATAATTT TTGCTCCAAT ACCTTTTTTA AACGATGAAT AACGCTGTTC 600

TTTTAGATCC TCAAAGAAAC GATCCTCTTT TAATTTCATC GCACTCTTTA ATCCTCTCGC 660

AAATGTATCC ATTCCAGCAA TGTGAGCAAG TAATAAATCT TCCATTTCAA AAGATGAaCG 720

TCTAACTTTA GAATCAAAGT TTATTCCCCC AGGTTCAATA CCCCCATTTT CTAGTATTTC 780

ATACATAGCT AATGTAACAT CATAAACATT AGTAGGAAAT TCATCTGTAT CCCAGCCAAG 840

CAGAACATCA CCTTGATTAG CATCAATTGA ACCCAAGGCA CCATAGTTTC GAGCTACATT 900

AAGTTCATGT TCAAATGTAT GTCCAGCTAA AGTTGCATGG TTAGCCTCTA GATTTAGCTT 960

AAAATCCTTT TCTAACCCGT ATTTTAAAAT AAATGCCATA GTAGTTGCAG CATCGAAATC 1020

GTATTGATGT TTTGAAGGCT CTTTGGGTTT TGGTTCAATC AAAAATTGTG GCTTGTGTCC 1080

AATTTTTTCA CCGTAAAATA TAGCCATTTT GAATAGACGC GCAATATTAT CTTGTTCAAA 1140

CTTCATATCA GTATTTAGTA ATGTTTCATA TCCTTCACGT CCACCCCAAA AAACATAATT 1200

TTCTCCACCT AATTTTTTTG AAACaTCTAA ACCTTTTTTT ACCTGAGCAG CTGCGATtAc 1260

GTATACGTTk GCATTATTTG TAGATGCTGC GCCGTTGACA TAACGAGGAT TTGAAAACaT 1320

ATTTGCAGTA TTCCACAATA GTTTAATACC AGTtTCaTCC ATCTTTTCTT TTATTAAATC 1380

TGTAATTTCA TCAATATTAG AAAAGAATTC TTTTAAAGAG TTACCTTCTG GAGCAATATC 1440

AATGTCATGA AAACAAAAAT ATTCAACATC TAGCTTTTCT AAAATTTCAA AAAAAGCTAT 1500

AACTCTTTTT TTTGCAGTCT CCATAGGAGA TTCTCCCAAC CaACTTCGCT TATTAACkGC 1560

TTTTCCAAAA GGATCTGAAC CGTCTTGTGT CATAGTGTGC CAGTATGCTA CAGCAAATCG 1620

TAAATGTTCT tTCATAGTCT TTCCCATAAT TATTTCTTCT GAGTTATAGT GTCGAAACGC 1680

GTACATATTT TTTGTGTTCG TTCCTTCATA TTTAATTTTT TCGATTTTTG GGAAGTAAAC 1740

CATGTTAAAA GTCTCCTTAT CATCTTTAAA ATTGTTATTT CAATTCGATT AATATTTTTA 1800

TAATTTATAT ACTATTGAAA ATTAATTAGT CAGAGGTAGT TTTAATTTTA CTCTTCCTCT 1860

TCTTCAGCAA TTTGTAACTT CGGTATTTTA ATACTTTCGG TACCTATTTT CAATAAATGT 1920

TCTACAAGAT TTTCCTCTTT TATAGCAAAG AATGATTCTA AAACCATTCC CAAATTAACT 1980

CCAGTTATTA CCTGAATTCT TGAGTCTTCA CTTGCTAGCA TCATGGCAGT ATTTGCTGGA 2040

GTCCCACCCA TCAGATCTGC TAAAATCACA ATTCTTTTTG CATCATTTAA AGTACCmATa 2100

ATTTTATCTA ATTTATTAAA GGTCCCTTCA ATACCATCAT CAGGCGTCAT AGAAACaACA 2160

GGATAaTTTA TTTGATCACC TAwGATCATT tGAGCCGAAT TCAAAATTTC TTTCGCCATA 2220

AGGCCATGGC TCATTAAAAT TACTTCGTTG GTCATAATGA TCTCCTTTAC AATATATCTT 2280

TTAAAAAAGT CTTTTTATCA CCGGGGGCCA TAATnGTGGT AATTCATATC TCGACTTAAT 2340

AGTTCCnCA 2349

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

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TACGGCGTCG AAAGAAAAAT AAATAGACCG TACTAAGAAT AAAAAAGCGA CTGAACTTTT      60
CAAAAGATCA GTCGCTTTTT TGTGCTTATT TTTAATTTTA AGCCCGTTTA AGCCGTTTTA     120
AGTATTTTTC TAGTAAAAAA GTACTTAGAA ATTAAAAACG GCTCTTAAAA CGCAAATATG     180
AGCCAAATAA ATAAATTTTA ATTTTTATCA GTACGAGCGA TTTTTTACGT ACTGCCCATT     240
TACATGCAAA TTTAAAAATT AGCAAAAAAT CGTTCCGAAT TTGCATTTTA AATGGGTAAA     300
CTTGCAGTTT AATCGCATAG TTCTCGCAGA GGCTAAAAAA TAAAAAAGCA CTGAAATATT     360
TCAGTGCTTT TTTTATTTTT CTTCTTCAAT TTCGTTGATT GTCTGATGAT TAATTTTTCT     420
TTTTTCTTCT TCGGTTAATT CGTGAAGTTC ACTCGCCAGG TACTCTTTCT GATTCCAAAT     480
ATAATAAATT TGATACAAAT ATTCAGTTGG ATCAATTTCT TTGAGATAAT CCAATTCTCC     540
GTTTTTTAGT TTCTTTCTCG CCTCTTTAAA AAGTCCTGAA TAGACTAAAA TCTGCTTACC     600
TTTTAAAGAT TTATAATACG CGTCAAATAT TTTTTGATTG ATAAGATAAT CGCTATCTTT     660
ACCCGAATAC TTCGCCATTT CGTATAATTC TTTGTTGTTA TTTTGCTTAA TTTTTTGAAC     720
ATGGACTTGC GTGATCTCCG GCATTCCTGT GACATCTCGC CACATTTCGA GCCATTCTTT     780
TTGTGAAATA TAAACCTTAG AATCTTTAAA ATAAGATTTA TTTACAGCAA TTAATACATG     840
AAAGTGCGGA TTAAAATCAT CTCGTTGcTT GTTGTATGTG aTTTCTAATT TTCTGACGTA     900
ACCTTTCATC ATCGCTTTAA CATTTTTTCT TTTCACTAAC TTTCCAAACG ATAAATTAtA     960
TTTTTTTATT TCaTCTTCTA ATTCTTCAGC TTTCACATTT GGTGTCGTTA AGGTTAAGAA    1020
AATAAACTCT TTTTTCTCTT CTTGCTTAAT GTACTGCATC ATCAACGATA GACCTAACGC    1080
ATCTTTTCtC GCTCGTCGCC ACGCACACAT CGGACAGAAA CGATTTTTAC ACATATTATT    1140
TTTATACAGT TTCTTTTTTG TCTGCTCTTT ATCCGTTACA AACGCTAAAA ATGTGTTACA    1200
GTCCTTAATC AGATCCATCT GTTTTTCTCC CACAAATTTA TTAATAAAGT TCTGAAACAC    1260
TTGATTTCTC TTCTTTTTCT CAGTATACTT TTCCATATCA GATATATAAA ACAACTGGTT    1320
CTGTTGCAAA GTTTTAAATA AAGAATAAAA TCCCTTACGG TATCTATGAT TTAAGCTGGG    1380
ATTCCCAATA ATACCTTGAT TTCAGTACAG ACCGAAAACC CGAAGAGAGT GCCTTCTTTT    1440
CGGGTTyTCT TATATAATCC TCGAATGGCT TCCATGCCTT TAATCGTGGT AGAGGCAGTG    1500
CGTAAACTTC GATAGAATTT ATTGCGTCTC TTTACTGGAC GATGGTCTTG TTCAATCAAA    1560
TTATTCAGGT ATTTAATGGT ACGATGTTCT GTCCCTTGAT AAAAGCCGTA TTCTTTTAGT    1620
TTCTTAAAGG CACTTGTAAT AGAGGGGGCT TTATCTGTGA cTACAACCTT CGGTTCATCA    1680
AACTGCTTCA CTAACCGCTT AAGAAAAGCA TAGGCTGCTT GTGTGnCCGT TTTTT         1735
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(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

AAGATTTAAA AGAGTCTGTC AACAGTTTAG AAGATAAGTT TTTAACAGTG GATGAATTAC 60
GAGCTTTTTT AAACTATGGG ATAGTTTATG AAGAGTTACC CATGTCTGTT CTTTTTCATG 120
TTTTGTTTTA TACTGGGTGT CGTGTGAGTG AAGCGCTTGC TTTACAGCCT CAAGaTATAG 180
ATTTTGAACG AAATGAAATT TTGTTTTATA AACAGACAGC AGTAAAAGGA AAAAGTAAAG 240
ATTTTCGAAT AGAAACTACA AAAACTGTTA GTTCTGCAAG AAGAGTACCC GTCACACCAT 300
TAGTAATGGA GAAATTACAA GAATTAATTG ATGTATTAAA TAAAACAAAA AGAAATAGTA 360
ATTTTGTTGT AGATGAAACT TATTTATTTG TTTATCTCGA TCCTGGAAAg CGTGGAGTTC 420
CTTATCGTCG TGAATATGTA AACGATCATG TTAAACGTTG TGTAGAGCGA TGTGGAATTA 480
ACAAAGATTT TCACACCCAT TTGGCTCGTC ATACTATGGC TAGTTTAGTG GCAGAgtAtT 540
GCmGTkGGGA TGkTTwAAAG GATCGtTTAG GTCATACnGA CAGTACAACC TCAAAAATAT 600
ATCGCCATTT AACATCAACT GAAAAGTTAA AGCCTCTGAC TGCTTTTAAT nCTTTAGAAG 660
GTTAAAAAGA TGGTGAAAGT ACTGGTATTA CAGGATTCTT GAAAAACATT TTTTTAATAG 720
GTTAGTCAAA GTGTAGTCAG AGGC 744

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

TGAAGAAGTT ATATTGGTAG TTTCnCTCTC nGAAAaAAAG TTArGCAAAa CAAtGGATaA 60
aGAGTATCmA GaATGCTAAT CCtTATTAGT TAAAGTTCTA TCTGGAAAAm GCaAAAGTAT 120
TTGAGACACA ACACGCAGCC TATAGAGATT CAAGTGATCT GTGTAAAGAA TTAAAATAAA 180
AAACGAACGT TCATGTTGAA ATTAGAAATT AAATGTTTTA TCATACTAAT AGTATAAATT 240
ATCTGTAATG GATAATTATT TTTTATAGAT TGAATAAAAT GTTCGTTCAT TTTATTGTTT 300
TGTTACTTAA ATAGTTTTGG AATTTTAAGG AGGAGAAAAA ATGTTTTTTA CTGGTAAAGA 360
AAGGAATTTG AAATTTGCTA TTAAGAAGAA ACACGGTGGC GGTGGTGCAG CATCAGTAAT 420
TATCGGATGT ATTATTTTCG GAAGTATTGC GTTTGGTGGG ACAACATTAn CTTACGCTGA 480
TGAAGTGCAT AATAGTATAA ATCAGGATAT ACAAGATTCT GGTAGTACAA TTATTGGAGA 540
AAATGATTCT TCTACCAAAT CAGCTGAGTA TAAAATGATT CATGAAATTG ATGGAACTAA 600
AATTAGTAAC GGTGAAAaTA GTnAaGAAaC AaCTACAAGT TCAGGAACTA TACTGGCTGA 660
AGAAGCAATA GAAAGTTCAA ATCAAAAAAA TTCAAAGACA AGTGAAGTCG AACAGGATCT 720
TCATAAAGAT GTATCAGGAT CTGAATCAGT AAAACAAGTA GAAACTTCTG ATTCTATAAA 780

AAAATCTGAA GAATCAGCTG TTAAAACATT AAATCTGGAT GATTCACAAG AGAATACTAA 840

TTCAATAACT ACCAAGGCAG AAAATGATGC GCTATCTACA GTTAATGATG AAAAAGTATT 900

AAATGAAAGT GATAGTATTA TCAAATCAAT TCCTTCGGAA ACAGAGAATG TCGATAATAA 960

TAGTAAAAGT GATAATAGGG ACTTAGTAGA AAACTCAGTG GAAACTACTA AGGAAATAAT 1020

GAAAGAGGCT GATAAAACTG AAATAGCTAA AAGGAATGAC AATATCTCTG TATTGAATGC 1080

TGGAACTGAA TCATTTAATG ATAGTGATAA AATAAGAAGA TCTAAAAGAG ATAATGAATC 1140

TCCTGTTCCA AGTTTGAGTA TTCAAATGCC AGTCACAAAA GAGATTTACG AAAATGATAG 1200

TACTATTAAA GGAAAGTCTG AACCAGGAGT AACGATAAAA ATTTATAAAA ATGGTATTGA 1260

ACTGGGGTCT ATTAAAGCAG ACGATGATGG AAATTTTGAA TATCCTCTAG AATCACAAGC 1320

TATCAAAAGT GATAACTACT CTTTCGTTGC GGAAAAAGAT GGAGCGAAAA GTATAGAGAG 1380

CTCTGTAAAT GTAGTAGAAA ATAAAGAAAT AGTAGGTAAT CAACGAGATG CGTATACTCC 1440

ATATGGGTTT GGTATATATA ATCGAGGTTT AGTTACTACT GATGATGGAA AGAAACATTA 1500

TACAGTTGAT ATGGAGGGGA ATTTrGCATC TGAAGCGTAC TTTGATCTTG CAGGCGGAAC 1560

AATGTACTAT TCAATTGATG AAAAATTTGC ACCATATGTT GAAAAAATAG TTCTAGATGG 1620

TAAAACAATT ATTTCTAAAA ATCCGTATGA ATTGCCCAAT AAAACCAATA TTTGGTCTTC 1680

TGGTATTCTT AGTACAGATA AAAGAGGAGG ATTGGTTCGT GCTGCTTTAG TGGGTCGTAC 1740

TAACGGAACA ATAGATATTT ATTTTAAAGA TGATACTCCT CAAGAAGTTC TCAATAGTGA 1800

AATACCTTTC CAAGTTTGGG CTAGATTTAA AGAGAAAAAA GAGGGAGTAA AAAATGATCT 1860

AATTTCTGAT TTTGATCTAA ATATTTTACT TCAAAACAAT AAATTAATAT TAAGTAAAGA 1920

TACCTTTTTC AAAGATGAAG ATATTGTCAA TAATAATGGT CCTAAAATTA GTTCTAATTT 1980

TAACTATACC AATAATACTA TTGATATTAA TTATGGAGTA AATACTGGTA ATTATGGCTT 2040

AACGATAGGG AAACGTAGTC CTTATAACTT GCATATTAAT ACAGGGAAAG AATTAAGTGA 2100

TTTAGTTGAT ACGATAAAGA TTGACAATAA AAATTATGAG TTCGAAAAAC TTCCTGATGG 2160

TTCGTTAGTG ATTAAAGATA TATACAAAAA GGGAATTTTA GGTGGAGCAT TACTTAACCG 2220

CCAAGAGATT ACAATCAGTT TAGGATTAAT AGCGAAAAAA AATCTGGGCG ATCTCATTGA 2280

TTTCAAACAA GAATTATTAA AACTTGATGT ATCTATTAGA GATAATACAA CCTTTAAGCT 2340

AGTAAAAGGA GAAGCTACAG AAGCTATCCG TAAAATAGAT TCCTCATTCG ATACATTTAA 2400

ACAGGAATTA ACGAAATGGA TTGAAAAAAG AGATAGTAAT CCACAGGAAC CTATAACTAT 2460

TAATTCTGGA GACAATACTT CTATAGTGGA TCCTAAAGAG ATGGTTGAAT TTGCAGTAAA 2520

AAATCCAACC ACAGAAAATA TTAATAAAGC ACGTAGTTTG GTTTCTAAAA TGTGGCTTTG 2580

GGACAAAAAC AAATATAATC CAGTTCTTAA TGCTGCTGAA GAAGTAAACA GATATCTTTC 2640

AACTACGTTA AATGGTTCAT CAAATGATGA TGGCTTGATA TTAAATAATA CTCATGCGGC 2700

AACTTTCGTT AAATTAATTG ATACGGATAA AGATGGGATA CTTGATAGAT ACGAAGCAAA 2760

CATGGGAATT GGAACCAACT ACACAAATGC TGATTCTGAT GGTGATGGAA AAAGTGACGG 2820

ATTTGAAATT TTTAATGATA CTGATCCTTT GGTGAGTCCG TACGATTGGT TTGATAAAAA 2880

TGGAGAAAAA ATAAAAATAG TAACAACCGA TACTGATACG ATAAGTGGAA GAATAGGAAA 2940

TAACAACTAT GATACTGAAA ATGTCTACCC TAGAACTGTT CAATTAATAA AGGTTACTGA 3000

TAACGGAGAA AATCTGATTT CTGAAATTAG TTCTTCTGAA GATAGAAAAG GGACTTTTGA 3060

ATTTACTGGA TTGAGTGGTA AATTAAGCAA GGGAGATAGA CTCGTTGTTA AAATTATTAC 3120

TAATGAAGTA CAAAGAGAAA TTGATCGACA AAGAAATGTT GTTCAAGTTG GTTATGATAA 3180

TCCAGAGGTA TCTGAAGAAG TAATTGTTCA GGGCGCACAA GTAACAGTCT CTTTTGACTT 3240

TAATTATAAT CAAACTGATC CTGACTTTGA CCGTCAACCA GTTACTCAAG TAGTAGAATT 3300

AGAAAAAGGT TCAAGGCTTT TAAATAGTTA TTTTACTCCA GAACGAAAAG GCTATAAATT 3360

TATTGGATGG AATACTGATA AACTTGGAGT AGGACAAACT GTCAATGATG GTTCTAGTTT 3420

TAATGAAGAT ATAACGGTAT TTGCTCAATG GGAAAAAGAA CCTAACCTAG CTGGAGAAGT 3480

ACATGCTCCA CAAGGTCCTA TTGAAGAAGG TAAAAGTATT GTTCTAAATA ATGTAGTACA 3540

GTCCAATAAA TCAGGGTCTG TAATTGTAAC TGGAGAACTT CCAAAAGGGC TCTTTGGGTT 3600

ATCTATAAAT GAAACAGGTA ATCTAATTGG TACTCCACTT ATCAATGACT GGATTGATGG 3660

AGAAAATAGT CGGGAAGTAA AGATTCCAGT TACAATTAGT AATGGTGACG AAAAGGTTAT 3720

GGTGGAAGTT CCATTAACGA TCCTGCATGA TACTCGAGCG GCAGACGCAG TAAAAGCAGC 3780

AGAAGACGCA GGCAAAGCTG GAGCAGATAA GAAAGCCGAA GTGGAAACCG ACGGTTTAGT 3840

GACTCCAGAG GAAAAAGCGG CAGTGGATGG CTTGAATGAC ACGACTACCG CGAAGAAAGA 3900

AGACGCAAGC AAGTTAGTGG ATGCCTTGCC AGAAGGACCA GTAAAAGATA GCTTGAAAGA 3960

TCGCTTAGAT AAAGTGACAA CCTCTGAAGT AACAGTGAAT GATGCAGATA GCAATGGCAA 4020

AGCGGACGAT GTAGATTTAG CTGAAAAAGC AGCGGCAGAC GCAGTAAAAG CAGCAGAAGA 4080

CGCAGGyAAA GCTGGAGCAG ATAAGAAAGC CGAAGTGGAA ACCGACGGTT TAGTGACTCC 4140

AGAGGAAAAA GCGGCAGTGG ATGGCTTGAA TGACACGACT ACCGCGAAGA AAGAAGACGC 4200

AAGCAAGTTA GTGGATGCCT TGCCAGAAGG ACCAGTAAAA GATAGCTTGA AAGATCGCTT 4260

AGATAAAGTG ACAACCTCTG AAGTAACAGT GAATGATGCA GATAGCAATG GCAAAGCGGA 4320

CGATGTAGAT TTAGCTGAAA AAGCAGCGGC AGACGCAGTA AAAGCAGCAG AAGACGCAGG 4380

CAAAGCTGGA GCAGATAAGA AAGCCGAAGT GGAAACCGAC GGTTTAGTGA CTCCAGAGGA 4440

AAAAGCGGCA GTGGATGGCT TGAATGACAC GACTACCGCG AAGAAAGAAG ACGCAAGCAA 4500

GTTAGTGGAT GCCTTGCCAG AAGGACCAGT AAAAGATAGC TTGAAAGATC GCTTAGATAA 4560

AGTGACAACC TCTGAAGTAA CAGTGAATGA TGCAGATAGC AATGGCAAAG CGGACGATGT 4620

AGATTTAGCT GAAAAAGCAG CGGCAGACGC AGTAAAAGCA GCAGAAGACG CAGGTAAAGC 4680

TGGAGCAGAT AAGAAAGCCG AAGTGGAAAC CGACGGTTTA GTGACTCCAG AGGAAAAAGC 4740

GGCAGTGGAT GGCTTGTTAG AAATAAAACA GTCTTCATTT ATGCCGTTTG AAAATTTATT 4800

TTCGACTACA AATGATTACT CACAGTTTCC TAAAACTGGT GAAAAATCTG ATTCTATTTT 4860

AACCATTTAT GGAGGTTTAT TATTCTTAAG TAGTATAGGA TTATTAGGAA TAAAAAAAAG 4920

AAAAAATAAT ACGAATTAAG TTTGTTTGTA TTCTTCTTTA AGAAAGGATA GGTGTATAAA 4980

TTTTATCAAT AAAAAGCTGA CTATTTGTCA AATAGAGTTG ATAGAATGAT AATAAAAGAT 5040

CATCTAAGGT AGGATTTCTC TTTTCTACTT TAGaTGACTT TTTGTTTAAA TATCAGATAA 5100

ATTTTGATTG GACCTGTAGT TGAATATAGA TCTGTCGTAG TTACAGAAGG TAAATCGCAT 5160

ACTTTTCAAT TCTAGAGGGG AAGTCTTGTT GAGTATTAGC TATTAAGCAT CATAGCCCAG 5220

TTTTGAATTG CCTAACCACT TCGCTTGTAA TTCTTTCATG CGTAAACAAA GTAGTTTTAG 5280

GAGTACATTC TCATTAGTTA AGTTGAGTAG CATTATCTAA TGCAAAAAGG TTTGGCTTTT 5340

AGCTCATAAT AATCTTTACT AAGTCTCCTC CTTTCTTCGA GTATTATTTC ATTTGTGTAT 5400

AAATTGCATC TTTTTCTTCT TCTAGTTTCA TGATTAACAA CTAAAAATTT TTTTAGAAGG 5460

ACACAAGATA ATACATTTAT GCTGTAATAG ATAAAGAGGA TAATTATGTT TAATCAAAAG 5520

GAAGAGAAGC AGTTCAAATA TGCAATCAAA AAGAAAAAGG GGGCGGTAGA GCATTTTTTT 5580

GTATTATCGG AGTAGTATTG TAAGAAAACT AAAGATTAAA AATAGCAAAC GGArATTATT 5640

TCCAkTTtCT TATTTTTGCA AAAAATGAAT GTTCATGtGT ATGAAAGTAA CCAATAAATT 5700

TATCTTTTCy CgAAGGAAGT TTATTTTTAA TAATTTGAGA GGGTGATTAT ATTGTGTTTT 5760

GAAAATAAAG GGTATTTTTT TGAAATCTCA GaCATTGCTG AATTTGTTAA AGTAGAAAGA 5820

AGGAAGCAAC GCGGCTCAGC TACATTAAAT ACTTATGACT ATATTTTGAT TAATATTGTA 5880

AAACAATTGT GTAAGCAGCA AAAAAAATTG ATTTACTTAA TAAACTCAAA GAATTTCAAG 5940

ACTATATTAA GCAATTTAAT TGAAGTGGAT GCCAAAATTT CTGATTATCT TTTTTTCTTG 6000

ATTAATTGTA GATTTGAAAC TGATAAAGAA GTAATAGAGT GTGTAGAAAG TGTAGAAAAA 6060

GATGCTCTTA GAGACTACTA TTGTGGGTTA AATTTCAGCG ATAACATAAA TAACTATAAA 6120

TTAATAGTTC ATACAACTAA ATATTAATTT TTTTTAGAAC CATGTTAAAG GACTATGTGA 6180

TATTTACAAT TCCATCTCGT ATGTGCTAAC CTTTTATCGT TAAAGCTATT TCGTTTATGT 6240

GTAGAAACGT GAGTTTTTGT TTCGTACGTT ACACGAACGA AAATGATTAA AGTCAATAAT 6300

GAAAATGGGA CGAGAATGGG ACAATACTCA GAAAAAAATC TGATTATTGC CCCATTTTTT 6360

TGATTTCAAA GTACACAAAA AGCACTCATT CCTGTAAGAT TAAAGTGACG AAACCCAATC 6420

AGAAAGGAAG CGAGTGCTTT ATTTTTAAAA TTATACCATC AATCAAACAA CTTTACCATT 6480

AGATATGGAA CAATATATTC CTGAAACAGA TGTCGCTTTT GCGGTCAATG ATTTAGTCGA 6540

AGCCATGCCA CAAACACTTT TTCTTAAATT AGAAGAACAA CTAGGATGAC TGGCCTACCA 6600

CCCTAAAATA ATGTTAAAAA TTATTCTATG TGCTTACACG CAGCGTGTTT TTTCAGATCG 6660

TAAAATTGGA TTTCTATTAG ATGACAGCTA TCGTATGCGT TGGCTAGCAA ACCACGAACA 6720

AGTCAGTTAC CGGACCATCA ATCGCTTCCA AAGTCAGGAA ACAACTGCTC ACCTTTTAGC 6780

AGAAGCCTTT GTCTTATTCC GCTGTCAATT AATCACCAAT CAGGTAATTG ACAATGAAGC 6840

GCTATATATT GATGGCACAA AAATCGAAGC GGATGCCAAT AAATTCAGTT TTGTCTGGCG 6900

CAAAGCAACA AATCAGTATG AAGCTTCTTT GGATAAACAA TCAAACGAAT TCTATCAAAC 6960

CCTTTATAAA GAAGAAATCT TGCCTTCTTT AAAAGAAGAA AACCAAAGTG ATAGATTGAC 7020

AAGCAACTAA TTGGAAGAAA TCGTGCATCA CTTGGAGACA GAATTAGTGG CGACAGAAGA 7080

ACAACTACAA AATGAGAAAA GGATAGA 7107

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

TGAATGGATT TGGCAATATG CTAAAAAAAA TAAGAATAAG TTACTGCTAG CTGTTATTTT 60

TGTCGTTATT AACGCTATTT TAATTGTTAT TATTCCATTG TTATCTGGCA GAATTGTAGA 120

CCAAGTAATC AATCAGGGGA AAACTGAAGA GCTTGTCCCA ATTCTTGGGA TTATGATTGG 180

AGTGACCGTT ATTCGGACAG TTGTTCGTTA TAGTTATCAA GTCTTGTTTG AATCGGTTGG 240

ACAATCTGCG TTATTTGACT TAAGAAAAGA TATGTATGTC AAACTTCAAG AATTAGATTT 300

TGATTTCTTT AATCATACAC GTGTTGGCGA CATTATGGCG CGAATGACAG GGGATACAGA 360

CGCTATCCGC CATTTTGTwT CTTGGGTCAC TTATAACCTC TTAGAATGTA TTTnATGGkT 420

CATCGCAGCC GTGATTGTGA TGGGGACGAT CAATTGGCAA TTGATGCTAG CATtAATTTT 480

AATTACACCT TTGATTTTTC TGTTAACACA AAAAATGTCG AAGGAATCGC ATCCGGTATT 540

TTTTGAGATC CGGGAAAGTT TTTCTCGGCT AAATTCGATG GTCGAAGAAA ATATTGGTGG 600

AAATCGGGTG GTTAAAGCTT TTTCTCAAGA ACCTTATGAA ATTGAAAAGT TTAACAAGCA 660

CAATGAAGAC TATAAAAAAT GGAATATGGC TTCTGCAGAT GTCTCAAAAA AATATTTACC 720

GTGGTTAGAC GGTTTTGCAG GTAGTTTAAA TGTTATTGCC TTAGTTCTTG GTGGCCTCTT 780

TGTAATTCAA GGTCGGATGA CAATTGGTGA TTTAGTGGCC TTTAACGGTT TTCTCTGGAT 840

GTTGAACATG CCGATGCGAA TGAGTGGCTG GTTGATCAAT GATGTGCAAC GCTTTACGGC 900

ATCGTCCATT AAAATTCGTC AGTTATTAGC AACGAAACCG AAGATTCCCA TTGCTCGGGA 960

AAAAGAAGCA GAACCAATCC AAGGCTATGT GACGTTTGAT CACGTGTCCT TTCATTTTTC 1020

AGATGATCCA GAAACCCCCA TTTTATCGGA TGTTTCATTT TCAGCAAAAC CTGGTGAAAC 1080

AATTGGTATT TTAGGGGAAA CTGGTTCAGG CAAAACCACT TTAGTTAACT TAATCGCTCG 1140

GTTCTATGAT CCAACAAAAG GCACTGTTTA TATTGATGGA AAAGATGCTA AAAGCTATTC 1200

TGTTCGTAAA TTGCGAGAAA ATATCTCCAT GGTTATGCAA GATGTCTTTC TTTTTTCCAA 1260

TACAATAGAA GATAACATTG CTTTTGGTAA CACATTGGCT AACTTGGAAC AAGTGCAAAT 1320

GATGGCTGAA ATTGCTGATG CtCATAGCTT TATTTCCAGA ATGCCCGAAG GTTATGCAAC 1380

AATTGTTGGT GAACGCGGCG TTGGCCTATC TGGTGGCCAA AAACAGCGGA TTTCACTGGC 1440

CCGTGCCTTA ACCAAAGATC CAGCTATTTT AATTTTAGAT GACACAACTT CCGCTGTTGA 1500

TATGGAAACA GAATCAAAAA TTCAAAAAGA ACT 1533

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 895 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

TTCTAGGCGG CGTACCCTTT TCCGGCTAAA AACGGTCCGG AAACTCTTGG AAACCCCTTG 60

GTTTTAACTT GGGTCGGAAA TACTTGGGTC nTAGTTTCCT CCAAACCGTC AATCCCCTGG 120

TTCAAAATTG GATTTAAATA ACACATCCAT ACGGAGTTTT TTCTTCTTTT TGCCCAATAA 180

GGAATGAACT CTTTTTGGgA ACGCAACGAC CTTCGTTAAG GTTTCTTCTA ACAAGCCGAA 240

ATCTTGTGCA GCGCGTGCTT TTAGCCAATC TGTATGTGCT TGGTTTAATA CTTTAACATA 300

TTCTTGCATA CGTTCAGCTG GAACATTTTT ATTCAAAGCA TATTCTTCTT TTACTTTTTC 360

AAAAACCAGT TTCCCTAATT CAGATAATTC TTCAGGGCGT GTCTCAAAAT AGGCCAATGC 420

TTCTTGAATA ACTGGGCCAA TACTTCGTTC AAAATATAAT CCGGTTAAAT ACCCTTCTAC 480

TTCTCCTCGA AAAGGACTAC TTTTTTCTGG CATCCCAGTT GATGAATCCC AGTCTAATAA 540

TGTCAAGGCA TTTTTTAGTA ATTGAATTTC TTTCACTTCT TGTAAAAATA CAGCTTCCTT 600

CATTTTTTTA CACCAGCTTT CTTAGTCTTC CCGTGGTTTT CTTGGTGGAC GTGTTCCCCA 660

GTATTGGAAT AAATCTGTTC GTAAGGCTCC GTTGTAAAGC TTcCGTTTTT TAGTAGCTTk 720

GGCACCATAA TATTCTTCAA AAGCAAGATC ACTCGTCAGT ATATACTTGc TCCAAGTAGT 780

TAACGGACGG AAAACATGGn CCATTCTTTA TACAACGGGG AACACTTCCT CTTCTCCTAA 840

ACGCTCACCA TAAGCGGGTA GCTACCATAC ACCATATCCT CTCGGTGGAA AACTT 895

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

TATGAATTTT GnATAAAAAT GGTGCCATGT ACAAGAATGC TTGGACAAAC AGCGATAAAT 60

ATTCATATTA TAGTACATCA GATGGCTCAT TAGCGGTTGG ACATCAACAA ATTGGTGAAA 120

ATAAATATAT TTTCGATAAA AATGGTGCAC TATATAAAAA TATGTGGGTA GATTTAGACG 180

GAAATCGTTA CTACAGTAAA GAAGATGGTG CTCTCGCTAT TGGAGAACAA ATCATTGATG 240

GAATCACTTA CATGTTTGAT GAAAGTGGGA AACTAGTTAA TAATTAATTT TTGAGAATTA 300

GAAAATTTAT TTTAGAATAG AGATGTAAAT CTGTTGCAAA GTTTAAGAAG ATATTCGGAT 360

TGAGATAGAT AACACAGCrA TrAAAACATA CCAAGATTaT GAATTAATCT CGGTATGTTT 420

TTATTTTTTA AAACCAAAAC AAACGTTTTT GTGTGGTATA AACCATATCA ATACTTCGTT 480

TGCCTAAAAT CTCGCCAtCT GCGTGAATGG TTTGTGGAAT CGTCGAAACA AT 532

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

AGTATCCAGT TTAATGCTTT GTCAATCGAA ATACAAGAAA GTGGnACAGC CGTTTGACGA 60

ATGTCCCACT TTTCTGTTTT ACTATTAACA GGTTTGTCTC AATGTTTGTG TAAAATGCTT 120

GGATGGTGTT ATAAAAGATT CCTGCGAACA TAAAGATTAA CCAACTAAAC CGCCAtCCCC 180

TAAAACAAAA CTmATAAATA GATAGAGTgC CACAACTAAG GGCCAATAAA TGGATGCAAT 240

AATTGCACCG ACAGGATTTC CCACAGAACC TTCCTCTGTT TTTGTTTGCT TAGGGGCATA 300

CTCAGGATGA CCAACATGTT CTGAATAAAA ATAAGTTTCA TTCAACAATT TATTAAAACT 360

TCCTTTAATT ACTCCACCAA ATATAAACAA GAAGACACCA ACCGATACTA AAAAGAAGAG 420

CCAACTAATC CCCATCGTTC CATTATAATA TTGTCCGCCC ATCATTTGAT GCATGGAACG 480

GCGCATCATC AGATGAAGGC CACTACTAAA GACAACAACT GGGATTAAAC CCAAAATACA 540

AAAAACTACG CCCGCTGCCA TACAAAAAAT AAATGATCGT TGAAAACTTT GTTCTCTTTG 600

TGCAACTTCT TTTTTTAACT TAATCGGAAT CAATCGTTGC CCCAGCTGTT TGTCCATTGC 660

AACAAACCGA TTACCAGCAA CAATAAATAA TGGAACGCCG ATTGCCACAC CTATGAAAAG 720

ACAAACTAAA CCAAGACCGT TAGAAAGAAC ACCACGCATA CCAACCAGCA AGCCAACACC 780

CACCATGATT GCAACAACAC CAAGACCAAT TTGAATCGCA CCTTTACGTT GGACAGCTAA 840

ATAGTCAAGT CCTTCCTCCA CTGrAATTTC TGGCAAACCG TTCATTGAAT CGTTTGGTTC 900

ATCCACTTGT TTATTTCTA AATTCAATTC TTCCATTAAT TCATCAATAG TACCAAATTC 960

AGArATAATT GTACCArTTG ckTCATTTtC CGATTTTCCT TGGCTGAGCA AGTCTTCATA 1020

ACGATCCTCA GCATTTGCTA ATrAGTCCGm CTTTAATTGT TTTGTTTCAG ATGTTTCAAC 1080

AACGCCTGAA AATAAGCTAT CAATAAATTC TTCTATAATT TTCATTTTC 1129

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

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AACCCCCGAT AATTACTCTT TACTCGCAAT TAAGCGAAAA ATTGATCGTT CATTTTTACC      60

TGATCATATT TCTTCCGTCT TATTAGATAC AGAGACGTTT GGTAGCAAGT TAGCCTTATT     120

ATTGCTTAAC AAACGCAAAG AAAAAACAGC CTTGATTAAT GAGGCTGAAA AATTGGTGCT     180

AGATCACAAA AATACATTAG GCATGTCTAG TGTTAATCCA CATAGCAAAA TGaTTGTAGT     240

GGGTAGTTTA AACGTTGATA ATTAtCTGTA TTCAACAAAT TTACCACATa ACGGCaAAAC     300

AAATTTTTTG tCTAGCTATG CTAAATTCCC CGGCGGAAAA GGATTAAATC AAGCTGTTGG     360

CTTAACCAAA CTGGGCCATC AGGCCACCTT AATTGGTTGT TTAGGCTCAG ACACAGATGC     420

GAATTACTTA tATAAAGAAT TAGAAAAATA CCACGTTACG ACAGATGGTA TCACACGTAT     480

TCAAGATACT GAGACTGGTC AAGCTTATAT TTATGTTGAG ACAAGCGGCG ACTCCATGAT     540

TTCAATCTTA CCTGGTGCAA ACACAGCGCT TACGCCTAAA AAAATCGCAC AGCAAAAACA     600

CCTATTTATG GATGCCAGTT TTTGTCTCAT TCAAACAGAA ATTCCTTTGT CTGCTGTAGA     660

GAAAGCTTGT GAAATCGCCC AACATTCAGG GGTACCGATT ATTTTAAAAC CAGCTGCTAT     720

TCATCATATT CCAGTGAATA TACTAGAAAA GGTTGATTTT TTCATTCCCA ATGAAGATGA     780

ATTATTGGAA CTTCAACCAG ATACTGGTAC ATTAGAAGAG AAAGCGGCGT ACTTCTTAGA     840

AATGGGCGTA AAAAATGTCA TTGTTACTTT AGGAAAAAAA GGCGTGTTAT TAAAAACACC     900

CCAAGTGTGC CACTATTTCC CTGCAACAGA AAATATAGCT GTGGATAGCA CTGGTGCCAG     960

TGACAGCTTT ATCAGCGCGC TCGCCTCCTA TCTTTCGAAA GgTTATCCGA CTGAAGCAGC    1020

CATTCAAATA GCAATTCAGG CTGCAGGATT TTCAGTTTCT AAAGAAGGGG TGATTGATTC    1080

TTTAGTTGAT CACGTCACTT TGGAAAATTA TTTGATAAAA AAAGAACCCG CTCTTTTTGC    1140

TCATCGTAAC ACCTGTATCG ACTGACACAG GnGTTTTCCT GCTGAATATC TTGTnATTTT    1200

CTCATnAACC AATGAGAATT GTGCTTTTTA TTACAATTTT ATTAGGCGAA CTATTATAAT    1260

AAAAGAGAAG TTATAACTAA GGG                                            1283
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(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

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TTTTCGGGAT TCCTAGAAAA GCTTGGACTG TAACTTTAAC TTGGTATTAA CGCGGGACTT      60
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CTTTTTATTC ACTGAAATCC ACGTCGTTTC AATTCTTGGG TTACCCTTCT ATAGCCATAA 120

TGTTGATGTT TTTTACGAAT CGCTTGAATT TCTTCTTCAA TGATTTGTGT TGAAGCTGTT 180

CTGTCGAGGC GTTTTTGCCA GTACATGTAA GTAGATTTTG GAAACCTTAG GGTTTCCAAA 240

ATATCTTTTA ATCGAAAGTG TCTTCGGAGA CTGTGAATGA TTCGTGCGAT TCGTTCATTT 300

TTTGTTCGTC CTCTAAACGC AGTCTCCTCA ATTCTTTTAA ATAGGCATTC TCAATTTTTA 360

ACATTCTATT TTCTTTTTCT ArTTTyTCTA CTTGAGATmG TTCACTTrtA rTGkTTkGGG 420

TTCATTTCGT TTCTTyTTAG ACATGGTAGG TGGACACCCT TTCTATTTAG AGAGTCCCTT 480

ACGCTAGACT TCCGATACGT TCTAAGCCAA TTCGCAATCA ATGATGGATT GTTCGTTTTT 540

AAAAGATTAG CAACTTCTTA ATAGGACAAC TTTATCGCAT CTAGCTTAAA TTGAACAGAA 600

TAATTCTTAC TTTTTTGACT ACGAAGTAGT CCTTTTTCAC CAAGTCTTTA TAGACATTAA 660

TCCATTTGTT TATTTGAGAA CAAATTTAAG TTTAAATTCA AAATTTTATT TTGCCATACA 720

AAAAAACTCA AAAGTTAGAT TTCTAGGTCT AACTTTGGGG GAGCACTACA GAACTGTAAT 780

TCTCTTAAGC GCATTTAATA TAGATTCAAT CTTTTGTAAA AATCCCTATA TTTTGTTTCT 840

TGAAAAATTT AATCATTTTA ATGAACTAGG GATGATCGAT TTCGAGAACA TAAAAAACAT 900

ATTAATACAG GATTGCTTTA TCCTTGATAC GTTTTAAGAG TACTCCGGTT TGTTGTATCT 960

TTTATTACTC CAAACGATGA TCCCGCAAAC GATAGCCCAC TCCAATCTCA GTTATCAAAT 1020

ATTCTGGTTT CAATGTATTA CTTTCGATCT TTTTACGAAT ATTAGACATA TTCACCCGCA 1080

ATGTCTGCGA GTCATTGCTG TAGGGGCCCC ATACTTTTGT CATCAAGGTT TGATACGCAA 1140

CTACCTTTCC CAACTGACGA AACATCAGCG CTAAAATTCG ATATTCGTTT TTTGTAAGAT 1200

GGATTTCTTG TCCCTTTTTA TAAACTAACT GTTTTTCGAA ATCAATTTTC AAGTCTTTGT 1260

TTTCCACGAC AGTTAGTGAT TCCGTTTGAA CGTTTTGATG GCGCAAAGCT GTACGAATCC 1320

TCGCAAGTAA TTCATTCGTT CCAAATGGTT TAGTTACATA ATCATCCGCA CCTAAATCCA 1380

ACGCTTTAAC TTTCTCCTCT TCATTATTTC TAGCAGAAAT AATGATGATG GGCAAATGCA 1440

TTCGCTTGCG AAGGATTTTT AACAAATCAA TCCCATCAAT GTCTGGTAAT CCTAAGTCTA 1500

ACAAAACTAA ATCAAACGAT GTTGTTTGAA AAGCAGTCAA TGCCTCCATT CCAGTACTAG 1560

CAATCGTTAA CTGATAGCGT TCCTGTCCCA AAACAACTTC CATAAAATCC GTAATATTTG 1620

GATCATCTTC AATCAATAAA ATGGATTGCT TCATAATTCT TCCCCTCACT TCAAATAAAT 1680

TCGAACCAAT GTTTTGCCCC TACCTATCGT CATTTCCATT TTACCATTGT GCGCATGGAC 1740

GATTGTTTTT ACAATACTCA ATCCGATTCC TAAACCATTT TTTGAGTCAA CCGGTACTTC 1800

ATTTGTGCCG GACAAGTTTG ATTGGATCTT TtGAAATTGT TTTAATGGAA TTTCGCCGTG 1860

ATTTTCAATT TCAAAAACTG TTTGTTCTTT TTCCTGATAG ACGTTTAGTT TGACTGGTAG 1920

ATCATTTTCT CCATGACGAA ACGCATTTTC TATCAGATTA AACAACGCTT GTTCAATCAA 1980

AATGGGGTCC GCTTGAATAA AAATGACCTC TTCTGGCAGG TGAATATCCA CTTGGCCGTC 2040

TGGATAGACC TTCCTCAAAT GCTTATAAAC AGCCTCGATG ACCTCTTCTA CTGGTTCAGC 2100

AGTTTTATTA ACCTTCATAG TATCCATGTT GATTCGCGTG ATGGATAAAA GATTTTCAAC 2160

CATCCGAATC AGCCATTGTG ACTCTTCTTG AATATCCTTT AATAATTTTC GCTGTGTCTC 2220

TTCTTTTAAA TCATTTCCAA TGCCTAATGT TTCAGCAATC CCTGAGATAA CAGTTAATGG 2280

TGTTCTCAGA TCATGAGATA CGGCTCGTAA TAAATTGCTG CGGACTTTTT CCCGTTCATT 2340

TTCTAACTCA ACTTGCTCTT TCTCATCTTT CAATTCTGTT TGTTCCAAGA TGACCGCAAT 2400

TTGAGTCAGC ACCAATTTTA AGTAATTGAG CTGATCATTT TCCAAATCAA GATCTGCATT 2460

TCGTTCAATG CCTAATACCG CCAACGTCTT CCTGCCTGCA GCAATCGGCA AATAGAATCC 2520

TTTAGCTCCA TTTAGTGTGT CTGTACCATT CCCAGCTTCT TTTTGGTTCT TTGCTGCCCA 2580

AAAGGCTACA GCTGCTTCGT CTTCATTATT TAATATTGAT TTTTTTTCGT TGATACAATG 2640

AACACTCTCT GTCTTCACTT GACGATCAAA AATAATCACT TCTCGTTCCA ATAATCTTGA 2700

TAAATAAGTG GCAGAAATAT CAAGAATTTG TTTTCGACTT TCCACTAAAA CATATCGTTT 2760

GTTCAATTCG TACAAAATTT CCATTTGGTG CTCTTTTTTC ATAGAAGTAT CTGCTTGTTT 2820

CTTTAATCGA ATCATTAAAT TACTGCTCAT CAGGGCAACA ACTAGCATGA GCAATAAAGT 2880

AAAAGGATAT CCCTGTTTAT ATACTGTCAG AGAATATAAT GGTTCGACAA AAAACCAGTT 2940

AAAAGACAAA ACACTTAAAA TAGAGGATAA TGAGCTCCAA AAATAACCGG ATGTCGTTCG 3000

AGCGACTAAT AATACGAATG AAATATAAAT AAGCATCAGA TTTTGATCGC CAACGTGGAT 3060

ATATTGCATC AATTCCGTCA CGACCGTCGC TAGAAAAACA CCACCAATTG CAATCACTAA 3120

ATCTTTTCCG CCACCCTCAA TGACTTTACG AGTCTTAAAA AATAAAGACC GCTTTTCTTC 3180

ATTGAAAGGA ATTAAATGAA GTTCCGTATC TTTCAATCGT TTTAACAAGC GATCATCAAA 3240

CGCTTCAATA AAGATTTTTT CATACCACGG CTGCCTTAGA TTTTTCCCCA TAATAATATC 3300

AGTAACACCC GTCATTTTTG CGAACTCGAC AATCGTCTCA AAACTATCAT CCTCTTCAAT 3360

ACTAATAACC TCCGCACCTA ATTTATCGGC TAAAGGAATG TTCGTTGGTG TATTTTCTTG 3420

CGTACGAACT TGAATCACTG TCCAATCGAC AACTAGACCT TGCGCTAAAC GTGCTGTCCA 3480

GCGAATACAT TTTTCGGTCA TTTTTGGAAA GGCATCGTTC ACCACCGTCA ATAATTTACT 3540

TTGTATCCCA ATTGTCTTTC CACTAATTCG ATTAATATGA TCCGACGCTC GCTGAATTGC 3600

TAATCCACGT AATTGGTCCA ATTTTTGTGG AATAAAAAAA TTTTTCAAGG CACGTTTCGC 3660

GTTTTCATTC GCATATATTT TTCCTTGTTC AAGTCGTTCG ATCAGCTCAT CGGGCTCCAC 3720

ATCAATCACT CTTATTGTCG CTTGCCGTAG AAAAGTGTCC GGCACCGTTT CCTTGACCTC 3780

AATTCCGGTA ACTTCTTCAA CGATATCATT CAAACTTTCG ATATGTTGAA CATTGACCGT 3840

AGTAAAAACA TCGATTCCTG CATTCAACAG TTCATCAATA TCCTGGTATC GTTTACGATT 3900

TCGAGAACCT TCCGCATTGG AATGAGCCAG TTCATCAATC AACACGATTT CGGGCTTCTG 3960

TTGAATGATT TGATCAATAT CCGGCTCTGT TAAAACCATT TGTTTATAAA AAATATTCTT 4020

AGGAGGAATT TGCGGTAATC CTTCTAATAA TCGATTGGTA TCTGGACGAT CATGAGGTTC 4080

GATATAGCCG ACAACAACAT GTTTTCCCAT CATCAATAAT TCATGAGCCT CTGTCAACAT 4140

ACCGTAGnTT TTCCCAACAC CAGCCGCAAA TCCAAAAAAT ATCCGCAATC GACCTCGGCG 4200

TCCATCGCCA GATTGCATTT CTTCTGTTGT CTGCATCAAC AGTTCTCCTC TCTTTGTATG 4260

CACAACAATT CCCTAACCAT TTTTGGTTAG AGAATTGTTC TATATTATAT TCCTAGTTTA 4320

TCTAATGCTA GGTTTAACTG CAAAACATTG ACATAAAATC GGTCTGAAAA CCAATCTTTT 4380

TGGCTATGTT TATCGATGAG TTTACGAATT GATTGTTGAG ACAAGCCACG TTCTTTAGAA 4440

ATTCGGGCAA CTTGAAAATG AGCTGCTGCC AAACTAATAT CCGGATCCAC ACCACTAGCA 4500

GATGCTGTCA CGAGATCATT CGGAACTTTT TTCTCTGCTG GATTTTTTTC CAATTCTGCA 4560

ACGGTGCGCT TCTCAACTAA TTGCTTTTGC TCCGCCGAAA CAGGTGATAG CTGACTAACT 4620

TCCTCACTAC GTCCTGAAAA ATATTTTGCC TGTTCAAAAG TTTGCCCAAT CAACTTTGAA 4680

CCAACAACTT GATTATTCAC TGAAACCTTA CTGCCGTTAG CCTGATCTGA AAAGAACAAT 4740

TGACCAATGC CAGTAACTGC AACGGTATAT AGCCCACCAA AAACGATCAG GCTAAAAATC 4800

AAAAAACGCA AACTGCCTAG AATACTTTTT TTCATTGTTT CTACTCCTTT ATAAAATGAT 4860

CAGCGAGAGA ATCAGATCTA TAATCTTGAT AAAAATAAAT GGTGCAATAA TTCCCCCAAG 4920

TCCATAAATC AGCAGATTAT GACTCAAAAT TTGACTGGCC GGTTTTTCTT GATACCTCAC 4980

ACCTTTTAAT GCTAGTGGAA TCAAGGCCAC GATAACGACT GCATTATAAA TGACAGCGGA 5040

TAGAATCGCA GTCAGTGGAC TACCTAATCC CATAATATTC AATCGATCCA GTTGCGGATA 5100

AATACTGTAA AATAGTACTG GAATCACCGC AAAATACTTA GCGATATCAT TTGCGATACT 5160

AAACGTAGTT AACGCGCCGC GAGTCATCAA CAATTGTTTC CCAATCTGTA CGACTTGCAG 5220

CAATTTTGTT GGACTGGAAT CCAAATCAAT CATGTTCCCC GCTTCCTTCG CGGCTTGTGT 5280

TCCTGTATTC ATCGCCATCG CAACGTCGGC TTGCGCTAAT GCTGGTGCAT CGTTTGTCCC 5340

ATCACCAGTC ATTGCAACTA AGTGACCCTT TTCTTGATAC TCGCGAATCA GATTCATTTT 5400

ATTTTCTGGG GTAGCTTCTG CCAAGAAATC ATCTACTCCA GCTTCCGCTG CTATCGCTGC 5460

CGCTGTTAAG GGGTTATCCC CAGTGATCAT GATGGTCTTG ATACCCATCT TACGCATATC 5520

AGCAAATTTT TCCTTTACAC CATTCTTAAC GATGTCTTTC AAATAGACGA CACCCATCAC 5580

ACGATTATTT TTTATAACTA CTAGAGGTGT TCCACCTGCT CGAGCGATTT TATCAACAAT 5640

CTTGTCACAT TCAGATGGAT AGTCCTCTCC TTTAGATTGT ACATATTTTT TCATGGTGTC 5700

TGCGGCACCT TTGCGAATCA CGTCACCGCG ATAATCAATT CCGCTCATGC GTGTTTTGGC 5760

ACTGAAATCG ATAAATTTAA CCTCTGATTG CTGGAATTCT CTTTCCCGCA AGTTGAAACG 5820

TTCTTTTGCT AAAATCACGA TACTTCGACC TTCTGCTGTC TCATCAGCTA AAGAAGATAA 5880

TTGCGCCGCA TCCGCTAACT GTTCTTCACT AACACCATGG ACTGGCAAAA AATCGCTTGC 5940

TCGTCGATTT CCCAATGTTA TGGTTCCTGT TTTGTCGAGT AAAAGAACAT CCACGTCACC 6000

AGCTGCTTCG ATCGCACGAC CACTCATGGC AATGACGTTT TCCTTCGTCA AGCGGCTCAT 6060

ACCTGCAATC CCGATCGAAG AGATTAAGGC CCCAATCGTC GTTGGCGCCA GACAGATTAG 6120

TAAAGCAATC ACAATAACCA GTGATAAAGC TTCTCCTTTA CCAGATAACT GACTGCTGAA 6180

ATCAGTAAAT GGGACTAAAG TAATTGATAC AGTTAAGAAA ATAATGGTCA AAGTAATCAA 6240

GAAAATCTGC AAACCAATCT CATTCGGAGT CTTTTTTCGT TGAGTTCCCT CTACCATGGC 6300

AATCATTTTA TCTAAGAAGG ATTGACCGTT TTCCGAGGTA ACACGAATCA CTAAATAATC 6360

GGAAACGACG GTTGTTCCGC CAGTAACCGC ACTGCGATCC CCACCAGATT CACGAATTAC 6420

TGGCGCTGAT TCGCCAGTAA TGGCACTTTC ATCTACTGAT GCAGCCCCCT 6470

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

CAATTAATTT GGAGATTTCA GCCATAGTAA TGCCTTTTTG AAATAATTGG ATAATGGTCG 60

TTTCTAATGA ATCATTGGTT CGCTTATATG CTGGTAGTGT TTGTTGAGAA AGTTCGCCAT 120

TCCGATCTCT AGGAATAGTT AAATTCAACT CGCCATATTC TGTTTTAAAT GTACGTGAAT 180

AATTCCCGTT ACGGGAATTT CCTGAATTGA ATCCATtTCA ATCATATTTT TCGTAATCTA 240

AAAAAGCAGT TaGCTCTGCT TGTAGAAGTG AATTAATCGC TCGCTCTAAA TGATCCTGAA 300

ATAATTCATC TAAATCCCCT TTATTGAGTA GTGTTTGCAT AATTTCTATA GTAAATTTAG 360

TCATGAGAAA GTCCTCCTAT AAAATTTCTG TGTGGTAACT TTAATTTTAC AGAATGGACT 420

TTTTTTTCTA CCCTAAATTT CTATTTACAC AAAATATTTT ACGCTATCTT TTATTTTAAA 480

ATATGGGATA TTATGATAAA CTAACTATGG ATGATATTTG AAAAAACCAT ACTGTATGTT 540

TGATTTAATT TTTATTTTTA AGCTCATATC GTAAGAATGG GACTTGTAGT CTCACTTCTT 600

TATGGAGGTG ATAATTATGA ACGTTGGTTT TATTGGAGCC GGCAAGGTAG GTTGTTCATT 660

CGGGAAGTAT TTCCAGGAAC ATAAAATACA AGTAACAGGA TTTTATAGTA AAAGCGAAGA 720

CTCGTCATTA GCAGCTTCGA ATTTTACATC TAGTAAACAA TATTTAAACT TAAGAGAATT 780

AGTAGATGAA AATGATACTA TTTTCATTAC GACTCCTGAT GGTCAAATTC AGGAGGTATG 840

GCAAGAAATT AAAAATTATC AAATCAAAAA CAAATTAATC TGCCATTGCA GTGGTGCAAT 900

ATCTTCAGAT ATCTTTTCAA ATATACAGGA CTATGGTGCT TATGGCTATT CTGTCCATCC 960

TATGTTTTCA ATATCAGATA AATATAATTC ATACAAAAAA TTAAAAAAAT CTTTTATAAC 1020

AATTGAAGGC GATGAAAAAT ATGCAAAGTT TTTATGTGAT TTCTTCAAAA AGTTAGGTAA 1080

TAGTACTGTA ATTGTATCTA AGGAGAATAA ATCTCTTTAT CATGCCGCAT CAGTAGTATC 1140

TAGTAACCTT GTGCTAGGAC TTATTAATAC AAGCGTTACA TATCTAATTC AATGTGGATT 1200

TACTGAAAAA ATGGCAATTG AAGCTTTATA TCCATTAATT GAATTTAATA TTAGAAATAT 1260

AAAAGAAAAA GGAATTATAG AAAGTTTGAC AGGACCAGTT GAACGTTGTG ATATTTCAAC 1320

AATTAAAGGT CACTGTGAAG TTTTATCAGA TGAAGACAGA GCTTTATATA TGCTATTATC 1380

AAAAAATGTA TTAGAGATAG CTATGTkrAA AAATATTAAT AGAGATTATA GTGAATTAGA 1440

AAAGTATTTA GGAGAGAGTT AGGAGAGAGA TAGATGAAAA ATACAGCAGT TACATTTAAA 1500

GAATCTAAAT TAAGAAATGA AAAATTAACA ATGCTTACAG CTTATGACTA TTCAACAGCA 1560

AAAATAATTG ATGAAGCTGG GaTAAATGGA ATATTAGTAG GaGATTCTCT TGGTATGGTA 1620

TGTCCAGGAC ATGAAGGATA nCACTTTCAG TAACCATGGG AAGCCTGATT CCACCATACT 1680

AGAGC 1685

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

GGGAAAAtAA akGyCCCCTT AtcCCTTTkG GTAtTCCsCc AgtGATAAAC yCCtGTTAAG 60

aTAGTGGCtA TATAAaAAAG GcmGrTaCTT AAGaAGaGTA TATTCaTGaT TyCCCyCCTA 120

GTTTAAAtGa AAGTCaTGAA TGaTTGTACC aAGATTTTTT AGAGAAGTTA AGATTGAATA 180

GAAAAGTAAA TACGATAAAA TTTTTATAGA CTGTTACGTT GAAATGTTCT TCAGAGACTA 240

TTTCTTCCAA TACCGCCTAC TAGATAGGTG GTTTTAATCA TTATTTTCGG AGGTTGTGTT 300

TTGGCCAAAA AGTAAAGATT TAATGGATGT AGGTTCATTT GTGAGCCCAT CTAGATAGAA 360

CGTTTCAGGA CTTTAGTGAG GCATGAAACG ATTCGATGCA AGCATTATCT GAAGGtGTCC 420

CTTTTCGGGA CCTACTCATG GTAATGCCTT TTTTTATTTG GTTCTGGTAG TCAAAAGAAG 480

TATAAACAGA GCCCTGATCA CTATGCAATA GACAATCCGT TGTTTGAGGC AATTGATCAA 540

ATGTATCCAG AACAAAATCC GTATCTTGCT TATCACCGAT GGTATAGGCG ATAAATTCAC 600

CATTGTATAA ATCCATAATT GAAGACAAAT ACAATTGCTT TTTACCAAAA GGCAGATAAG 660

TAATATCTGT TACCAATTTC TTTAAAGGAG CGTCTGAAGA AAATTACTTA TTTAGCTTGT 720

TCTCGACAAC CGTGTAAGGT TGTCCCACTT TACTGCGTTT CTTCATTTTC ACGCGACAAT 780

TCTAATGATA TTTCCGCATA ATCTTTTGTA CGGTGTTTTT ATTTACTTTG TATTCCTGAT 840

TAATCAACGC AtAATCTTTC GATAGCCATA TCGAAACTTA TGCTGGAAGC AAAGTCGACG 900

AACAGCTTCt TCAAGAGGCG TTAACTTTCC CAAGTCTTTT CGATGAGTCC AACGATAATA 960

AGTAGCTCGC GAAATGCCGA AAAGTTGACA CAATGCAGTA ATGGGTAATT TTCCTTTCAT 1020

TCTTTTAACT AATTCTACAA ATACTTCTGG CTCCACGTTC TTTCCAATTC TTTGAACTTT 1080

TTAAGCACCT CAATGTGCAT TTTTAAATAG TTATTTTCAT TTTTAAGCTG CTGTTCATTT 1140

GATAGATTTT CTGGACCTTT TCCATAAGCA TATTTTTTTC AACGGGTTGA ATCAGACGAT 1200

GATGATTCTC GCCATTACGA TACCCCAACG CCACCATGTG TCAATTTGTG TTTTGTTTTT 1260

AATTCCTAAT TCTTCCATAA TCGTTTTTAC AGGAATATTC TCTTTTTTCA TCTGTATAGC 1320

CATTTCTTTG ATGTAAATAG GATAAGATAC TCAATTTCTC ATTGAAAAAG CACCTCCTAG 1380

TTAAATTCAT TTTAACGTGA ATTCAACAAG AGGTGCTTTT yTTGTCTCAG TTTATTGGGT 1440

CAGTTCCCTA TTTGTTTGGT CACTTTTATT TTAGCAAAGG TGTTCTTATT TTTATACAAA 1500

AAATAATCCA GATGTCAATy AATCTTATTA ATGGTATCGG AATTTCAAGC nCTGTTGnAC 1560

AAAnTT 1566

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

CAATAAAGGT TTCGCTTAAC GTCCCAAATA AAACTGATAA AAtmAGAATC ATCcAGAAGA 60

TTAAATAAGC CAGAAAAATA AACGGTTAGA TAATACTTTG TCCATTGTGT TTTTCCTGAT 120

TGATCTTCCT GATCCATATC CATAATATTT TTTAGAATCC AATCGATTAG CATATCGCCC 180

TCCTcTTCAA GTATTGCACT AAATTATAAC GAATATAGCG ACTAATAGAT AGATAATTCC 240

TTAATTAGTC ATTATCCCTC CCTAAGTAAG AAATAGTGCC TTGACCTGAG TATAATATCT 300

TCTTGAGACT GGTACTTCCG TTCCGTCTCT CATAGTTAAA AGATGCGTTT TATAATTTAA 360

TTTTGACGCA TATTTTTTAT TGATGATGAT TGATTGATGG ACTCTAATCA AATCTGGATG 420

CAGTTGTTCA ATTTTTGATA ACGTTCCATA AAATTCTCTT TTAAAATTTT TACCAACCAT 480

TGACACACGA TGATCGTATT CCGTTTGAAA GAAATAAATA TCATTAATAT CCATTTTTAT 540

AGAAGACGCT TTTAAGTTAA TGATAATATA TTCACTTTTT GTCTTTATAT TTTCTTTTTG 600

TTGAATATAT GCATCGACAC ATGTTTCGAC CTCTTTTTGG AAATCTAGAA AATCCACGTT 660

CTTTTGAATA AATTGAAGAG CTGAAACCAT ATATTTGTAG GAAGTTAAAA CTAATTCTGT 720

GTGAGTAGAA ATAAATACAA TCAGACTTTC ACTGTCTGTT TTTCTGATTT CTTTAGCAAC 780

CTCAAATCCT GCCTGGATAT GATTGTTCAT TTGAATATCT AGGAAAAAGA TATTTAGTTG 840

GGCGTCCTGG TGTGCCACTT GTAATAATTC ATCTGAACGT GAAAATAAAT GGATTGTTTC 900

ATTATAAATA TTTCTTGAAT GTAGGATATT TGTTAACAAT ACTTCTAACG CTTTTGCTTG 960

AATAATTTGG TCTTCTAATA TATAAATAGC CATTTGTTCA CTCATCCCTT TCTCAAGAAG 1020

ATATAAAATT ACACAACAAA AGACAAATGA TTATAATGTT CAATCAATTT ATACACCAAT 1080

AAAAGAGATA AAAAATTGAT TGTCTGTTAG TATATTCACA TAAATTTAGT ATAGCGATTT 1140

CAGTAGTTTC CTGCAAACAA AAACATAAAA TAACAAAGGA TCAAGAAAGA GTACTTTGGA 1200

CTATTCATCT TTTTCTAACG AATCATGAGG ACTATTGTCT CTTCGTTGAT GAAAAACAAA 1260

GAATCAACCG CCAAACTGTT CTTGTCATTT TATACATGAC AAAATCaATT CATTGGTCGA 1320

TTCTGGTTAA TTTAATTTGT TAGTcACACA TGGGATCAtt GTACTAAtTt TtTACTTA 1378

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

TAAAATATCT AAACCACGAC GACCTCTCAC CCGTTTTAAA CTGTCTCCAG AATCAGCAAT 60

GTATTGTAAT TCATATAAAA CAAAGTTAGG GATGAGCAAA ACACCTTCTA AAAAGCCTGT 120

TTTAGCGATA TCGTAGATTC TGCCATCAAT GATGACACTG GTGTCTAAAA TTTTGTATTT 180

ATGGAAGTTG TCTTCCACTT TACGTTCCAA CATTTGTCCT TCGGTGTCTT CCGTATTTGC 240

TTTCTTTTGG CGAGGTGTAA AAACTTTTTT CCACTCCTCA ATCCGTGTTG TTCCCATTCG 300

GAAACCTAAG TAACCCAGAA TAATCATAAC TAGAATTGGC AGTAAACTAT TCACGACAGG 360

AATTTGTAAG TTGTACATTG GAATGGAAAT AATGACACCA ATTGTTAAAC CAATGATGGC 420

ACCAATACTT CCAAATAATA AATAGGTTAA ACTCATTTCA TTTAAAGCTG CTTCGATTTT 480

TTTGACAGCG GAAACAATAT ACTTTGCTAA CCCTAAAGAT AAAATAAAGA AAATAATTGC 540

ACCGATTAAT CCGTTCGTAA AGTTATTGTT TAACCAACTG TTATTGCCTT GCTTAGCCAT 600

TTCCCAAGCC ATTGGGAAAA GAGAAATTCC TAAACTTGCA CCAGCAATGA TCATCAGCAA 660

CGTGATGATT CGTTTTTGCA TATAGCCATC CTCCTCGTTT ATTTAATAAA GACGTCTAGT 720

GTTGTGGGGC GTACAAAAAT CATACGCCAC CAAAAACCTA AACGGATTAT TTCTACTTTC 780

ATTATTTAAA AACTTTTCTT AACGTTTCAC CAATTGTTGA AACGCCAATA ATTTCAATCC 840

CTTCAGGCGC TTCCCAGCCA CCAAGGTTAT TTTTAGGGAC ATAGACTTTT GTAAAGCCTA 900

GTTTTTGCGC TTCACGCACT CGTTGTTCAA TACTATTCAC GCGGCGGATT TCACCAGTTA 960

AACCAATCTC ACCAATGAAA CATTCCGAAG ATGAGGTTCC TTTTTCTTTA TAGCTAGAAG 1020

CAATACTGAT TGcTAACGCT AAATCAATAG CTGGTTCATT AATTTTGACT CCACCAGCCG 1080

CTTTTAGATA CGCATCCTGG TTTTGTAACA AAAGGCCTGC CCGTTTTTCT AAAACCGCCA 1140

TGATTAAAGA AACGCGATTA AAGTCCAACC CGGTGGTCGT TCGCTTGGCA TTGCCAAACA 1200

TCGTTGGGGT AACTAACGCT TGGATTTCCA CCAAAATAGG GCGTGAACCT TCCATTGCTA 1260

CCACAATTGA AGATCCGGTG GCTCCTTCTA AACGTTCTTC TAAAAAGACC TGAGAAGGAT 1320

TCATAACTTC AACCAATCCA TGTGTCTGCA TTTCAAAAAT ACCAATCTCA TTCGTTGAGC 1380

CAAACCGATT TTTGACAGCC CGTAAGATTC TAAAGGTGTG ATGCTTATCT CCTTCAAAAT 1440

AAAGAACCGT GTCTACCATA TGTTCCAACA TCCGTGGCCC TGCGATAGAC CCTTCCTTCG 1500

TTACGTGTCC GACAATAAAA ATGGCAATCC CATTCGTTTT TGCCAGTTTC AATAATTCGG 1560

CAGTTGTTTC *TCGGACTTGA CTGACACTAC CAGCAACGCT GgTAACATCT GGCTGCGTCA* 1620

TTGTTTGAAT CGAGTCAATA ATGACATAGT CTGGTTCTAA TTTTTCAATG GCTCGTGATA 1680

TTTCGTGCAT ATCTGTTTCT GCGTATAAGT AAAATGTCTC GTTGACGGTG CCTAanGCnt 1740

CCGCTCGTAA TTTAATTTGC TCAGCACTTT CTTCACCAGA AACATATAAA ACCGTACCAC 1800

CTGTGGCTGC TAATTGTTGC GATACTTGTA AGAGCAATGT TGACTTACCT ATTCCGGGAT 1860

CGCCACCGAT TAAAACTAAC GAACCTGGAA CAACGCCACC ACCTAAAACC CGATTCAGCT 1920

CCACTAATTC AGTTTTTACA CGAGGCTCTT TTTTAGGTAT GACTTCAGAT AGCCGTTGTG 1980

GTTGTGTCTT TTTACCAGTC AAACTTACTC TAGCACGACG ATCAGAAGTA TCTTGAATAA 2040

CCTCTTCCAC CATCGAATTC CATTGTCCGC AATTAGGACA GCGGCCGAGA TATTTTGGAG 2100

ACACATACCC ACAGCTTTGA CATTCAAATT GAACTTTTGC TTTTTTTGCC ATGTAGAATC 2160

TCCTTATCTG TTGTTTATTT TAACATTTAT TAAATGGTTT GAATAACGTT GCCTACTGAA 2220

AAAATGGGCT TTATTTTTGT CCAGACGAAC CAAAACCGCC CGTTCTTTCT GCCTCGACTT 2280

GGTCATCATC CGCTAATAAA AACGGCTTAA AAATCCCTTG GCCAATTCGT TCACCTTTTT 2340

CAATGACAAC ATCTTCATAT CCAAAGTTTA AAAATTGGAA CATGATATGT CCTTCGTTAT 2400

TCTCGTTATT ATAATAATCA CTGTCAATGA CTCCGACACC ATTCGCTAAA AGTAGGAATC 2460

GTTTTAGCGG GTTCGAAGAA CGACTTACCA ATTCTAAATA TTCAGAATCA GGCATATACG 2520

CCTTAATTCC TGTTTTAACT AAAATTGGTT TGGGATTTTC TCCAGCTTGT TGTAACTTCC 2580

AAAGACTTGG TACAACGACC GTTTCGGCTG CTTGAAAATC ATACCCCGCG GCACCTTTTG 2640

TTGCTCGTTG TGGGACACTC AAGCCCTCTT CTTGATACTT AGAAATAATC TCAAAACCAC 2700

GTTGTTTCAT ATTCATTCTC CCCTACTGTC TAAACTACTC CTATTTTACC ATAATCTCTG 2760

ATACTCTGGT TGTTTTTAGT AAGTTTCTCA TTTCTAAAAG CCCAGTTAAT CTAGACTACG 2820

CAAAAAAGAG GAGAATTTTT GTTTATTTTC CTTCTTTTAG TCTATCATCT TCTCTTAAAA 2880

TAAACAGACC AAATCCCAAA AAGTCCCAAG ATTCCCTCAA AAAGTTCACA CTTTCATTAA 2940

ACTTTCTTTA CTATTCATTA TTTAGCACTT TCTAGTAGCC GCTGATTTTG TTATAATGAG 3000

TGTCAAATTT TACTGTAAAA AGAAACGAGG CACTTATGAG AAACAAACTC CAACAGGCCA 3060

AACGAATTGT GATCAAAGTC GGAACCAGTT CTCTGATTTA TCCCAATGGC AATATTAACT 3120

TAAAAGCAAT TGATCAATTA GCCTTTACTT TGAGTGATTT AAGCAACCAA GGCAAAGAAA 3180

TTATTTTAGT TTCTTCTGGC GCAATTGGTG TCGGACTGAA TAAATTAAAT CTATCTGTAC 3240

GCCCAACGAC AATTCCCGAA CAACAGGCAG TCGCTGCAGT CGGCCAAGCA GAATTAATGA 3300

ACATTTATAA TCAGCGGTTT TCAACCTATA GCCAACAAAT GGCACAAGTT TTATTAACTC 3360

GTGATGTTAT TGAATATCCT GAAAGTCGCA ATAATGTTAC CAATACTTTT GAACAACTGT 3420

TAAAAATGAA TATTATTCCT ATCGTCAATG AAAATGATAC TGTCGCAATT GAAGAATTGG 3480

ATCACTTAAC CAAGTTCGGG GATAACGATC AATTGTCTGC CATTGTCTGC CAAATTGTTC 3540

AAGCTGACTT GTTAGTTATG TTATCAGATA TTGATGGTTT CTTTTCAGAC AACCCTACTG 3600

TCAACAAAGA AGCCACGTTA TTTTCTGAAA TCAATGAAAT TAATGAAGAC TTGTTCCAAT 3660

TAGCCGGTGG TAAGGGAAGC CGCTTTGGCA CTGGTGGGAT GTCTAGTAAA TTAAAAGCTG 3720

CTGAACGTGT GTTAGCTAAT CAACAGGCGA TGATTTTAGC AAACGGAAAG CAGCCAAAAA 3780

TCATTTTTGA AATTTTAGAA GGAAAAGATA TCGGTACGTT ATTTATTAAA GGAGGGCATG 3840

AAAGTGACTG ATTTAAAGCA ACTAGGGCAA CAAGCTAAAG AAGCCTCTTA TACGCTAGGC 3900

TTGATGGATA CTCGTCAAAA AAATACTTTG TTAAACAAAA TGGCCGCAGC CATTGAAGCC 3960

AATGCACCCC GCATTTTACA AGCAAATGCA TTAGATTTAG AGCAAGCCGC TACCCACGGA 4020

ATTTCTGAAA CAATGCAAGA CCGCTTACGT TTAACAGAAG AACGGATCAC AGCGATGGCT 4080

GAGGGCATAC GCCAAGTCGC TACTTTACCC GATCCAATTG GGGAAGTAGA TAAAATGTGG 4140

CGCAATGAAG CGGGACTGTT AATTGGGCAA CAACGCGTGC CTTTAGGTGT TATTGGAATC 4200

ATTTATGAAT CGCGGCCAAA CGTGACAACA GATGCCGCTA GCCTTTGTTT CAAATCGGGA 4260

AATGCTGTTA TTCTTCGAGG CGGAAAAGAA GCGTTTCACT CCAATCAGAT ATTGGTGACA 4320

ATTTTACAAG AAGCGCTAAT CCAAGAAGCC GTTTCTCCCC ATCTCATTCA ATTTGTTGAT 4380

GATACTTCTA GAGAAACAGC CCAACAACTT ATGCGCTTAA ATGACTACTT GGATGTCCTC 4440

ATTCCGCGTG GCGGCGCCAA CTTAATCAAA ACTGTTTTGA CAACAGCCAC TGTTCCTGTT 4500

ATTGAAACGG GCACGGGCAA TTGTCATATT TACGTGGACA AAGACGCCCA GTTAACAATG 4560

GCAACTGAAA TTATTGTCAA TGCTAAATGT CAACGTCCTT CTGTCTGTAA CGCCGCCGAA 4620

ACGTTATTAA TTCATCAAGA GGTGGCTGAA GCCTTTTTAC CAACAATTGA AAAAGCCTTG 4680

AAGGAGTTTC ACGTGGAACT TCGGGCAGAT GAACGTGCGT TAGCAATTTT TGAAGAAGCC 4740

ATTCCAGCGA CTGAACAAGA TTGGGAAACG GAATTTCTCG ACTTTATCTT AGCAGTGAAA 4800

GTCGTTGATT CTTTGGACGA AGCCATCCAG CATATTAATC GCTACAATAC AAAACATTCT 4860

GAAAGTATTA TTAGTGATAA TTACTTTGCC ACACAACAAT TTTTACAACA AGTGGATGCA 4920

GCCGCTGTTT ATGCGAATGC TTCAACTCGT TTCACGGACG GTTTTGAATT TGGATTTGGC 4980

GCCGAAATCG GCATTAGTAC GCAAAAATTA CATGCCCGTG GACCTATGGG TCTAGCAGAG 5040

CTTACTTCGA CAAAATATGT TATTTATGGA AATGGGCAAG CACGTTCTTA GAAAGAAAAA 5100

CCCTTGATTT AAAAATCAAG GGTTTTTCTT TCtCCTCTCT AATGTGCATT TTTACACATG 5160

AGATTGTTCA CAGTTCCACA ATCTATTCTT GATATTTTTT TTGAATCCTC ATTATACTTT 5220

CTACATATGC TTGTTTCACT TGGACTGGAT CTAAAATTGT CACTTCTTCA CCAAAGCCCA 5280

TAAAATAGTT GGCTAAAAAT TGTGTTTCTG TTGGATGAAT CTGTCCAACT AAAAAACACT 5340

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GCGTGGGCGT TTCTTCCAAC TGAATATTGT CAAAGCGATG TTTATAAAAA AATTCTTTGC      5400
CTTTTTCTGT AATGATTGCT TTAAATGGAA TCGTACGTGC CGTCGTTTGT TGATGGCGAT      5460
ACGATTCTTT CAATTCTTCA GTCGTAAAAT CCAGTGTTTG GTTTAATTGC TGAATAGCCT      5520
CCATAAAATC ACAGCGGTAA GTACGCCAAG CCTTTTTAGT CACATCATAG CCTGAACAAT      5580
ACCAATACCC TTCTAAAATA GTTAACCGGG TTGGTAAGAT TTTTTTCGTT GTTGCTTCAT      5640
ATCTGGTATA GTTAAACTGA ATTACTTGTT GCGCCAAAAT ACAATGAAAC AGCTGCTCTA      5700
AATTGCCTGG TGCTTCTACT TGTTCAATTC CTTCGTAATA GACGACCTTA CTCATTTGAC      5760
TGATTTTAAA TTGGGTTGGT TCATCTAAAG AATGCAATAA TTTTTGCTTA ATTTGCTGAT      5820
AGGAATGACC AAACGGTGAC TCTGCGACTA ATTTCAGTAA TTGTAACGAA AAAAAGATTG      5880
CTAACACTTC ATTTTCGTTA AAATAAATCG GCGGCAACAA CGGTTTGTTT AAAACTCGAT      5940
AGCCACCATA ACGACCATTC TCCACATATA GCGGCACGCC TAAATTTTCC AAAGCTTCAA      6000
TATCCCGCAA AGCTGTGCTT TTAGAAATCC CAAAAGTTTT CATTAACTGA TTTAAATTAA      6060
ACTGAGGATG GGTTCTCAAG AAAAAAAGTT CCTGATTTAA ACGTTCTGAT TTTTTCATTT      6120
TTCCCTCCAT CGGTGTCACT TTTTGACACC TTTTATTGTT ATGCTTATCT TATCAATCTT      6180
AGGAGGTTCA AACAATGAAA AACACACAAT TTGCCCTTTT TATGGTCTTA AACGGaCGAG      6240
CAACGGaAGC CTTGACGTTT TACCaAGAAG CCTTTGCTGG TGATATTCTT TTTAAAATTA      6300
CTAATCAAGA ATTTAAAGAG CGCTTAAATC CTTCTTTGAC CATTCCCGCT GGCGAAGAAC      6360
ACTGGCTTTC TCACTCGATT TTACAAATGG ACACTTTTCA ATTACAACTA GCTGATAATC      6420
CTTTGTTTGC AGGAATGAAT ACCACGCCCA CAGAACAATT GACCCTCAGC TTAACCGTCA      6480
ATAGCCGTCA CTCTGCCAAA ACAATTTTTG AAAAACTCAC GTGCCATCCC GAATCCTGTA      6540
TTATCCAAGA ACCAATTGAA AATGAATTTG CAACATTTTA TGCGATTGTG AAAGATCCTT      6600
TTGGTTTAGT CACTCAAATT ACTCATGAAA AACAAGCAGA TCCTACCAAG AAAGGAAGTT      6660
AGCCGAAGAA TGCGAACCTA TGAATCAAAA GAAGCCTTGA TTGAGGCCAT TCAAATAGCT      6720
TCACAAAAAT ATTTAGCTGA ATTTGCAGAA ATTCCTGAAA CACTTAAAGA TCACCGAATT      6780
GAAACAGTAG CTAAAACACC TTCAGAGAAC TTAGCCTATC AATTAGGTTG GCTCAACTTG      6840
CTGCTTTCTT GGGAAGAACA AGAACAACGT GGTCTGACCG TTCAAACGCC AGCTGAAGGC      6900
TATAAATGGA ATCAACTGGG CGCGCTCTAT CAATCATTTT ATCAAACCTA TGGACAAATG      6960
AGTTTAGAAA GTCAGCTGAT TGCGTTGCAA GACACCTTAG AAAAATTACT TCATTGGATT      7020
GACTCGCTTT CCGAAGACGA ATTATTTTTA CCTCAACAAC GGGCTTGGGC GACCACCAAA      7080
GCACAATGGC CTCTTTGGAA ATGGATTCAC ATTAATAGCG TTGCCCCTTT TACTAGTTTC      7140
CGAACGCAAA TTCGCAAATG GAAAAAAGCT TGTCTTTAAA AAGTTATCCA CATTTTTTCA      7200
AAAAAAGCTT GACAAGTATT TTTAAATTCT CCACAGAAAA CTTTGTGGAT GAAATTTCTT      7260
ATTTTTTCCA AAAAACTTTT CCACAATGCT TATTTGTTCG ACATTAAATC TTTGTAAATT      7320
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CTAGAAAAAA GAAGATGAAA ACGTTGTTTT AATAACGTTT TCATCTTCTT TCAACTTTAG 7380

GGATTCCTTT ACTTTTAGCA AACAGGACTT CTGAACTTAC GTCTGTTTTT TTTAGCAACT 7440

CGAAAACTTA TCCTTGTGGA TAAACCGAGA TAAAAAGCTT TTTTGTGGTT TtCAACAGAG 7500

TTATGCACAA AGTTATCCAC AGGGCGTTTT CAGCAATTTT TCGGAGAATA TTCGTTGTTT 7560

AATCTGGTGA TTTAGCATTT GAATGTCAAT CCCTTACTAC TAATTCTTCT tCACTCCACC 7620

CTTAGGATCC TAATAAAATT TTAAAGTkTT cTcTAtTGGT ACATCArATA AAGAGTATGr 7680

kAAACTATAG GTACTT 7696

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

CTCCTATACA AACATAGGCT ATTGCTCAGA AATGTCGAGA GACACCAATG AGTAGAACAA 60

GACTGGTCGA GGAGAAGGCT TTTCTCAAAA TAGCTAAGAG TGATCTTTAC GTTGTATAGT 120

GCTAAAGCTC AACGTTCATG TTGATGTATC TTTTTAGTCT CTAGTCAATC AGTTAAGTAA 180

GTACTTTTAT TTAAAATTAA GAGAGGAGTG AAAGTATGAC TACTATGTTA GCAATCATTG 240

GAACTGTTGC AATCATCACA GTTCAAGTTA TTGAATATAA TATGACAGAA ATTCATATTC 300

CTACTGCAGG AACATTTAAT GACGATGATG CAGAACCCCC ACATTCTTCT GTAACCCTTG 360

TATTTATTCG CACTAtACyT AtCACTCTCT CACTTAACTT TCCATCTCAt TTTTTTGAGA 420

wGGkTTTTTT ATGkATyCGr GAAAATwATr AACmAAAAAG ACyGtTAAAy CAATGATTTA 480

ACAGTCTTTA GTATACCGGC GGCCGGGGTC GAACCGGCAC TCCCGTGAAG GAACTGGATT 540

TTGAGTCCAG CGCGTCTGCC AATTCCGCCA CGCCGGCAAG ATATTTTGGA AGGCGGTAAC 600

CGGATTTGAA CCGGTGATGA AGGTTTTGCA GACCTCTGCC TTACCACTTG GCTATACCGC 660

CATATTCCAT TTTTGTTACm AAAAAACTGG GGTAGCTGGA TtCGAACCAA CGCATGACGG 720

AGTCAAAGTC CGTTGCCTTA CCGCTTGGCT ATACCCCAAT AAAATTACAA AGGGCGACCG 780

ATGGGAATCG AACCCACGAA TGCCAGAGCC ACAATCTGGT GTGTTAACCA CTTCACCACG 840

ATCGCCGTAA TCTTAAAAAG TGTATCTATT AAATAATTAA ATGGCAGGGG CAGCAGGAAT 900

TGAACCCACA CCAACGGTTT TGGAGACCGT TGTTCTACCT TTAAACTATG CCCCTAAAAT 960

GGAnGAAAGT GGATTCGAAC CACTGAA 987

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

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CGCACCTCAC GATCGTAAGC AACAAATTTT TCCGTAAATA GCAAGGGATT TTCCAAGCCT     60
AACGCTTTAG CAAAGGTAAA CAAGCTTGTT TCTTTTAAAG AAGCTGCTTG AATTAATTTT    120
TCATCTGTTA AAACAGCAAC TGGAGTCGCA TCTGCTAGTA AACGTCCATC ACAAACTACT    180
AACGCACGTG TTGTATATTC CAACATTAAG TGCATATCGT GAGTGATCAT TAAAATAGTC    240
ACACCTAAGC GGTTCAATTC TTCTAAAAAT GTCATCATTT CTGTATAATG TTTAAAATCT    300
TGCCCAGCTG TTGGTTCATC TAAAATTAAT AATTCAGGTT CTAAAACTAA GATTGATGCA    360
ATAGTTACCC GTTTTTTCTG CCCAAAACTC AACGCAGAAA TCGGCCAGTT CCGGAAGGGA    420
TACAGCCCAC AAATATGTAA AATATTCGTC ACACGTTCCT CAATTTCTGC TTGTGGCACA    480
TCTCGTAAAA CTAATCCTAA AGCTACTTCT TCAAAAATCA TTTTTTTAGA AATCATTTGA    540
TTGGGATTTT GCATCACATA ACCAATTTTA TCTGCACGTT CTTtGATTGA ATAATTGGAA    600
AAATCCTGTC CTTCCCATAA AATCTTGCCA GATTGAGGCG TGATGAACCC GCAAATTATT    660
TTAGAAAGTG TAGACTTCCC GGcACcATTT TTTCCTACAA TGCtGATCAT TTCtCCAwGA    720
TGaATAGTTA CwGAGAAGTC ATCTAACACT TTTTCACCG                           759
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(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

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ACCGACGCCT AAATCCTTTT GCTTCAAAGT AGACTCCATT GCCATTCGCG CATGAAGTTT     60
CGTATTATTT TCTTTGCTAA GATGACCTAA ATAAATGCGT TTTGTTTTAT CACCTAACAC    120
ATCCGCCATC ACAAGAGCAC CATCATCATT GGATAAATGG CCTTTATCTC CTAAAATCCG    180
TTGTTTAAGA CTCCATGGAT AAGGTCCTGC TCGCAAAATT TCAATTTCAT GATTGCTTTC    240
GACTAAATAA GCATCTGCAT TTTCAATCGT ACCACGAATA TGATCGCTAC AATAACCTGT    300
ATCCGTTAGA ACAACAAAGG AACGATTATT GCGATGAAAA CGATAAAATT GAGGCGCAAT    360
CGCATCATGT GAGACACCAA AACTTTCAAT GTCCATATCT CCCAAGGTCA AAACTTTGCC    420
CATTTCAAAA ATATGTTTTT GAGCGACATC GACTTTGCCA ATCATGGGAT CCATCGCTTG    480
CCACGTTTTT TCATTGGCAT AGACATCTAA CTTATATTTT CGCGCTAACA CGCCAACGCC    540
GTGAATGTGA TCCCGATGTT CATGTGTAAC TAAAATCGCA TCTAAATCTT CTGGTTTGCG    600
ATTGACTTCT GCTAACAGTG AAGTGATTTT TTTGCCACTT AAACCCGCAT CTACTAATAC    660
TTTCTTTTGG TTGGTTTCAA TAAAAAGGGA ATTGCCTGTA CTGCCACTGG CAAGAACACT    720
GATATTAAAA GCAAACTCTG AATCCATTTA AAACTCTTCC CTTCTACATT ACAACATTAA    780
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CGTGTTTCAT TATACAACGG ACCTTAATGT TTTTCCACCT TTGGCACAGT ATTATTTGTG 840

ATGATGGTAT TACTTACGGC ATTCACCTGT TCAATTTCAA CTGAATCTTC ACCAGTAGAA 900

ATTCCTACAA ACCAGACTGG AACGTATACA TTTTTCTCAC GAATTTTATA AATTCTTGaA 960

TAGGCCAATT TAAtGAATGT TATTTTGGAA TTACTAgGAA TCCGGTTATT CATATAGAGC 1020

GTGTCTATCG CATCACGATT GGAATATAAA TCCGTTTTGT CTCGTAACTC TTCAATATTT 1080

TCAATGTGCG TTTGCGAATA TTTACTAATT TGCCATAATT CACCTGACGA ATCTGCTAAA 1140

ATACTTAnTT TTGCCGGGTC GnnCCCGAAA A 1171

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

GCAATCATTG TATTGGGATA GAGGTTAAGn CCTAGGGCAT CCCCATCTGG AAATGCTGTA 60

TGGTCATGGn CATTCCTAAC CAGGATTAGG AnGGAGGGAT CGCAATTyCC ATCTCGTTCC 120

ATTTAATTTT GCTTAAGGAT TGTGCCATCA AAACACCAAC AATAATCAAC GCTGGTGCTG 180

TAACTTGCGA AGTGACAACT GCTAACAAAG GAGAAAATAG CAAACTGAAA ATAAATAAAA 240

TCCCGGTTGT AATAGCTGTG ATTCCTGAAC GACCACCCAC AGCAATCCCC GCAGATGATT 300

CGACATATGC GCCAACTGGC GATGTCCCTA ATAGAGAACC AGCTAACATC GCTGTTGAAT 360

CAGCGGCTAA AGCTTTCCCC ACACGCGGCA TTTTATTGTC CTTCATAAAA CCTGCTTGAT 420

TGGCTAAGCC CACCAACGTA CCAGCCGTAT CAAAGAATGT TACTAATAGG AACGTTAAAA 480

CCACGACCCA CATTTGAaTC GTATTgATAT CTTTCACATG TCCTAACGCC ACTAAAAATG 540

TTGGTTCTAA aCTTGgCcGC TTGAAATAAt CTTATCAGGC ATTGGAATAA CGCCTGTCGC 600

TAAACCAACA ATCGTTGAAa TCGCCATCCC AATAAAAaTA CCACCCGGTA CTCGACGAAC 660

TAACAAAATT GCAGTTACGA CTAAGCCGAC AATGGTAACC CACGTTGAAC CAACATTCAA 720

AGGTCCTAAG CCAACGAGTG TCGCATCATT AGCCACAATT AAGCCACCTT GGCTTAAACC 780

AAGAAAAGCA ATAAACAACC CGATCCCACC TGaAATGGCA AATTTCAAGT CTGCAGGAAT 840

TGCATCAATA ATTAGCTCGC GTAATTTAAA AATTGTAATT AAAATAAATA TCAATGAAGC 900

CACAAAAACG CCCGCTAATG TCGTTTGCCA AGGAATCCCC ATACCAACAG AGACTGAATA 960

AGCAAAGAAT GCATTAATTC CTAAAGCTGG TGCTGTCGCA ATCGGATATT TCGCCAACAC 1020

ACCCATTAAA ATACAACCTA AGGCACTCGC TAAAGCGGTG GCAGTAAAAA CAGCGCCTTC 1080

GTCCATGCCA GAAGCACCAA GTACGGTTGG ATTAACGAAC AAAATATACG CCATTGAGAT 1140

AAACGTGGTG AAACCAGCTA ACATTTCTCG TTTCATATTC GTATTCAATT GTTCAAGTTC 1200

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AAAATATGAA CTTATTTTTT CTTTCATGTT CCGTCCTCCT AAAATCTAAA TATTTTACAA    1260
TGTTCGTAAA ATATTCAATT TATTAATGAA ACAACGTGCT TCCTTGAGTG GATATTATTA    1320
AGCACGAATA GCCCCATTTT ACTTGATACA ATAGGAATTT GCAACAAAAC ATAATTAGTT    1380
AAATACACAT AGTTTTGATC AAAAGCACAG ACCAAAGCAC AGACCTTTTT TAATCCATCA    1440
CGCCAATAGT TACATATTAC GTTTACTGTT TTTTAAACCC AACGGGAAAA GAATAGTTAT    1500
ACCTGATATA CCTATACTGA TAAAAAAATA AATGAGGTAA CTTGTCCAGT CAGCGGTACC    1560
CCCATCTATA TAACCTGAAA TTGAAAAATA TGAAAaCAAA ACTATCACAC TGACTAACCA    1620
CTGATATCTT AACCTTAATT TTAATTTTAT TGTCATTACG TAATACATCA AATACACGCC    1680
TATCAGTACC AACCATACGA TGTAACTACT GATAGAATAA TGACCATCGA ATAAGcCCAC    1740
ACTAGATTAA TCAAAATAAT CAATATTATT GGTAGTAATA CTTGACATAA AGTGTTAGAT    1800
CGATAGATGC ATACTATTTT ATCGATAATT TTTTTCATTG TTTGCTCTCC AAAAGTTTAT    1860
TTTTAATATA AGCTAATAAA GTTCCTAATT CAATTACTAC CCATGCTGTT AACAGAATAG    1920
TCCAGAATAA ACTTCGTACA TAGAATAAAG CTATAAATGT AAATATTAAT ATTGCCAACT    1980
GACTGATTAT CACTAATAAA TCTTTTTTTT GGGAAAATTT ATAAGCTAAA AGACTGCACA    2040
CTATGCCAAT TACTGGGATA AAACGAATAT AACTAGGAAC CCCTTCCATT GGTACAGTAA    2100
ACAATAGAAT TATAGAATAC CAAAGTTCAT CAGGAACCTT CGACGATAAT GCCCTTATTC    2160
TTCCCCAATT CATAAGTTAA TCCCCCTTTT TCATTCTCTT ATACTTGTCT TCTATACGCT    2220
TATCCTGTTT TTTCCCGCCT GCATGAAAAG CTAGAATAAT CATTGCCTCT GTAATAACAA    2280
ACTCCCATAC TGACCAATGA AAAATAACTG TCATCCCTAG AATTACTAAC ACAGCTGATG    2340
CTAGAATAGC ATCTTTTGTG CCAAAATCTA TCCCTATAGG TAACATAAAA AACCTCCAAT    2400
CTCACTTTTT TTATCCTAAA GACATTGCCA AAATAAATAA TATCCAAGGA ACTAAAAAAC    2460
TAAAAGCACT TAAAAGATTA GCGACAAGCA ATATAAGTTT TAACCCTAAG TGCTTTATGT    2520
ACATACTAGG AATAGCTCCT ATCAAGCCAA TTGGTAACGT CCACAACAAA TCAAAGGCAC    2580
CATGATAGGG ATTGTAGAAA AAGAGGTACT TAATCCATAC AAGTATATTC AAAAGAACGA    2640
ATAGGACACT CGCAACAACT GCTGATCGAT TATTTAGTTC TATTTTCATA GTTACTGACC    2700
TCTTTGGTTT TTATTTTAAT TATATCAGAA AAGACTTCAC TGATAAAAAT CTTTTCTTCC    2760
CCTCAAACAA ACGAGCTATA ATAAAGTAAC TAGAAAACCA GCAAAAATAA TTTGTAATAA    2820
TTTTAAATTA TTGTGCTTTT TTATATTTTA GGTATAAAAA AGGTAGCCGA CTATCCGACT    2880
ACCTTTTAAA CACTATTCAA TTACAGTAAC ATTTACCGCT TTTGTTCGCC CTTCGTATTC    2940
TGCGGTTTCG TACTCCACTG CTTGGCCTTC AAGCAATTTT CTAAAGCCTG GCATACAAAT    3000
ACCTGTTTGA TGTACAAAAA TCTCTGATCC ATCTTCGGCA ATAATAAAGC CATATCCTCT    3060
TTTATGATTA AAACTTTTAA CTGTTCCAGT TTTCACTTAT ACTTCCCCCG TATTATGATT    3120
TAAGTTGCCC ACGATCAAAT TTCATAGCTC TTTCTACTAG ATTAGGAGCT GAAACATAGC    3180
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TTGAAATGCC TATTACACTT CTGTTATGGC GAGTAACTCC GATGATTTTA TTTCCTTCGT 3240

CTACTACCTC ACGATTATAG ATTGCATTAG CTTTTACTTT AACTGATTTT ATAAACATAG 3300

CCTTTTCATT TAATTGTTTA AGCAAAAGTG CTATTTCTTG TTCCACGGGC TCTAGTTGTT 3360

TTTCAATTGC TTGTCTGTAT TGAGAGTCAA TATCTCCTAC TTTATTAGGA AAATGAGTAA 3420

AACAAGATTG CTGTAGCTCC TCGCGTTCTT TCTTCATTTG TGTTAGTAAA TGATTATTTT 3480

CwGTTAAAAG CCTGTTTATT TCAGGTTTTC TCTTAAGACT ATCTACCGTA AAAGTTTTCG 3540

TATTTTCTAG CGTTTCTAAC TCTTTCTCTA AGACAGATTT TTCCTGtTCT AAATCATTAA 3600

TCACTTTATC TACTCCGCTA AAAATTTCTT TTAGCTCGGA AATAAGCTCA ACTTTTCCCG 3660

GAATATCGTA GTTAATTTCT ATCATTTTAA TAGCACCCCT TATTTATCAT ATTTAGACAT 3720

GATTTTTTTA AATGGATCAG GTTTATCTTC TTTCTTATCC TCTTTATCTG ATTCCGTAGA 3780

ATCACCTAAG CTTTCTTTAA TCAACTCTTC TAATGCTTCC GAAGCTTTAT CAATGTCAAA 3840

TTGCCCTTCT TCATCTACAA ATTCCTCTAA AACTTTTTTA ATATCTTCCG CTGTCATATT 3900

TCTTACCTCT TTCATAATTT TTTATATATT TTGGTGAAAT TTCACCGAAA TAAACATATT 3960

CTGCTTGATA CATGATATTG CCTAATTGAA AAGCGTCATT TACTTTGTCC TTGTTTGTAC 4020

ATAAGTGTGT ATGGAATTGC nGnATCCAAT AAACTAGCAG CCGTGTGATC TGGTTCGAAT 4080

ATTAGCAATG GCAGCATTCC GATAACACAA TATTACTTAT TAACGGCACn CCAT 4134

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

AATTTTTTTA GTTCGTCTGT GGCGTTCTAA GTGCAGCAAA TAATCGTCTT GCAGTTTTAG 60

AAGGTCTGAA TATACCTGAT CCATAGTCTT GCTGGCCGAC AAAGAGAGAG AATAAATAAA 120

TGAAATAGGA AGTGTTTCAA TTTTyTTGTT GCGAGTAATC CAAGAAGAGA CAGTTCCTTG 180

AGAGAAAGCA TGTAATTCAC AAAATTCTTC TACAGTAATC CCTAGTTGCT TGATAATGTA 240

TGCGTTGaTA GGGTGTGGAT ATACAAAGGT TTTTCTmGGC ATGGTGGGTA AGCTTCCTTT 300

CTTAGGTTAT TAATGCGTTT GCAGTAATAT TGTACTAAAA AACATGCAAT AAGGGAAGGG 360

CGTACCTGCT TCTTTTTTGT TGACCTTCTT TAATAATGTG TTATACTAAT AATGCGGAAG 420

ACATAAGTTC GATATGAmCA GCACAAkAGm CCAAACcTGT GACGAGGTTT GGGCTATTTT 480

TTTCGTCTTG CGGATAGACG TGTGGGCTAG GACAACTTGC ATGGTTATCT GCTAATCATC 540

TAACCAATGG TCAACTAGTA AGATTACTAG ACCCACAAAA AGTGGGGCAA TAACCAAAGA 600

CATAAGTTCG TACATAAACA GCACCCCCAA TCGGAGGCAA GTTGCCGAAA TAATTATAAC 660

ATAAATTCGA ATATACCTAT ACAGTAGTAA ACCTTCAGTG TTTTACTTCA ACTTTTAGCT 720

CTCTTTTTAG TACGTATACT CGTTTACATA ACGAACATTT GTACTTACCT GAATCACTTG 780

ACACTCTGCT CGCAAGACAC CCaCACGCAC ACTGTACGTA TGCAACGCCA CTTATTTTAT 840

TGTnGTCyTT AATCACTGcA CCCtGGTAGT TAAaTTyCTT CATAAAATTC TCCATCATCG 900

TAATAATCTT TCATAAAAGC ATCGATTGAT yCTtGTTCTT CATCTGATAA TTCTGGAAGT 960

ACGACGTCTG CGAAAGGATT TTCCAATGTA TCTACAGCAG ACCA 1004

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

CCCCTTyCAA ATAAgCtCGT TCgTGCTGGT CGGGCCakGA ATGCCgGTGT TTAcTTTGTC 60

aCGCaAAATA GTGaCGATTT aCTGGATGaA CGCTTGAAGA ATAATATCGG ATTGAAATTT 120

GCTTTTCGTA GTACCGATAT TCaTGAAATC aAGAAGACTT TGGAATTTTT TGGGTTGGAT 180

CAAGAAGATG AAAGTAATCA AAAACGCCTA CkAGATTTGG AAAACGGCCA ATGCTTGATG 240

CAGGATTTGT ATGGTCGGGT AGGTGTGGTT CAGGTTCACC CGGTCTTTGA AGAACTCTTC 300

CATGCCTTTG ATACTCGCCC ACCGGTTCAA GAGAGAATGG AGTGAAGGAG ATGAAAAGGA 360

AAATTTTACG GATTGTAGGC ATTGTTTTGA CTAGTCTATT TTTCCTCATC ATTCTTTTGA 420

GTTTAGTTGG AAAGGTAGCG GAAGCGACTG GATTAGTCGA TGATACAGTG AAAGCTGGTA 480

ATCTCTATTC TCAATATTCT CTTGGTAACT ACCAACTAGA TTTTTTTGTA GACAATTCTT 540

GGGACTGGCT ACCTTGGAAC TGGGGGGATG GTTTAGGAAA AAGCGTGATG TATGGTCTCT 600

ATGCCATCAC AAATTTCATT TGGACCGTAA GCTTGTATTT GTCGAATGCC ACGGGTTATG 660

TGGTTCAAGA AGCTTATAAA TTGGATTTTA TTTCAGATAC GGCAGAAAGT ATCGGGAAGA 720

ATATTCAAAC TCTAGCCGGG ATTAACGAAA ATGGACTTCA GCCATCTGGT TTTTATTTTG 780

GCTTTTTGAT GTTAATGATT TTGGTTTTAG GCATTTACGT AGTCTATACA GGATTACTTA 840

AACGGGAGAC TACCAAAGCA GTGCGAGCTG TTATTAATTT TGTAGCGATT TTTCTACTTT 900

CGGGTTCCTT TATCGCCTAT GCCCCTAACT ACATTACGAA AATCAATGAC TTTAGTTCGG 960

ATATTAGTGA ATCTGCATTG AGTCTTGGCA CTAAGATTGT CGTACCAAAT TCTGAAAGTC 1020

ACGGTAAAGA TAGTGTTGAC TTAATTCGTG ACAGCTTATT CTCAATTCAA GTCCAACAGC 1080

CGTGGCTCTT GTTGCAATTT GATGATTCCA ATGTAGAAGA AATTGGCGAA GAGCGAGTTA 1140

ATAAAATTCT ATCCGTGAGC CCGGATGAAA ATAAAGGGAA GGATCGCGAG GAGGCGGTTA 1200

AAGCCGAAAT TGAAGACAAT GAAAATGCAA ATTTGAGTAT AACAAAGACC ATGAGCCGAT 1260

TAGGGACCGT GGTTTTTTTA GTATTGTTTA ATATTGGAAT TTCCTTCTTT GTCTTTCTAT 1320

TGACAGGAAT AATGCTATTT TCCCAAATTC TTTTCATTAT CTTTGCGATG TTTCTCCCAA 1380

TTAGTTTCCT GTTGTCCATG TTACCGACCT ATGAAAGTTT GGGAAAGAAA GCGATTGTTC 1440

GCTTATTTAA CACGATTATG ATGCGAGCGG GAGTGACATT GGTCATCACG ACAGCATTTA 1500

GTATCTCTAC GATGTTTTTC AATATTTCAG CAACCTATCC GTTCTTTATG GTAGCATTTC 1560

TACAAATTGT AACCTTTGCC GGGATTTATT TCAAATTAGG CGACATTATG AGTATGTTCA 1620

ATCTCCAAAG TAACGATAGT CAGTCTATGA GTAGGCGTGT GATGCGAAAA CCTCAAATGT 1680

TAATGAACCG TAAATTTCGT CAACTCAATC GAAATGTTGG CCGAGCGTTG GCTTTTGATG 1740

GCGGTGTAGC AGTTGCAGGT AAATTAGCAA CTGATTCTAC AAAAGAAAAC AGAGGTTCAA 1800

AAAGCAAAAG ATTATCTAAT CGAAGAAACC AATCGATACA AAGTAATCAT GAGCAAAATA 1860

CTGATCCGAA GAAACAAGAA AAGACTACTA ATAGTAGAAC CACTCGATTG AATCTTATGG 1920

GTAGGAAAGC TGGAAAGGCA ATGGATTCAA AATCTATCGT GAAGGACAAA GTAAAACAAG 1980

CAAAAGACCA TGTAATTGAT ACGCCAACAA ATTTGAAATA TAACCTGCAT AGAGGAATTG 2040

AAAAGGCGAA AAATGCCCCA GGGGAATTTA AACGCGGGCT TGTGCAGGAG AAAAAAGAAC 2100

GAGAAGAACA AAGAAAAGCT AATCACCAAC AACGGCAGAA AAGAATGGAT GAAAAACGCC 2160

AAGTGTTAGG 2170

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CAAAGAATAT TGGAGGACAA AATGATCAAT CAACCAAATT CAGTTGATCA ACCAATCCTG 60

ACGAACCAAG AAAAAATGGT CAAAGGCTCA GCTTGGATGA CAGCTAGTAA TATTATCTCC 120

CGCATGTTAG GGGCGATTTA CATCATCCCC TGGTACGCTT GGATGGGCGA GCACGGAAAC 180

GAAGCGAACA GTTTGTTTTC AATGGGGTAT ACGATTTATG CCTTATTCCT AATGATCTCT 240

ACCGCCGGAA TTCCAGGTGC GATTGCCAAG CAGACCTCGC ATTATAATTC ATTGAACGAA 300

TATAAAwTTA GTCGACAGCT TTTTwATCGk GCCTTACaAC TAATGGGtGG CTTAGGTGTG 360

GkTTTTGCTA ttGtGATGTA TTtGGCATCT CCGGCATTAG CAGCTTTGTC TGGCGGAGGA 420

CCTGAATTAG TTCCAACAAT GCGTyCATTA AGTTTAGCCG TTTtAGTTTT CCCArGCATG 480

AGTGTCATTC GCGGTTATTT CCAAGGAAAT CAAGAAATGA TGCCCTTTGC TTTATCACAA 540

ATTGTTGAAC AAGTAGCACG AGTTTTTTAC ATGTTATTAA CTGCTTTTAT TATCATGAAA 600

GTCTTTGAAG GTAATTACGT TACAGCGGTG ACCCAAGCCA CTTTTGCGGC ATTTATTGGG 660

ATGCTCGCAA GTTTTGCGGT TTTAGGTTAT TACATGTACA AACAAAAACC ATTATTTGAT 720

TATTTAGAAG AACACAGCGC CAATGAACAT GAAATTGCTC CAAAAGAGTT ATTGATTGAA 780

ACTTTTAAAG AGGCGATTCC TTTTATCGTA GTCGGCTCAG GAGTGACTGT CTTTAAACTT 840

GTCGATCAGT TTACTTTCTC AAACTTTATG CGTTTGTTTA CGGaTTATTC AGATACCCAA 900

TTACGAGAGC TTTTCGGTAT TTTTAATGCC AATCCGGACA AATTAACCAT GATTGTCGTG 960

GCTTTAGCGA CTTCGATTTC GGCTACTGGa TTACCGTTAA TTACAGAAGC GGTCACCTTA 1020

AAAaATCACC GTGAATTAGC GCGTTTGAtT AGTAATAATT TACmACyTTT TGtGkTTGTA 1080

ATGtGCCAGC AACGgTCsGt ATGATGTTTT AGCGnCACCA CTATACACTG GTTTTTACAT 1140

G 1141

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 965 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

TTAGATATGC CCTTATCAAG TCAGGCTCTG TATTTTCATT TAGCGATGCG TGCCGATGAT 60

GATGGATTTA TCAATAATCC CAAAAAATTG CAGCGAATGG TCGGTTGTGG GGAAGACGAT 120

CTAAAATTGT TGATGGTTAn AAAATTTATT CTAGTATTTG AAAGTGGTGT GATCGTTATC 180

AAACATTGGA AAATTCATAA TTATATTCGC AGTGATCGTT ACAAACCAAC CTTGTATCAA 240

GAAGAGArAA ATCAGATTGT TGAAAAAAAT AGCAAAGCTT ATACGTTTAA AGCAGAATCG 300

TCTGTCGGTG GTCAACCAGC TGACTACCAA CGGTTACCAC AGGAAAGCAT AGTCCAGTCT 360

AAGTTAGGTC AGAGTCAAGG GCAGTAGTTC AGAAAACGAT TGTTTAAAGA TGATTTATCA 420

TTTTaTGAGG AAAACGGCTT gGTACACTGG CCTCAAAAAC AAGCCArGAT TTTaAGTATT 480

GGTTGCAAGA TTTTATACAA AAAGGGGCTA GCCAAGAGGA AGCATGCCAA TTAATCTTGC 540

ATGcTTTAGG AATTGCCGTC GATCGAAATA AACGGAATTA CGGCTATGTA AATGCTATTT 600

TGAAAAGTTG GGAGCAACAA AATTATTTAT CCGTACATGA AGTTCTGGTA AATGATAAAA 660

AACAAGTGTT GGAGCATGCG CCGCAAATGA CAGAAGAATA TCAAGAGTTA GGTTTTTAAA 720

GAAAGGAGGA AATCAGTATG CATGCGACAG ATCnAACTTT TCCAATACTA TTGAGTCAAT 780

TGTTAGAAAA AGTTGAAGAC CGTTGTCCTG AATGTGGCAG TGAACAATAT GTTTGGCCAC 840

AAAAAAATAA AGATGGCACm GAACGTTGTG CCCCAACTTG TTGGTCGTGT GGGTAtAAAA 900

TGCTAAAAAA ACATGAACAA nGAGCCAATC AACAACGTTC TCAAGAGAGT TTTATGGCAC 960

GTAAC 965

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GACAAATGCT GCTGCCGCGA AAGGATCGAG AGACCCTTAG TTGGTTGAAC AGGAATAATC 60

GTGAAGGTTA TTCATAATGT AGCTGATACA TGTTATCTAC GCCCTATAGT GCTAAAGmTC 120

AACGATAGAG AATCTTATTT AAAGATGGTA TTTTGGGACG TACTCTATTG TTGAGTAGGT 180

CCTTTTTTGT GTGTTTGGCA AAAAAGCAAT TATTCACTGG AAGTATAAAT AAGAAAAAGA 240

AAGGATGACT GTCATGGAAG ACCCTGGAAG TGAACAGAGA AACAAAATAC AGTCACCAAT 300

GAAAGGAGAA GATTTTAGCG CTCTTTTCGG CAGGTGACCA CAACCTTGGA GGAAAAGAAA 360

ATGATGAACA AAAAAACAAT GGaTATGAGA AAAGCAACCA AAGaTCAAGa ATTACGTAAA 420

TTGGCTTTGC TTTCTGAACG GGAATTAATG ATGGAATTAC GGACATCTGA AAAAGGACTC 480

TCGAATGAAG ATGCCGAAAA AAGATTAGAG GAATTTGGAC CAAACGAaGT TTCTGCACAA 540

AAGCCAACCC CAGCAATTAT TTTATTTTTA AGTGCATTCA AAGATCCGTT TGTCTATGTC 600

TTAGCCTTAT TGATGGTCGT TTCAACTTTA ACGAAAGATT TCGAAGCCGC TATCGTGATG 660

GGCGTGATGA TTTTAGCCAG TGTCTTGAnT GCTTnATACA AGAGTATCGT nCTCAA 716

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

TAGACAATTG GTCCCCACTA CAACTATCCA GTTATAACnA AGAGCGCCCA CTCGAACCTT 60

TTTCTGTAAT ACGCCTAATG TCATTACCAT CATATTGCCT GTTGCTAACT CACCACCAAC 120

AAAAGTAAGC GCTATCAACC CAACTGGAAA TAAAGCTCCA CCCAGAAAGT TGTTAAAcTT 180

CCCCmTTCTG TGGGGGCAGT TCCaGTGATA CGAATAAACG CCAAGTAACC CAgTGCAaTA 240

CAAAAACCAG CCaTGATGCC TAAAATACAG AGTCGAACAA ACGATAATTT CCCTTTCATT 300

TCTGCCTTAT CACCTAAGCT TGCAACTATT TCTTCACTAC TGAAAAAATC CATTACGATT 360

CCTCCTTTTT ATCGATACCA CTGAGACAAT TCTTCTTTTC GATTGACATT TTTAAGTTGA 420

TTCTCTTTTG ATAGTTGCAC CGTTTTTACA GATAGACGCT CAAATTCTTG CCGAATCTGA 480

TAGTTATTTT GCGCAAGCTG TTTTTGAAAT GTTGGTAAAC AAGAACATCG ATAAAAGCCA 540

AATAATGGTT CTTGACGACC TTCAAAGTCA AAGATTGTTA CTTGATTTTG TCCACGCTTA 600

GAGGCTAACT GATACACAAG TTTAGGAGAA AAAGTTGGTA TATCACAGGC AATTACAAAC 660

ACTTCAGCTT TCTGAGTATA GTTCATTGCT GTCACAATCC CACCTAATGG CCCCTTTCCA 720

AGATACATAT CTTGAATGAT TGTGCATTTT CTAAACGCCT TAGGAAATTT TTGACTATCA 780

TTCGTTACTA AAATAACCTC TTCGAACAGT TCCATTAACT TTTCAGCTGT TTGCAAGATC 840

ACGTATTGCC CTTGAATTTT CAATAATGCT TTATCAAATC CCATCCGTGA ACTTTTCCCG 900

CCGCATAACA GCACTGckGT ACAATCAGCA ATAATTTTCG CCACCCCTTT TACCATAATn 960

Tnn 963

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

CACATCCTCT CTAAGTTTTC TTCTACATCG TCGGAAAGCT CGTTTTCTTC TAATTCTATA 60

TTTTCCATCA AACAAATAGC TGTTTCTATC TCTTCAATCT CATCTAATAC GCTCTCTATA 120

AGCCTGTGAG GGCAATTAAC CTCTTCTTTA TACTTGAATC GCCTAATGAG CAATTGTTGC 180

TCTAAAGGCT TAAGAGTAGC CCAAAACCGC TCAAAATGTT TTTGTCGAAA TAATGTGCGT 240

TCGATTCGTT TATCTATTAG CTCTAGCTTT AACAAAAGTT TTTCCACTTC TTTATCTGGT 300

CGGAAGCCTT TTGTAGTCAT TCCTAACTCA TCAAACACAA TATGCGTTGC CATATTTTGG 360

CTGAAAAATT CAATACGCCT TAATTTTTTT ATTGAAAGCA ACTTTTGCAA CACTAACGGA 420

AATGAGAGAT AGTTTTTTAT AACAATTTCA TCAAATGGAT CCATTGACAA CGTTCCTCTC 480

TTTCCTGAAT TGTCTTTTTT AGGCTGCCGA AAGTGCCGAC TTTTTTAGGT GTCTGATTTG 540

TCAGATTTTA AACAAAAAAG AGGACACAAG ACCTCACTCA ATTAAGAGTA AGCTGTCTCA 600

TATCCTCTGG TTCTTCCTAG TAAGATACAT AGCGCTAGAA TAGCAAGATA TACTTATTTA 660

ACTGTCTTTA TTATAGCACT TTTTTCGCCT AATAGATAGT TTAGACTGCT AATTCTTAGG 720

TAAAACATGC GATGTAATTG TATCGTATTT TACTACCTTC CCATCTTTTA CAATCAACTT 780

AACTTCCCCA AATTTTGGTA GTTCTACCAC TTCCGTTTTT TTACTGTTAT CAATGTATAC 840

TTTATCCATG TTAGCCTCCT GTTAATAAAA ATCTTTTAAA TTCTTTAGTT TTCTTAATAG 900

TAAAAATAGC TGTGCACGTT GTTAAGTAGC TCTTTAGCAC TCCTTAAGAT GCATAATTGT 960

GTTTGTTTTG AAATATTTTA ATTATACAGC GTTAGTAATT GTTAGTATTC ATACTTTTTC 1020

ACACCTAATT AAGGAAAAAG TCAAGTTTAG TCAAGTTTTT ATATAGAATA AAACGAGATC 1080

TTGTAAGGkT CTTTTTTAGG ACGGAAGAAG CGGAAGATTT CATGCCGTTA TTTCTTCTTC 1140

AATCTTTTTA GTTTCTTCGA TAATCGCCGT TTTTCAATCT CTTTAGCGTT GTTCCCTTTA 1200

GAAGCTCTAC GGTCTTTAGA CTGCACATTT AATGCATGTT TTGTGCCTGC TGGTTTTTTC 1260

TCTCTAATCA TGACTATTAT TCCTCCTCAT ACCAAATAGA AATAGTTGTA ACTGACGTAA 1320

CCTCCTCAGa ATCTCCGTAG CTTTCCCCaG TCTGTTTAAT GTGTTTGaTT TCAATATACG 1380

GGTTCTCCTC TAAAAAATCG TTTAATTCAC GCTCTAACTT GTTGATATTT CCtCTTTGAA 1440

AAATTTTAAC TTTCATAATC GCTACTCTCC TTGTCTTATA ATGTACAATT TGTAGTATTT 1500

TGTAGTATTT AAAATTTGGG TTGACTATCA AGATACATTA TAAACTCATC CGAACATAAC 1560

AGAAGGAAGG TAAATTTATC AAAAAGATCT ACGTACAAGC TCTCCTGATT CTCAGTAAGA 1620

TTATCTTTTG CTAAGGCAAA GTAAAGCCGA ATCAATCGCG CTAATTCTCC TTTAAGCTGT 1680

TCGACACTCG AAAAATTTTC ATCTTCTAAT AAAGACTGTA CAATTACTCC TTGCATGCCT 1740

CCTGCAGCTT CTTCTAACCA ATTAGGGTCT TTTTCCATTT CCGCTAAAAC GATAGGGGAA 1800

AAATGAGAAA TATCTCCAGT AAAATGACCT CGTGTAAAAG CCAGCATATT GGATAAAAAA 1860

CTTCTTGTAA TTTCTTCATA TTCAAAATTC GGTTCTTTTT CTGTTGATAA TATAAGCATA 1920

AGATTTCCTC TTTTCTTTAT CTTTTTTTGT TTTATTCGTT TGGTAACTAA TTCTAAAAAA 1980

AACTGGTTAC CGCTTAAAGC ATTGGGGGAG TAAGGATAGA GCCATTTGGT AACTAGTTAC 2040

CAATTCTTTT TACTATTCCT CAAACTTTTA TTAAAACTTT ATTTACAAAT TTCAATAGAT 2100

AAAATTAGTA ACTGGTTACC AAAACGCTCC TCCCTCACTC TCCCAAGGGG TGGGAGTGGT 2160

AACCGATTTA TTTTGAATTG GTTACCATTT TTTTATAAAT TTCTCTTCCC TCTTACTCTC 2220

CCAAGGGATT TGGTCGGTTA CCAATTTATT TTTAAATCGG TAATTTAACT TATCAGCTTT 2280

AAATCGTTTC TTACTAAAGA TTGGTAAGGC ATTCCATTTT CTGGTGGTTC TTCATAGCTG 2340

AAAAAATCTC CCAATGCTTT TATTTTTTCT ATCTCATTCA CACTATATTT TATTTTTTTA 2400

TTTATCCAAC TATCCCCTAA TAAATATGTG AACTGTTTAG AAAATTTAAT TTTACTCAAT 2460

GGTTTAAAAT TATTTTCCTT GCAAAACTCT TTATATTGAG AGTAAACCAT ATAAAAAGGG 2520

ATTTTGTTTA TTCCTAAAGG CTTGAATACT GTTTCTCTAA AATCAACTAG AGGGTCATTT 2580

TCTTGTTTAT ATTCTTCTAA AAGTTTTTTG GAAACATCAG GTACTATAAA ACGTTCAAAA 2640

TCCATGTTTA CCGCTTTATG CAAAACGTAT TCGAGCACCT CTTTTCGGTT GAtATACTCT 2700

TCTTTTATTC TCCAATCATC TTTAGCACCT TCAAATGAAG CATT 2744

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

ATTnATCTTT TTCnGGCTCG GAACCAATAG ACCCATTTTG CCATTCTAAA CTGATCTAAA 60

ACGTAATAAA ACAGTTTGAT CCATCTGGAT TGATTTCAAC CCATTTAGGT AGTTTGTAAG 120

AACGTTTAGC CAAATTTCAA TACTTCTTTA ATTGGCAAGC CCTACGTTCC TATAGATAAA 180

CTTTTTGCTT TTAATTGTAC ATTACCATTC GCCATCACGT AAGGATCAAA ATATAAGTAA 240

AAAGGAATGT CATGCCCTAA CACCTGAAAT GTTCCATTTA ATAAAGCATC ATTTTCTAAA 300

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TAAAATTTAT ATTTGATCTC CGAACCTTTT TGAAAGTCGG CTAAATAAAA GTCAATCAGT    360
TTGTTCACTT GTTGTTTTTT TGACTGAATG GTGACGACTG GCTCGCCTTC TTTTTCAACA    420
ATTGCTGGTA TTTTCTTTAA ATCTGGTTCG CGAACTTGTG TTGCTCGAAA TGTCACGAAA    480
GCTACACTAC CAATGATTAA ACCCACTAGA ACAAGAAAAG CGATTTTCCA GGGATTTCGT    540
TTAAGATTGG TTGGTTGTGT CTTTTTAATT GATTTACTTG TTTTTGGCTT TTCTTCATTC    600
ATTTTATTCA CTACCTTCTG ATTTGGTTAT CCATTCTTTC TCTGTCTTGA CCATTTCATC    660
CCGGACAGCT CCGGCCATAA TTTGGTAGCC AAGATTATTC GGATGGAAGC GATCTTCTTC    720
ATATAACAAA TTGTTTAAAT CCTCTTTGCT AGCACTACTT CCTGTAGTTT CTGAGTCACC    780
ACCAGTTACG CCAACTTCAT CGCCACGACC TTTATAGAGT AAATCATTGA TAGGAATGAA    840
ATAGGCTCGT TTTTGCTCTT GAACCATTTC TTCGGTTGCy TGATTCCAAT TATCAACGAT    900
TTCTTGCATT TCTGTAATTT CGGAAAAGTT TAAGTAGAAG GGATTGTAAA TTCCTAAGAC    960
ATAAATAGGG GCCTTCTCGT TGTACTCTCG GATTTCTTCA AGTAGTCGTC TTACTCGGCG   1020
TTGATAGGCT TTTtGTGGAC GATTGAACGA GCTGACTTTC AAGTCGAAAA TATTACTACT   1080
AATTACTTTC ATTAAGTCAT TTCCACCAAC CGTTAGCGTA ATCACGTCCG CAGAGGCAAG   1140
GCCCTTTTGA ATTTCAGGTT TCTCTTTGAT TCGTTTTAAA ATTTGATCAC TACGATCCCC   1200
ATTTTTCCCA AAATTGTCTG TTTGAACACC GTTCAAGTTG TAGTGTTCTT TTAAATCATC   1260
TGCCACAATA GGAACAAAAC CTCCACTATT CGTCAAATCG CCAATTCCTT CAGTTAAAGA   1320
ATCACCGATA GCTGTATAAT GAATGACTTC TTTTTGATTT TTTTGAGCAG TTGTGGCCAC   1380
TTTCTCTTGC TTTAATAGTG GCTTTGCTTT GGGGATGGCC ACACTTAACA ATGTAAAAAC   1440
ACCTAGCGCA ATGAGGATAG GTGTTAAGAC GGTCAGCAAA ATATGCTGTG TTTGTTTTTT   1500
CATCTTCGTC ACTTCCTTTT AAATAAACCA ACAAGAAATT TTCCTTTTCT TGTTAGAAAG   1560
AGGTTGCGTC TACTCGTTTA AGAGTGAGAC CCAACCTCGT TATTTCTTAG TCTGTATAGT   1620
ACATAATAGC AAAGGCATTT TTcCTGTATG TGTTGCAATG ACTGGaTTCG TATGTAATAC   1680
GGGaATATCC ATGTCTTTaA AGATTGCTTG TAATCCTTCT TtGAATCCAT TtGCTAGTTC   1740
TAGCCCATCC gCATGAGAAA TGCCAATTTG TCGAACATTT GGAATCTTAC TTAATTCTGA   1800
TTTCAATTCG TCAAACCATT TATTAAACGT TTTAACGCCT CGGCCTTTCG CTACAGGAAT   1860
CAATTCCGTA TTTTCAAAGT CCATGACAAC TTTCATATTA AAAATGTTTG ATAATAATCC   1920
TGTTGTACGG CTGATTCGTC CACCTTTAAC CAAATTATCC AATGTTGAAA TGCCAATGTA   1980
TAATTTAGTA TTTTGTTTGA CGCGTTCAAT TTCAGCTAAA ATTTCTGGAA CACnCGCTCC   2040
CGCTTGTGCC AATTTTGCTG CTTGAATGAC TTGGAAAGAC AAACCTTGGT CTGTAAAATC   2100
GCTATCAATC ACCGTTACTT TACTTGATGA TAAGTTGCTA GCTTGACGGG CCGCTTCAAn   2160
CCGTT                                                               2165
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(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GGTGAAGCAA CCCTTCTGTT GCTCCACCAA CTCCTAACTA GACCGTTTCT CGATGCCTTA 60

GATTATTTTG ATTCTTTTTC GCCTGCTTCT AAGTAGCTGA CATCATTGAC TTTATCCAAA 120

GTATATTCGC CATTTTTGTA ATGAATTGTT GTGACACTAG CATTCTTCAA ACCGCCTTCT 180

GGGACTTTAA AATCATCAAA TAAAGTTGCT AACAACGCTG AAATACTCAA GCCATGAGAG 240

ACCACTAAAA CATTGCCATT CCCAGAATTG GCTGATTCTG TGGCAACAAT TTTATCTAAG 300

CCTTTTTTCA AACGTTTAGT AATTGTAGCA TAGTCTTCTG CAGGCCAGTT ATTCTTGCTT 360

TCCTCGCGCT GTTGATCCAG TTTAGCTACA CTATTGGCAA AGGATTCAGG AGTCATGTTT 420

TTCATAAATT CTTCTAAGGA AACACCTTGA TCATCAGCAA TATCCTGCCA CATTGTCTTA 480

TTTAAATCCC CTTCATAGCT ACCAAAATTA AATTCACGTA AATCTGGGTC ACGCACGACT 540

TCAAGGTCTT TGCCTGCTTT ATTTTGATCT AAAATAAGTT GAGCAGTTTG CAAGGCGCGG 600

CCACTATCAC TACTATATGC ATTTTGAAAG GCAACATCTT TCAGTCCAAT CCCAGTTGCT 660

GTCACAACTT TTTCACCTTC TGGTGTTAGG ACCGCATCTG ACCATCCTTG TACGCGGTCC 720

GTCGTATTTA ACATGGTTTT TCCGTGGCGC ACAATGTAAA GAGTTAGTTC TTCAGGTTTT 780

GTCTCtTTTT CTTTTGTCGT TGCTTGCTGA TTTTTACCAC AACCAACCAT TACTAAAATG 840

GCCAGAAAAA GCATCCCCAC AATCGTCAAT CGTTTTTTCA TTTTTTATTT CCCCTCATCT 900

TCTACTCTGT TGTTAAGTTT TCACCATTAC TAGCGATAAC TTGTTTGTAC CAATTAAATG 960

ATTTTTTCTT AGTTCGTTTC AAGGTTCCCT GACCTTGGTC ATCCATGTCT ACATAGATAA 1020

AGCCGTAACG TTTTTTCATT TCGCCAGTCC CTGCTGAAAC TAAGTCAATA CAACCCCATG 1080

GCGTATAACC AATTAAGTTA ACCCCGTCTT CTTCTATTGC GGTTCTCATG GCTTCAATAT 1140

GTTGTTTAAA ATAATCAATG CGGTAATCGT CGACAATCGA GCCATCCTCT TGCAATGTAT 1200

CCACCGCGCC AAACCCGTTT TCAACCACAA ACAATGGcAT ATTGTAACGA TCTGACAACT 1260

GACACAATGA AATTCTTAAC CCTAAAGGAT CGACAGCCCA GCCCCATTCA GATTCTTGCA 1320

AATAAGGATT TTTAACCGCA GGCATTTGGT TGCCTCCGAC ATATTTTACT TCTTCGGGAT 1380

AAGCAGTCGA AACAGTCGAC ATATAATAAC TAAACCCGAT ATAATCAACT GTTCCTTTTT 1440

GAATAATCGC TAAATCATCT GACTCCATTT GAATTGTCAT TCCTTCACGC TCAAATTCTT 1500

TGAGCTTATG CGCTGGATAA TAGCCCTTAG CCTGGACATC CATATAAAAT TCTTGCTCTC 1560

GGTTAAATTG AACAGCTGCT ATCACGTCCT CAGGTTTGCA GGACAAAGGA TAACTTGGAA 1620

TATAAGCCAC CATCATACCA ATTTGGAAAT CTGGATTGAT GGAATGTCCT AATTCAACTG 1680

CTTTCGCACT TGCTACAAAT AGATGATGCG CTGCTTGATA TTTACTTTGT TTATCATTAT 1740

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TGTGAATCCC AATTTGCGTC CAACTTCTTA AAAAATTAAT TTCATTAAAA GTCATCCAAT     1800
ACTTCACTTT ATCCTGATAA CGTGTAAAAA TGGTTTCGCA AAAGAAAACA AAGAAATCAA     1860
TCACTTCACG ATTTTTCCAA CCATCATATT CATCGGCCAA ATACATCGGA ATATCAAAAT     1920
GGTTAATCGT CACAACGGGC TCAATTCCAT GGCGCAGCAA AGCATCAAAA ACTTTATCAT     1980
AAAAGGCTAA GCCTTCTTCA TTAATCTCTT TTGTTCCATT TGGGCAAATC CGGCTCCAGG     2040
CGATAGACAG CCGAAAACAT TTGAAACCCA TTTCTGCAAA TAAGGCGATA TCTTCTTCGT     2100
AATGATGGTA AAAGTCCGTC GCTACATGAC TAGGGTAGTA TAATTCTTCA TCGATATAGC     2160
CAATCGCTCC TTCGGGTAAT GCTTGATCGC GCGTACACGA AGCTTTTTGG CCTTCTTTAG     2220
TTAAATACGT AATCCGTCGC GGTTCTGTTT GACTACCACC AGTAATTGCA TCTAATGTAC     2280
TCAGACCTTT GCCTCCTGAA AGgTAGCCAC CTTCATATTG GTTAGCAGCT GTTGCGCCGC     2340
CCCATAAAAA ATTTTCTGGA AATCCCATAA AATCCCTCTT TCCCTCTGTT TTTAGGCATC     2400
ACAAAGAAAC CATCAAGGGA ATTGACGCTG GCAGAAGAGT CCTTGTTTTT TCTACCAACG     2460
TCAAACGCCC TTTAATAGTT GCTAATTTTA TTAATTACTT AAATCTTCAC CATTTGTTGC     2520
GATTACTTTT TTGTACCAAT CAAACGATTT CTTCTTGCTT CGTTTTAACG TACCATTTCC     2580
TTCGTTATCG CGATCCACAT AGATAAAGCC ATAGCGTTTT TTCATTTCAC CTGTTCCAGC     2640
TGATACTAAA TCAATACAGC CCCAAGTCGT ATAGCCTAAC AAGTCGACAC CATCTTGTTC     2700
AACAGCATCT TTCATCGCTT GAATATGCGC CGCCAAATAA TCGATACGAT AATCATCGAC     2760
TACATCACCA TTTTCGTCTG GTGTGTCTAC CGCTCCTAAG CCATTTTCAA CAATGAATAG     2820
TGGTTTTTGA TAACGATCAT ATAAGTCATT CATCGTAATT CTCAAACCAA GCGGATCAAT     2880
TTGCCAACCC CATTCACTGG CTTTTAAATA AGGATTTTTC ACAGAGGCAA AGATGTTACC     2940
AGCTGTTTGT TCATTAATTT CTGGATCTGT TGATGTGACA CGAGAAGAAT AATAAGAGAA     3000
CGAAATGAAG TCCACCGTAT GTTCTTTTAA AAGTTCTTCG TCGCCTTCTT CCATTTCAAT     3060
TTGAATACCT TTACGGGCCA TTTCTTTTAA AGCATACGCA GGGTATTCCC CACGTGATTG     3120
GACATCAATA AAGAAATAAT TTTCACGATC TGCTTGTCGA GCAGCGAAAA CATCTTCTGG     3180
TTTACAAGTA TAAGCGTAGT TGGAACCAGC CGCTAACATA CAACCTACTT GGTTTTCAGG     3240
ATCTACCTCA TGAGCAATTT TTGTCGCAAT TGCACTTGCT AGTAGTTCAT GATGGGCCGC     3300
TTGGTATTTC ACTTGTTCTT TGTTTTCGCC TTCTTCAAAG TATAGACCTG CTCCCATAAA     3360
TGGTGCATGT AAAATCATAT TAATTTCGTT AAATGTTAAC CAATATTTGA CTAATCCTTT     3420
ATATCGGtTG AAAATTACAC GGCAAAGATT TTCATAGAAA CCTACTAACT TACGACTACG     3480
CCAAGCGCCA TATTCTTCCA CTAAGTGCAT TGGGcAGTCA AAGTGTGTAA TCGTTACTAG     3540
TGGCTCAATC CCATATTTAT GACATTCTTT GAATAAGTCT TCATAGAACT TCAAGCCTTC     3600
TTCATTCGGC TCTGTTTCAT CTCCCATTGG AAAAATTCGA CTCCAAGCAA TGGATAAACG     3660
GTATGTTTTA AAACCCATTT CACCAAACAA GGCGATATCT TCTTTATAGC GATGATACAT     3720
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ATCAATCGCC TCTTGTGCAG GATAGAAATG TTCCTCATCA AAGTTAAACA TTTTCTTTTC 3780

ACCAGTGATT ACTGGAAAAC GATCTGGACC AGTTGGCGCT AAATCGACGT TTGCCAAACC 3840

ACGTCCGCCT TCGTTATAGC CACCTTCACA TTGATTGGCT GCTGTTGCGC CACCCCATAA 3900

AAAGTCTTTT CTAAATGCCA TAAATTCTCT TCCTCCACAT CTTTTTATAT TAAAGCGGTC 3960

AGCAAATCAT CACTTGTTGA AACTTCATTA CTGCCGACTT CCAAAATATC TAAATAATCC 4020

GCTGTATTCG TCACAACGAT TGGAATTTGT GTACTAAACC CAGCTTTTTT AATTCCTTCT 4080

AAATCAAAGG TTACTAATGT TTGACCTTTT TTCACGCGGT CACCTTGTTT TACAAAAGCT 4140

TCAAAGCCTT CGCCTTCTAA TTGAACTGTA TCAATCCCAA TATGAATCAA TAATTCTGTG 4200

CCGTTATCTG AAATCAAACC TAATGCATGT TTTGTTGGGA ATAGTGTGAC AATCGTTCCA 4260

TCAAAGGGTG CAACCACTTT ACCTTCCGTT GGTTCAATCA CGACCCCATT TCCTAATGCT 4320

CCATTTGCAA AAGCAGGATC CTCTGCATTT TTTAAAGATA ACACTCGTCC TTTGACTGGA 4380

CTTGTAATAT TTTCTTTTTT AATCGTTGTT TTATCAATAA TCACTTCTTC TTCCTCAACT 4440

GTATTGTCTT TCCAGAAGAA GAATGTTAGA CCAAAACCAA CGACCGCTGC AATGGCAATT 4500

GCAATAAAGG ACTGGATCAT CCCACTTGCA TCATCACCAT TGATAAAGTT TAGCACACCA 4560

AAAATTCCTA AACCACCCAT TGTATAAGCT GTCACATTGT TGATCATCAA ATATAAACCA 4620

CCGACAGCGC CACCAATCAT TGAATAAATA AATGGCCATT TTTTTGGTAA AGTGATTCCA 4680

TAAATTGCTG GCTCTGTTAC ACCAAAAATA CCAGAGATAA TTGCTGGCGG ACACAAAGCT 4740

TTTAACTTTT TATCTTTCAA TTTGAAGAAC ATCGCTAAAA CAACCGCTGT TTGCGCAAAA 4800

CTAGCTGCAA ATGATCCCGT TAATACTTGG CTTGAACCTT CTTGTGTCAC TTGCATAATA 4860

GCTAATGGCA CAACGCTCCA ATGTAAACCA AAAATAACTA AGACTTGCCA GAAGAAACCA 4920

AGAATCAAAC CATACAAAGC TGGTGAGAAA CTCATTAATG CTGTAAAGCC AGCGCTTAAT 4980

AAATCTGTTA GCATGCTAAC GATTGGCCCA ATTACTAAGA AACCAATTGG TAAGGCAATC 5040

AACAAGACGA AAAACGGTAC TAAGAACGTT TGAACAACTT CTGGAATAAT ACGTTTAAAC 5100

ACTTTTTGAA CTTGTGCCGC AAAAGCAATA ATGAAGATGA TTGGTACGAC ACTACTTGTA 5160

TAGTTCGCAC CGACCCAAGG AATCCCCATA AATGTATTAT AGGCAGGTAA ACCGAATAAA 5220

TTATACGGTG CTGCGGCTCC GGCACCCGCT GTTGTTTCAA AGGCCGTTTG TAATGCACTT 5280

CCTTGAATCG TTGGGTAACA TAAAGctGCG CCAATCACGA TCCCTACCAT TGGATGCAAC 5340

CGGAATTTTT TAGCTGCTGT ATAACCTAAA ATAACTGGCA TAAAGTAGAA AATTGCATCG 5400

CCAATCCCAT TTAACATGGT ATAAGTCCCT GACGTAGCCG TATAGAGCTT TAAGAAAACC 5460

AATAAGGCAT TTAACCCTTT GACCATCCCA GCCGCTGctA ACGCCCCTAA AAAGGGTTGG 5520

AAACAACCAC TTAAAATATC TATTAAGCGA TCAAATAAAT TCCCACTGGA AGCTTCTTCT 5580

TCACGTTCTC CTGACAAGCC TGCAATACTA ACTACTTCTT CGTAAACGGC TGGAACATGG 5640

TTCCCAATAA CGACTTGGTA TTGTCCACCG CTTTTCATAA CAGTTACCAC ACCGTCCATA 5700

TTTTTTAAGA CATCATCATT CGCTTGACTC TCATCTTTTA ATTTGAAGCG AAGACGTGTG 5760

ATACAATGTG TCAAACTATT AATATTCTCT TGCCCACCGA CATTTTTTAC AATTTTTTCT 5820

GCTAGTTCAT GATATTTTCC CATCTTTTTT TCCTCCAAAA ATTTATTTTC ATTTGAAGGT 5880

TTAGCCAACT GAATGTCACT ATCCAAAGTG GTGCGTTTAT TGTTCCGTTG TTTGTACAAT 5940

TCGTGCAATG TGAATCGTTA GGTACAAGCG TTCTTCATTT GAAACTTGAT AGTCATAGTT 6000

CTCATTTAAA TACAAGCTGA TCTTTTCCAC GCAACGATAG GCGTTGAGAT ATTTCTTTTT 6060

GATTACCGCA TACAGTTCTT CATCATCATT TTCGACAACT TCACGTTGGT GTAATAAGCG 6120

ATAACAGAAA AATTTTAATG TGTGCTAAAT CGATAAAAGT AGACAGAGTC TTCATCAAAA 6180

CTTACCTTAA AATAGTATTT GACGATATTT GTAATCTCTT GCATCAACTT TGTCAATTCG 6240

TAAATATTAC CGACTTCTTC CTCCATCTCC GCATTTACCA AGTGCAATGC GATAAAACCT 6300

GCCTCATCCG TTGACAATTC CATTCCTACG CGCTTTTGTA CCATTTTTAA AGCATTTACT 6360

CCTACTTCGT ACTCTTCAGG AAAAAAACGT TTAATATCCC ATAATAATAA ATTCTTAATT 6420

GCAATTCCTT GTTTTTTTCT TTCTAAAGCT GTGTACAAAT GATCCGTCAG AGAAATATAA 6480

ATGGTATCAT TCAAACTCTT TTTCAACGTT GATTTTGCAT AAACAATAAT GTCATCCGAG 6540

AGTTTCATCA TCTCTAAAGG AATATTTCCT AACAATTCTT GAAACTTAAG TGATGTTTCT 6600

TGATTGGCTA AATAAAAAAC TTGATCGATA CTTTCATCAG GAACCCAATC CCCAATGCGT 6660

TTCTTAAAAG CAATTCCTTT GCCCATAACA ATTTGCTCTC GTTTATCATC ATCTAATGTA 6720

ATAACCACAT TATTGTTTAA AATTTTGTGA ATAATCAATG CCCCACCTCC TTTGTGTTTC 6780

GTTGAAAAAA GAAAAACCCA ATTTCTTCAA AAAGAACGAC ACACCTGTCG CTTCATGAAA 6840

AAATTAGGTT TAGCTTGTCT TTAAACAATC ACTATCCATC TATTTACTTA tCCCtACaTC 6900

CaAAGAATAA CATATTTACA ACAAATGTCa ACGCTTTCAA CGACATTTTT TTGTAATAAA 6960

AATAAAAAAA GCATACAAAC ATTGTTTGTA TGCTTCACTA TGaCCCGTAC GGGACTCGAA 7020

CCCGTGTTAC CGCCGTGaAA GGGCGGTGTC TTAACCGCTT GACCAACGGG CCATTAAAAA 7080

GAAAAAACGG AGAAGGAGGG ATTTGAACCC TCGCGCCGGT TTCCCGACCT ACACCCTTAG 7140

CAGGGGCGCC TCTTCAGCCA CTTGAGTACT TCCCCAAGAA ATAAATGGGC CTAAATGGAC 7200

TCGAACCATC GACCTCACGC TTATCAGGCG TGCGCTCTAA CCAGCTGAGC TATAGGCCCC 7260

AAATAAGAAA AAAGCGGGTG ACGAGAATCG AACTCGCGAC AACAGCTTGG AAGGCTGTGG 7320

TTTTACCACT AAACTACACC CGCAAATTTT TCTTGGATGG CGCGGGACAG AATCGAACTG 7380

CCGACACATG GAGCTTCAAT CCATTGCTCT ACCAACTGAG CTACCGAGCC AAAAACGGTC 7440

TGGACGGGAC TCGAACCCGC GACCTCCTGC GTGACAGGCA GGCATTCTAA CCAGCTGAAC 7500

TACCAAACCA ATTCGTTTTT GCTTTATGCA AATGTATGCT TTAAAAAATA AAAGCAATTG 7560

CGGGGGCAGG ATTTGAACCT ACGACcTTCG GGTTATGAGC CCGACGAGCT ACCTGACTGC 7620

TCCACCCCGC GATAATTAGA CCAAGGAAAC TTAATTCCTA AGAAAGGAGG ATAAGGGATT 7680

CGAACCCTTG CACGGTTTTA CCCGCCTGAC GGTTTTCAAG ACCGTTCCCT TCAGCCGGAC 7740

TTGGGTAATC CTCCGTAACA AAACTATGAC CCGTACGGGA CTCGAACCCG TGTTACCGCC 7800

GTGAAAGGGC GGTGTCTTAA CCGCTTGACC AACGGGCCAT TTTATAAAAT TATGGGCCTA 7860

AATGGACTCG AACCATCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT 7920

AGGCCCAAAA AGAAAAGCGG GTGACGAGAA TCGAACTCGC GACAACAGCT TGGAAGGCTG 7980

TGGTTTTACC ACTAAACTAC ACCCGCATGG CGGTCTGGAC GGGACTCGAA CCCGCGACCT 8040

CCTGCGTGAC AGGCAGGCAT TCTAACCAGC TGAACTACCA AACCATACTT TTCTTTTTAT 8100

GTGCTTTTGA AATCAAAAGC AATTGCGGGG GCAGGATTTG AACCTACGAC CTTCGGGTTA 8160

TGAGCCCGAC GAGCTACCTG ACTGCTCCAC CCCGCGATAA TTAGACCAAG GAAATTTAAT 8220

TCCTAAGAAA GGAGGATAAG GGATTCGAAC CCTTGCACGG TTTTACCCGC CTGACGGTTT 8280

TCAAGACCGT TCCCTTCAGC CGGACTTGGG TAATCCTCCA TGATAAAAAT AAAACTATAA 8340

ACAACGTCAC AATGGACCTT GTAGGACTCG AACCTACGAC CGGACGGTTA TGAGCCGTCT 8400

GCTCTAACCA ACTGAGCTAA AGGTCCAGGC TCTTCCAAAT GTATAATCGC GGCGGAGGGG 8460

ATCGAACCCC CGACCTCCCG GGTATGAACC GGACGCTCTA GCCAGCTGAG CTACACCGCG 8520

AAACTCTTAT ATTAAAATAA GAATGGAGCC TAGCGGGATC GAACCGCTGA CCTCCTGCGT 8580

GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GGCCCCATAA AAATTATTAT CGGGAAGACA 8640

GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC 8700

CCGTATATAA CTAATGCACC CAAAGGGAGT CGAACCCCTA ACCTTTTGAT TCGTAGTCAA 8760

ACACTCTATC CAGTTGAGCT ATGGGTGCTA AATATAAAAC AATGCCGAGG ACCGGAATCG 8820

AACCGGTACG GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC 8880

ACCCCGGCGT AATGAATTGG CTAAGCGGAA AACGGGGTTC GAACCCGCGA CCCCCACCTT 8940

GGCAAGGTGG TGCTCTACCA CTGAGCTATT TCCGCAAAAT GGTGCCGGCT AAAGGACTTG 9000

AACCCTCGAC CCTCTGATTA CAAATCAGAT GCTCTACCAA CTGAGCTAAG CCGGCTAAAT 9060

ATGCGGGTGA AGGGACTTGA ACCCCcCAnC CTTGCGGCGC TAGATCCTAA ATCTAGTGCG 9120

TCTGCCAATT CCGCCACACC CGCAAATGAA ATATGAATAT GAGCCGTACA GGGCTCGAAC 9180

CTGTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAACGGC TCAAAAAATG 9240

GAGGTTAACG GGATCGAACC GCTGACCCCC TGCTTGTAAG GCAGGTGCTC TCCCAGCTGA 9300

GCTAAACCTC CAAAAACAAC AATTCGCGTG GCGACGTCCT ACTCTCACAA AGGGAAACCC 9360

TTCACTACAA TCGGCGCTAA GAAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGGTGTATC 9420

CTTCTCGctA TCGCCACCAC ACTGGGTGTT GTTTCTTATT GAGTTGAATC TTCATTCACT 9480

CAAAACTGGA TTGAAGTTTG AATCAAAATA ACCAAGTTGC TTTTACTTAT CCATTCTTTG 9540

GTTAAGTCCT CGACCGATTA GTATTGGTCC GCTCCAACTA TCACTAGCCT TCCACTTCCA 9600

ACCTATCTAC CTAATCATCT CTCAGGGGTC TTACTTTCTT AAAGAAATGG GAAATCTCAT 9660

CTTGAGGTGG GCTTCACACT TAGATGCTTT CAGCGTTTAT CCCTTCCCTA CATAGCTACC 9720

CAGCAATGCC CTTGGCAGAA CAACTGGTAC ACCAGCGGTA AGTCCATCCC GGTCCTCTCG 9780

TACTAAGGAC AGCTCCT 9797

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1807 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

CCTCTTTCGT ATATGTnnCT GTTGTAACGT AATCTCTTTT CAkGATGTGT TCyTCcTAAA 60

AGTTGTTTTT GTTTACACAT TGACTTTACC AAGTTTAGCG AAGAGTTTAC TATCCACCAA 120

AAGTTAGAAA ACGCTTTCTT TTTCGGCGTA ATTTTTCATT AAAAAAAGTT TATTTATGGT 180

TATAAACCGT TGGTACACCA GGGGTTTATA AAAGTTTAGG CGGATTTCTC TCTAATTTCT 240

GACCAATCAT AGATTTGAAA ATGGTATAAT TATTTTGAAA AATCATTCAC TTAAAATAAA 300

AGATGAAAGG GGTTTCCAAT CGTGACATTT GTTTTTATTT ATAACATCTT GTTGATTATT 360

TTATATTCGT TTACTTCAAC CTTTACCTTA AATCTTTACT TGAAAAATAA ACAACCGATT 420

TTTTTATTGC TTCTCTTTTT AATGGTTATT TTTATTTGTG ACAATGTGAT TGTTTATATG 480

ACTGAGTTCA TTAATTCGTT TGcAACCGaa TATaATCaGa CCTTTATGAC CGCACCTTTT 540

TTAAAgACCA TCATTTTTAy TTGkTGtAAT TTTGCCTAnC TGGCTATTAT CAATACTATT 600

AGTGGTCGTC CTTTTAAAAA TTATCAATTT GTCTGGTTAT TTTTAATTGG TTTATGGATG 660

CTAGCTATTC CATTTTCACA AAATTCCGCC TTAAAAGTTT GGTTGTACTA TTTACCCAAT 720

CAGCTATTTT TAATTTACCT TGGATGCTAT GCGCTCTATC AACTACGAAT AGATCCTTTA 780

TCAGCCCTTG CGAAAAAATA TCTTCGTTTT ATTGGTTGGC TAAGCATTGG TTTCGGTGTG 840

GCGATTCTTT TGGAAGATAC CtTCGTTATT TTTAACATTG ACCAATATTC TGATATTGTC 900

TTTAAAATTA ACAACCGAAA CGTTTCTGAA GATATTTATA CAATCATTCT CTCCATCGCC 960

ATTATCTACT TCTGTAATCG TGATTTTCCT CTGTCGGTTC TTGAAAAAGA CGCTGCTAAA 1020

TTGGAAGAAA ATCAATCAGA TGAACCCGTA CTTTTGGCGC CTTTTTGTGA TGCCTATCAA 1080

TTAACGCAGC GAGAACGAGA AGTGCTTTCG TTACTTTTAG AGTGCAAAAC AAATCAAGAT 1140

ATAGCCAACG AACTATTCCT ATCAATCGGG ACAGTAAAAA CACATATCCA CAATATTTTC 1200

GTTAAATTAG AAGTAAACAA AAGAGCAGAA GTTTTTGTCA GTTATCAACT TTTTTCTCAA 1260

CAACAAACTG AACATTTAGC GAGATAATTA AAAAGGAAGC CTCTCCGTGA TCGGTGGCTT 1320

CCTTTTTGAT TAACTATTTT CTTGTACTTG TCGAACTCTC TTTTCAATTT CTTGAAAGTT 1380

AATAATTTTA GCTTGGCGAT GAATTTCTTT TCCTTCATAG TATAAGATAA TGGTCGGTGC 1440

AGAAAAAGCA TTTAATTGTC CAATTATTTC TGGACTTTTA TCAGCTTCTG CAATGTATGT 1500

AGGAAATTCA TATTTTGTTG CAATTTTTTC GACAATCGGT TTATCAACTG TACAAACACT 1560

ACAATTTTTT GCTGTCAAAA AGACGGCTTG TAGACGATtG TCTGTAATTT TTTCTTCTAA 1620

TcyTCtAATG TTGTtACATA TTCCaCTGaA TAGCCCTCCT TGTCyTTTGt CyAAAATAAC 1680

AGATTTACyA GCAAAATAAC AACTTAtTGt TTGGcyAGGa AkGCyTTAAC aAAAaAGTTG 1740

tCGcCCaTTT TAtaAAkGGG GsGaCAACTT TTTACTGGAT AACCGCTTAT TAAnTAAAAA 1800

ATTTAnG 1807

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

TGAAGTCTGG TTCACCATTG TTTGAACAAA TTGATAAATC CATCGACAAG AAAGTGAATT 60

TATTCTCAAA CAGCTTTTCC CGCTACGCTG TTCGTGCAAT GCTTGCTTGT CTATTTTTAA 120

CGTTGGGAAC AGCCGTTGCT TTTGCAATCG CAATTAAAGG AGAAGGAATT TCTCATAGTT 180

TAGGGAAAAT GCTTTACGCC TTCATGTTCA GTTGGtCACT TGTGaTGATT TTATATATGA 240

ATGCCGAACT TGGtACCTCG AATATGTTGT ACATGACTGT TGGGGTCTAT CGTAAAAAAG 300

TCAACTTTTC CTTAgCTGCA AAAATTTTAT TTACCTGTAT CTTATTCAAT TTAATTGGTG 360

GCGTCTTGTT TGGCTTCTTG GTATCACTTA CGGTGCCGTT CCAAGATTTG CCAAAAGATA 420

GTTTCTTCTT TACATCGATT GCTGGAAAAT TAGAAAAAAC CACCCTACAG ATTTTAGTTG 480

AAGCTATGTT CGCCAATATT GTAGTTAATA CAGCCGTATT AGTGAGTATG CGAATGAAAG 540

ATGACGCCGG CAAAGTCGCG GCCATTATTT TCATTATCTT TATCTTTGCG TTCCTTGGTT 600

TTGAACACGT GATTGCCAAC TTCCCAGCCT TAAGTTTAGC TTACTTTGCT TCGAACGGCG 660

CAATTGAAGC TTTCACAGCT GGTAATGTTG TTCATAATCT GTTCTGGGCC TTTATCGGTA 720

ACTTTATCGG TGGTGGCTTA ATTATGGGTC TCGGCTATGC cTGGTTAGAT AAAGACACAA 780

AAaCTTAACG TATTTkGATT AATTGACCAA CCAACTATAC TAAAACATGG ACACTGTTTT 840

AGTATAGTTT TTTTATnATA AG 862

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

GAGGTTGTCG TTGTCCCATG ACACTCACTC CTCTATAAAT GAATnTATTA CaCTTATTAT 60

GTTACTACTA TTTTACAAGG TGTCAAATAT TTTCATCGTG CTTTCTGAAA ACCATTTCAA 120

TGATAACTCC ATTAAAAACA ACGTATCACT TGATTGTCTC TTTTTTGGTG CAAAATTGTG 180

CCTTTTTTGT ATAAATAAGT CCCTCGTTTT CCCACAAAAA AACCGCTACT TTTTCATCTA 240

GTTTATAAAA AAGTAACAGT TATAAATTAT TTTTTCTTTT TCCCAATCGA GAGAATCCCT 300

CTTTTTATGA CATCAAAGAA ACTCAAAGAT TGGACCATAT GATCTGGGTC AACATATTCA 360

CGAATAgctC GTAACACTCG CkTCGGCkCT TTTGAAGCAA ACGTATACGT CCCATTTTTC 420

TTGGTTTGAA TCGCATAACG AGGaATCCAT TTTCCTTTGa ACaTTACCGG AA 472

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

TATAnTTTTC AGCAATCGTT TCAAATAACT TAAATAATGT CATGAAAATT TTAACATCCT 60

TAACAATTGT CCTGACCATT CCGACCATCA TCGGAGGAAT TTACGGCATG AATGTGAAAC 120

TCCCTTTTGC AGAGCATGAA TATTCTTTTT GGATTATTTT TGCCATCACT ACCTTAATCT 180

GCGTAATTAG TATTCGAATT TTAAAGAAAA AGAATCTCTT ATAACTTTAG GTTGCTGTTT 240

TCAGGAAAAG GTTGTACACT ATTAGCAGAA ATTAAAAAGG ACGTGTCATT TATGAACGAC 300

AAAGAACAAA GTCGCTTTTC AAAAATCACG AAAGTCGTGG TTTGGCTAAT GCTGATCGCA 360

ATTGTAGGTT CAACTGTTTT AACAGCGATT CTTAGTCTTT AAACTGGAGA ACTTTTTCAC 420

ACATTAAAAG TAAAAAAACA GCCCCTTCTA TCAATTGAAA GGGCTGTTTT TTTACTTGCT 480

CAAATAGAGC GGCTATTTTT TCGCCATCGC CAACAGCTCT TGTGCATGTT CAATGGTTAA 540

TTTCGTAATT TCACTTCCTG CGAGCATACG CGCAATTTCG TTTACTCGCT CTTTTTCAGA 600

TAAAATTCGG ACGCTTGTTT CTGTCCGCCC CGCCACAATT TCTTTTTCAA TAAAATAATG 660

TTCATCGGCA ACGGCCGCCA CTTGTGGCAA GTGCGTGATA CACAACACCT GCGAATTTTC 720

TGAAATTTGA TAAATTTTAT CGGCAATCGC CTGTGCTACT CGGCCACTAA CTCCTGTATC 780

CACTTCATCA AAAACAATAC TAGTGATCCC TTGCGTTTGA GAAAAGATTG TTTTCATAGC 840

CAACATCACT CGCGAAAGTT CTCCGCCAGA AGCCACCCGA ACTAACGGTT TTAATGGTTC 900

CCCTGGGTTA GTAGTAATAT AAAATTCTAC TCCGTCTAAG CCATTTTCTT GTAAATGCTC 960

AAGTTCTGTA AAGCGGACTT CAAATTCAGT TCGCTCCAAA TATAGTTCTT TTAATTCGGT 1020

TAAAATTTGT TGTTCGAGCT CTTTGGCTAG GCGCTTTCGT TC 1062

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

TTCCTGATTG AAGCAAAGAG AGGTGTAGCG CTATGGAAAT GGAACATATT AATGAAAATA 60

CGATTCGTGT GTTAATTGGC AACGAAGACC TGGCGGATAG AGGGATTACT TTTCTTGACT 120

TACTAGGAAA CCACAAAGAT GTTGAAAATT TCTTTTATAG TATTTTAGAA GAAGTTGATG 180

TCGAAGATGA GTTCCAAGGC AGTGAAGCAG TCACTTTCCA AGTCTTGCCT AAAAATGATG 240

GTTTAGAACT GTTTATTAGT AAAAATGTCG CTATGGACGA CTTGTCTTCC TTAGAAGGTC 300

TGAGCGAAGT CaATGCAGAT GTTAGCGAAT TGATTCGCAA ACAAATTGAA GCAGACAAAG 360

CAGCCGCCGA TGAACTTGAC GAGATGGAAG CCACAGATGA AACAAACAGA AATGTAATCT 420

TTGAATTAGA TAATTTTGAA GCGATGATTC AATTATCCAA AGAAGTCTTC ATGCAATCTG 480

TTTTGACTAA CTTATACACG TACAACGATC GTTATTACTT ACAAGTTTTG TTCTTAACCG 540

ATGAATTAGA AAAAACAAAT GTTGACAATG AAATTGCACA GATTTTAGAA TTTGCTCATA 600

AAACAACTGT CACTCAGGAT ACTTTAGTCG AATATGGCAC TTGTATTATG GAACGCAGTG 660

CATTGGAATT AACACGTTAT TACTTTAATG ATTAAGCAAA AAAGCAAAAA CTTTCGAGTT 720

TcTTkTTkTT tGGaTGAAAA TTAAGAAACT TTGCGTAGTT TATTTATGAG AGGTGAAAAT 780

CATGTTAACA GCTTTAACGG CAGACAACCA AGAATTATTT TCTTTAATCG ATTGCTCGAT 840

TGATGAATTA ACACAGATAC GAAGCGAACA AGCTTTTGTG TGTCCAATGT GTCATCAATC 900

GGTCATTTTG aAGGCAGGCC CCATTAAAAT ACCCCATTTT GCTCATCGTA AAAAGAATAG 960

TTGTTGGtAC GAAGCAGAAG CTGAAACAGA AGAACACCTC CGCTTGAAGC AGCTTTTTGC 1020

GGAAAAGTGT TTACGCGAAA AGCTGTCCTT CCAAGTTGAG GCATACTTAC CCACCTTGAA 1080

GCAACGCCCA GATTTACTCA TTGGGGAAGA TAGCCATTGA AATTCCATGG TAGTCCATTG 1140

GCCATTAAAn CGTTTGGTAG AACCGGACGG AGACTTAATC AAACTCCATG GCTAATnGAG 1200

TGGTTTGGGA TTnTGGTGGA CCGATTAAGG CCTAnAG 1237

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

GCTATTCAAG ATGAnTTAAG CGATACTAAA GACGAAATAC GTGAAGTGAC GAAACAAGCG 60

AGAGAAGAAA CAnAAGAGTA TAAAGAAATC TTAGAAAGTA AAATAAAAGA CCATAACAAA 120

GTGGTTGATA AATCGAATAC AGCGCTAAAA GTGATGACAA AAGGCGTTAC AAATATATTT 180

TTTGTGCTAA TTATTTTTGT ACTTGTAATG CTTGTGACAG GTCCGATAGG TCATTTCTTT 240

GGTATTGAAC ATTTATATAG CTTTATTAAT GGTTTTATTG ATGACCACGA AAGTGCATGG 300

CGATATTTGA TGTTGATACT TTATGCAGTA CCCTATGTAT TCTTCGCTAT CATTCTGTGG 360

CTCATAGCAT TGTTTTTTAG AGTATTTAAT GACCTTTAGG TAGATTTATA TATAAAAAGG 420

GCTAAATACG CAAAATACCC CCTTAAAATG CAAAATAAAT GCAAATAAGG GGGTAACTCC 480

TTATGAAAAA ACAACTAATA GTATTATAAC ACGTTTTTAT GCCGAGAAAA CTTATTGGTT 540

GGAATGGGCT ATGTGTTAGC TAACTTGTTA GCGAGTTGGT TGGACTTGAA TTGGGATTAA 600

TCCCAAGAAA GTACCAACTC AACAACACAT AAAGCCCTGT AGGTTCCGAC CAATAAGGAA 660

ATTGGAATAA AGCAACGAAA GGAGTTGAGT AAAATGAGTG AGAAAACGAA GAAAATCATT 720

CGAGTATCAT TAGCTTTTTC ACAAGTAGTA GTGCAATCAT TGATAGTTTA TTATACTTAC 780

CAGCAATATA AATTATCTAA AGAGAATTAA GTTTTGATTA TGTAATAAGT TTTGGTACTA 840

AAAAAGACTT GATCTAATTA GACCAAGTCT TTTGTTAGTG TTATATTAAT AACAAAATAA 900

AAATAAGAAG TCGCTCACTC CCCGACCAAA GTTTGTGAGC AAAATAAACA GTCGATGTTT 960

GTTTCTTAAT TGTATATCTT GATATTAAAC GATTTAAGAT TATTCTTCAA GATATATATT 1020

CGCAAATGTA ATTGGAAAAG CGACTTCTTA AACAAAATTA AGGAGTCGCT TTTTATGGCA 1080

AAAATAACGr wAAATGAGCA AGAAAATTTG GTGGAAAATT ACACAAAAAA ACCGGCGTAC 1140

TCCAAACTAG TCAAGTCCAG ACTCCTGTGT AAAATGCTAT ACAATGTTTT TACCATTTnT 1200

ACTTATCAAA ATTGATGTAT TTTCTTGGAG AATAAATCCA TTCATCATGT AGGTCCATAA 1260

GAACGGCTCC AATTAAGCGA TTGGCTGATG TTTGATTGGG GAAGAT 1306

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

CTATTTAATC TTGCTCACGT TGTTTTCTCT TGGCTGCTCG TTCTGCGCGG nGGGCAGCCC 60

TTCTTGCTTC CGCTTCCGGA TCAACTACGC GTTCTTTTTT CACTCGTGGC TTCTCGTTCT 120

CTGGCGTATT TATTTCTGGT TCACTTTGTT TTTCAAGTTT TGCTCGAATT TTTTCTTCTT 180

GACCAGCTAA ACGAGCATAA TTATAGAACC GTCTCTTAGC ATCATTAATT GTTTTATTAA 240

ATAACAATTC CGCTGTATCT GGTTGACTGG ATTCTAAGGA CGCAAAGCGA ACTTGTTGGC 300

GCATAAACTC TTTCATTAAT GAAAAATCTG GTTTTTTGAA ATCCAATATC ATTGGTTCTT 360

TGCCTTTTTC TCGCAATAAT GGATTATAGC GATATAAAGA CCAGTAACCT GAATGAACCG 420

CGTCTTTCGC TTCTTTCAAC GTTTGACTCA TCCCACCTGC TAAACCATGT GTAATACATG 480

GTGTaTAAGC AATAATAATC GATGGTCCAG gGAATTTTTC TGCTTCTTCA AAAGCTTTAA 540

TCGTCTGCAT TTGGTTTGCA CCTGAGGCAA TTTGAGCGAC ATAGACATTT TCATAAGTCA 600

TTGCCATCAT CCCTAAATCT TTTTTAGAGG CATACTTCCC ACTGGCAGCA AATTTCGCAA 660

TCGCTGATGC CGGAGTTGCT TTGGAAGTTT GGCCACCTGT ATTGGAATAG ACTTCATTAT 720

CTAGAACTAA CATATTTACA TCCGCGCCAC TAGCTAACAC GTGGTCAATA CCGCCGTAGC 780

CAATATCGTA AGCCCAGCCG TCTCCACCAA TCATCCACTG ACTTGGTTTA ACAAAAAGAT 840

CTTGATCGTC ATAAATTGCT TCCAATAAAG GTTGATTCGT TTTTTCTTCA AGCAAAGCTG 900

CACGTAATTT AGCTGCACGT TGTTGCGTAC CTTCACTTTC GGACAGATGT GCTATCCAAT 960

CTTCCATCAA TAAACGTAAA GAATCACTGG CTACAGAAAA AGCTTTGGTC ATTTTACTAG 1020

CTAAACGTTC GCGACGCGCT TGCGTTGCTa ACAACATGCC GTAACCAAAC TCGGCATTAT 1080

CCTCTAAAAG AGAATTTGAC CAAGCTGGAC CTTGTCCTTG TTCATTAGTA GTGTAAGGTG 1140

TCACACCCGC TGCAGCACCC CAAATCGATG AGCAACCTGT TGCATTAGCA tCAGCATTCG 1200

GTCACCAAAC ATTTGCGTCA ATAATTTAAC ATAAGGCGTT TCGCcGCAAC CAGAACAAGC 1260

ACCAGAAA 1268

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1060 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

GTTTTACCTT AAAACAAAGG GCAATCAGTG TTAAAACAAT AGTCATTAAA GGAGCAGCAC 60

CTAAATCAAT TAAAGGTTTA AAAATTGTAT TTGCTAGGTC AATAATCGTA TTCATTTATT 120

TTCTCCTTCA TAAGCTAAGA TAACAAAATT TTTATCTTAG TTTTGTTATT GTTGACAGTG 180

AAGCGTAAGT AATTAGTCTG AAAAGGAAAT CATTTGTTTA AAGAGTGAAT GATACTTTCC 240

ATTTGTTGAT AAACAGGTTC AGCCATTGCT GGAATTCGAT AAAGAATTGC GCCTGCATCA 300

ACTACAGGAA TCGTGATTGG GAAACCCAAA TCTGTTTTGG CGATTTGGGC GAAAATATCA 360

TAATGGGATA GCATCTCTTG ATTGATATCT TTAATCATTA CGGCATCGCA AGAAACTTGG 420

TAGCCTCTTT TAGATAATTC TGTTTCTAAT GCAGATTTGA TTTGATGGCT AGAGTTTACC 480

CCAGCCCCAC ATGCAGCTAA AATTTTGATC ATGTTAAATC TCTCCTTTAA AATTTTTTTG 540

TAAAAAACGA TAAACTTCTT CTTTATCTTC ACATTGAAAA AAAGCCAATA GTGATGAACG 600

GTCTGTCGTG TTAATAAAAT CCaTGATAGT CGCTAAAAGA CCCGTTTGTT CAATACCGTT 660

TTCATTTAAA ATCATGAAAA GAAAGGrAAC aGAGAGCGTT yCATCTGGGr TAATCATGtT 720

AtGAAATgAT AAGGATTGTT TcAATTTAAT nCGGGATAAT TCTTGTCGTC CGTACAAAGG 780

TACTTTCGGT ATGCGGAATG GCGATATTCG GTAGTGCAGG ATCAATCGGT GTTAAACTTA 840

AACCAGTCGG ATAGTTGTGT TCTCGTTCCA ATAAATTAGT TAGAAAATnC AGGTGTAACT 900

AATTTCTTTT TTAACAAGTC TAAATAAACT TCTTCAAAAA CTTCTTCTTG TGTTTTTTTG 960

TTTGAAATAT AGGTAGTATC TAATGAAAAA ATCGATGTTT TAATAACCAT AGAACCCCTC 1020

GTTTCTTTAA TATATTATTA nTTATTTACA AGTATAATAT 1060

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

AnATnCCAAA AGAATTAAAA GACAAAAATT TACTTTATGA AAAACGTATT CCTCCGAAAA 60

AACTCTCTAC TGGTGAATTC AAAAACTATC CAAACAGATT GTATTTAGGT AAGCTGGAAG 120

TTTCAGCAAC AGATGTTTAC GCCATCAGTA ATGCTAGCTA TACAAATGAG TTTCCCGAAA 180

GTGGGAAAAA CCAACCTTCG GATAAACATG ATAAAATCGG CGTTTCTTTC GAAAGTGGGA 240

AAAACCAACG TCCAGAAGAA TCCAATAATA CCAGTACTTT GTTCGAAAGT GGGAAAAACC 300

AACCCAATCT ATATCTAACT AATTCTTTAG ATACAATAGA TACAATAGAT ACTGAAAAAG 360

AACGATTGCA ACAACAATTA TTGCTCGATC AATTTTCAGA AGTTCAAGAG CATACATTTC 420

TTAGCAAAGA TAGCTTAAAA TTTATTGCTG CCTTTTCTGA TACTATTCAA GAAGCCCATG 480

AAATGGTwGG AACAATTATT CGTGCTAAAA CTAAAGTAGA AAAAGAATAC AATmTCGTTC 540

TAATTGGTGA AGATTATCAA GAAGAaATAG ACAAATGTTT GCGACGAGTG ATGCATAAaA 600

TCAAGACGGA TTCTACTGTT AAAAGTCCTA AAGGCTTATT TTACAAGTCT TTTTACAATT 660

TATTTGTTGA ATGTGCACTA GAGAAAAAAA GTCAATTGAA CAAGAAAAGT AATTCTAACA 720

CACCAGGAGT AATCACTCAT AACTGGGTTG AAAATCaATa AAGTaGCTGT TTaGTaTGaA 780

TTTAAATTTA TGGAGGAAAA TTATATGTCT TTTGAATCTG AAAATAAAAA CGTAGAAAAA 840

ATAATTGTGT CTAATAAAAC GTATTATCTT GTTGGGACAA GTCACATTTC AGAGAATAGT 900

GTTAAACTTG TTAAAGAGGT TATTGAAAGA GTTCAACCAG ATACTGTTAG TATCGAGCTA 960

GATAAAAAAA GATATGAAAA ATACACTAAC TCTAACCAAT GGGGAAATAC AGATATAATa 1020

AAAATTATTA AAGAAAAAnA ATtAGTTGTT CTAATATCCA ATATTGTTTA CAGTGCATAT 1080

CAAAAAAAAT TAGCAAATAC TAAAGGAACT ACTCAAGCTG GTGAATTAAT TCAGGCAATT 1140

AAAAGTGCTA AGGAAATAGG AGCAAACATT CAATTAATCG ATCGTGATAT CCAAGTTACT 1200

TTTAAAAGAA TGTGGCGTCA TTTAAGCTTT TTGGAAAAGC CAAAACTTTT TATGACATTT 1260

TTTACTGAAT TTGATGATAT TGAACAAGAT AAATTAGAAG AATATTTAGA GTCTGATAGT 1320

TTTGACAAAG TATTTATTTC GTTATCAAAA AAATATCCTT CGCTGTATCA GGATATGATC 1380

ACGGATAGAG ATAAGTATAT GTCTACTAAA TTGAmAAATA ATTCAAGTCA AGTGAATGTT 1440

GTGGTGGTTG GGAAAGCTCA TATGAaAGGa ATTAAAGAGA AGTTAGAAAA AAGAACAGAG 1500

TTTTCCTTAG ATAATTTAAA TGAAATTCCA CCAAAAAAAT TArGTmCTAA ATtATtAGaA 1560

TTnCC 1565

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

CCGTGGAACC TTCTAAGTCA CCACCAATGA TTCCAGGTAG CCCCATTAAT AAAATATCGT 60

TGGATAATAG GCTCTTTTAA CnCGATCAGC ATCCCACGTC CCATAATTAA TAATGCAAGC 120

CTAAAACAAT ACTCGGAATT TGAATAATAA TATGTGAACG GAAGGGGTTA ATATCTCTTA 180

ACCAATGCAC TTGAGTGAAG GCTTCTGGAA TAGTGGCTAG GAGCACCATC ATAATTCCTG 240

AAAAATAAAG TAAAACCACT TCTAGCTTGT GGGCAATTTC CAAAGTAATT TGTTTTAGCA 300

GTTGACGATA ATGAGTATCC AACTTTTGGC TTAAGTGTTT TGTAAAGAAC AAACAGCCAA 360

TTAAGAACGG AATAATATAA TAGAATAAAC GATAGAGCAA TAACCACAAA ACAATAATTT 420

CACGATCGAC ACCTAAGTTG CTCAGTCCTA AAATCATCAT GACATCAAAA CTACCTAAAG 480

CCCCTGGAAT CATCGAAGCA ATCCCAATAA TCGAAGCTGC TACATATAAA GGAACAATAT 540

CAATTAAAGG AATCGGTACA TCTAATAAGT AACCAATACT GATAAAGGTA ATTAAAACAC 600

CTGTCCATTC TAAAAACGAA GGAAACCACT AGAGATAAGC GTTTTTTGCA TCGAGGGTAC 660

CAAnGGACTA TTTTTTTGGG AATGTAAATT AGTTAAGTAC nGGAATTAAG CCGCACCTAA 720

TTACCnATCC CATATTGCTG TAATAAGCCT CTTTGnTCAA CTGACCAGGG AAAGCAAGAT 780

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1610 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

GAATGTGGAT TTAATTGATC GTGATGTGTT TGGTTATGCT GTTGATAAAG GCTGGATGTG 60

TGTCCAAGTA TTCTTTGTCA GACAAGGAAA ATTAATCGAA CGTGATGTAT CGATTTTTCC 120

ATTTTATGAT GATGCCAGTG AAGCATTTTT AACTTTTATT GGACAATTTT ATCAAGAGAA 180

TGAGCATTTT GTGCCAAAAG AAGTCTTGAT TCCTGATGAC ATTGATAAAG AAAGCGTCGA 240

AGCTTTATTA GCTACGAAAG TCTTGCAGCC GCAACGGGGA GAAAAGAAAA AACTGGTTAA 300

ATTAGCCAGT AAAAATGCTG CAGTTGCTTT AAATGAAAAA TTCGATTTGA TTGTACGGAA 360

ACAAGAACGA ACAATTGGCG CAGTTGAAAA ATTAGGCAAT GCGATGAACA TACCTGCGCC 420

CATTCGAATT GAAGCATTTG ATAATTCAAA TATTATGGGA ACAAATCCTG TTTCTGCGAT 480

GGTTGTGTTn ATTGACGGAC GGCCAGCTAA AAATGAGTAT CGAAAATATA AAATAAAAAC 540

CGTCCAAGGT CCTGATGATT ACGCTTCTAT GAGAGAAGTC ATTTATCGCA GATATTCACG 600

AGTTTTAAAA GAAGGCTTGC CTTTTCCTGa TTTAATTTTa ATCGATGGTG GTAAAGGTCA 660

AGTCGATGTT GCCAAAGATG TGTTAGCCAA TCAACTAGGA GTCGATATTC CTGTAGCTGG 720

ATTAGCCAAG AACGACAAGC ACAAAACGAG TGAACTTTTA TTTGGTCCAA ACTTAGAAGT 780

TGTACCATTG GAAAGAAACT CACAAGAATT TTTCTTGTTG CAACGAATCC AAGATGAAGT 840

CCATCGTTTC GCCATCACAT TCCATCGTCA ATTACGTAGT AAAAATAGTT TTGCTTCCAA 900

ATTAGATAAC ATTGAAGGCT TGGGACCGAA ACGCAAAAAA AATCTTTTAA AAGAATTTAA 960

ATCGCTTAAA AATATTACGG CAGCCAGTGT TGAAGAATTA AGAAAAGCTG GGTTACCTGa 1020

AACTGTCGCA AAGAATGTGT ATCGTCATTT GcATCAAGAA ACAACCTCTG AGATAGAAAA 1080

ATAAATGAAA ATGaaCCAGa CCmATTaGGT GCTTTTCCTA ATTTGtCTGG TTTTTTTATT 1140

CAATTTTTTC ATGAAAAGTT GAACTCTCAA GAAAATATGA TAACGATTTC TTTCGTGATA 1200

TACTAATACT AACTTAAAAG AGAGGACGTC TGATCATGAA AATACTAACA CCCGTTTATC 1260

AAATAAAATT TAAAAAAGTA CCAAATCAAT TACTGATTGA TGAGCGTTTA ATGAATGAAT 1320

TGGGTAGATG GCTGAATCGT ACAGGTCGAA TTTGGGCCTG TCAATCATCA AAATCGGCAA 1380

AGGAATTTAA AAATACATTT TATGAAAGTA CAGGCTTGTC CGCAAATGAA GTGTATATTT 1440

CTGCCGAGAC GGATGGCCTT TTTCGTTaGC AGAAATAAAG CGCTGTTAAA GTGCACATCT 1500

TTCCATAACA ATGTCATGnC AGCCACACGG AAGTACGTTG GTACTAACAC GGTTGAAAAn 1560

GAAGGGGCGT TAGTGTAnGG AAAGGTAGCA ACCTTGGGAT TAACnGTGAC 1610

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

TGAATAATAA ATAAAGGAGA GAAACAAAAT GAAAGATACC TTTCGCTTAG AAAACCAGAC 60

GATTTATTTT GGTACAGAAC GGGCAATTTC AGCCAGCCCT CAAACGATTT GGCGCTACTT 120

AACTGAGACA GACAAGCTAA AACAATGGTT TCCAGAATTA GAAATTGGTG AATTAGGTGT 180

TAACGGGTTT TGGCGGTTTA TTCTGCCCGA TTTTGAAGAA ACAATGCCTT TCACTGATTA 240

TGCAGAGGAA AAATATCTGG GCGTGACTTG GGATACTGGT ATCATCTATT TTGACTTAAA 300

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AGAACAAGCA CCTCATCAGA CCCTGTTAGT CTTTTCAGAA TCTCTCCCAG AAAATTTTAC     360
AACACCTCGC CATAAAGATA TCGCTGGTTG GTCAATTGTT CTCAACCGCT TGAAGCAAGT     420
AGTTGAAACC CCTGATGCAG CACCAGAAAA AATAGATTTT CCGCAAATAG AAAATCATTA     480
CTTGGaAAAA TTAACGAATT TAGAAAATTA AAAAGTGTGG CACAACGGGT AAATCACCCT     540
CTGTGcCACA CTTTTTAAAA ACGTAAAATA CGCTGATAAA CAAATAAACC TAAATCAATT     600
AAGCAAACAA CAAAAATTGC CAATAATACA AAAGAGACCC GCAACTCTGC GGCGTACATC     660
CCTCGTAAAC TAATTGTTGC CAAACATAAC CCAAAAATCG TTGCCATTGT CACTTGTAAC     720
ACGGTTCCTG GTTTTAGGGC ATAAACAAAA ATGCCAATCA AACTAGAAAC AATGAGGTGT     780
GTCAGTGGCA aTTGAAGCCA ATTGACAACA AACAGACTAA GGAAACATCC TAAAAGAGTC     840
CCCCAAAAAC GTGTCTTAAT ACGCGTGTTC ATTTCTGCTT TCACTGGATG CAAGAGTAGA     900
AAAACATTCA TCGGAATCCA AATTATTTTA ATGCCTCCTA CACTCCACAT TAAAATAAAA     960
CTCAGTGTAA TGGTGAAACT CATACGAATA GCTAAACGAA ATCGTgCACC CTTTCGTCAG    1020
GACTTTCTAA AAATTGTTTG AAACTTGTAA TCCCAAAAAA AATCTGTTGT AAGTCGTGCC    1080
AGAAATTAAT AACTGCCAAT TTTTGTTGCT TCATATTTAA TTGAATGCTT TTAAAAAAAC    1140
GAACATGGCC CCTACTCTTT AAGCTAGTTA GCTGACGTAA TCCTGTTTGC CACCAAGCGT    1200
TTAATGTTAA AGCCAATAAA AAAAGAC                                        1227
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(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

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AGGATCCCGC ATATTTAAAG CGCTCGTGAT nCAGTCAATT AAATCTTGAG GTGTGACTAC      60
CATTGTTGCT CCAATATCAC GAGCTTTTTG TTCTTGTTTC CTCTTTTCAT TTGTATCTTG     120
ATCTATTATA TCGCCAACCG ACGTGAGGTG ATGTCCAATT TCCTCTGCAA CCGTACTAGT     180
TAATTCTCTA GGATGTTGTT GAGGATTTAA ATACACAACA TTGTTAATAT ACAATCCTTT     240
TTGCTTTTCG GGCATGTTTG GTTCAAACTT ATACGTTAAA TCTGAAAAGC GAGCCATCAG     300
TTCTTCTGAA GTTACCATTT AAACACCTAC TACTTTAATT ATTTGTGATC GCGTTTCTTA     360
ATATAATCAA TGAAAGAGAG AATCTCATTC ATTTCTGTAT CTGAAACGTT ATCGTCTATA     420
TGAGCAGCGA CGGTTAATTG TTTTTTTGAT AAGGAAGTAT CTTCAAAACT TTCTCTCCCA     480
TGTAAATAAT CTAAACTTAC ATTGAAATAG TCAGCAATCT TATTTTGGAT ATCTATATCT     540
GGAGTTCTTC TTCCTTGTTC ATAGGAAGAG TAAGTCGTTC TAGCTACACC AAGTGCATTT     600
GCAACATCAG TTTGTGTTAA TTTTTTTTGT TTCCTTAATT CTGTTAAACG TGTACCGaAC     660
ATAATGTTAC CTCCTACGAT TCGTTATGTA CATATAATAC TACGCAATCT GAGTAGTTTG     720
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AAGTTAAATA TATTAAATGT GTCAAAAAGA GTAATTAATT GTTGACATGT GTCAGAATGC 780

GTAgwATTAT AAAAGTACGC AATACGACAC ATAAAGGAGG ACACAAAATG AGAGATTGGC 840

TATTGGAATT GCGTATAAAA AATAAAATGA CTcAAGAAGA GGTTgCCgTT aAAgCGGaAA 900

TTTcAAGAAC CaCGTATGCA TCTATTGaAC AGGGAAGAAG AAGGCCATCT GTGGaAAGTG 960

CTATGCGAAT CGCATCAATC TTaGATTTTg aTTgGACAAT TTTTTTTtGa GTAAcTATGA 1020

CTCGTTATGA CTCTTTATAT TTGGATAGGA GGTGAAAATA TGCCAGAAAA ACAAAAAATG 1080

ATTGATTTCA TTTTGGAAAT CATGCCAAAC GTAAAGCTTA TTGTTGAACT AGCmACAGAT 1140

GATCAGTTAG TTCGTCTGTA TGrACAAGCA CAGGATAAGT TGAACTATCm ATTGGATCTA 1200

ATCTAATTGT ACaAAAAAAT ACATCATATA AAAAGATGGT TAATTAAGAA AGGAAGAAGT 1260

AAAAGTAAAT GTCaATGTCa GTAATATTAA GAAAGTCGTT AATCGAAGTT CTTAATAAGA 1320

AAAATGAAAA GAAGAAAGAT GTAGCaCGTG AAATCAGTAC ATCTCAACAA TCATTGAGTG 1380

ATTGGACTTC TCAGAATAAT GTTAAACCAG TAACAATTGA AAATGCTCTA AGGCTTAGTG 1440

ATCACTTTAG AGATTCGACT TTCACAATGG AAGTTATTCA TCAGTTTTTT GGAATGTTTA 1500

AAACTTGCGA TGGAGATGTT TATCGAAAAG ACCCTTCGTC ATTGGACCGA TTACAGAAAA 1560

TTGAATCTAA TGAGAGAnnA GCATTGAAGC ATGACATAGA AAGAATTGTT TTGAAAAAT 1619

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2082 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

ATCCCGCAAG TCGTCGGTnC TAAAGGAAAA CTAGGACGAA ACAATGTAAT TTTTACTTTA 60

TCTTTGGCTT ACTATGCGTC AAAAATTGAA CAAGACCGCT GTTTTGATGA TATGGATGTA 120

TTCAACAGTT CTTTGAATTA TCCTCTATCA GTTTCAGAAA TAAAGAGAAT TGTTAAGAGT 180

GCTTACTCAG GTAAATATAA AGGCGCAAcA AAACCTATGT GCAAGAACTA GTGTCAAATT 240

GGGGATTAGA ATCGTTATCT GAGGAAAAAA TGTTTACACA GCAAAGAAAT ACTTGGTACA 300

AATTTAAGAA GGAACGTCAT AAAAGAAAAA AATCTCACCT TTCCGAATGG AAAAAAGATA 360

TTTTAGATTA CCTTGAAACC CAGTGTTATA GATATCGACC TGAAGTTAGT ATGAAGAAAA 420

CAGATTTGCA AGCGGCTGTT ACTTTCAATG GGCAATCGAT TCCTAAAAGA TCACTTGACC 480

GTGCACTACA AGAATTAGTG GCCGAAGGTA AATTATTTGT ACAAACAAAA GCCGGTAGGG 540

GTGGAGGACT AGTAGTTGCT ACTCGGAAAG CATTAATTCG TACAGTTATT CAAGTAAAAC 600

AGCAAGTCAA ATATGCTTAT AAACAGGGTA TTAAGACATT CTTTAAAGAA GCTGATATGT 660

TAGTAAGACT GTTTGAACAA ACTGATAAAn ACAGTCAAAG AGCCAGAGAA TACAAGCAAT 720

TAAAACTATG GAACACTGGA TAAATTTAAA CATGTCAACT GCCAATACAT TATATTTCTT 780

TTATACTTAA CAGCTATATA ATTTTTGTAT TATTTTTTTT AGTTATTTGT TAAAATTATT 840

TTATACAAGC CTTATTATTT GGTTAGTAAC TTTTAACAAC GGAGGGTGAT AAAAATGAAG 900

AAGTACAAAA AGTTTTGTTT TTTAGGTGTT TGGTTATTAC CTTTGGTTTT AGCTAGTTGT 960

GGTACAAATA CTGCTACAAA TGATTCACAA GATATAACCG AAAAAAAAGT AGAACAGGTA 1020

GCGACTTTGG CTGCAGGGAC ACCTGTTCAA AGTTTAGATC CAGCAACTGC TGTTGATCAA 1080

ACGAGTATGA CTTTATTATC CAACGTGATG GAAGGTTTAT ATCGATTAGA TGAAAAAAAT 1140

CAACCGCAAC CAGCAATTGC AGCTGGGCAA CCAAAAGTGA CGAATAATGG CAAAACATAT 1200

ACCATTGTGA TTAGAGATGG CGCTAAGTGG GCTGATGGTA CACAAATAAC TGCCAGTGAT 1260

TTTGTGGCTG CGTGTCAAAG AGTTGTAGAT CCTAAAACAG CTTCTCCAAA TGTGGAACTG 1320

TTTTCTGCTA TAAAAAATGC CAAAGAAATT GCTTCAGGAA AACAAGCAAA AGATACTTTA 1380

GCAGTGAAAA GTATTGGTGA GAAAACATTA GAAATTGAAT TAGTTGAACC AACACCTTAT 1440

TTTACTGATC TGTTATCCTT AACGGCTTAC TATCCAGTAC AGCAGAAAGC AATTAAAGAG 1500

TATGGGAAAG ACTATGGTAC TTCTCAAAAA TCAATTGTAA CAAATGGAGC ATTTAACTTA 1560

ACAAATTTAG AGGGAGTAGG CACTTCTGAT AAGTGGACGA TTTCTAAAAA TAAAGAGTAC 1620

TGGGATCAAA AAGATGTTTC TATGGATAAA ATTAACTTCC AAGTAGTCAA AGAAATTAAT 1680

ACAGGAATAA ATTTGTATAA TGATGGACAA CTAGATGATG CACCTTTGGC TGGGGAATAT 1740

GCAAAACAAT ATAAAAAAGA TAAAGAATAT TCAACAACAT TAATGGCCAA TACAATGTTT 1800

TTAGAAATGA ACCAAACTGG GGAAAATAAA CTTTTACAAA ACAAAAATGC CCGAAAAGCG 1860

ATTAGCTATG CTATCGACCG GGAAAGTCTA GTTGAAAAAT TACTAGATAA TGGGTCCGTT 1920

GCTTCTGTTG GCGTAGTACC AAAAGAAATG GCTTTTAATC CAGTAAATAA nAAAGATTTT 1980

GCTAATGAAA AATTAGTGGA ATTTnACAAA AAAAAAGCAG AAGAATATTG GGGATAAGGC 2040

AAAAAAAGAA ATTGATTTAT CCAAAAATAC TCTTTAGGTT Tn 2082

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1091 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

AAATGACTTG ACTGTTGCTT CAGTTGnCAG CATTCACCTT GCTTTTAGCA GGCTGTAACA 60

CAACCAATAA TAAAGGCACG ACCGCAACGA GTGATTCTGT CGCTAAATCC AGTGAAAGCA 120

AAACAAAGGA TTCGGTCGAC TTAAATTCAC TAGATTTACC ACAACTAGAT GACAAAGTTG 180

CCGAAGATCA AGACTTAGTC CAAATGGTTA CTTCAATGGG AAATATTGAA ATCAAACTAT 240

TTCCTAAACA GGCTCCAAAA ACTGTCGAGA ACTTTATGAA ACATGCCAAA GATGGCTATT 300

ATGATGGCTT GACTTTCCAC CGCGTCATCA ATAACTTTAT GATCCAAGGT GGCGATCCTA 360

GCGGTGATGG aACTGGCGGA AACAGCATCT GGaATAAACC ATTTGAAGAT GAATTTTCAA 420

ACCAGTTATA TAACATTCGT GGCGCGTTAT CAATGGCGAA TGCaGGrCCT AATACTAACG 480

GCAGTCAGTT CTTTATTGTC CAAAATACAG ATGATCAATC TGATGGTCTT TTATATGATG 540

ATTATCCAAA AGCAATCATT GaTGCTTACa AAAAAGGCGG CTATCCTTCT CtTGATAAAA 600

AACaTACTGT TTTCGGTCAA GTAACCAAAG GAATGGATAT TGTCGATAAA ATTGCCAAAG 660

TCGAAGTTGG TGCCAACGAT AAACCAAAAA CTGATGTTAA AATTGAAAAA ATCAATATTC 720

TTCAAGAAGC AAAAAAATAA CAAAAAGTCA GAACGTACGC TGAAGATACG TTCTGACTTT 780

TTGTTATTTT TGAATCGCTT GTAATGCCTT TcTGGtACTT GGkCyTGkTT GACCTCyTCa 840

TACGTATTGA TGTGGGcCCC TTwATTkGrG mCTTTtAGaT AATGrTCTGk TTTTAAwTCa 900

kGGTCCGCTG tGaAAGkTAw TTCyCgCGkT TTGCCTTCCT CATCTGCGGC TACTTGCGTA 960

TAACTAGCAA TTCCATAGCC ATTAACGCTA ATCGGCTTTC CTTGTTTTAA CATACACATT 1020

TCCTGCTTTA AnCCAATGGG ATTTAAATGA TCCTAnCACA CCAGCTAAAT TCGCCAGAGG 1080

TCCnCTCCTG C 1091

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1575 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

ATTTCGTTCA CTGGTAAATT GAGATATTTC AAAACACCTT CTCGATTTTG AACTTCATCA 60

AAACAAATCA CTGTACCAAA ACCAGTACCA TCTTCACTAT CATCCAAATC ATTTGTTGAT 120

TGTGTAATCA ATACTAAGAA ATTATTAAAC GAACGTCCAA TACGTTTCAT TGATTTTAAA 180

ATCGCTTTAC CTTCTGGCGA AGATTGAAAA ATCCAAGATT CATCAAAGAA CGTCACTGTT 240

TCTTCTTTTG GATTTCTTGA ACCAAACTTC GAACAAAATG TTCCTAAAGC AAACATCAAT 300

GTAACAGAAA GACGTTTATT TTCATCTAAA TTTTCATTTT TATCAGTTGG TAAGTCTAAG 360

TCCTCAATTT CTAAAATTGT TACTTTCTTA TCGAATGATA GACCCTCAAC ATCACCATGA 420

GAAAAAGCTA ATTCTAAAAC TGAACCTTTA ACAGTCGACA AAATAAATCT ACCCATATCT 480

TTCACGTCAG AAATTTCACT TTCCACTAAT CGCTCAATTA CATGCCAAAA TCCAACCTTT 540

TTGCCTTCTT TCCGTTCTAA AACAACTTTC GCAATCGCTT CATTAATTTC TGTTTTTTGC 600

TTTAAATTCC ATGTTCCTTC GTATATATTG GTTAACATTG CTTTAGTTGT TGCAATCGCT 660

TCTGTTTCAT CAAATAAAAC AATCGGGTCA AGCACGCCAT GGTTTTTCGT ATCACGAACA 720

TCTAAAGTGA CGAAATTAAA GGACTTCACa AAATCAACAT CTAAAGGATA TTTCTTTTGA 780

TATTCAGGGT CATTAATTGT GTACATAAAT TGCTTTCGCA TTTCTTTTTT TGGATCAATG 840

TATAACACTC TGTCTTTTAA AAGTGCCATT TGCATAAATA AGGTTTTAGC CGTCACTGAT 900

TTTCCATTCC CAGTATCACC TGTAAGCGCC CAATGTGGGT TGTTTGTTTT CTTTCCATCA 960

ACCCCTTCTT TATTTGCTAA TAGCATGTTC ATAAAAATTA GATTTTTTGA ACTAGAAATA 1020

ATAGATTTTC TATCTTCTTT TTCTTCCAAA GTTGTATCCA CTCGTCCAAG GTAAAAGCCT 1080

AACTTCGTAC CTGCATGAAG TGAAGTAAAG AAATTCAACT CGGCAAACGA TTCAATCGTT 1140

GACGTGTGTT GCCAACGAGA AGTCTGCATT CGCAAAAAAT TACCAAATAA GGTTGATTGA 1200

AATAAATAAG GATTATCAAA CGTTGCTTTA ATAAGTGGAA TATCTAAACT ATCAAAACGA 1260

TTGATTAAAT ATTTTTTTCT TGCACGCATT TGTTTTTTCG TGCTACCACT AACAACAATC 1320

ACTGCTTTCC AGTCAATAAT ATCCACACCA TCATCAATTT TTTGGTCTAA ATCGTCaAGT 1380

GATAATTGAC CTTCAACAAT CTTTCGTTTT TGTTTAGAAC CAGCTAAGTG TGCTTCCTGC 1440

ATGATATTCT TAGTGCGGGT TCTTGCACGT GACGAACGCC CAGACAGTGC TAATTGCCCT 1500

TTACTTTCTG CAAAAGTCGC TTGAATCTTC ACTTCGACTG GGAAAGGCAT TTTTTGAACG 1560

ACCTCTAAAA AATGT 1575

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

ATGGTCATTT AAATTTGATT GAACGCATGC GnAAGTTATT TGACGAATcA TTTAtTGGCG 60

TTTTTATAAA TACAAGTAAG CAAACATTAT TTACGCCAGA AGAGAAAAAA TATTTAATTG 120

AAGAAGCAAC TAAAGAAATG CCAAATGTGC GTGTTATTAT GCAAGAAACC CAGTTAACTG 180

TGGAAAGTGC AAAATCATTA GGGGCTAATT TTTTGATTCG TGGCATTAGA AACGTCAAAG 240

ACTACGAGTA CGAGAAAGAC ATTGCTAAAA TGAATCAACA TCTGGCGCCA GAAATTGAAA 300

CGGTTTTTCT ATTAGCAGAA GAACCATATG CACATGTAAG TTCCAGTTTA CTAAAAGAAG 360

TTTTACGTTT TGGGGGCGAT GTGTCTGACT ATCTTCCTCC CAATATTTAT CATGCGTTAA 420

AACAAAAGAA GAATGACTGG aGCTAAAATT ATGAATAagA AAACAGAAAA ATTTTCGTTT 480

AAATCaCTCA TTCCAaTGGT ATTGGCATtG CtGCTAATTG GTTTGTTTAT CGTCCCAATT 540

CCTTATTATA TTGAAGGACc AGGAACGACA GAAAATTTAA AAGAGTTTGT AACTGTCGAT 600

GGAAAAAAAG ATACGCAGTC TgGTGCTTTT TATTTAACAA CGGTGGGCAT TCGTTCGGCC 660

ACTATTTTTT CTGCCATAAA AGCAAACTTT TCGGATTTTC AAGAAGTCAT GTCCAAAAAA 720

GAATTAATGG GTGATAGTAG TAATAGCGAA TATAATCGAA TTCAACAATA CTATATGGAT 780

TCCTCAAAAA ACGCCGCAAT TGAGCAAGCC TTAAAATTAG CGAAGGTTCC ATATGAGATG 840

AAATTTAAAG GCGTCTATGT GTTAGCGATG GAAGACAACT CAAGTTTTAA AGGAAAAATT 900

GAAGTTGGCG ATACCGTGAC AGGCGTGGAT GGTAAATCTT TTAAAAGCAG TGAAGAATTA 960

ATGAATTACA TTAAAGCACA AAAAGTGAAT CAAAAAGTCA CTGTTCAATT TATTCAAGAT 1020

GGCAAAGCAA AAGAAGCGAC CGGCAAATTA ATTGAATTGC CAACAGATAA AAAAGCGGGG 1080

ATTGGTATTG GTTTGACCGA TCaTACAGAA ATTGATTCTT CTnTCCCAGT ATCTATTGAA 1140

GCGGGTGATA TTGGTGGG 1158

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

AATCAATTCG TGACTGTTCG GAATGCCTTG AATTGGTCTT TCAATATCCC TGTCGTTCAT 60

GTTAATAATG AGCTAAGAAA AAAAATGGGT GATGaTAATT tCyCTTACAA TCACTACTTA 120

AGTAAAaTGA ACTATCCAGC TTCAGATGCT TGGGCTTACG AATCTGCGCC ATTGGGTTCA 180

GTAGAAACAA ATGTTGTAAC ACAAACAAAC GGCTTCCAAG CGCTTGCTAA CAAAGGTAAA 240

TATCAAAAAG CCTACATGAT TGAAAAAATC ACAGACAATA GCGGACATGT GGTCTACGAA 300

CACAAAGATG AAGGAACGCA AGTTTATTCA CCGGCGACCG CTTCTATTAT GAATGACTTG 360

TTGCGCTCAG TGGTGGATTC TGCGAATACG ACAAAATTCA AACCAACGTT AGCTGGCTTG 420

AATCCTCATC TAGCTAGTGC TGATTGGGTC GGAAAAACTG GGACAACTGA TGAGTTTAAA 480

GATTCATGGC TGATTGTCTC TACCCCAACT GTGACACTAA GtTCTTGGGC AGGACATGAT 540

CTACCAGCAC CAaTGACGAT GACCAGCGGC GACAATAATG GGAATTATAT GGCGAACTTA 600

GCCAACGCGC TGTACTATGC GAATCCAGAA TTGTTTGGCA TTGGTCAAAA ATTTGAATTA 660

GATCCAAGCG TTATTAAATC AAAAGTTTCT GaATtTACTG GTGAAAAACC TGGCTCAATT 720

ACCTATAATG GTGCCAAGTT CAACACaCCT GGCAAAACAA CGACTTCATA CTATGCCAAA 780

GATGGTGCAC CACAAAGTAC CTATAAATTT GGGATCGGTG GAACAGACAG CAATTACGCT 840

TCTTACTGGG GAAATCTTGC TCCACGTGCC ACTACAAATA ATAACAACAA TAACAATAAA 900

AACAACGATA ATAAAAAGAA TAATAATTAA CTCGCTAAAA TGAGCCAGAA aaCGTATTTT 960

cTGGCTCATT TTTAGGTATC AAAAAcGGCT AAACTAAGAG TTAaCGCTCT TAGTTTAGCC 1020

sTTtAATTCA ATTTATTTTG TTGAACCTTT TTGATCAATT CCATAAGGTA AAACAcTGTT 1080

TTTTCTTCAA TTtCTTCTTT GTTCATTAGT TTTGTTAATA AACGCATTGA CACGGCACCG 1140

ATATCATATA AAGGTTGTGT AATACTTGAT AGACGTGGAC GAGAGACTTC TGTAAGCAAT 1200

GAGTTATTGC TTGTAATGAT TTCAAATTCT TCTGGAACTT TCACACCAGC ATCTAGCATC 1260

CCATCTAATA AGCCAATTGC TAGCTCATCA TCTGTAACAA AGGCAGCAGT TGCCCCACTA 1320

TTACGGACAC GCTCAGCCAA ATTAATGCCT GCTTTAAATT TATATTCAGA TTCAAAAACT 1380

AAGCCTTCAT TATAAGATAA GCCATTTTCG GCTAAAGCTT CTTTGTAGCC TTTCATTCGG 1440

TTTTGACCAT TAATTGGATC GATTAATGCA CCACTAACAA AAGCAATTTT TTTGTTTCCA 1500

TTTTTCGCTA AAGTCGCTGT TGCATCTTTC GTTGCTTCTG TGTAATCAAT ATTAACGCTA 1560

CCAACTTGTT CGTCTGGATC AATTGAACCT GCTAAGACAA CAGGTGTTTT TGAACGTGAA 1620

AATTCACCAC GAATATCATC TGTAATGCGA TGACCCATAA AGATAATCCC ATCTACTTGC 1680

TTGGCAAGTA AATTGTTTAA TACAGTAACT TCTTTTTGAT CGTCTCCATC TGAATTAGCT 1740

AAAATGATAT TGTATTTATA CATTGTAGCT ACGTCGTCAA TGCCACGTGC TAATGAAGCA 1800

AAAAATGCAT TACTAACATC TGGAATAATG ACACCCACTG TTGTCGTTTT TTTACTTGCT 1860

AAACCACGTG CGACTGCGTT AGGACGGTAA TCTAAGCGAT CAATCACTTC TAAGACTTTT 1920

TTACGCGTTG CTGGTTTTAC ATTGGGATTA CCATTGACAA CACGAGAAAC AGTAGCCATA 1980

GATACATTTG CCTCTCTAGC AACATCATAA ATTGGTAATT GTTTGTnTTT CCATGTTTCT 2040

TCTCCCnATA AATATGAATT TGGnTCTCAT TTTCTGAAAA CAnCTGGTTA CCATTTCTGT 2100

CCTAGCCC 2108

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

TTTTGACTTT TAATCACTAT TTTGCAAAAA AnTCAGACTT TTTTCATTAT-TTAAGAGACn 60

TCCCGCAAAA AGAACTTTTC TTTTTTTGCT ATTTCTAGTA AAATAATTCA TTGAGAGCAA 120

AACTATACGG AGAGGAGAGA GTTTCAATGG CAACAGGTTG GGTAGTATTA ATCGCAGTAA 180

TCGCTTTATT AGTAGGCGCT GCAGGGGGCT TTTTCCTTGC ACGCAAATAT ATGCAAGATT 240

ATTTCAAAAA AAATCCTCCC GTTAATGAGG ATATGTTACG CATGATGATG GCATCAATGG 300

GTCAAAAACC GTCAGAGAAA AAGGTTAGAC AAATGATGCA ACAAATGAAA AACCAAGGAA 360

AATAGTAAAG GTTATTCAGG TAATCATGAA TAAGTGTAAA AACGGGCTGA TTTTCAGTCC 420

GTTTTTTTGT TGTTTTGCGG GAGAATAGGA TAATCTAGGA GGAAAAGAGC GAAACGTTTA 480

ATCAAAAACA ACAATAACGA AGAAACCTTC TAGCTCGAAA GTAGTCTTCG TAGAACAACA 540

AAGTAAAAGG AGGGACAACT GAATGTCCAT ATTCAAAAAA TTAGGCTGGT TTTTTAAGCA 600

AGAGAAAAAA AGTTATATTA TTGGGGtTTT CTCATTAATG ATGGTCGCTC TTGTTCAATT 660

AGTCCCGCCC AAAGTTATTG GCGTCGTTGT AGATGAAATC GTTaACAAAG AAATTCGCTT 720

AACGAAAATT ATCGTGTGGG TTGCACTCTT GATTGGTGCT GGGCTTGCCC AATATCTTTT 780

TCGCTATATT TGGCGGATGC ATATTTGGGG GAGTGCGGCT CGTTTGGAAA AAGAGCTACG 840

GACTCAATTA TTTCATCATT TCACAAAAAT GGATAGCATC TTTTATCAGA AATATCGGAC 900

AGGTGACTTG ATGGCGCATG CAACCAATGA TTTAAATGCC ATCCAAAATG TTGCTGGAGC 960

TGGGATTTTA ACGTTTGCCG ACTCTGTGAT TACGGGAGGm ACAACGATTA TCGCAATGGT 1020

TCTATTTGTC GATTGGCGCT TAACATTAAT TGCTTTATTA CCGCTGCCTT TATTAGCCGT 1080

CACTTCACGA GTTCTAGGTT CTAAGTTGCA TGATGCCTTT CGAGATTCAC AAGCTGCTTT 1140

TTCAGCGATT A 1151

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

AAAATAATGA AGGAGAATAG ATATGGGAAA ATTTCAAGTA ATTGATCATC CGCTAATTCA 60

ACACAAACTA ACAATGATTC GCGAAAAGAA CTGTGGGACA AAGGTTTTCC GCGAaGTTGT 120

CAACGAAATT GCTATGTTAA TGGCTTATGA AGTATCACGG GATATGCCTT TAGAGGATGT 180

TGTCATCGAA ACACCGATGG GTAAATCAAC ACAAAAAACA CTTTCAGGGA AAAAAGTAGC 240

AATCATTCCT ATTTTACGTG CCGGCATTGG CATGGTTGAT GGGATTTTAG AATTAATTCC 300

AGCAGCGAAA GTTGGACACG TTGGACTTTA TCGTGATGAA GAAACATTGC AACCGCATGA 360

ATACTTCGTG AAATTACCTG AAGACATTGC AAGTCGTCAA TTATTTGTTG TTGACCCAaT 420

GCTAGCAACA GGTGGTTCCG CAATTATGGC CATCGATTCA TTAAAAGAAC GTGGTGCTAG 480

CAACATTAAA TTTGTATGTC TAGTGGCCGT TCCAGAAGGT GTGAAAGCTT TACAAGAAGC 540

GCACCCAGAT GTAGATATTT ATACAGCAGC TTTAGATGAG CGCTTAAACG AAGACGGCTA 600

TATCGTTCCT GGTTTAGGGG ATGCTGGTGA CCGTTTATTC GGAACAAAAT AATAACAAAA 660

AACCGTTAGg TAACCGATTA TGGkTACTAA CGGTTTcTTT TGCyTAAAGA mCTTycTAGG 720

TGTwTAtAAA AAtaaA 736

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

CGAAAGCTAG ATACGGCGGT AAGTAAGCAA TCGATTATCG ATTGACAACT ACGAGCAAAA 60

GCTGAGACAC ATGTCTCCAG CTGACTATCA TAGGATTTAG taTGTGGGAC AGCAGTCAAG 120

CATGACTTTT GTCCCACATA TTTTCTTTTA TATAATATGG TGGCTCAACT GGAAAAGAAT 180

ACTTCTTTTC CGTTCATTAT GTTATGATAG ACAAGAAAAA AACACCAAAG GAGAGAGAAG 240

AAAATGACGA TCAAAGAATT CATTAAGAAA AGTCGCTTGA AAACATGGGA CGTTATTATT 300

ATTGCTATTT TAGTTCTTGG TTCTTTTCTG CCCCTTGTTG TTTTTGCCAT GCAAAACCGT 360

GGTCAAGAAG CGGCTACGTA TCAAGCAGTC TTGAAAGTAG ACAACAAAGT AATCAAAGTC 420

TTTGACTTAA AAAAGGACGG CCCGCATTAT ACATATAAAT ACGAAGCAAA AGACGGTGAT 480

TACAACCTGA TTGAAGTAGA TGGTGATCGT ATCCGCGTGA AGGAAGCCAA CTGTGCTGAC 540

TTAGTGGATG TTCGACGAGG CTGGATTTCC AAACCTGGTG AAACCCCGAT TGCCTGTCTA 600

CCCCACAATT TGTTTATCAC CGTGGAAGCT TCTGATGGGA GTGAAGACGG TAGCTTAATT 660

TATTAAGCAC GACAACTATG AGCAAATTAC ACAAGAATAT TTATATTGCT ATGCTCGTTG 720

CCCAAGGGGT CATTATTGGC TTAATCGAAA ATATGATTCC TTACCCTTTC GCATTTGCTC 780

CTGGGGCAAA GCTCGGTCTA GCAAATTTAA TTACCATTAT TGCGATTTTC ACCATGCGTA 840

AgcGTGATAG TTTTTTCCTG GTCTGTTTAC GTTTGATTTT AACGACATTA CTGGGCGGCA 900

CACTTTCGAC CTTTTTCTAT AGTGCCAGTG GTGCCTTATT AAGTTATTTC GGCATGTTGC 960

TTGTCAAGCA GCTGGGGCCA AAACGGGTCA GCATTATCGG GATTAGTGCC GTTGGTGGTT 1020

TCTTACACAA CGTTGGTCAG TTGCTAACGA CCTCTTTCTT TGCTCATTCG TGGGCGCCGA 1080

TGCTGTACTT ACCAnTTTTA TCTCTGTTTg GGGTtACTCT CGGGGaTGCC ATTGGGgATT 1140

GCCGCTaATn ATtACyACAA CATGTcCAGA CGTTACGAAA ATTCCAACTG AATTATGAAC 1200

AAACAACGAA ACATAACTGG AGTCAATTTT TCTAATTGAA AACCTGTCCG CCACAATTAA 1260

AGGAGTCATC TTATGAATAT ACATCCTATG TGGAATACCT ATCCTACGTT ATCAAAAGAA 1320

TTAACAACTA CTCTTCGCTT GATGGAACAA GCGGTTCAAA TCGATAATCA AGAGATTCAA 1380

GCTGCTGTCC ATGACATGAT TCATTCTGGC GGCAAATTGC TACGTCCAGC CTACCAACTG 1440

TTGTTCTCTT ATTTTGGTGA ACAGCGGGAC CCTAAAAAGG CGACAGCGTT AGCGrCTTCC 1500

ATTGAATTAC TGCATACCGC CACGTTAGTT CACGACGATA TTGTCGATGA AGCTGATACG 1560

CGTCGTGGCT TGCCAACATT GCGTTCGCGC TTTGGAAATA GCACAGCCGT GTATACAGGC 1620

GATTATCTTT TTGTTTGCTG TTTCAAGCTC TTATCTGATT ATTCTTCTTC ATTAAAAAGC 1680

ATTCAATTAA ATTCGCGCAG TATGGAAAAA GTCCTGACTG GTGAGCTTGG TCAAATGGAC 1740

AATCGCTATA ATTTCGAGGT AACGATTGAC CAATATTTAA AAAATATTTC CGGGAAAACA 1800

GCGGAATTGT TTGCGCTAAG TTGTTTTGTC GGTGCCTATG AAAGTGGCAC CTCCCAACGT 1860

TTTGCCAAAC GTTGTGGTGA AATCGGCGAA AATATCGGAC TGGCTTTTCA AATTATTGAT 1920

GATATTTTGG ACTATACACA AACTGTGACG CTATCGGCAA ACCCGTCTTA GAAGaCGTAC 1980

GTCAAGGCGT GTATTCTTTG CCCTTGATTT ATGCACTTGA AGCCAATCGT GAAGTCTTGT 2040

TGCCACTTTT AATGAAAAAA GAAGCCTTGA CCGATGAAGA AACACAGGAA ATTTATCGTC 2100

TTGTCCATGA ACTAGGTGGC GTAGAAAAGG CCCAAGAATT AGCCACTCAT TACACAGAAA 2160

AAGCGCTGAA AGAAATCAGC AAACTTCCTG AAACAAAGGC CCAAGCGAAA GAACAATTGT 2220

ATGAAATTAC ACAAACGATT TTGACAAGAG AAAATTAAAA AAGCCGCTGG ATCCTATTGA 2280

GGATTTAGCG GCTAGCTTTT TAGGTGATAT CTTGGTATAA TAAACACGAA GAGAGCGTAC 2340

TAGACATACG CTCTCGGGTA GACCGTTTAA GACGGTAGCT TGATTTTGAT ACGGAAATAA 2400

ACCCGTCAAT CCTTGCTAAA GATTATGACG GGTTTATTTT TTGTCGTTTT TATTACTGAT 2460

TTTGACAATT AATGTTGTTA CTTATACAAC TTAACTACTT TTGATGCTTC ATTCCATCTC 2520

TAATTTGTAT TACCTAGTGA ATACATGTTA TACTAATTAA AAAATGGAGG TGTTAGCTAT 2580

GACATCAACA AAAACAAGAA AACAAGGAAA CTCATTAGTT ATAACAATTC CTGCTACTTT 2640

AGGAGTTAAA GAAGGGGAAG AATTTGTTAT TCTTCGCAAA AATAATGGCT CCATCGCATT 2700

GATTCCAAAA GTAGAAGATT TTTTTGAAAA TACTGCTGAA GGAGAGTTTT ATCTTCCTGA 2760

ATTAGCGATT GATTATTCAC CTAGCGGAGG AGAAGTTGAT GGGCTATAAA CCAACTCAAA 2820

GAGATATTGT TATTATCGAC TTTGCGCCTT CTAAAGGTTA TGAAATCAGA AAACGACGAC 2880

CTGCTCTCGT AATGAGCAAA GACAGTTACA ATATTTCAAC AAATTTAGTT ATTGTCTGTC 2940

CAATAACCTC GTTGGATAAG GAACGTCCTT TTCTTGTCCC TATTTATAGC GAAAAACTTC 3000

ATACCTCCGA TAATGCAGTA AGTAAAGTGA ATACGCTCCa AGTCTATTCA CTCGACTATA 3060

CAGAACAGGC ACAACGCAGA ATAAAATATG TAGATACGTT AGACGAAGAA ACATTTTACG 3120

AAATTGCTCA AAAGTTTTTA CAAAACTTTT CTTTTGCTGT TTAATTCGGC TTCAACTGAA 3180

CACGCATATA TGATTTACTA TTCGACTTTT CCGTTTCAAC TTGCTATAAT AAACACGAAG 3240

AGAGCGTACT AGACATACGC TCTCGGGTAG ACCGTTTAAG ACGGTAGCTT TAATTTATTG 3300

GTtAATAAAC CCGTCAATCT TCGCTAAAAG TTATGACGGG TTTATTTTTT GTCGTTTTTA 3360

TTACTGATTT TGACAATTAA TGTTGCGAAA gcAATCGCAA GCATCAATGC TTCAAAGACA 3420

GTCACTACTA TTCCTTTCTA GGGAAAGAGC AAACAAGCAA AAACATTGGC AGTCCCCCTT 3480

TTTTTGAGAA ATTGCCACCG TCATAAACTT CCTACTTGTG TAGTATAACA CATTTGTACC 3540

TTCCTAGAAT ACGCTTACTT TCCTGATTAT TCAACAGCCG CTTTCTTTTG TAATAAAAAT 3600

CGCGCACCGT TTACTGGGAT AAAACGATTC AGCCAACTAA AATTTTTTAG ACTAAACAGA 3660

CCGACCATCT TTTTTGATGG TCGGTCTGTT TAGTCTATTG CTCCGCCTTT ACTCCTTCTC 3720

CGACAATGCT CGCCAGACAT CAAATGTTTG TTTTAAGCCT TGGACATTAT GAACACGTAA 3780

AATTTCTACG CCTTGTTGTG CTGCATACAA GGAAGCAGCG GCTGAGCCAA AATCACGGTT 3840

GGCTGGTTCT GGTTCGTTCG TTAAAGCGCC AATGGTTCGT TTGCGAGAAA CGCCGTATAG 3900

TAACGGATAA TCTTGGTAGC GAAAGGCGTT AGGATCTTTT AACAGTTGAA GGTTTTCTGC 3960

GACAGTTTTA TGAAAGCCAA TCCCTGGATC GAAACAAATT TTTTCTAAGG AAAGCCCATA 4020

TTTTTGGCAT TGTTCAATTT TTTCTGTATA AAATTGGTGC AACTCTTCTT TTAAAGAAAG 4080

CGATTGGCGT TTTCTAGAAT GCATAATCAC AACTTGGACT TCAGGATATT GTGCGAGGAC 4140

TTCTGCCATC CCCGGAGTGT CTAATCCTTT GATGTCATtA ATCATTGTGG CGCCAgcTTG 4200

GATCGCGGCT TCCGCTACTT CGGGATAGTA GGTGTCCACA GAAATCGGCG CTAGAGAAGT 4260

CTCACGTATT TTTTTTATTA ATGGTAATAC TCGGTCTGCC TCAACTTGTG GAGAAACTTC 4320

TTCGTAGCCA GGACGTGTGG ATTGGCCGCC AATGTCTAAA ATATCGGCCC CCGCTTCTAG 4380

TAGATGAAGC GCATGTTGAT AGGCCACGTC GACCGTTGTG TAGCTACCGC CATCAGAAAA 4440

AGAGTCGGGG GTCGTGTTGA CAATCCCCAT AATTTGGTAA TTCTTTTTTA AATCAATCAT 4500

TGTCACATTG CTCCTTTATC TGCTGAATCA TCTTTCGTAA AGCCCGTATT CTAGGACTTA 4560

TCTTCATTCG TTCACTCGTG GACAACTCCG CTAAGGTTTT GCCTCGGTCT GGTAAATAAA 4620

TAATCGGATC AAAGCCATAA CCGCCTGTAC CGCGCGGTTC AACTAATTCA CCAGTCAAAG 4680

TGGCTTCCGT TTGCAACAGT TTGTCGTCAT TGAGTACATA GACCAACGTG GCTGATAAGG 4740

TTAACTCTCG GGTCGACTGT TGCCCTTCAA ATAAGTGCAA CAGTTCGCGG TTCTGTTCTT 4800

CCGGATTGGC TGAATGGAAA AAGCGGCTTG TATGAATACC TAATAAATCA GGAAAAGCAG 4860

TTAACGTTAA GCCGCCATCA TCACCTAACA CTGGGCGGCC AATTAATTGT TGGAAAAAGC 4920

GAGCTTTTAG ATAAGCATTT TCAGCATACG TAGTGCCAGT TTCTGCAGGT TGTTCTTGAC 4980

TGGTTGTATA CTTTCGATAA GAGACAAGTC GAATAGCGGG GTCCTTAAGT CCTGATTGCA 5040

TTTCTTTTAA CTTACCTTGG TTATTCGTGC CAACAATGAT TTCCATTTTC TAACGTATCT 5100

CCATTAAAAA TTGATTTTTC CACTCTTGTT CTTTAAATAG TCCGGTAAAT TGAAATGTTT 5160

TGGTGCTACT TTGTGGTGTT TTCACGCCGC GCATCGTCAT ACACATATGT TCCGCTTCAA 5220

TGGCTACTGC AATGCCTTTG ACGGGAATAT TTTCTTGGAG TTTGCGGGCA ATTGTCACTG 5280

TTAAATCTTC TTGAACTGTG GGACGTTTGG CACAATGTTC TACTAATCTT GGTAACTTGC 5340

TTAGTCCCAA TACTTTGCCA CCTTCTGGCA GATAAGCGAC ATGTACTTTT CCATAAAATG 5400

GCAATAAATG GTGTTCACAC ATTGAATAAA AGGCAATATC TTTTACTAGA ACCATTTCGC 5460

CTTCATTTAA GCTATCAAAT AATTTATAAT CGTCAAATTC AGGTTCGGTT AATCCACTAA 5520

AAACTTCTGC ATACATTTTA GTACGCGTTT GGGTGTATCA AGGAGTCCTG CCCGTTGAGT 5580

ATCTTCCCCC ACTGCTTCTA AGATTGTGGT AACTGCCTGC n 5621

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3807 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

CAnATATCCA ACAATGCTTG GAATCTCCTC CGCTTTCCAG TGTAAAATGT ACTTGGGTCA 60

TGGTAAAAGT CCCCCTGGGG TATGGTTTTT GGTCGTTAAA AACCATGTAC CGTAAAAGGA 120

CTGTTATATG GCCTTTTTAC TTTTACACAA TTATACGGAC TTTATCTAAT GATTCCCTAA 180

CAGTATTTTA CAATTACTTT TnTATTTGCC GCCTTTCCCC AATAAGGCGG TATCTTTTTG 240

CATAAAAATA TTGAATTAAA ATGGTATTGT CTACGTACGC ACTTTTGGAC ATTTTCACAT 300

AGATCTCCTT TTTACCGAGA AGGTGGCCAT TTTTTTGTTG AAAATTGAAA ATGAGTAAAG 360

TrATATTATT ATATAtTAAG CTATAACTAT AACCAGTAAG AACTATTTTA CCTTAATAAG 420

CTAGCTCTTG CTTGGACCAT TAGCTCAGCT GGTTAGAGCA AACGGCTCAT AACCgTTCGG 480

CCACAGGTTC GAGTCCTGTA TGGTCCATAA AATATTTAGT GAGTAACAAG GAGTATTTCT 540

CATTTGAGAG ATAAGCCTTG TTTTAGTTGT AGTAATCCAC CTTTATATAT TCGAAGTTGG 600

ATATCATTTG AAAACCAAAT TAGTGATACT CAGACTTTTT TAGTTAATAT CAAAATCATA 660

AAATCTCTAT TTGACAGTGT TTGTTCACGA AAAAATAAAA AGAGTGTTCA TTTATAACTT 720

CTTGAAAGAG GAAGGTTATT TGTCTTAAAT GAATTTATAG GATAACGGTT CTTAGTATAG 780

AATGTAAAAA AAGCCAGCCA GTATTTGGCT GGCTTCTGTG GTAAAGCGCA GCCGTTTTCC 840

GCCAGTTGCA CTTTAGGTGC GTGTTAGCAC TTGCTTCAAT AAAGAATTAA GAATTACTAT 900

TATTATGCCA TAAAAGAAAA ACTTTGAATA GATATGGATA GCAAAAAACC AGTGAATAAA 960

ATTCGACTGG CAAGATAGAT TTTGGATAGA ATTCCTTGAG GAAAAGTTAG AATTATTATG 1020

CCACCATGGA GGAATAGTTG CTATGATGTT GCTATCAGAA ATTGATTACA AAAAGACAAA 1080

AGTAATGTTC ATCGATTATA AAAAATGTTG AATTTTACAA CGTATGTGAT GTGTATAAGT 1140

ACATTTGCAA TCTCCTATAT TATTTGATAT TCCACTTTGT GAATGTTAAT GGAGCATAGA 1200

TTAATTGGTA GAGCAGCGGT CTCCAAAACC ATCAGTATAG GTTCAATCCC CATTGTTCGT 1260

AGCATTGCTA CTTAAATAAA AGAATCGCCA ATAGATGTTT CTGCTGAATT CAGGATGAGT 1320

CACTAGATTG CAAGTGTTCC TTTTTTATTT GGCAGAAGAA TGAAGAATTA TGTATAATAA 1380

CTTTTGCAGA AAAGTGAAAA GATAATGGCT AATCTCTTGA ATAAAGGGGT GATGCCTATG 1440

GTTCATAGCT TTATCTCTAG ATGTAGTAGA CATGTCTGGA TTCGAAATAT TATTGCTAAT 1500

GGTTGCATTC GTAACGCTAG TTTTGCTGGG GATAGACCGT ATGAACACAA AAAATAACCA 1560

TCTCACTTGA CGGGGCGTAg CTGGTTATTA AAACTAATTT ATGACAGTAA CCGTCTTTTT 1620

AACGGTTCTA CATAAGGATA TGTTAATAGC ACATTTTTTT CTATATATAT TATACCATGT 1680

AACAAAATAA ATTCATTCAA GATTACTCAA CATAAGTGAG TGGTCTTTTT TGTGAATAAA 1740

AAAGCCACTA GGACAGGGAA CCTAGTGGTC AGGGTAGCAA ATATTATTAG TCGTAAGTGT 1800

ACAATAAAAA TAATTTTTAT AGGAATATTT AATCAACATC ATAATACTAT TATTATAAGG 1860

AGTTGCTACT CAGAATTATT ATATCAAATA CTAAAATAAT TTTGCAATAA AAAAGTTATA 1920

CACTAAAAAG CCACTAGGCT GTGGGCCCTA GTGACTAGGT AGCAAGCATT TTCAATTGGA 1980

GTTTTACACA AAATTTGAGG ATTATTATAA TACTTATCTG AATCGATAAa TTATCATATA 2040

TATAGGGAGT TGCTACCCAA TGTTATTTTA GCAGAAAGCA ATTTACTAAA TCAAGTACAT 2100

AGAATTTAGA GAAAGTAAAG AAATACATAT GTTAACAAAG GATTAGCTAG AAATGTGGTG 2160

AGGCCATGGC AAAATATACA AAGTGGCTAA CTGATGAAGG ATTAATTAAA ATTGAAAGGG 2220

TGAGCACGAG AGGGTCTCGC AGATGaACGA ATAGTACAAA ATATTGGGGA TTAAAAGACC 2280

AACCTATGAT TGaAAAAATA AATATTCTGa CATTACTGAC ACCCTAAAAA GaGAAAAAGA 2340

AGTTGTAGAT TGCCAAGTGG AAAACGCACT ATTTAAAAGA GGTGCAGGCT ATGAATACAC 2400

CGAAGTTACA AAAGAACTGA CAGAAAATGG GATAAAAATC ACAAAAAAAG GTTACAAAAC 2460

AATTGAATTA TATTGAGATT TAAGGTTTTT AATGGAAAGC ATGTCACTTT TAAATTTTTG 2520

ATCTGAAGGC ATAGCATAGA AAATTATTTT AGAAAATTTT GTGTAGCCAA CAGGAAAGCA 2580

TCAAAAACGC GATCTTCAAA AGTATGCTGC ATGTGTTGTA GTTAACTTAT TACCATTTGG 2640

TGGCGTTGTT TGGGATATAC TTAATTGTGA AAATCTAATG CAGGTTTTAA TTAATCCGTT 2700

GCAATGAAAA AAAAATTATG GTTATGATGT TAAAATACTT TTAGATGTAG GGAAAAGAAG 2760

TTTAACTCCT GAACAATTTG CAAAATTCAA TGCTTTAACT ATTGCAGCTG GTATAGCAAT 2820

TACTGCTGTG GCTTATTAGG GAATTAATTA GTTGAGCGGT TATGTGAGTA TATACGATTG 2880

TTAGAAGAAA AAATAATATC ATTTTTAAAG TTTTTAAAAG TTAACCCTCA GAATAATTGT 2940

TTTACATGTT ATAGTTATTC ACACCCTATT TTAAATAGTC TTCCTTTTAG CCTTTTGGTG 3000

CAGTGTTTTG AGATAAAGGA CTATTCTGCT TTAGGGTTGG ATTCTGGATA TTTATTTACA 3060

ATAGAAGCTG AGraAAAATG CTATTATCAT ATTGCTAACG TAACAGGAAA TGATTTTTCT 3120

ACTAGAAATT TTTTCGAACG GTATTGAAGG AACmATAAAT TGAATAAAAT ACTGGAAGAA 3180

ACAAGTGACA TACGAAATAT TATTATATTA ATAGACCTAA TGGGAGGAAC ACCTGCAAAT 3240

GTAACTATGA TCAAAGCAAG TATGGATAGA mGAATTCAAG TAGTAACTGG AATGAATCTA 3300

AGAATGGTAT TAGAATCTTA CTTTAAAATT AATGAAGAAA AACTTGCTGA GCATTTAATA 3360

GAAATAAGTA TAAGTAGTAT TAAAATACCT GAGATACAGA TTAGTGGCGG AGAAGAGTAA 3420

TTATGATGTA ATAATCTTAG CAGCGGTGGG GTGTGATCTA TATACAAATA TTAATATTTG 3480

TGTTAAACAT TTTTTTGATA TAAGAATGTT GTCCAATCAA ATTCTAGAAA TATTTTAGAC 3540

TATAAAATTT ATTATACGGG GAAAATACAA CTTTTTAGAT AAAGTCCGTA TAATTGTGTA 3600

AAAGTAAAAA GGCCATATAA CAGTCCTTTT ACGGTACAAT GTTTTTAACG ACAAAAACAT 3660

ACCCCAGGAG GGACTTTTAC ATGGACCCCA AGTACATTTT ACACTGGAAA GCGAAGGAnG 3720

ATTCCAAAGC ATTAnTGGAA TAATTCCGGT AAAGGGATGA CGGTTCCTAA AAAAATATTT 3780

TAACCAACGG GAATTTAATC CACCAAT 3807

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

CGTTGCACGT GTCACACATA CTTGnACTTT GCnGGCACTC TTTAGAATCC TTGCnATGAC 60

AAGATGnTGA TTGCTGTGGT CCGTGCACTT CAGATAACGA GGAAGCTCGA ATGACnGCGC 120

TTCCCATCGT GACAACATCA AATAATTTTT TCGTCCGTAA ACGGTTTCTA ATCTTTTGGT 180

CTTGTTCCAC GTTGGCGTTT GCGTTCTTCA CGTTCAATGC GTAGACGTTC GCGTTTTTCT 240

TCAGGATTTG GATCACTGAT CACTGTTCCT GCTTCAATTT CTTCTAACGC ACGACCTACA 300

CTTTTTACAG AATCAAAGGA TTCAACGGTT GGTTGAACGC CTTCATCTAA TTCATGCGCA 360

CGTTTGCTTG CTAAAaTAmC CAAAGAaTAT TTkGAAGGGA CTtCTTTTAA CAATGAGTCA 420

ATTGACGGTT TTmACATCAT AAGGCTACAT CTCCTCTAAC ATTTTAATAT ATTTTCCAAT 480

TACACGGTCA ACACGGAAGT GCTnCACTCG CGATAATGTC TTTAATTCGT TGCACGGCTr 540

AAGGAACTTC ATcATTCACT ACCGCATAAT CATACAGCGC CATCATTTCG ATTtCTTCTC 600

TGGCCACAGC CATTCGkTCT TCAwTCaCAG ACATTTCGTC TGTtCCGCGG CCAaTAATTC 660

TkGATTTTAA TTCCGCTAAA TCGGGGGGTG TCAAAAAGAT AAATACGCCA TCAGGCACTT 720

TGTCTTTGAC TTGTTTAGCC CCTTGGACTT CAATTTCTAA AAAGACGTCT TTGCCTTCAT 780

CTAACGTCTG GTTAACATAC GTTAATGGTG TCCCATAATA GTTACCAACA TATTCCGCAT 840

ATTCCAACAT TTCTCCAGCT TCAATCATCG CTTCAAATTC TTCTCTTGAA CGGAAATAGT 900

AATCTACTCC ATCCACTTCG CCTTCTCGCT GTTTCCGAGT GGTCATTGAG ATTGAATATT 960

GAAAATCATT TTCTTCACTG TCGAAAATAG CCTTTCTTAC AGTCCCTTTC CCCACTCCTG 1020

aAGGACCTGA CAATACGATT AATAACCCGC GCTCTGaCAT AACGACTTCC TTTCAAAACa 1080

TAATTTCACA GTATTAGTTC yAwTTTGcAC TTTTTTTCTG CAATTTTCAA GACTTyCTtG 1140

GAGATtCACT GAAAAAATAm CATTTCTTCT TTAATTTGGC TTTCATAACT TGTTCTTTTT 1200

TTAAACAAAT TACCTAGAAT TCCTATACAG GCAGCCATTT TTTAAGTAAA ATGAAGTGAT 1260

GACTCCTTTA GGATGAAAAA ACGTGAATAA GAAAGGCTGA GAAACATCGC ACGAATTAAA 1320

CCATTTACAT TGTTTCTGCT AGGCTTAGTT GTCAGTTGTG GGGCTnTTTT GCCCAACCTA 1380

CTGTGACTCA CGCAGAAGAG ATATAC 1406

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

CATTAATCGG CCTACACACC CATAAnGCCn TTTCTCTATA AGCAGTAAAC GCCCTAACTG 60

ATTATTTTAC GkTGCGtATc TGtGaCCAAT tAGGTtATAT AaTAACTGTt GGTACGTtCC 120

tTTTCCGTTg ATCCATCACC CATAAGCCAG ATTGATTTTT yCCTTGAATA GkTCCCGTTA 180

ATCGCATCAC TTATTACCTG CCATAACAGA GTAGTTATTT GTGCATCTCC GCAAGCAATT 240

TCGTTCAACC AGCTCTCTAC ATCCCAATCA TTAAATTTAG GTAACGACGG ATTTTCTACA 300

TATGCGGTTG CAATTTTTGA TGTGAATACA TAATTGGGCG TAAACGGTTC TAGTTGTTTC 360

GTTTTAAGGT TAAATACCCC GTTTTTCACT GGTATAAGAT ATCTTGAGAC CGTTTTAGGC 420

TTTATTTTAG CTTCTTTCCA AATGTGAAAA ATAACATCAT TTACsGCTCn AGCATTGGGG 480

TTCGGGTCAG CCACCCAATC ACTCGGTTAA TTGGGTTCAT TGGGGAAAAA GCCTCTTTGG 540

CGAACAAGCA ACGnGATTCT CCAA 564

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

AACTATGCTG AGTCTAGGGT TATTATTAAC TGGGTGCGGA CTCAAGGAGG CACAACTGAA 60

AAATCCAGCG AACGAATTAG TAACAAACCA GTTAAAATTG TCGCTGTTGG TTCCACCGCT 120

TTACAACCGT TAGTAGATGC TGCGAAAGAT CAATTTACAC AAGAACATCC TAATTATACA 180

GTTTCTGTCC AAGGTGGCGG CAGCGGAACA GGACTTTCGC AAGTTGCAGA TGGCGCAGTG 240

ACCATTGGAA ATTCCGATGT GTTTGCCGAA GAGAAAGATG GCGTGGATGC CTCTAAATTA 300

GTCGATCATC GGGTGGCCGT GGTCGGTATG GGACCAGTGG TCAACAAAGA AGTCGGCGTG 360

AAGAATTTAA CGAAGCAACA ATTGATTGAT GTCTTTACTG GCAAAGTCAA AAACTGGAAA 420

GAAGTGGGCG GCAAAGATCA AGAAATCGTC GTAATAAACC GCGCAAACGG AAGTGGCACC 480

CGAGCAACAT TTkAAAAATG GGGCTTAGAT GGAGCTAAAC CAGTTCmATC ACmAGrACAA 540

GtTCTTCgGG AcAGTTCGTA AAATTGTTGA ACAAACACCA GGaGCAtCAG CTATTTAGCT 600

T 601

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 708 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

TCATGGAAAC TGCAAGAAAG CnTAAnAAAT TCCTGAAGTG GAAAGAATTC TTTAGACTTT 60

TCTCGTTTTA ATTTAACTTT TCAATAAACC ACGATCATTT TGACAATTTC CGCATAGAAC 120

ATATTGCCAC CATTTTGATA AAGGTAACCC CCATTGTAAA CTAACGCTTG CCAACGATAA 180

TAACGATATT TCGTATTTTG GTCATTTCCT AGCAACGGTG AAAGGACTTC TCTTGAATAT 240

TCTTCTGCTA ACTCTGTCGT GTGTTTCCCG CCGCGTTCTT TAACAAACTG AATATAATCC 300

AGTCCATAAT TATATGCTTG TACGCCTGTC CACTCATCAC AGCCAGCTTC TTTTGCTTTC 360

GCTAACGCTT CCGCGAGAAA TTTGACGCCA TGTGCGATAC TTTCCTCTGG TGTTTCAATC 420

ACTTCTTGTT GTCCATAAAC ACTTTCACTG CTCTGCATAA TATCGCCAGA TTTCCCTTTA 480

GATTCTGTAT AGATAATCGC TAAAGCTAAT GTTTTGTATT CAGGTATTTT ATTTTTTTTG 540

ACTTCTGCTT CTACTTGTTT TTCAAAGGTC ATTACCGTTT CAACATTTTG ATGTATTTTA 600

TAGCCAAGAT AGCCAAGACC AGCAACTAAA CCAACAAACA AAAGTAGCAT GATTTnATAA 660

ATTATTTnTC TTACTCTACG CATCGAATCA TCCAAACTTT TTCTTTTA 708

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

TTGAAAAAAT CACAATTTAA TGATTTATCC ATTACGGAGA TGCACACAAT CGAAGCAATT 60

GGTATGTACA AGAAAAAAAC GTCTTCAGAA GTAGCCAAGG AACTGTCAAT TACCGTCGGA 120

ACACTTACTG TAGCGATTAA CAACTTAGTT AAAAAAGGCT ATGTTGAACG TTTGCGTAGT 180

GAAGATGATC GACGTGTAGT AAAGCTTGGC TTAACCAAAA AGGGAAAATT ACTTTTTAGA 240

GTCCATCAGC ATTTTCATCG TGAAATGGTT AAAAACATTT TGAAAGGCAT GGAGCAAGAA 300

GAAGAACAAG CGCTGTTAAG AGCACTAAAA AATCTTCATG ATTTCTTGCA AGAATACAAA 360

TAAAAAGTGA GGATCCCCAT GaAGAATTAT GCACGAATTA GTTGTACAAG CCGTTATGTT 420

CCAGAGAATT GTGTCACGAA TCACCAACTG AGTGAAATGA TGGaTACCTC TGATGAATGG 480

ATACATTCGC GAACAGGCAT TAGTGAACGT CGCATCGTTA CGCAAGAAAA TACGTCTGAT 540

TTATGTCATC AAGTCGCAAA ACAGTTATTG GAAAAATCTG GAAAGCAAGC AAGTGAGATT 600

GACTTTATTT TAGTTGCAAC AGTGACACCA GATTTCAATA TGCCTTCTGT TGCTTGCCAA 660

GTGCAAGGCG CAATTGGCGC CACTGAGGCC TTTGCTTTTG ACATCAGTGC AGCGTGTTCT 720

GGTTTTGTCT ATGCCTTAAG CATGGCAGAA AAACTAGTCT TAAGTGGTCG TTATCAAACA 780

GGTCTAGTAA TTGGTGGCGA AACATTTTCC AAAATGTTGG ATTGGACCGA TCGCTCCACA 840

GCGGTGCTTT TCGGTGATGG GGCTGCCGGC GTCTTGATTG AAGCGGCTGA GACACCGCAT 900

TTTCTAAATG AAAAATTACA AGCAGATGGA CAACGGTGGG CGGCTTTAAC GTCAGGCTAC 960

ACGATCAACG AAAGTCCTTT TTATCAGGGG CATAAGCAGG CGAGTAAGAC GCTACAGATG 1020

GAAGGACGTA GTATTTTTGA TTTTGCGATT AAAGATGTTT CACAAAATAT TTTATCACTC 1080

GTGACGGACG AAACCGTGGA TTATCTTCTA CTACATCAAG CAAATGTGCG CATTATCGAT 1140

AAAATTGCAC GTAAGACGAA GATTTCCCGC GAGAAGTTTT TAACGAATAT GGATAAATAT 1200

GGCAATACCT CAGCTGCTAG TATTCCTATT TTGTTGGATG AAGCAGTTGA AAATGGGACC 1260

TTAATTTTAG GTTCCCAACA ACGCGTGGTG CTAACAGGAT TTGGCGGCGG CTTAACATGG 1320

GGCTCACTGC TCCTAACGCT GTAAAAAACT GTTCACATAT AAATGAAGAA AATGACTATT 1380

TTGGAGGAAT ATACACATGG TATTTGAAAA AATTCAAGCA ATTATCGTAG AAGAATTAGG 1440

AAAAGATGCT GAAGAGGTAC AATTAACTAC AAACATTCAA GAAGAATTAG ACGCGGACAG 1500

CTTAGATTTA TTCCAAATCA TTAACGAAAT CGAAGATGAA TTTGATGTGA AAATCGAAAC 1560

AGAAGATGGC ATCCAAACCG TTCAAGATTT AGTAACATAT GTAGAAAAAC AACAAGCAAA 1620

CTAATACATG AAAATAGGGG GCTGGGACAT TTAATTGCTA AATGACCCAG TCCCTAAAAA 1680

AACAAGTAAA TAAGCCGTAA AAATCCTTTT TTACTTGAAT GAAGTGTACT TATCTTAGAA 1740

CTAAAGGACG TATAAAATCA ATGAATCAAG AGTTATGTGA GTTGCTTGGA ATCAATTATC 1800

CCATTTTTCA AGGCGGTATG GCTTGGGTAG CCGATGCTTC ATTAGCAAGT GCCGTGTCAA 1860

ACGCTGGTGG ATTAGGGATT ATTGCTGGCG GCAATGCCCC AAAAGAAGTC GTAAAAAAAG 1920

AAATTAAAAA AGTTAAAGAA TTAACGGAGC AACCCTTTGG TGTCAATATT ATGTTACTTT 1980

CACCTTTTGC CGATGAAATT GTCGATTTGG TTTGTGAAGA ACAGGTTCCT GTCGTAACGA 2040

CAGGTGCAGG CAATCCACCC AAATACATGG CTCGTTTTAA AGAACATAAC ATTAAAGTAA 2100

TCCCAGTAGT TCCTTCAGTT GCTTTAGCAA AAAGAATGGA AAAAATTGGT GCCGATGCTG 2160

TCATTTTTGA AGGAATGGAA GCTGGTGGAC ATATTGGCAA GTTAACCACT ATGAGTGGCT 2220

TACCGCAAAT CGTTGACGCT GTGTCAATTC CTGTGATTGC AGCAGGTGGG ATTGGTGATG 2280

GTCGTGGTAT GGCTGCGGCC TTTATGTTAG GTGCTGAAGC AGTCCAGTTA GGCACACGTT 2340

TTTTAATTGC CAAAGAATGC AACGTTCATC CAGATTATAA ACAGAAAGTT TTAAAGGCAC 2400

GTGATTTAGA TGCAGTAATT ACCTGTCAAC ATTTTGGCCA TCCAGTGCGT ACTTTAAAAA 2460

ATAAATTAAC CGCTCAATAT AATCAATTAG AAAAGCAAGA ACTCCAAAAA GAAGTGCCTG 2520

ATTTAGAAAT GTTTGAAAAA ATTGGTCAGG GCGCTTTGCG CAAAGCTGTC GTTGACGGGG 2580

ATATGGATTA CGGTTCCGTC ATGGCGGGAC AAATTGCCGG GTTAATAAAA AAAGAAGAAA 2640

CAGCCCAAGA AATCATTGAT TCACTCATGT CTGAATGCAA AGCGATTGTA CATAAGATGA 2700

ATCAGCGTTG GGGCTAAGTG AATAATTTTA ACAAAAAATG AGGTGTCGTA TGAAAACAGC 2760

GATTTTATTT AGTGGACAAG GAGCCCAGTA TCAAGGGATG GGTGAAGAAT TATATCACCA 2820

AGAAGCGATT GTTCGGGAAA CTTTCGATGA AGCAAGTCAT ATCTTAGGTT ATGAGATGGC 2880

AGAACTTTGT TTTACTGAAA ATGAACGTTT AAATGAAACA GAATATACGC AACCTGCTAT 2940

TTTAACAGTC AGTGTCGCAT TTTACCGTCT TTTGCAACAA AAAGGACTAA CGCCTGATGT 3000

CGTAGCGGGT TTAAGCTTAG GGGAATACAG TGCTTTGGTT GCCAGCGGGG CTTTGCGCTT 3060

TTCAGAAGCA GTGGCCTTGG TCCaAAAGCG CGGTCAGTAC ATGACAGAAG CAGCACCACA 3120

AGGAACTGGC AAAATGGTTG CTGTTATGAA TGCTGAGCGT GAAGTAATTG AGAAAGCCTG 3180

CCAAGAAGCC AGTGCTTTCG GAATTGTGGC TCCAGCAAAT TATAATACAC CACAACAAAT 3240

CGTGATTGGT GGTGAGGTTG CTGCTGTTGA TCAAGCGATG ACACTTCTCA AAGAAGCTGG 3300

TGTGAAGCGA ATGATTCCGT TAAATGTGAG TGGCCCTTTC CATACGGCGC TGTTACAACC 3360

AGCATCAAAA AAATTGGCTC AGGATTTAGC AAAATTGAAC TTTCAAACGA TGCAAATTCC 3420

TGTCATTAGT AATACGACTG CCGAAATTAT GCCCCAAGAG GCAATTCAAG CGTTATTGGA 3480

AAAGCAAGTC ATGTCTGCGG TACGTTTTGA AGACAGTATC GAAACGATGA AGGCTATGAA 3540

CGTAGGAACG ATGATTGAAG TTnGgtCCAG GGrAAACATT aACyGGtTTT GtTaAAAAAA 3600

TTGACCAAAC AATTGAAATG CACCGTGTGG AAGATGTTGC CACATTAACA GAAACG 3656

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

CCACACTTCa sCsTCCTGTA TAAGAGGAAT CAGATTAAAT TCTATAAACA TCTTTTAAAT 60

GTCTTTGCTC CAAAAAATTG ATGTCTAATC TTTAGAAATC ATTGTCTATC AGAATTATTC 120

TTAAAAAGTT TGATTTTTTT AATCAAGAAA GAGCTAATTT CTTCCAGAAC TCATATCATC 180

ATATTTTGCA ATGGCTAAAC AACTCAAAAT CGTTATACCA AGCAAACATC CTATAAACAT 240

GCCTAACAAA AATAAAAACA TGGTTAACGC CACCTCTACA TGaTTCAATA GACTTAAATA 300

AAAAAAATGr AGTAATCTTT CAGTATTTTT TATATTTTTT TACAAAAGTA GTTAAGTGTA 360

tTTGAACATA TCTTTTGaAC AGTaATaATA AAGAGTGGtA gACGGAGCGG TT 412

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

ATCCATGACT GTTTATCAAA CGTAGCTTTA CCTGTAGCCT GTTCTTTTCG TTGCTCGTTT 60

ACTTCTCTTG ATTCTAATAG TTGGAAGCTT TCTGTGACAA CCTCAGTTAC ATAAATACGC 120

TGGCCTTGTT GATTCTCATA GTTTCTTGTT TGAATGCGAC CAGTTAAACC GATCAGAGTC 180

CCTTTTGTTG CATAATTTGC TAATGACTCT GCAGCTTTCC GCCAAATAAC ACAGTTGATA 240

AAATCTGCTT CCCTTTCATT GTTAGCATTG GTAAAGTTGC GATTAATGGC CAACGTAAAT 300

TGACCTACGG CTGTTCCACT TTGTGTATAC CTTAAATCTG GGTCTTTTGT TAATCGTCCA 360

ACTAATGTAA CGTTATTAAT CAAGATTATT TCCTCCTACT CCTATAGTCA TTAATATTTT 420

CTTGTATGGA TTtAATAAAT CATGCTATCT AATAACTCCT AATCATTATA ACATGTGCTA 480

ATCTACTTTn CTTTTATTCT ACTAGTCTGA TTTCCCCTCG CAATCTCTCT TTAAACATTT 540

TATTTTCTAA CTTTGTATTG GACTTTTTCT TTATGGAATT GGACAAGTAG CCCATGTTCA 600

TATCTTTTTT TCTTTTGATA CAAGAAGTTT CCTCGACCAA TTAGaTAATC AAGAAAGCTC 660

TTATTATCCC ATTTTAAAGA AAAGAGCGTC CACACAAGGA CGCCCACTCC TACTATAAGA 720

ATCAACCAAA AATTAGCAAT AATTGTGGTA AAAAAATTGA TTTTAGCGAC AAATGAAATA 780

ATCGCGAATA TCAATAAGAG AATAAGGATA CCAATACCTA CAAAAATTTG TTCCAATCGA 840

ATGCCGTTTG GCGCAAAAGG CAATGCTACC CCTTTGATAC TGTAAATCTT GTGAGGTTGT 900

TTAAATTCTC 910

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

CCCnGAAAAA AATATTCAGT TTGATCAGAT TGATTACACA aTGTACAAAm CArGTsCCGG 60

TATCCAATTA ATCAAAmCAT CTGAATATAA TAAACTCGCA AAATTTATAG ATGAACCAAC 120

TTTAACAGGT GAGAAAGTAG TTAATTTATC ACAAAAAGAT GCTCCTTCTG CTGCATCAGT 180

AGATGTCAAA TCTGTTCAAT TGGCAAATGA TCAAGTTTTA AACATTGATA AAACAGAAGA 240

AACCAATGTA TTACCGACTT TTGGCGGTGT GGTTGTTATC CCAGATAGTA CCTCAACAGA 300

TGGAATCAAA GCGGAAACAG AAACAATTTG GCAGCCCAAA GCAGGAACCA ATCGTGAAGA 360

ATTGATAAAA GCAGAAAATA TTATTGGTGA CAAGTATCCC ATGTTAGTAG GAACAGCTGC 420

AATGTCGGCA GCCATTACGC AATATTATAC GCCAGTTCTT TTTGTCGGAC TATTTATCGG 480

TATTGTGTTC TTTGTTTCGG CGGGTAGTTT CTTATACTTC CGTTTATACA GTGATATGAA 540

TACGGACGTT GAAAAATTCA AGATGATTTA CAAACTTGGC TTGACGAAAA AAGAATTGAA 600

GAAAATGATT TACCAACAAG TAGGTATTTT ATTCTTTACC CCAATTGTTG TTTCATTTAT 660

TCATGGAGCT GTTGCTTTGA AAGCAATGTA TGCTGTCTTA GATCAGCCAA TGCAATTAGC 720

TGGCTGGGAA GTTTTAGGCG TTTTCTTATT GATTnCAGGT CGTTTACTAT TTAATTGCCA 780

GAACGTT 787

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

TTCCCGGGGC CAGCACCAGA TAAATTATGG ATCGATTAAT GTCCTACCAC TCCTTGGATn 60

TTCAACTrGG CAAtCATGAT ATGATTTGGC TGGCTGCTTA TAGTGGTTCA CTGGCTTGTT 120

TAGCCAATGT AGTACGTATT TGTGCTCGCT ATGGAAATTT AGATTTGTTA GAAGAACGTT 180

ATGCTATCGA TTTAACCGCC TTAAAAAAAT TTAGTTTAGA AACGTATAAA GAAAATCCTG 240

CTTTTGCACC CAAGAAAAAT CCCTATCGTG CGTTAACTGA AGCTGAAAAA CAAGTAGCGA 300

TGCGTGTGCA CAAGCCATTG CCATTATTCA AGAAAAACTA GAAGGCCAAA TTATTGGTCG 360

ACGCCCTGaT TTTAACTTGG CACATCGGtA CGCTTAGATA AGATTCAAGG GGaAACTATT 420

ACTTTTGACG AATGTCGTTA TACATTAATT AACAGCTGTT TCCAAACCGT TTCTGAAGAG 480

CAACCTTACC AATTAACACG TGAGGaAAAA CAGATAATTG ATGATTTATT AACGCAATTT 540

CAGTCTTCAC CGCGGTTAAC AAAACACATG CGCTTTCTAA TGGAAAAAGC TTCTCTTTAC 600

CTTGTGTATA ATCAAAATTT ATTGATTCAT GGCTGTCTGC CTCTGAATGC GGACGGTACT 660

TTTCAAGCTT ATACATTTAA AGGCCACTCC TATTCAGGAA AAGCTTTAGT TGACTTCTTT 720

CAGGAAATGT TAGAAGAAGC TTACGCTCAG CCTGCTAGTA CAGATGACTA TGCAACAGAT 780

TGTTtATGGT ATCTTTGGTG TGGCGAAGGT TCCTCATTAT TTGGTAAACG AGCTATGAAA 840

ACCTTTGAGC GTTATTTTCT CGCTGAAAAA GAAACACATT ACGAAGAAAA GAATCCTtAT 900

TACTCTTTGC GT 912

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

GAAATATCTT GTGCTTTTTG TTCAAGACTT GCGCATCCTG ATAATAGCAA AGTGGCTGCT 60

GTTAGCAGTA GCCACTTTTT TCCAATAAAT AGTTTCATTT CCTAACTCCC TAACTTTTTT 120

TCCGTTTTAA AGAATACTCA ATTTTCTTTT TTTCTAACCT ATCAAACGTT AATCCTTCAA 180

CAGCTCGTTC CCATTTTGTT TGTTGTTCTG TACGTTTCTT TGTACTGTCT GCATATATTT 240

TTTGTAAATC TCCATTAACC ATGAGTCACT CCTCCTTAAA ACGGTAAGTC ATGATCTGAA 300

ATCTCAATAG AACTACCTTC TAAATCTGGA AAGGGTTGTT GCGTATTGCT TTCCTGCTGC 360

CCAACTGGTG TAGGATTAGA AGCGTTAACA CCACGTTGTT GACTAACTTC TTTTGACTCT 420

AACAATTGGA AGCTTTCTAC AACCACTTCT GTCACATAAA TACGTTGTCC TTGTTGATTC 480

TCATAGTTAC GTGTTTGAAG TCTACCCACA AGACCAATCA ATGTTCCTTT TCGTGTATAG 540

TTTGCTAAAG TTTCTGCAGG TTTACGCCAA ATCACACACT GgAATATAGT CTGCTTCACG 600

TTCACCATTT TGATTCGTAA AATTCCGGTT AACkGCTAGT GtAAAAgCsG CAACAGCTAc 660

ACCaCTkGAC GTATAACGTA AATCACAATC TTTTGTAAGT CTTCCTACTA AAGTCACATT 720

ATTAATCATT TAAAAAACCT CTTTCTATTA TTTTTTTAGA AGTGATAGCA ACTGGTACTA 780

TCACTTCTAA ATATTTACTG TTTTACTAAA CCACCAAACA TATTTTTAAA CTTGATTTCA 840

CCAAACTCTG AAAGGAACGG ATCCGTTTCG TTTAAGCCGT AAGTGTATTG GTAATTCTCT 900

ACAATACTTT GATAATCCAT TTCCCAGTCC TCTTCATACG GAGATATATA AAACAAGTAC 960

AACATTGTTA TATCCCCCAT ATACTTTTGT TCAATCGCAT AGTATACAAG TATATTGTTT 1020

TCTTTCTCGA TAATTTCGAT TGCTTTTTTT CGTTCTTCGT TGATCCAATA GTTGGCGCCT 1080

AGATATGATT TTCCCGAAAA ACTAATTTTT CCTTCCTCAA TAAATTGTGC AATTGTTGGT 1140

TCATGAATAC CTAAAATCTT CATTCTTTTT CTTGCTTCCA TTTTCATTTT TtCTAAATTC 1200

AATTGAATCC CTCGTTTCTG TTTATCTTTA TAATCATTAT ACCATACATT GTATACAATG 1260

CATAGTATAA TAATGAGGAA TATTGACAAA TTTTGGkTTT TTATATACTA TATTTTGTAT 1320

AGTATATATA GGAGGGTAAT TCAATGAAAG ATCTTTCTCG TGAAGAAGTT TTAACTTATT 1380

TAGAAAACAA TGTGGTAGAT AAACAAGGTG CTGCAAAAAT TACAGGCCAA TCATTAAATG 1440

CCTTCACACA ATCCGTAAAA TTGAATGCAA TTAAGCCTTA CTTTGAAATT AAACATGTAA 1500

ACGGTGAACG ACCTACTGTA CGCTTGTATC ACGTAGACGA TTTAAAGGAA TACGCAAAAA 1560

ATAAACGAAG ATAAAAGAGA ACTCCCTTCT TTTATTCTCG TTTATTTTTT TATATAAAAT 1620

CCTTAGTTTA TTTTAnGACT A 1641

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

TGTGCCCGAC CATTACGAGA GAGCGCACAC GATGCTGCCA TGGCCGATTG AATGAAAAGA 60

CGnGCAGnTT CGTTTTGATA CCAGGAACTG GAGAGAACGG nACAGCAAGT GAAGAAGTGG 120

CTAGAGGAAC AAATTGGAAA GAAGTGAATA TTTTTTTAAT GGCGTAAAAT GTTTTGAAAA 180

TTTCAGAAAA AACAGTGAAA GTCTTkGTTT ttATTAAAAa aTGGCAAaGa TTCAaCGAAG 240

AmCCAGTTCT AAaGrCCTaG TAATaGCGCA ATTTCATGtT ATAATATAGG CAACAAAAAT 300

TATACAGAAT AGAAGAGGTG AACGTTATGC GTTGTCCaAG ATGTCATCAT AATAATTCCC 360

GTGTTATTGA TAGCCGTCAA GCAGATGATG GACGTGCAAT TCGCCGTCGT CGTGAATGTG 420

AAAATTGCAG TTATCGGTTC ACTACATTTG AAAGAATTGA AGCGGCGCCA TTACTTGTAA 480

TCAAGAAAAA TGGGGATCGT GAAGAATTTA ATCGTGATAA AATTTTGCGT GGGCTCATTC 540

GCTCTGCGGA AAAAAGACCC GTTGCTATGG AACAAATGGT TCAAATTGTC GATAATGTTG 600

AAAATCGAGT GCGTAGTTTA GGGGAAAATG AAGTCTCTAC AACGCTTATC GGTGAATATG 660

TGATGGAAGA TTTAGTCAAT CTAGATGAAA TTGCCTACAT CCGCTTTGCG AGTGTTTATC 720

GACAATTCAA AGATATGAGC GTGTTTTTGA AAGAGTTACA GGACATTGTC GACAAAGCAA 780

AATCTTCTTC TCCTGACTCA GAAAATTAAA AAGGAGGTCT TTCTTTGAAA GGAAATCGGC 840

AAAGAATCCA ACCAAAAAAT ATTTTTCAAG CGGTTATTGA TTCACCGCTT TCTGATCAAG 900

AGAAAGAGGT TTTAACCTTT TATATCAACC AA 932

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

TAAACCGACA GCACGGCCTG AACCGTTCAT CAAAGCAAAA GCGACAAAGA TAAACCAGAT 60

ATTTACCCAA TAGAACATGC CAGATAAACA GAAGGCAATT GTTAAACCAA TTGTAGCAGC 120

ACTTGATAAC CAAGTGAATA AACCAGCAAT CAATGCTAAA gCAATACATA CTTCAACGAT 180

TGTCATGAAT TTTTGCATGA ACAAAGCAAC TTCTTGGTTT GGCATCATAA ATTTCATTAC 240

GCTTTCGAAC CATTTAGGCA TGTGATCAAA CACTTGCATT GGTGTTTCGC CGTAAGCGTA 300

gcTTAAAcCA AAGTGCGCTG CTTGTGTTGC CGCATCGGCA CCACCGCTTG CCGCCGCATC 360

CGCCGCACCA CTTGCAGCaG TTGTTGcTGT TTCAGTTGCT TGAGAAGCAC CTGTTGTTAC 420

TTGTTCTTGT AACCAAGGGA ATGGGAAAAC GACTTTATCT GTGAACCAAG AACCGTCACC 480

AAACCAAGTG CTTGGTTTCA AGTAATCGCC GTTGCCGACA ATTTTCTTCA TTGATTCGAC 540

TAACCAAACC ATACCATAGA AGACACGTAG CGGAACACTC CACAAGACAT TGCCGTAACG 600

AGACGTATGT CCGCGAGCAA CAGAACGATC ATCTTTAATA TGGAAGATTT CGTGCATAAT 660

GTATTGGAAC ATGTAGTAAC CAGAACGAAT ATCAAAGAAG TATTTCAAGT TAACGATATG 720

TTTCATAATG ATGGCTAAGA AACCACTCAA ATGAATTTTA TCGAATAAGT T 771

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

TTTCTCTTAA ATAATGAAAA AAGTCTGATT TTTTTGCAAA ATAGTGATTA AAAGTCAAAA 60

ATATACGCTC TTAAATGTCA ATAGGACCTT TAAGAGCGAT TGTTGCTTTA GTTTTGTCCT 120

TGAATTTTTT CTAATAATTC TGGATCAAAT GTTTGATTTT TTAACATCGC AATTTCAAAG 180

CCGTAAGGGg CCTTTTTATT TTTTTTGTCT TCTCCGACAT AAGGTGTTTC TAAAATTTTT 240

GGTAAAGCAG TTAATTTTTC ATGGTGAACC ACACCGTTTA AAGCTTCAAA ACCAATAGTG 300

CCAAAGCCAA TATTGGCATG ACGATCTTTA TGTGAGCCCA TAGGATTTTT AGAATCATTC 360

ACATGAATAA CTTTTAAACG ATCCAATCCG ATAATTTTAT CAAATTCAAC TAATACGCCA 420

TCAAAATCAT CTTTTACATT ATAACCTGCA TCaTTAATGT GGCAgTATCC AGAGTGACAG 480

AAAGCyTATC ATTTAGCGTA ACTCCGTCAA TAATCGCAGC TAGTTCGTCA AACGTACGGC 540

CGATTTCGGT TCCTTTACCA GCCATGGTTT CTAAAGCGAT TTGAGGGATT TGCTCTTTCC 600

nCAAGACTTC GTTTAGACCT TTA 623

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

CCGCCTTTCT CTAAGnGTAA AACAAGCCAA TGTTTCATGT GAACATTGGC TTGTTTTACT 60

TACTATAATC ATCGCACTTT ATTtGyCGTt CTCTGCGGTA GTCGTATTCy TGGATACGGG 120

GACTTAACCA ACCTTTTTTG GCTGTTTTTC GTAATTGATG ATCAAATCTC CCTGGTGGTG 180

AACTATCTAG TAATTCATGG GTACGATTAT TCCGATTTGC ATAATTAAAC GATTCACCAT 240

TCAAGACTTT TTCCTGGTAT TCATTGTTTT TGGCCGCTTG aTAATAAGCT GGaTTACTAA 300

TTAATCTGCC TCGCCAGTCT TCAACTAACA CATCCCACTG GGgTCACAAA GGtCCCTTCT 360

TCcATTCaAA ATAAACTCAC TGTGaAAATT AGGTGTCAAT CGTTTCTTAt TAATTAAAGA 420

ATAAGATGCC CCCTCAGGGT ATTTGTTGTG CAAACGAGCA GAGCTTTTTT TCAGCTTCCG 480

CCCACCCATC CCCTTGCGGC TTGGCCGCAA AAACATAGCG TTTTAACGCC TGTTCATCGG 540

TGTCCCCTTC TTGTTTAAAA AAATCGCGGA TATACGTGAT ATTTTGACGA TCAATATACA 600

TTCTTAATTG ATGTATCTTT TTCGCTTTCT CTTGGTTAAA GCTCCCAAGA AGACCTAACG 660

GATAGGCTTT TTGAACTGTT TTTGCCAACA AATCCCAAAA CGTCGCATGC GGTGCAACCG 720

TcTTCGAGaA ACGATAAGGT CCTACTAATT GCAACATGCC ATGCTGATCC AACACTGCAC 780

CTAATTGCCA TAACAGTAAC GAGAGCTTTT CTTGCGGACG ATAAGCCGAA AAGCGAAATA 840

ATCGCTCATA CGCTGAAGAG CCCACTTCTT CCACTTCAGA AAACAGTTCC GCGACTGCTG 900

TTTTCGCTTG CTCAAGTGGC AAGAAACGCG TGTCTTTTAT GGCGCTTTCC ACTAATCCAT 960

AAACAGCTTG GCGGTCCCAG CCAGCGTCAA TCGCCGCCTC TACACCAGCA CTCATTGCTT 1020

GTTGTAATTC TTGCCAACGT CCCATCTTCT CGCCGCCTTT TCTTATATAC TTCTTCTATA 1080

ATGATAATCC TTTCCCCACA AAATGCCAAC TGCTTTAACG CAAAAAAACA ACCCGCCCTT 1140

TGGGGAAGGG CGGGCGGAGG AGTTAAAAAA ATGAAAAAGT GTTTTGTTAA GGGTTTTGTG 1200

TATCGGGTAT GGTTAAATAA TAGCCGTTAA AATGTGAAGA AACTATGGTA AAA 1253

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

GTnTCAATGG TGATTGAAGG TCAACATTTA GTAGAAAATG GGTTGTTATA TGTGGCTTAT 60

CCGAnAAAAG GCAATAaAAT GTATCCAACC TTTGTCCACC GAGATGAAAT TTTTCCAACA 120

TTACAAGTAA ACGAGGCAGA TGGGTATATT AAAGGCTCAA CCTTAAAATT TAATCGCATG 180

GTTAGTTTAG ATGAGACTTT TACGGTTGTC GGCATGAAGA ATGTTCTTAA AAAGCTAGCG 240

AAGAATCAGA CCAGTTCTGC TGTTGGGGAT TATGTTCAAT ATTTACCGGA AATTGAAGCG 300

TTGGTACAAA CAGAACCAGC TGCTGCAGCG ACATtCGCTG CATTAACGCC TGGTTATCAA 360

AAAgAGTGGG CGCGGTATGT ATTTAGTGCA AAGCGAGCGG AGACACGGAA AAAGCGGCAA 420

ACTGAAATGT TAGTCATTTT AAAAGAAGGC TATAAAACCm AAGCGCTTaT CAGCmAAGGA 480

rGAAtAATGG CGCAGTCAAT TGAAACAGTT ACAGCATACA TCGAAACAGT GGAACCAACC 540

nGnCGAnTGn CTA 553

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

AAAAAATCGT CGCATATTTT TCTTCGATAA TTTCAGCTAA GCGTTTTCGA AAGTGTTCGT 60

TGAAATTATT GTCCATGATA GTTAAGAAGA AAGATTTGTT CTCTTGAATA TTAATATAGA 120

GTTGCGTCAG AAGTTCTTCA ATGTGCTTCA CGCGGACACG GTTGCCATTA ACCAGTTGTT 180

GCGAATCAAG AATAGCGGTA AAAGCACTAA GCGTAAAGGT GAAGATTGCA TCATATAAAT 240

GCTGTTTGTC TTTAAAATGA GCATAAAAAG TCGCACGATT AATCATAGCT TCATCAGCAA 300

TATCCTGAAT CGTCACCGCT TCGTAGCCTT TCGTTTCTAC AAGTTTAAAA AAAgCTTCAA 360

TAATCATTTT tCTGGTTCGT TGTACTCTAA GGTCTGTTTT CTTTGCCATC ATAAATTCCT 420

TTCGAGATAG TCAACATTCG CGGgAAACTT tGTkGTTawC tCACaAAATA GGGTAAATkG 480

CyTGTtGCAA ATCATTTAGA ACCTTTCTAA AATAGGTATA TCnATnATAA CCAACAGTTT 540

GTnTAATAAT CCACCAACTG TGGAAAAATG AnGGGG 576

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

GAGCCTGTGA CTGTTGAGGT AmACGTTCAA CTTCTCTTGA ATGATAATCA TTTGTCTCTT 60

TGATTGCTTC CGTTAACTCA CCTAGAGGAA ATGCAGTTGG CCATTTCAAC TGAAATGGGC 120

GATCTATATA ATCATTATAA GGTGTAAATT CTTTTTTAGT TTTTTTCATT GGTTTATCCT 180

CCAAGACCAG TGTTGCCACC AGCGTGACCA CCAACTAATC CGGCTCGATT CACAGCTGTT 240

GCTCCATCTA AAAGAGAAGA AGCGTGAATC AAGGCTTTGA AGCCAAATTT TCGACGTATT 300

TTATCGATCA AAAAATCTAA TTGGGTATTA ATAATTTGTT CTTCAGGAGG GGAGAAGAGA 360

TCCAATTGAA GTGTGGTATC CCAAACCAGC TTTCCmAAGG AGACTCCTAA aTTTCGAATA 420

TCCATACCAG GAACATAGTT TTCTCGAAAA AGCTTCAATA CATGTTCGGT TAACACTTTT 480

GTGTTGTTGC TACGAGCGAT TTTAAGCTGT TTTCGCCAAC CAGACCTGCC CAGTCCATCA 540

ACTTGTCCTT TAGAATAACC AACAAAAATT GAAACACACT CAGTTTGACA GTTTGAATTT 600

CTCAACCTGG TTGCTACTTG GTCTGAAAGT TCCTTCAGCA CTAATTCAAT TTGATCTC 658

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 940 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AAAGAATCTA TCAAATAGTA GAGAAATATG GATATATAGA ATAAAGATGT AGCATATAGT 60

TATGCAATTC TAAAGAAAAA GTTTTGTCAG GAGTAAATCA AAAATTTGAA CTTGGGAAGT 120

TTTATGCGAT AGTAGGAAAG TCAGGAACAG GAAAATCTAC ACTTCTTTCC TTACTTGCTG 180

GaCTTGATAA rCCTCAAACA GGAAAAATAT TGTTTAAGAA TGAAGATATA CAAAATAAAG 240

GATATAGTAA TCATAGAAAA AATAATATAT CTTTAGTATT TCAAAACTAT AATTTAATAG 300

ATTATTTATC ACCAATTGAA AATATTAGAT TAGTAAATAA ATCAGCAGAT GAAAGTATCT 360

TGTTTGAACT AGGTTTAGAT AAAAAACAAA TAAAAAGAAA TGTTATGAAA TTATCTGGTG 420

GACAGCAACA AAGAGTAGCT ATTGCTAGAG CATTGGTATC AGATGCTCCA ATAATACTAG 480

CTGATGAGCC TACTGGTAAT CTAGACAGTG TTACTGCTGG AGAAATAATT AATATATTAA 540

AGACATTAGC TAAAGATAGA AATAAATGTG TAATAGTTGT AACACATAGT AAGGAAGTAG 600

CAGATTCTGC GGATATCATT TTAGAACTAA GTGGTAAAAA GTTGAAAAAA GTAAATAAAA 660

TGAATTTGGA GGTTGAATAA TGATAAAAAA TGCATTTGCT TATGTAACTA GAAAAAGTTT 720

AAAATCATTA ATTATCATAT TAGTTATTTT ATCTATGTCA ACTTTAAGTC TCATTAGTTT 780

ATCTATTAAA GATGCTACGG ACAGAGCTTC AAAAGAAACA TTTGCTAATA TAACaAATAG 840

TTTTTCTATG GaGwkAAaTA GACAgTAAAT CCaGGAaCcC TAGAGGtGGG GGrAATGTaA 900

AGGTGaGaTt TAaAAgAaTC TCAACnGATA GTAAGACTCC 940

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

TGAAAACGAC TAGGTGATTC AAACTTTCTG AAATTCTAAA TTGAATCATA CCAGAAGAAA 60

CTGGCCGAAC CAATAAAGTA AGGACAATAT ATAAGCCCAT AATGATACCA TTGGCTAAGA 120

CTGTTCTTAG CTTTCGATTG GCTTGAAACG AATTTTGCAT ACTTTTTCCT TCTTTCTCCG 180

AGTTTTTTTA CAAGGGATGG TTGATGAACC TTGGTTACAA TTGCAACAGT TCACATTCTA 240

ATATGGAAAG TCAAAATAGT CAATGAAAGC CCTGTTTTAC TTTGCACTTA TTTGCAGGTT 300

TCACCTCTCA TGCATTGTTT CGTGCCTTTT TCTAGTCATT TTTTACTTTT TTAAGCAATC 360

TTTATTCGCA GAAGTTCCTC CCTCTGGTAT AATGGACAAT AGCGATTCAA AGGAGGAGCT 420

CAATGaACAT TCACTACTAT CTTATTATCA ACGAGCAGGC AAGTAGCGGC AATGGCCGAA 480

AAGTCGCTAG AAAAGTGATT CAACAACTCA AGCAACAAGA ACTTAAATAT ACGGCTCTTT 540

ACACTGATTA CGCTGGACAT GAAAAAGAAT TGACGAAGGA ACTTGCAGAA ACAACTTTAC 600

TTCCTTGGTC TGaAGACTTA GACGTTTcAA CTTTTCCAAT CCTAGTCGTG CTAGGCGGCG 660

ATGGCACACT ACATAATGTC ATTAATTCAT TACTTCCATA TGATTCAACT ATTCCTTTAA 720

GCTATATTCC ATGCGGCTCT GGAAATGATT TTGCACGAGG GGTGGGATTA TCAAGAAATA 780

TTGATAAAGC ATTGCATCAA ATCCTGCGCA CCAGACGACC AAAAGAAATT CAAACAATTC 840

ATTATGTAGA AGCCAACCAA GAAGAAATCG GCTTAGCCAC CAATAATGTT GGCTTAGGGT 900

TGGATGCgGC AATCGTGGAA AAAACCAACG AATCGTCATC AAAAAAAGCC TTAAATAAAT 960

TTAAGCTTGG CTCGCTTTCC TATATTTCTT CAATCATcAT GTCyTTTTTA GACAAAAAGG 1020

CTTcCAATTT TAGTTGAAaT GAATGGkAAA CAATACmCaT TwAATCGTGC TTTCCTATGk 1080

ACGGTCACAA ATCaTCCTTA wTTTGGcGGG GGCGTGnnnA TTATCCGACG GCCAATCCTC 1140

GCAAAGCAGT CGTGGACTTA GTTGTCGTGG AACGAATCAA TATTTTTAAA ATTTTGTGGC 1200

TTATTTTCCT AATTGTCGCC AAAAACAAGG GAAATCTAAG CATTTTCATC ATTTTCAATC 1260

AAGCAAAA 1268

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

GGATGCTTCA GCTCTAGGAC CGATGGAATT ATTCATGTTT TTCGGTAAAC CTACGACAAA 60

TTTCGTGACT TCGTATTCTT TCACCAATTC ACCTAATCGC TCAAAACCGA AGTTCTCTTC 120

CTCTTCATTG ATGCGAATAA TTTCGATGCC TTGTGCTGTC CAACCTAATA AATCACTAAC 180

AGCCACACCG ACTGTCCGTG AACCTACATC TAGCCCCATG ATCCTCATTT GATATCGATT 240

CCGTGGTTCG CTAAGTAATA TTTGGTTAAT TCTTCCATGA TTTCATCACG TTCATGACGA 300

CGAATTAAGT TTCGAGCATC TTGATAACGA GGAATGTAAG CCGGGTCCCC AGAAAGTAAA 360

TACCCTACTA TTTGGTTAAT AGGATTGTAT CCCTTTTCTT CTAATGCCCG ATATACGGTT 420

TCTAACGTTT CACTGATTGC TTTTTTTCGA TTATCATCAA AATCAAAGCG TACTGTTTCG 480

TCTGTAAAAC CCATTTTACT ACACCTCACT TCTACTTTTA TACAATTTCA TTTtACTAGA 540

AAAGAACCGA AACTACAAAC AAAATTcTTC TCCTTCTCTC tTTTTTGkTA TTCyTAGkCy 600

TTatTAATAA ArGCTtCGkA AAAAAATGAC AGCCATCGAT AATTTTAAAA TTATAAAAAC 660

AAATACACAA CTTTATAAAA CAAGAATAAA ACTCTGCTAA ATCGCCAGAA TATCACCTTT 720

CCCTCCAATT CATTTTGCGA AAAAATCGAC GTTTTTCTTT TAAAAACTTT TAAATATCTA 780

TGATTAAATA ATATCAGCCT TTTAATGTTA CAATTCGCTA ACAATCTGTT TACGATGTAA 840

ATTTTCGATT GCAGCTGTTA TTTATTTCCT CTTTTTGGTT CGTTTGTAGT ACACTAGAAG 900

AAAATACATA AAGTGTAGGC CTGCCGCAnG GACTCCGnCT CCATTTGGTT TTTACTTTTT 960

AGTAAACCnG TTTGTTAGCC GGGTAAAAAT TGnGGATCGT AAAGCGATGG C 1011

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

TCTnTTTTAT TCTAAGATTG TCTACTAAGC ACTTTTGTCC TAGTAGCGTT TTGGTTTCTA 60

ACTTTATTAT TTACAGGGGA AGAAAAAATA AAGCACACCT TTACTGTGAT TCCAAAAATC 120

ACGTGTTTAT CATAATATAT TTTTGTTTCA ATCCCAAGTA TTCTGCTCAC AAAGTGTCGC 180

TTATTTAATA AACATTGCAT CGCCAAAACT AAAGAAACGA TATTTTTCCT CAATAGCATG 240

TTGGTAAGCA GCCAATGTTA AGTCTTTTCC TGCAAAAGCA CTCACAAGCA TCACTAACGT 300

AGATTTTGGT AAATGGAAGT TCGTTGAAAA AGCCTCTACG ACTTTAAATT GATACCCTGG 360

TGTGATAAAA ATATCGGTCC AGCCACTGTC AGCCTGaATT TCACCATTAA ATTTTGTGCC 420

AATTGTTTCC AACGTACGAA TAGAAGTTGT TCCAACCGCA ACAATCCGaC CGcCTGCTTG 480

GCGTACTTCA TTTAATTGCT TAGCCGCTTC TTCAGTTAAA CGATAGAATT CGCTATGCAT 540

ATGATGTTCT TCTATATTAT CaACGCTCAC GGGACGGAAT GTTCCTAAAC CGACATGTAA 600

AGTTAAATAA ACGAGATGAA CACcTTTTGC TTtGATCTCT tCTAATAGTt CTTTtGTAAA 660

ATGCaAACCC GCTGTTGGTG CTGAAGCTGG AACCCATTTT CTTCAGCCAT AAACCGTTTG 720

ATAACGATCT GGGGCCATCT AGACGGTCTT TGGATATATG GGCGGGCAAT GGGCATTTTC 780

TCCCTAAACG GATTCCTAAA AAAnTTCTAA GGAAAATTAC CAnnCAnAAT TTGAAATTC 839

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

CnATTAGATG GTTCCTACTA CATTCATTAT GAGACACTAG CAGCTGGTGT CTCTTTTTTA 60

TTTGTAAGTA TTAGTTACAC TTGACCGAAC GTTCGTTCTC GTTTATAATA TAAATTGTAA 120

TCCTTATGAT TATATCTACT AGAAAGAAGT CAAGAAAAAT GCTTGTTTTT CTGTCTTCTT 180

TTTGATTTAA TTATTTTAGT AGGTATAATT AAtAcGGAGT GTTTATTAAA TGGTAAACAA 240

GAAGAGACAA GTAAGATTTG AATTTTTCCa GGTCaATGGA AAAGCTCAaG AAGGAGAAAA 300

AATTGTAAAA GGACTTTTCG ATCTATATCC aTTAGCTGAT AGGATAAATA GTATAAGTAA 360

CTATACTGAT AGAGATGTTA TTCTTTTTGG GGAAAAAGTT AGAATGGACA GATTTTTTGA 420

GGTTTCTAGT AGTCCAGAAT TATATGCAAT GCATTTTACT AGATTAAGAA ATGATAAACC 480

TGCGTATGTA GAATTAAATA ATGAAGTTTT GAAAGAAATT CCGTTAAATC CTGGAGAATA 540

TATTGCTGAG GATATTAGTT GCTTGTATGA TAGAGAGCTA TCTGTTTTAA TGGtACAAAG 600

AAATATTCAT AGTTTGTCAC CTTCAGGTAT TGrAGATTAT TTTACTGAAA TGAGTGATGA 660

TTTAGTAGAG ATTGAATTAT TGCCAGTkGT AAATAAaGAG ATTATTAGTA AnGCCTTAGC 720

TAATGAAAAA TTTCGTAAAC TAGAGTTAAG AGCAGGTTCT ATGAATACAA CTAGTGATAG 780

AAGTGGATTG AGAAAAGTAT TAGGTCCTTT TATGGAACTA TTTGAGAAAT TTGAAGGTAC 840

AAATTTTGTT ATAGAAATTA GTTCAGGGAG ATCAAAAAAA GATTTATCAG AAGATCAAAT 900

GAAAGAAGTA ATAACAGCAA TTGAACAAGA TAAGAGTTTA TTTAGTTCAG CAATTGTTTC 960

AGCAAAAAAA TCAAAAGAGG TACCTGTTGA AAAGTATGAT TTAATAAATG GAAAGCTCTA 1020

TGTGTATCGT TCTTTTGATT TGCCAGATGG TGCATTTTTA AAATCAGATA GTGTTATAGA 1080

CAATATTAAA AATTATTATT TTCATCCTAA TGAAGGTGGG TATAGAAAAC AAATTATCGA 1140

TGCTGTAAAA TAGTTTAAAG AAGAGGGTGA GATATCCTGA 1180

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

GTAGACCTAT TCATCTAACT CAATATCATT CACATAGTnT TTTAATCTnA GGTTATTGTC 60

TTGAAGATTA GGATGAAGCC TATCAATCCC CGAGTCAATT AGAGCTATGG TTATATCTTT 120

CCCTAGTTGT TCTTTCACTG GATCAATATG AGATAAAATT TTTTTATATG GCCAATTAAA 180

AGACTTAAAA TCTTTGTTTA AAATATTAAT GTTTAAAATA GAACTATTAA CTTCTTCAGG 240

TTTAAAATCT GGTAATTTTT TCCCTTCCGA AACATTAAAA TATTTACCTA TAAACTTCCT 300

ATCACTATCA TCCAGGTTTT TAAAACTAAC TAATCCTATT TCCTGTATAT AATCTACTTT 360

TTCAGAAGAT AATTCAGACT CAATTTCTTC TATAGCAGTT GTTTGCGAAT TATCAATAAA 420

AAATGAAATA TTATTTGAGA GATCTGATGC ATAACCTGTT GTTCCTAATG TTAAAAAAAT 480

ATATGAGATT AAAATATAAG TCAATCCTCT TTTTTTCATT TTGTACCTCC AAATTGTTGT 540

TTTTTGTAAT ACAGTGAACG ATATAACTCG CTATTTTCAA TAAGATCTTC ATGCTTTCCA 600

ATACATACTA TTTCACCATT ATCCATTAAT ATAATTTTAT CAAAGTTTCT CACCGTACTA 660

ATTCTGTGAG CAACAGTAAT AACTGTTCTT TTCTCATCTA ATAAATTAGA AAAAACTTCA 720

AATTCTGAAA TATTATCCAT TGCaGATGTA GGTTCATCTA AAAGTAATGT ATTCACATTA 780

GAATAGAACG CTCTAGCTAA AGCAATCTTT TGCCTTTGAC CACCAGAGAA ATTACTACCA 840

TTTTCTGATA CTATAGTTTT CTCATACTGA GGAATTCCTA AAAGTACCTC ATCCATTTTT 900

GATTTACTCA TACTTTCTTT TAGTCTTTTT TTCTCATTTA TAGAAGAATT CGGTTTAAAC 960

TCTAAAGAAA TATTTTTTTC GATAGTTTCA TTAAAAATAT GCGCATTTTG ATTAACATAA 1020

AAAATGTTTC TTCTATTATT GGAGTTGTTT GATAAAGGAT AGCCTTCATA CAATAtTTCt 1080

CCATTAGAAg GTTGTAACaA TCCaGCCAAT AGTTTTAGTA AAGTAGATTT CCCTGACCCA 1140

CTTCTACCAA CAATAGCAAC TTTATCCCCT TTTCTTATGT CAAAAGAaGG GAGCGTCAAT 1200

AATTTTGTGT AAATAAATTG TCCTCCTGcA AAATAATTAG TTACTCAGTA AACATTGaAA 1260

CTAATGTATC GGTTACCTGT TGaAAACCTT TATGGcTtCT GTTTAGAAAT TTTTGaTtGT 1320

ATGTATCAAA AAkGCTGACT AGrAAGCGkT CTAGTGawTC TTCATTTTGA AACTGCTCTT 1380

TTCTACGGCT GTATCTTTTA ATTTGCTTAT TGAAAGACTC GATTAGATTG GTTG 1434

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

GTAGTCCCTA CAGTTCTTCT ATTTATAAGG yTTCTCGTTT AGACAAGCCA CGTTCTAAGA 60

TTTTTTGGCT TCTAAGATAC TCTGAATTTT CTGTACTTTC AGAAAAAGAC AACTCTGTTT 120

CGATCTCCTC TGACTCAATA CAAATGAGTT CTTTGCCATA CCATTGTGCT TTATACAACA 180

ATTTAGCTAA AAATAAAGAC CAAGCCAGTT CAGAACGATC ATGTTTTGGC GGCCGCTCAT 240

TACTGTGaTG GGcTTTTTCA ATACAAATAA CATCGTAACT TGaAACCAAT TCCGTTGTAA 300

TTTTGTTTAA AATATCCGTT CGTTGGTTGG cTATTTTTTC GCGAATTTTT GCGACTTTTA 360

TTTTTTGTTT TTGATAATTT TTTGCTTGCG AAAGATCGAC ACCTTTTTCC AAAGCAATCA 420

TTTTACGCTT GTTTAATTTT CGTTCTTCTT GACGTAGTTT TTGCTTTAAA TGCTTTGAAC 480

AATAGCTTTT TTCGAAGCTT TCACCATTCG AAAGCAGCGC AAATTTTTCC CTACTGCTAC 540

AAATTCCCAC CATTTTTTGT TGCTTTGTTT TCGTTTCAAT CGGCGCTTCA CACAAAATGG 600

AAACATAATA ATTGTGACTC GCACTCATAG AAATAGTTAC AGATTTTAwC TCCCCCAGCG 660

GTTGGcGGTG TACCTTCATT TtAATTAAAG ATTtCAATTT AGGTACTTTC AAATAACGAT 720

TATCCAAAAT TTTGACCGTG CCATGTTGAt TGTTCGTAGT GTAGGAATGC ACCGTTTCtT 780

TCTTTTTCTT TTTTGGAAAG CCCATCCCTT TTtCCCGATA AAAATTTTTA AAGGCTCGAT 840

CCAAATAAAC TTGtGCATTt GCCAAGGCTA AACTATCAAC TTCTCTGAGG ACAGGGTATT 900

GTnTCTTATA TTTAGCTGGC GTTGGCATTT TAAACGTTTG TTGAGGATTT TTTCGCATCT 960

CTTTGTAGAk ATCAATCCGG GCTTGTAACA TTAAATTATA CACCAA 1006

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

TGGTAGGTGA AGAGGTGATA AGGTGGATAA AAGTATGAAA ATAAAATGGA AGCAGAATTT 60

GTTAGTCGCA TGGATTGGTT GCTtTTTTAC AGGGGCGAGT ATTAGCTTAG TTATGCCGTT 120

TATTCCAGTA TATGTTGAAC AATTAGGGAC GCCTAAGAGT CAAGTAGAGT TGTTTTCTGG 180

ATTGGCAATT TCTGTCACGG CGTTTGCTGC TGCGATTGTT GCACCGATTT GGGGAAATTT 240

AGCTGATCGA AAAGGTCGGA AAATTATGAT GATTCGGGCT GCAGCAGGAA TGACGATCAC 300

AATGGGGGCG TTAcATTTGT CCCTAATGTA TACTGGCTGT TGATTATGCr TTTTATGAAC 360

GGGATTTTAT CCGGCTATAT TCCTAACGCA ACAGCGATGA TTGCGTCGCA GGCGCCAAAA 420

GAGAAAAATG GCTGGGCTCT AGGGACATTA TCAACAGGTG CAATTGcTGG GaCGTTAATT 480

GCGCCATCGA TTGGCGGTGC GTTGGCACAG TGGTTTGGAA TGGAAAATGT CTTTATTATT 540

ACCGGCGTTA TTTTATcATT ACAACGTTGT TGACTATCTT TTTAGTTAAA GAAGATTTcA 600

ACCAGTTGAG AAAAAGGATT TATTAACGAC GAAAGAAATT TTTAGTAAGA TGGATCATGT 660

TTCAGTATTG ATgGTTTGTT TGTGACTACG TTAATTTaCA ATTAGGAATT ACAAGTATCA 720

GCCCAATCTT AACGCTATAT ATTCGtCTTT AAGgGCGATA CAGAGAAgTA TTATtTGTTA 780

GTGGTTtGAT gTTcGATGCC GGCGTTCAGC AATAATTCTC TCCnACCTTn Gn 832

(2) INFORMATION FOR SEQ ID NO: 598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

CTTTTGGGAC aATnTGrTaC CTAtrGCgCC tTaCaATTrG CaCnGTACGT TTCCmTGtCG 60

CaAATAATGG caTCCgCGTG CaACCCCcAT GTGGTAGAmG GAATCTATGG CaATGATGaA 120

AATGGAGCTT TaGGAAAAAT TTTAAAAGAA ATTGAACCAA AAGTTTTGAA TAAGGTGAAT 180

ATTTCTGAAG ACCAGATAGG AATTCTTCAA CAAGGTTTCT ATAATGTGGT AAATGGAACT 240

AGTCCTTTTA CAACTGCACG TGGTTTAAAA TCAGACAAGT TTTCGATTGC TGCTAAAACA 300

GGGACCGCCG AAACGCAAGC AACAGATGCT AATGGAGTAA ACCATACAAC GGTTAATAGT 360

AACTTGGTGG CTTATGCGCC GTACGAAAAT CCTGAAATTG CAATTAGCGT TGTTTTACCA 420

CACTTAAATG ATGAAGCTTC CAAACCAAAT CAAACGATTG CCAAAGAAGT TTTAGAAGCG 480

TATATGGAAA TGTACAAAAA ATAAAATTTG TAAAGTAGAA CTACTTTACA AATTTGCCCA 540

AAAGGGTAGT CAAATGACAA AAAAAATGGT ATGATATTCA AGTCTAAGAA ATCTCTTGGA 600

AAGATCAATT ATTAGTAGGA GGGGAAAACA TGCGCGTAAA CATCACTTTA GAGTGTACTT 660

CTTGTAAAGA ACGTAACTAC TTAACAAATA AAAATAAACG TAACAATCCT GATCGTTTAG 720

AAAAACAAAA ATATTGCCCA CGTGAAAGAA AAGTTACTTT ACACCGTGAA ACTAAATAAT 780

TTATTTGAAT ATAGCCTAGA ATCCTTGCTT TATAAGGGTT CTAGGCGCTT TTTTTGTTGT 840

TAGGAATTTA CTGATTTAGT TATTGATGTA GATTTGCTAT TTTAAAAATT TACATAGCTA 900

CTGAAAGCAT CTGTTGCTTC TTTAGTAACT TCATCAGAAA CATGAGTGTA AGTATCCATA 960

GTTATTTGTA AAGAAGAATG TCCTAAACGT TCTTGGATTA TTTTAGACCT AACGTTATCT 1020

GATTCGAATA ATAATGTTGC GTGGGTATGC CGAAAACCAT GACAACCAAT AGAATGTAAG 1080

TTAGCTTTTT CTGCCAATCT TTTAGAACGT TGGTAAATGT CTTGACTTCG GGACATGGTA 1140

CCATCAATTT TTGkAAAAAT GaGTtGTGTT TTAAATCCAC CTTTTTTCAT TAAAGCTTCA 1200

TGCTGTCTAA GTTTCCATTT TTTTAAGATA TAAGCAGTCT TGTTATCAAA AGAAATTTTA 1260

CGAATAGAAT TGGGAGTTTT AGGATCGTTT ATAGTCAATC CATTTGTACT GATAGCAGTA 1320

GTTTTATTTA TATTAACTAC CTGCTTTTTT AAATCAATAT CATTCCAATT CAATGCTAAA 1380

GCTTCACCAA CACGTATACC AGTAAAAGAA AGTAAGCGAA AAATAGCACA GTCTAAGTCG 1440

GCATAGTATT TTAGAACTAA ACTTTCTTCT TTGGCTTGAT TGGCAATGCT ATCAGCTGTA 1500

TTTAAGAAAT GTTCCAGTTC GTCTTTTGTA TAGAACTTTC TTTTTGTATk CTTTtCTAAT 1560

TTCTkTAGCG AACTAGGTTT AGTTATTTTC TTAAATGGGT TTGAGTCTAT TATTTCTAAA 1620

CCAACAGCAT AGTCACAAAC AC 1642

(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

AGTGATCTTT ACCCTTTCCG CAGATACCGC AGCCAAAAAA GAACTACAAC GGATTCTTTT 60

GCAGTATAAT AGAAAATAGA AACGAAAGAA CAGGCACCAA CACAAAGGAG GTATTTTTAT 120

GAAAGTCACT CAnCTTTCTA GTGAAaCCCT TGACCGAGCG CACGAACGTT TTGAAGAAAC 180

ACTTGCGCAA ATGACCGTTG CCGAAGCAAA CACGATGCCC GCACCATTAA TCAAGTCTGT 240

TACTTGGCTG ATGTGGCACc AGCCAGAGAA TTAGACCTAC AAATTTCCGC ACTTAATCAT 300

AGTGATCCGT TATGGCTTAG TCAACACTGG ACAGAAAAAT TTGCCTTGGA TTTGCCAGAT 360

GAAACAGAAG ACTGGCATCA CACACCAGAG GAAGCGGCGA AAGTCGTGGT GGCAGAAAAG 420

CAATTGCTTA GTGACTATTT GGCTGCCAGT GTGGCACTTA CCAAAAGCTA TTTAGACCAA 480

ATCAAAGAAG AACAATTGTC AGACGTGATT GATAAAAATT GGACCCCGCC GGTGACTAGA 540

CAAGTCCGTT TAGTTTcAGC GATTGATGAT GCAtGATGCA TTCTGGGCAA GCCGTTTATA 600

CACGAAGATT AGTCATTGGA AAATGATAAA TAAGCAAAAA CCAAAAATGC TTCTGCTTAA 660

GCGGAGCATT TTTTATTGAG AGAAAAATAC ATAn 694

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

AATTAATTTG ACATAAAACC AAGTAGAAAG ATAACATTCT TTATCTAATT CAGTTATATA 60

TCACTTTTTT TGCAGGTGCT TCAACAGTTA AGATTTCAAT AGAAACTGGA CTATTTTCTA 120

ATATACCyTC TTCTTTTGCA TGTTTCCtAC ATAAATTATT TTTTGTAGAT AGTACTCCTA 180

TGTCCTATTG AAAATATTTG TATTATAATT TCTGAATCAC AAATATTAGC CAATATTCGA 240

TAATTTCCAA TTCTGTAACG CCATTCACCA CTTCTATTTC CAGTCAAGCC TTTTCCATGT 300

TGACGAGGAT CAGTAGTTCC TTCTAAGTTT TTTCTAATCC AAGCTACTAT TATTCTTGCC 360

TGATTTCTAT CCATTTTTTT TAATTGTTTC TGCGCTTGTG GCATATATAC AACTTTATAT 420

TTCATTTAGT AAATTCTCCA TTTCCTCTTG AGAAATACCA ATCTCTTTTT TCTCTTTGGA 480

AATTTCTATT GCGTTCCGTA AGgTTTTTAA ATCAATTTCA TCTTCAATTT TATCTAATAC 540

AGCTTTTCGA TAAAGTTCAG TTAATGAAGA ATTATGAGCT TTTGCATATT CTAACACAAG 600

TTCTTTCTCA TCCTCAGGaA TTCTAAATGT AATTGkTGaT TGaGACATCt TATTACCTCC 660

ATTCGCACTT kGtAAtAACa TTGTATTAAA AACAAGGGGA TTTGGCAATA CAATGTTATT 720

ATAAATGTGA TGATACTCCA ATATATAGAA TAAACATGA 759

(2) INFORMATION FOR SEQ ID NO: 601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

ATTCATAAAA TTGGCATTAA TATTAATCAA ATGGCCCGTC TGGCCAATCA GTTTCATGAA 60

ATTTCGTCTG AAGATATTAA AGATTTGACC GATAAAGTAC AGAGTTTAAA TGCGCTGGTT 120

CAGAGCGAAT TAAACAAATT AATAAAGAGA AAGGAACAAT CGTAAATGGT GTATACAAAA 180

CATTTTGTTA TTCATACATT TGATAAATTA AACAATGCTT GCTCATATAT TGAGAATGCA 240

GAAAAAACTG AAGTCACGAA TGATAATCCG TCTGAACACT TGGAACATTT ATTTCAATAT 300

ATTGTGAATG ACGATAAGAC GTACATGAAA AAATTAGTTT CTGGGCATGG CATTGTGGAT 360

CCAACAAATC CTTATGAAGA ATTTAAATTA ACAAAATTAC AAGCAGCAAT TCAACGAAAA 420

ATCGGGTACA CATTCGATCC AAAATCAGAA CGATTGCTTC CGCCAACGTT AACAGAATTA 480

GAAAAAGGCA ACGCgctTTT AGCACACCAT TTAATCCAAT CCTTTTCTCC AGAAGATGAT 540

TTAACGCCAG caAAAAATAC ATGAAATAGG GTACAACACG GTGATGGAAT TGACGGGTGG 600

AGAGTATGAA TTTGTGATCG CCACACATGT CGATAAAGAA CATTTACmCa ATCmTAtTAt 660

TTTTAGGTTC CAACCAACTT TAAAAACCAG G 691

(2) INFORMATION FOR SEQ ID NO: 602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

TTTTACnTCT TCTATGTTAT TTATnTCTAT ATTATCTATA TATTCTTCAT AGAAATAGGT 60

ATTTCTAGTA ACTTTTTTAA CTATATAAAT ATCTGCCTCT AATTCTTTAT TTAAAAATTC 120

AAAAAAATCT CTTAATTTAT TCTCGCTATT AATCTTTGGC TTGTATACTA TCTTCTTTCC 180

ATCAGAAAAA GTTAGTGTAG AAACAGTTTT TCCGCGACTA TGAGAGTCTC CCTGTGATTC 240

TGATATAGAG TTAAGCTCTG AGGATTGTAT GTTAAAACAA TTTTGTATGC TAGGTAAATC 300

TTCAGTCACT CTTATAAGCA TTTGTTTAGT ATTATCTAAA AAATATCTCA TTCTAACAAC 360

AGTAATACGC ATCAACTCAG GATAGCATGT ATAAAAAGCT ATTATATCTT TTTTAGAGTT 420

AAATCTTTTT TTTAGATAAT AGATAAATCG CTTGCTACTA TCATTTCCCT TTAGAGGTTC 480

ATTTTTTTTA AAAGTATGCA AATCTAGCAC TAATGTTTTA CTTGTTAAGT GAATAAGCTC 540

TTGTGTTAAA GTTTCTAATA AATTAATAAT GAATTCTTTT GTACAAATAT TTAACTCTGA 600

GTTTAAATCA AGTAAAAATA AACGaGCATA CTGTAAGAAA TATCTAAAAG GATAACTAGC 660

ATCTACTTCT AATAATTTCT CTTCACTATC ATTATAAGAA TCTAAAATGG aTTCAAAAAA 720

AAtATACCAT GaTTGaTcTk gTAATGTAtT GAAtTGCAmC TTCTTTATCA GGAAAGTTTT 780

CAATAGGTGT TATTCCTAAT CCAAAATTAT CCAGTGATTC ATATTTATAT TTAATCAAGT 840

AGTCTAAATC ATCTTGTTTA AGAACACTTT TTCTTTCTTT CCAAGCTTGT AAATTTTTAA 900

TGTCGTACTT CTCTTTACCA CTTTGCTTTA GTAAAAAACA TCTTTCATTT ATGCTTAAAA 960

CATTTATTAA ATTATCTTCC ATGTAAGCAC TCCTTTTTTA TGTATAAGAG GGCTAGTTTC 1020

ACTAGCCCTC TTAATATATA AATkAGCAAA ATTTAGCTGA AAATAATGCA CCTACTCCTA 1080

AGCCTATGGT AAAACATGCT GGAGTTGTCT CAGCCTGAAC ATCTCCACTA CCTTGAAtCG 1140

CTTCCATTTC TTCTAAACTT AACTCTTCAA AAGAAGGACC AACAAGTTCT AATTTATTAG 1200

AGTAATAGTT TTCTTGATTT TCCTTATTTA GCACTGTGCT TCACCTCACT AAGTTTTATA 1260

GTATATTTTA ACAATGTTTT AAAGACACAA CTACAGTTAC TCCAGTAAAA ATACCGCCAC 1320

CAACCCAGCC ACAAGCAGCA CTACTTGCTG CAGCTGTCGC CGCaACAGCA CACACCGGTG 1380

TTGTCTCAGC CTGAACATCT CCACTACCTT GAATCGCTTC CATTTCCTCA ACACTTAGTT 1440

CTTCAAAACT AGGrACTACA CTTAAATTTT CCATAATTCT TACCCTCCAT CATAAAATTG 1500

TTGTATATTG CATAACATAA TATGTTACAA TTTAATATTA TAGAGCtTTT AATCTTTTGT 1560

CAAGTGACAC TTGACAAAAA GGAGGAATCA AAATGGCTAT TTTTATTTTT TTATTGGATA 1620

TCATTTCTGT AGTCTACTTn GTTTTTAATC TGAnTGATTC AAAAAAaGaT GmGCGAATTT 1680

TATATwCaAT TTCtTTAACA TCTACTTACA TGTACTTATT TATTAACTTT TCCATACTTA 1740

TAGTAATTGC TATTTtTCTT TTACTACCTA ATGTTATTAC TAAAAACTAT CTATTTAATT 1800

TTATCTACTA TTACTTCTCT CTATCAATGA TATTGCACTC TCTGTTACTA CTTTTTTTCA 1860

ACAAGAGGAC TTCATAAATG ATAATCAATA ACTTAAAATT AATTAGAGAG AAAAAAAAAA 1920

TTAGCCAAAG TGAATTAGCT GCTTTATTAG AAGTTAGCAG ACAAACTATT AATGGTATAG 1980

AAAAAAATAA ATATAACCCT TCTTTACAGT TAGCATTAAA AATTGCTTAC TACCTGGATA 2040

CTCCACTAGA AGATATTTTT CAATGGCAAC CTGAATAAAA AAGATTTTTA AATTTCACCA 2100

CAGAATATTT AAATTAAAAG AAAGGTGCTT CGTATGAAGA AAAAGTTTAT ATCCCTTCTG 2160

ATTTTATTTT TAGGAATAAT TGTTGGCATA GTAACAGTTT ATATTTTAAA GCATAAATAA 2220

TTATGACTGT TGTTTTATAC TTTAATCATA ACTGATTTTT TATCAGTAAA ACCCTCACTT 2280

ATGATTACAT TCATTTAAAT AAAAACTAGG CTCAAATGTA TAGTAAAGAC TATCTCTTTT 2340

TTTGGGGGAG ACAGTCTCTA AGGTTATAAC TTATTTTAGC CTTTCAATTG CCTTGATATT 2400

ACTTTTATTT CAAGATTATT TAACATGGAC AAATACTTCT GAATCTTTTA CATAAATGTC 2460

GTGGTAATAA TTAGATTTCA TTAAGTCACT TTCTTCTTTA TTCAACGCGT TAATATCAAA 2520

GATCTCCATG TTCACATTTA AGCCAGTGTA CGTTCTAAAT AAAAACTGAT TTGGCCAATA 2580

AAGGGCTTCA TTTGGTGGAA CCAGTTCTTT TAATATAGGA TAATTCTTCG AACTATTGAC 2640

AAATACTGGC GAATCCTTAA ATAAAGAGGT ACTATGcACG GTCACcGTGt CACGGTTCAC 2700

TAGATCTTTT AAATCACCGG CTAATATCAT ACTTTGTCGT TCAAAAGATT CCTTTTGGTG 2760

ACTTAACGCA CTAGCATAAA CAAATGTAAA AGATAAAAGG TAAACACAGA AAAGGCAAAC 2820

CGCTGTTTTT GACACATAAC CTACCGCGGG TTCTGTTGCA AAGTTTTAAA TAAAGAATAA 2880

AATCCCTTAC GGTATCTATG ATTTAAGCTG GGATTCCCAA TAATACCTTG ATTTCAGTAC 2940

AGACCGAAAA CCCGAAGAGA GTACCTTCTT TTCGGGTTTT CTTATATAAT CCTCGAATGG 3000

CTTCCATGCC TTTAATCGTG GTAGAGGCAG TGCGTAAACT TCGATAGAAT TTATTGCGTC 3060

TCTTTACTGG ACGATGGTCT TGTTCAATCA AATTATTCAG GTATTTAATG GTACGATGTT 3120

CTGTCCCTTG ATAAAAGCCG TATTCTTTTA GTTTCTTAAA GGCACTTGTA ATAGAGGGGG 3180

CTTTATCTGT GACTACAACc TTCGGTTCAT CAAACTGCTT CACTAAcCGC TTAAGAAAAG 3240

CATAGGCtGC TtGTGCCCGn TTTTACGnAC CAAT 3274

(2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

ATTCCACGAG CCATAGCAGC ATTTGCAATA TCTGTTGGAT CACCAATTAA GATTnGTTCT 60

ACTAATTCAT CAGATTTTAA GCGGGCAGCA GCACCTAAGA TTCTAGGATC TGTTGCTTCA 120

GGGAAAACAA TTTTGATATT ACGGCGTACG ACTTTAAATT TTAAGCTATC GAATAATTCC 180

ACGATAAACC CTCCAGTTTT ATATTTACAA AATCCATCAT ACACTATTCT CAAAGAAAAT 240

AACAGTTTTT TCTAGCTGTA TTAGTCAAAA AAACCAATAA TCCGATAAAC TTTTCACAAA 300

CTAACTCTTC TACACTATAA CAGCATACAC TGTTACACTA CACTGTTTCA GGAAGTTGCC 360

AATCAATCGG CGTTTCCCCT AAACGTTCTA GAGCGGCATT CGCTTGAGAA AACGGACGTG 420

AGCCAAAAAA ACCACGATGT GCTGACAATG GACTTGGGTG TGGCGATTTG ATAATCACAT 480

GCCGAGTCGT ATCAATCATT TTAATTTTTT CTTGAGCAGG ACGTCCCCAT AAAATGAAAA 540

CAACAGGTTT TTCACGCTCA TTCAACTTTT CGATAATGAC ATCTGTCAGT TGCTCCCACC 600

CTTTACCTCG ATGGGAATAG GCTTGACCTG CCCGAACGGT CAACACAGTA TTTAATAATA 660

ACACGCCTTG TTTGGCCCAG CTTTCTAAAA AGCCATGGTT GACTGGTTGG TACCCTAAAT 720

CAGCTTGTAA TTCTTTGTAA ATATTCGCAA GAGATGGCGG CACTTTCACA CCTGGCTGGA 780

CAGAGAAACT TAGTCCGTGT GCTTGATTGG GTCCATGATA TGGATCTTGT CCCAAAATTA 840

CTACTTTTAC TTCTTCAAAA GGGGTTAGTT CTArCGCTGA AAATAAATGA TACATATcTG 900

GATAAATCGT TTGTGTCTGA TATTCTTTTT TCAAAAATTC CCGCAATTCT TGATAATACG 960

GTTTTTCAAA TTCAGCAGAT AAAATGTTTT GCCAACTATT GTGAATAATT TCTTTCATAA 1020

TGCTCACTCC TTCGCTCTCT AAGCATAACG AATTTCTCCA AACCTGACAA GAAATTTCTG 1080

GGTACTTTCT CTTGGAAAAA CGTGGTAAAC TATAGGTAAG CTTTAAATAG ATAATGAGGT 1140

GTAGAGAATC GATGATTAAA TTAATTGCTT CAGATATGGA TGGAACACTT TTAGATGCAA 1200

AAATGAGCAT CACAAATGAT AACGCTTCAG CAATTCGCGA AGGAwACGTT TaGGAaTCgA 1260

ATTTAtGGTT GCTACTGGCC GCGCATAtAC cGaAGCGAAA CCCGCGTTAG AAGAAgCTGG 1320

aATTGACTGC GCCATGATTA CTTTaAACGG CGCCCAAGTG TTCGACAAAG ATGGACACTC 1380

ACTTTTCACG GCTGGGATCG AAAAAGAmAC AGTAACAGAA GTACTAACTA TTTTGAGTCA 1440

ACACAATGTT TACTATGAAA TCTCTACAAA TAAAGGTATT TTTTCTGAAC ATCAAGAAAA 1500

AAGAATTGAA AACTTTGCCG CTCATATTGC AGAATCCATG CCCCATTTAA CTTATAAAGT 1560

GGCGATTGCC ATGGCTTCAG CACACCTATC TTTATTGCAT ATTACCTATG TTGATCGTTT 1620

GGACGACATT TTAAAAGATG ATTCGATTGA AGTCCTTAAA ATTATTGGCT TCAGTATGGA 1680

TGGGCCGAAA GTATTAGGTC CTGCTGGGAT GGAAGTAGAA GAACTAGATG ATTTGGTTGT 1740

TACCTCTTCT GCGCTTAATA ATATTGAAAT TAACCACCGC CTAGCACAAA AAGGGATTGC 1800

AGTTGCGCGC GTCkCTAAAG AACGTGGGAT TCCCGCTGAA CAAGTCATGA CTATTGGTGA 1860

TAATTTAAAT GACGTCAGCA TGATTCAATG GGGCTGGGGT AAGTTTTGCA ATGGGGCAAT 1920

GCCGAACTGG AATTAAAAGA ATACGCTAAA TATGAAACAG CCACTAATTa GAAAAgGTGT 1980

TGGCGArCaT CCgCGTGCAA TAAGAGAAGA TTtGTAATAA GCACTaCCAG TTACAGCACT 2040

CATTTATATA TAGAAAGGAG ATCGTGTCGT GTCTGAATTT TTTATTCAAG AACAACAGTT 2100

AGGAAAAGTT ACGCGAACCA TCGTGAAAGA CCAAGCAGGC CGTTCACTTT TTCTATTGGT 2160

GGGGCGCTGG GGCACACGAG GAGATGCGCT TTCTTTATAT GCAATGAACG GAGAAATTTT 2220

AGCCAGTATT AAACAAGTTT CTTGGACTTT TGGCACACGA TTTGAGTTAT ATCAGCGTTT 2280

TGAAAAAGTG GGTACTCTAC GGAAACTGTT CAATTTGAAT GCTGATTTCT ATTATGTTCA 2340

AGGCCTTCAC TGGGCAGTTG TTGGGGATAT CAAAGCGCAC CAATATTCAA TTTATCAAGT 2400

CCATAAAAAA ATCATGTCAA TGGATAAAAC CATGCTTTGT ACAGGCGACT ATTTTGTTTT 2460

AATGTTGTC 2469

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

GAATCACCTC AGAGTTAATT TTGTCAAAGC AGGTTTTTCC TAAAAATATA GAAATTACTT 60

CTTTTTTAAA TGTAGTATTT AATGTGGAGT TTAAAAATTA TGTAATGAAA TCTAGAACTT 120

TGATTTTATC AAGAACTGTA CGTGTTATAG AAGGATGCTC AGAGAATGAA TATCAGAATT 180

ATAGAAGAAA ATTATTAAAC TTTGTAGAAG AGTATTATGA GTCGGAAGAA GTGTCAAAAA 240

ATATTTCAAA ATCTTCTATA TCGAAATGGG TAACAGGAGA ATAATAGCAT GTATAATCAC 300

GTTTATTTAA AAGAAGATAT AGATGCTTTA ATAAATGAAT TTGGAAAATT GAATGCTGAG 360

GATGaATCTT TATTTAGaTT TCTAAGTAAA AAGATTATAT TCTTAAAGGA AATAAAAATA 420

AGTATAGTAA ATACTACTGT GATATTTTAT ATAGACCAAA TGATATCGGA TTTAATGTAC 480

TTAATGGCTA GTTATCATAA GGGTGAAGTG AGATATTTTT ATTTAAATAT TAGATCAGTA 540

ATTGAGGCAT TTTCCCGTTT GTTTAGTGAG GTAGAAACAA GTACTAATAG AATAACTATG 600

ACAACTTTAT TAGATAATAT AGCTAACTAC ATTACTTTAA ATGATTTGCG TGATAGTnAA 660

GAGGrTtCTC TGGACTATCC TAGACTAAAA GGTCTTTATA GAGAATGCTG TCTTTACGTA 720

CACGGAAATA TTAATGCnAA ATATTCATTA ATTGAGTTTT ACAACGAGTT GCTTAATGAA 780

GAAATAACTA GTGCTCA 797

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

TCTGCGTTAT AGAGCTTAAG AGGTAATnAT nCAAnATCAT TGCAATCAAG GTGGTAnCGC 60

GAGCAATCGT CCTTGACTGC AATGGTGTTT TTTGTGTACA CAATCTGCCA CTTAAGAGGG 120

TACAAAATAT AAATAGTTAA TTATTAATAG AAAGTAGGAA AATCAATGAA AGAATTAACA 180

AGTAGTCAAG TTCGCCAAAT GTATTTAGAC TTCTTTAAGT CTAAAGGACA TTCAGTAGAA 240

CCAAGCGCTT CTTTAGTACC AGTAAACGAT CCAACATTAT TATGGATTAA CTCTGGTGTT 300

GCAACCTTGA AAAAATATTT TGATGGCTCT GTTGTGCCAG AAAATCCAAG AATTACGAAT 360

GCTCAAAAAT CTATTCGTAC AAATGATATT GAGAATGTTG GGaAAACGGC TCGTCATCAT 420

ACAATGTTTG AAATGTTAGG GAACTTCTCA ATTGGAGATT ATTTTAAAAA TGAAGCGATT 480

CACTGGGCTT GGGAATTTTT AACTGGTGCT GAATGGCTTG CTTTTGACCC AGAAAAATTA 540

TATGTGACTG TTTATCCGAA AGATACAGAA GCAAAACGCA TTTGGCGTGA TGAAGTTGGT 600

TTATCTGAAG ATCATATTAT TGATGTAGAA GATAACTTCT GGGgATATCG GTGCTGGTCC 660

ArTGGTCCGG ATACGAAATC TTTTATGATC GCGGCGAAGA ATTTTTAGAT ATTCCAGAAG 720

ATGATCCAGA AAaTTATCCT GGTGGCGAAA aTGrACGCTA wTTAGrAATT TGGAmCTtAG 780

kGTtCyCyGG AATTTAATCA TACACCAGAA GATACGTACG AACCATTACC ACATAAAAAC 840

ATTGATACGG GCATGGGCTT GGAACGTGTT GTATCTATCA TTnCAAGATG GCACCAnCAA 900

ATTTTGGAAA CTGATTTATT TATGCCAATn CATTCA 936

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 890 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GCTGTTCCGG TTCTTCCTCT AGTTCCTTGG TTaTcAAAAa CGATATCTGC TCGTTCTTTT 60

TTCATTTCAA TCGGCCATkG GCTAGCAATT CGkTGTTGCG CTTCTTCTTC TGTTAATgGT 120

TTCGGGCCAT CAGACGCTCT TTnTGAATCT TTTCTGGTAC ATATACCACA GCAACTTGAT 180

CCATGATCGC CTCATAATGA GCTTCATAAA GCAGAGGAAT ATCAACAATA ACAAGGGCGG 240

CTTTCTTTTT AGCTTCTTCA ATTTGACGTA AAATTTCTTT TCTTAAAAAA GGTTTCAGCG 300

TTTCATTTAA CAACTCTCTT TTTTGAGGAC TAGCGAAAAT TAATTGTCCT AATTTTTTCC 360

GATCCAATTC ACCAGTTGTT AATACTATTT CTGGTCCGAA AGTTTCAACG ATTGCGGCTA 420

AGGCTGGTTG CCCTTTTGCA ACAATTTCGC GGGCGATAAT GTCGCCGTCA ACAATTGGAT 480

AACCTGCTTT TTTAAAAAGA GCAACAACCG TACTTTTACC TGTCGCAATC CCTCCTGTAA 540

TGCCTAAAAC TTTTGTCATT TCAATCGACG ACCTTTCAAT TGTTGGCATT GTGGACAATA 600

ATGCGTACCA CGTTGTGCCA CTTTTGTTTT AACAATTGGC GTACCACAAC GATTGCAAGG 660

TAAGCCTGTT TGCCCGTAGA CATTCAACGC TACTTGAAAA GTCCCTGCTT CTCCTAACGC 720

GTTTAGAtAG GTGCGGAtGG TGGTtCCACC TGCTTCAACA GCGCGTGCCA AGACGTCAAT 780

GATTGCTTGA TACAACGTAG CAACTTCCGC AGTTTTAAGG AATCTGCTGG TTGTTCTGGA 840

TGGATTTGCG CTTGCCAAAG TGCTTCATCT ACATAAATAT TCCCCAAACC 890

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GCCAACGTTA GGGAACCAAC CAAGGCGTTT nGGACCAACT TTGGAAAACT GACGGACTAA 60

AAGGGCCTCC nGATTATCTA AnGGCTAAGG CCnTAAGGGA ATCCGAATCC CCTGTCATTG 120

TGTAGCCGTT TAACGCACCA TATACAGAGA TTAAAATCCC AATAGTTACG ATTTTGCCGC 180

CAATTGGTCC AAAAATAGCC ACAGAAGCAT CCGAAGCTGC ATTCAAATTC CCAGCGATTT 240

GCTCAATTGG TAATGTTTTT AGAAACACAA AATTAATTAA GGCATAAATT AAAGTAATCA 300

ATAACAAACC AAAAATAATG GCTTTAGGCA AGTCTCTTTC TGGTCGCTTC ATTTCACCAG 360

CCACGTTACC CACACCCAGC CAGCCATCAT AAGCAAACAT GGTGGCGACT AAGGCGCCAC 420

TAAAAGCAAC TAAAAAGCCA GTATTCGcTG TTGTTTCAAC AGGAAAAAGT GAAACAGCTA 480

CTTGTCCGGG AGTAAATAAT CCTACTAAAG AAATcAAGGC AATTGGAATC AGTTTTACTA 540

CCAATGTCGT TGATTGGACC AAAGAAGCAA TTTTTGTTCC TAATAAATTA ATTATCGTGA 600

TACTGGTTCC CGCAAGAATG GCAATTGGAA TCAATAAATT TGCCGATAGA TGAAACAAAT 660

TGATTAGTTG TGTACTAAAA ATAATGGATA ACGCCGAAAT GTTGGCAGGA TAATAAATGA 720

TACTTTGTGC CCACCCTAAA AGAAAACCAG CTAATTTACC ATATGTATAT TCAATATACT 780

TCACTGCGCC ACCTGTTTCA GGGATTGCTG TAGCAAGTTC GGCGCTGGTT AATCCTGCAC 840

AAATGGTTAA gGCACCACCT AACACCCAAG CAAAGATAGC TArACTAGCT GACTGTGCGT 900

GTCCAACGAC ACTCGCAGCT TTAAAGAAAA CACCAGCGCC AATCACCGTA CCCATTACCG 960

TGGaTAACGc ACCAAACGTT GTTATCTCTC TTTTTAATTG CTTTTTCTCC ATrGcTCCCt 1020

CATTTCATTT AAACTTAAAA AGCGTAACAA AATTTCCACT TTTTTGG 1067

(2) INFORMATION FOR SEQ ID NO: 608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

TACCCGTCGC CAATGGCTGA CAATGGATAT GATATTtCAG ACTATTATGG TATTTCTAGC 60

GATTTTGGTA CAATGGCAGA CTTCGATGAA CTCATTGAAG AAGCAAAAAA ACGAAACATA 120

AAAGTTATTT TAGATTTGGT GGTAAACCAT ACATCTGATG AACATGCTTG GTTTCAAGAT 180

GTTTTAAAAA ATCCTCAAAG TCGTTTTCGA GACTTTTATA TTATAAAAGA AGGACGAGAA 240

GCACCTACAA ATTGGCGGTC TAACTTCGGT GGTAGTGTTT GGGAAAAATT ACCTGGGGAA 300

GATGCCTACT ACTTTCATGC CTTTCATAAA AAACAGCCGG ATTTAAATTG GGAAAATCCT 360

GAACTACGCA AAGAAATCTA TCAAATGATT CGTTTTTGGT TAAACAAAGG AATTGCTGGT 420

TTTCGTGTAG ATGCGATTAA TTTTATTAAG AAAGATTTGA CTTGGACAAA CTTACCTGCT 480

GaTGGGGcAG ATCAATTAGC CAAAGTAACA AAAGCTAGTA GAAACATGCC AGGAATGAGT 540

GACTTTCTGA ACGAATTAAA AGAAAAAGCT TTTGCTGGCT TTGaTAtTGT CACAGTTGCC 600

GwArCGGCCG GCGTCAATTA TCTAAATTTA TCAGAATTTA TTGGAGAAAC AGGGTATTTC 660

GACATGATTT TTGACTTCAA aTGGGCTGAT TTGGAwGtGA AATCAGGAAG CGAATGGTTT 720

TATAGAATCG ATTGGtCTTG GAATGATTTA CGCACATTAA TTTTCAAACA GCAAGAAGCC 780

ATGCAAGAnG C 791

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

AAGACGACGT tCCAATGTGT AAwTGAACAC AACCTGTTTT ACAGTGGTGT TGCCTAATAC 60

GGATTGCTAC TTGCTCAGCm ATTTCTTTTA CGACCAGTyC GATTTCATTT CTTCTAGTAT 120

AATCTCGTGG TAACACTTGT GAATTGCCAT AAGATTTTTC CTTTGACGGT TCTAGTGGTA 180

TTGCTATGTC AGTTCGATCA ATACCATTTG CATGGAAGTA CAGCTGTAAC CCAATCACGC 240

cTAAACGGCT CTTAATGGTG TATGGATTCC AATTAGCTAA ATCTTTGATA CTCATGATCC 300

CCATTTGGTT GAGCCTTTTT TTCATTCGAG AACCGATACC CCAAAAGTCT GtCATTTCAG 360

GAATATTCCA TACTTTATCA GGAACATTTT GATACGTCCA TTCGGCAATA AATCCTTCmT 420

TGkTCTTCGC TtCGTTGkCT AArGCAAGTT tGGCTAACAA GGGATTATCT CCGACACCTA 480

CTGCAGCAAT CAATCCTAGC TCTTCTTTAA TACGTTCTTG GATCATTTGA GCGAGCTTCT 540

TTCTACGTTG GCTTCGTGTT CCTTCAGTCG TAAAAAGATT CAGTGATCGG GTCACTTTTA 600

AGATTGATTC ATCGATCGAG TAAATCAGTA GATCTTCATC AGCCACATAT CTTCTGAAAA 660

TATTATTTAC CTGCATATTT CGCTTGATAT ATAGTTTCAT ACGTGGTGGA ACAACATGTA 720

GTGTTTTAGG AAATGGTTGT GGTAAAtCAC GkGGTCTACT CACATTtGTA AtACCATACC 780

GCTTTTTkGC TTCAGGAGAA GAAGCTAATA TCAATCCTGA ACCAGTATTG TCACCTCGAC 840

TCATAACAAC AAGTTCTGTT GTTAATGGAT CTAAATTTCT TTCTATACAT TCGACACTCG 900

CATAAAAAGA CTTCATGTCG ATTAGAAAAT AATCATTTAC TGGTTCTTTC GAATAATCAA 960

ACATGAATAA CACCCCTTCT TTTTACATTA TACAAACGTA TGTTCGATAT TGTAAAGAAG 1020

AAATAGCTAA ACACACAAAA AAAGAAGCGT AGGTAAACTC TTACCCTGCT TCTTCTTTTG 1080

ATTTGTATGA TCAACTCATT GtATCACTTT ATTAAATAAT TTGAAAATcT AATaAAAACT 1140

CTCACTCTAA AAGAGTGAGA GCCTGCAAAT TAGAGTACGG AATTCTTTGA GAGTTCCGTT 1200

CCTTAATATT AACAAATGGT CTTAAAGCAT ACAAGGCGAA TTA 1243

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 586 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

TAGATGnAAT nTGAAGTGAC TGGTGAAAAT CGACATATCA TTAATGGCCA TACACCAGTT 60

AAACGAACAA AAGGCGAATC GCCAATCAAA GCAAATGGCA CGCTTCTCGT AATTGACGGC 120

GGCTTTTCAA AATCTTATCA GACAATTACT GGGATTGCTG GTTATACATT GTTGTACAAC 180

TCGTTTGGTT TACAACTGAC CGCGCATAAA TCTTTTTCTA GTAAAGAAAC AGCCATTTTA 240

AATAATCAAG ACATTCATTC CATCAAACAA GTCATCGATC GCCCCTTACA GCGGCTATTG 300

GTGAAAGATA CCACTATCGG CAAAGAGCTA TTAAAGCAAT CGCAAGCACT CCAAAAACAA 360

ATGAAACAAA ACCAGTAGTG CCGTTAAAAA GACGCTTGCG CTCTTATCCG AAAAATGATT 420

AAATGGaGGA GTTGAGAAAA ATATCTATTA GAGAAACGGA AAGGGTTTtA CATTGAAGAa 480

CAGCmACTCT CACTTTACGG CACCATTTTC TTTCTTTGCT TTnTCCTAAT TGTGGGCTTC 540

TTCTnCTCAA GTCGTGGCGA AGATTATGCC AAAGATCTGA ACAAAA 586

(2) INFORMATION FOR SEO ID NO: 611:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

GCACGCrCAA CTTTCAAGCA AAAACGAATT GGGAACTATA AAGAAACAGC CGATTGTTAT 60

TCTCTTCAAT CGGCTGTTTC TTTATTTATT TGCCTTGTCA TCAGTGTTTT CTTCTGCAGC 120

AATCCGCGCT TGAACTTGTT GACGTAAAGC TTCTAGTTCT TTTTCTTTCT TTTCTAATTC 180

AGCTAAATCT TCAGAAATTT CATGGGCTTC TTCTGCTGGC TTAGGTTGTA AAAAGACGTT 240

TAAACCAATC GCTATAAAGG TCCCAATGAA TGTATCCAAC ACACGTTCCA TTGCATATTG 300

aAAGGaATCG CTTTGCGGaA TACTTAAAGA AATCATTaAA AGTGTCGCAG TTGCaGAAAT 360

GATCCCAGCA TTGTTrTTAA TCCCATCAGA AACAACGaTG aCGaTAATGA CTAAAAGTGG 420

T 421

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

TTTTTCAATA AATAgTTATA AAGATAATAT TACTAGAATT AACGAAGAAT GGAATCAATA 60

TCAGTCAAAA GAGACCATTA ATAAAATAGT AGAGTTGGTA GAGAGAATCT TGGGGGGATT 120

TTGTGAAAAG TAAGGTACGC ACTGAATATA TTGGGGGATT ACCAGTTGAC GTATTAACAC 180

ATCAAGAAAT TATGGATGAC TTAGAAAGTT ATCTCAAAGC TAAAGAGAAA ATGATTGTmA 240

CTAGCGTTAA TCCGCAGATT TCATTGTTAG CATTTGAACA TCCAGAAGTT AAGTTATATT 300

TGAAAAGAGC AACTCATCGG ATTGCAGATG GGATAGGTGT GGTCAAGGCA TCGAAGCTAA 360

TGGGTGGGTC TATTCGTGAA AGAGTTACAG GAATTGATGT CaTGGATAAT TTTTTAGAGT 420

ATGCAAATCa ACATaAGGnA CGAATCTTCT TGTmTGGTGC aAAGCAAGAA GTAGTTGAAG 480

CAGCAGCTAA AAATATTCCA CGACCATATC CAGGGATTGT TATTAGCGGT ATTTTACATG 540

GCTATACCAA GGAAAAACAG CAGGAATTGT GGACCAATTA ACCAAGCTGA ACCAGGTTGC 600

TTTGTAGCAT TGGTCnCCGA ACAAGAGTTT TTGGACAACA TTGTCnCCTG ACACTATGAT 660

TTAGACGAGC GGnCTTGCGT TACTGGn 687

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 889 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

CGGCTTGAAT TTTTTATTCT TCTATAGTAG TTACAGCAAC TTTGGAAATC TTTTCTACAA 60

AGGCATCAAG TAAATCGACA ACTGCTTGTT GTGTTTCGAC TTGGTTAATC GCAACTTTCA 120

CTTTGGCTGC TCGCGAGATT CCTTTTAGAT AGTAAGAAGC ATGTTGGCGA AACTCACGGA 180

CCGCAATTTT TTCACCTTTT AAATCCACTA ATCGTTGTAA ATGAACTTTT GCAATGTTAA 240

TTTTTTCAGC TGGTGAAGGC TCAGGCATCA ATTCACCCGT TTCCAAGTAT TCTTTCGTCC 300

GTTGAATCAT CCAAGGATTG CCCAAAGCAG CTCGACCAAT CATCACACCA TCCGCTCCAA 360

CATATTCTAA CATGCGTTTA GCATCTTCAG GCGTTTTGAC ATCGCCATTT CCCATAAAAG 420

GAATGGTTAA ATGCTTTTTC ACTTCCTTTA AAACGTCCCA GTTGGCTGTC CCTTCaTACA 480

TTTGGACACG TGTCCGACCA TGCATAGCAA tTGCCGAAGC CCCTGCTTGT TCGGCAGCCA 540

AAGCGTTGTC TACAGCATAT AGATGATCTT CATCCCAGCC TGTTCGCATT TTTACAGTGA 600

CCGGCAAAGA AACTGCCGAA GAGACTGCGT GAACCATCTC ATGCACTTTA TTCGGATCCA 660

GCAACCATTT CGCACCAGCT TCAgCTTTAA TTATTTTATT GACAGGGCAG CCCATGTTAA 720

TATCAATAAT CGCCGCTTGG TATTTTCTTC CACAAACTTA GCAGCTTCCA CTAATGTTTC 780

GTTATCTCCA CCAAAAATTT GTACACTTAA AGGATATTCC CGCTTCATCA ATATATAGCA 840

TTTGCTAAGG TTTTTTGGTn TCTTnATTTT AAnGCCTTTG GTCACTAAT 889

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

TGGTGATGAC TTTGTTTAGA ATACAAGTAG GATTTTGCTA CGACCGAAAT AAACATAGCC 60

ATAATCCCCA AGCCTACTGT AGCATAAATC ATGGTGAAAA TTTTTCCCAA GTCAGTAACT 120

GGATGCACAT CTCCATAACC AATCGTGGTT AACGTCATGA AACTTAAATA TAACGAATCT 180

AATGGCGACA ATTTTTCCAC TGTTGAATAA AAAATAGTCC CACTCAACAA CGTGGTTGCC 240

AGTAAAAAGA ACAAGGCACG AGTGTCTTCT TTTTTTAAGA TACCTAAAAA AGATGAAAAT 300

AATTTTTTGA CAGAAATAAG TAAAGATAGC AAAAAAATGA CCTCTTTCTA TTGTTAATCT 360

CTTCTTAACG TTAGCACTTT TTAGATGAAG TTCAACTTTT TAATTGGTGT GGTTAAAGAA 420

AATTTATTTT TTTGTTATTT ATAATACACT TCATCTAAAA ACAACCCTTG TGCAGGAGCC 480

GTTTCACCTG CGCCTTCTCG GACTTTTGTT GCGAACAATT CATCAATTAT CGCTAATTCT 540

TTGGTGCCTG CACaATTTCT AAAAGTGTCC CAACGAGGAT GCGGACCATT TTATGCAAGA 600

AACCATTGCC CACAAAAGTG AACTGTAACA TTTCGCCGTT TCTTTCAATC GTAATCTTTT 660

CAATCGTTCG AGTAGTCGAT TTTTTGGtTT TTTTCAATGC TGAAAAACCA ATaAAATCAT 720

GGGTCCCTAT TAATTTTTGG CAAGCTTGTT CCATTTTTTC TTGATCCAAC GCTTTGGGAA 780

AGTGAAAACT ATGATACCGT TCAAAGGcAT TAGGAATTgG GcTATTCCmA ACATAGTAGC 840

TGTATTGTTT GCCTGTGGCG TTATACCGTG CATGAAAACG TTCAGGCATT CTGGAACTTC 900

TTTAACAACA ATATCGCCAG GTAAATATCG ATTAAAAAGG ATAACATTCC GGTGTTGTAA 960

GTGACCAGnC GTTTAAAATC GCTACTGGAC CACGG 995

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TCAACCATTG TCGGCGCCAA TGCGTTTAGT TTATATTGGC TTTTGTTATC TGAAACAACA 60

GACTCAGAGG AGAATGGCTC GCTGTTTCAT GCAGATTTAA TTAGTTTGCT GGACTTGAGT 120

TGCCAACAAT TAGAAGAAGC TTGCTACAAA TTAGAAGGCA TTGGGTTGCT AGAAACGTAT 180

AAAAAAACAG ATCGGGAATT AGGAGATTGT TATTTATATT ATTTAAAAGC ACCTGAAACA 240

GCCGCTCGTT TTTTTAAAGA TGAAGTGTTA GCTTTAGTGT TATTTAATCG GGTTGGaCAA 300

CGGAAATTTG ATCAATTAGT GCAAAAGTTC CAACCGCATC CTACTAAAAC AGAGGGCTAT 360

CAAAATGTTT CCGCTAGCTT TCaAGArGTT akgCCTTarr GrAgACaAAT TGTTTcCGAA 420

GCGAAcCGrT TGACcACGAT ccAGrAACtT TTTCTCAAAA G 461

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

CAAAATTTGT TAAAACGAGA TATTGCCAGT nTTTTAAGAC AAATGCACGG TTTAGATTAT 60

ACAGATATTA GTGAATGTAC TATTGATAAT AAACAAAATG TATTAGAAGA GTATATATTG 120

TTGCGTGAAA CTATTTATAA TGATTTAACT GATATAGAAA AAGATTATAT AGAAAGTTTT 180

ATGGAAAGAC TAAATGCAAC AACAGTTTTT GAGGGTAAAA AGTGTTTATG CCATAATGAT 240

TTTAGTTGTA ATCATCTATT GTTAGATGGC AATAATAGAT TAACTGGAAT AATTGATTTT 300

GGAGATTCTG GAATTATAGA TGAATATTGT GATTTTATAT ACTTACTTGA AGATAGTGAA 360

GAAGAAATAG GrACAAATTT TGGAGAAGAT ATATTAAGAA TGTATGGAAA TATAGATATT 420

GAGAAAGCmA AAGaATATCm AGATATAGTT GAAGAATATt ATCCTATTGa CtATTGTTTA 480

GGAATTAACA ATATTAAACC GGAATTTATC GAAATGGTAG AnAAGAAATT nTAAnAGG 538

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

GCAATCAAAC GCGTACGTAC AAGTGCTAAC GCGAATGCGA AAAATTCATC TCAAACAAAC 60

GCAATGCtAC AGaATCAAGA AATTTGAAGA AGCTGTAGCT GCTGGAGCTG ATAACGTCGA 120

TGCTTTATAC AACGAAGCTG TTAAAGCTGT TGATATGGCT GCAACTAAAG GTTTAATCCA 180

TAAAAACAAA GCTAACCGCG ATAAAATTCG TTTAAGCAAA TTAGCTAAAT AATGTGAGAT 240

AGAAGTTAGC ATTCATGTTA GCTTCTTTTT TCATCCAAAA ATGTCCAAGT CTGTTTTCAC 300

AAAGACTCGG ACATTTTTTT ATAAAGGTGA ATCAATCCAC GGTAAATCCG TTGTGAGATG 360

TTGACTAAAT AATTTAGTCT CTTCTCGCAA AGCTAAACGT TGTTGTCGTC TCGTTTCATA 420

ATTGGAACAA ATCAACTTTT CTTCTGCAGT TTCTGGGACG ACTGCCGCTA ATTGGAAGTC 480

ACTTTCGGGA TTCATATGAG ACGGAATGGC TACAAAAGTT GTAAAACAAG TCGCCGCTAA 540

ATAACGCTCT CCAGTTGTTA AATCTTCTCC TACAACTTTA ACAAATACTT CCATCGATTT 600

ATGATGCACG CCAGAAACAA ACGTTTCAAC ACACACTGAG TGATTTTCTT TTAAAGGTTT 660

TAAAAAATTC AAGTTATCTA AAGATGCTGT AACTGCCCCT CTCCGACAAt GTCGTGAAAC 720

GGAAATGGAT GCGGCGTCAT CAATTAAAGA CATTAATTTC CCACCAAATA GTGCACCAAA 780

GGGATTTAAA TCAAAGGGrA ATACACGATG TGTTTGAATA ACTCGTGATT CTCGACAAAA 840

TTtTTCTTTC GTCATTAACG ATTCCTCTAC TTTCATTTAT AAACTTTTCC ACGCTTTACT 900

TTAGCTTACT TTACCATTgA TGCAATCCTT ACTTTTTAGG AAACATTTAA AAAATAACAA 960

ATTTGCAAGT CCCATTTATT CATTTTTAGG AAAGTTGCTG TATAATAATA ACGGTTAAAG 1020

AACTTTTAAG GAGATGGaTA CACaTGAAAA wTGCaATTGC TGGTGCCGGC GCTATGGGCA 1080

GCCGTTTAGG AaTTAkGTtG CATCAaGcGG rAATGakGTA ACTTTAATCG ATCAATGGCC 1140

CCGCGCACAT TGAAnCTATT CGTA 1164

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ATTnTCCCAT TCCTTGTTTC AATAAAGCAC TGGAATCTTT GACCGGACGT GTAGTTAACT 60

AAATATCTAT TACTAAACTC TTCTTTCGTC GAAGTATACC AATTTCTGTC AAATGTAGAG 120

TAAAATAAGC ATTCTCTATA TTTTTTCTGA GCTTTTAAAT AATAATCTGA GGTATCTTCT 180

ATCCCTATAT GAATATTCAT TTCCCTATAG TCTATATCAT CAGCAACATA AAACGACAAA 240

TCATTTTCCG AAAACATAAT AGCGGGTATA AAATCTCCTT CGCCAAAAGC TCCTAACAGT 300

CCAGGTTCCG ATAATTGCAT TTTAGCTTTC ATAAATCTAG GTAAAAATAT ATCATCAGTT 360

TCTACTTGTG AGATTGCTCT AAGTTCCATT GCGTTAAAGT AAGCCATTGG AATATTTCTA 420

TATATATTAC TTAATTTAAG TGAAATATAC ACACTTCCTC CTAAAGTATG AACTATTATA 480

ATTATGAACA ATTGATTATT CATAATATTA TGTTTATTTA GTTTTTCTAC TATTAATTCT 540

ACTCTGCTGG TTATTTTTTC TGTATAATCA ATATTTTCTT CTATACCACC AAAAATACCA 600

AAAGCTATAA GTAATTTATC ATTGGCAATA TTAAAAATTG CCTCCTTATA TTTTCTTTCA 660

TCCAGTAATT TTATAGCAAA ATTATTCTCA GCAATTTTTT CATGTTTCAA TCTCTTAAAA 720

GACTTTCTTA TATCATTCCA CATTTCTTCA AATACGTATA CTTCAGATAT TATTGTGGCA 780

ATTTTACTGG ATAATGCGTT AGCGACaGAT GTTATGTCTA ATATAAGTAC GCCTTCCCCA 840

GTATCCAGAT AAaGGCTTAG TTAAAAAGAG GATGTTGGTT TTGGGAAAAT GGTTTTTGCT 900

TTTCTAAATC AACATCTTCC TTCAnTATTG GATATTnCAT GTATTCCAGG TAATTnGTTA 960

ACTAAAAAGC ACCAAGTTTC CATAAAACC 989

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2013 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ATTGATCAGT GAATATTATG TTATGTAnCG nTTCTTTAAA CCAATTGCTC TTGATGAAAn 60

ACAAAATTTC TCTAGTGTTC AGCTATTCCT TAACCTTTTT ATATTTAATG CTTTATTCAT 120

GTTTGTTATG CTAACAAACT TTCATCAAGT TTTTGTAGGA AAAGAATTTA TTATTTTTGG 180

TAGTTTCATG GGTGGAATAT TTACGATTTG CTTAAAGGAA CAACTAAAAG AATACCAGAA 240

GCTAATGAAT CAATTTATAG ATATAAAGAA AGAAGTACAT TGATGAAAAA TAGAATTAGT 300

TAGAACAGCC ATGTATGGTG AAATATTGTA GTATATTACT TGTTAAGGAC GATGAACAGG 360

ATGAGTATCA AAAAATATTT ACTTTTTTAT ATTATTAGCA CATGTGCCAT TATTTTTGTT 420

TCTCTTACTT TTTTCTTTTT ACCTCTAAAA TCGATTGATT CTAGGAGTTA TGAAGTACTT 480

CATACGATAT CTCAATATGG AGTAATTTCT AATAAAGATG AGTGGAGGAA TATTTTAGAA 540

TTAACAAGAT ACGGTAGAAA AGTAACTAAT GTGGATAATT TAAATACATT AGTATATGGT 600

GTTAACAAAC ATAGTTCTGT AAAACAAATA AGTAGTGACA AAGATATGGA TAATATGGAA 660

ACTCTTAAGT TACCAAGTAT TTCAAAGTAT GAGGATCTTA CAATTATTAA CATTCCAAGT 720

GTCTATAGCA ATGATGATAA CTTCTCAATT AAATATGCAT CAAAGTTGAC AGATTTAATC 780

GAATATACTT CTGGTAACAT TGTTTTAAAT TTATCAAATA ATTATGGCGG GCTGAAAGAA 840

CCTATGATTA TTGGTGCGAG TTCTTTAATT CCTAATGGAA TGCTCTTTAG CAATATTAAT 900

AATAAAAAGG AAAAGTATCC TGTTTACTTA AAAAAATGGT AAATTATTTG GTGGCATTCC 960

AGGAACGATT AACGAACTGA ATCTTTATAA ATTATCATTA CACAAAAAGA AACTAGGGAA 1020

AAAAGTTGCA GTTGTAATAA ATAATAACAC AGCAAGTGCC GCTGAGAGTT TACTTTTAGC 1080

GTTAAAGAAT AATCCmAATG TAAAAGTTTT TGGTATGCCT TCTGCAGGAT ATACTTCGGT 1140

TAATyTAGGA CGTTTTTTTA CTAATCAAAA TTCCGATAAT TATTGGTGGt TTGTATATAC 1200

TGTTGGCTAT TATGAGACAA TAAAGCCCAT AAAGGGAAAA TGATTGTTTA ACAATCAACC 1260

TGTCCCGCCA GATTATTATG TAGATTTATC GATGTTAGAT AGAAATACTC AAGATATTAC 1320

ACAATTTTCT AATACCAAGA AACTATTCAA AGAAATAAAA AATTsGATTA ACTCTGATTG 1380

AGTTGAAGGT ACATTAAAGT AAATGAATTC TTAATGTATA GTATAACTTG TAAGCATAAA 1440

ATTTTTATAG GAGAAAGGCT TTTGCTAAAA TTATATTGTG GTAAAAGTCA CATGAAAGTG 1500

GGGGGGAGAA TCGATGACGA AAGGGAAAAA AATTTTGTTT AGTTTTATTT CTTTAGTTTT 1560

TGGAACTTTT TTATTTGCAG TATTTGTTCA TTATCAGTTC ATGTATTCAT TACCTATTTA 1620

TTTTATTAAG TTTGAAGAGT ATCCTTTTAT AGGGAATTAC ATTCAACTAT ATTTGTACTG 1680

GGGTAGTGTT ATAGGTATGG TCTTTATCCT TTTATTTATT TTAGGGATTG TTTTAAGTCC 1740

AGCAGAAGTA ACATCCGTGA AATTAAACGA TGACAAAGGA ATATTAGAAA TCAAAAAAAG 1800

TGCTATTGTA GGAATTGTTC AGTCGCAATT AGATCAGTCC AATTTATTAA GGGATTCAAA 1860

AGTAAATGTA AAAATGTATA AGAAAAAGAT AAAAGTACGT ATTACAGGAA ATACAAGTGA 1920

CAATCTAGAT ATTATAAATC AAACGAATCA ATTAGTAAAA AATATTGAGT TATATCTTAA 1980

AACTTTTATA GGATTAGATA CTTCAATAAA AGC 2013

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

ATAAATTTCT GGTGTTnAAA AAGTTCCTTT AATTTCTTTA TAACCTAGTA TAGATAAnTC 60

ATCACTnATA TACGnATATT CAATATTAGG AATTTTTACA TTAGTTTCTA AATTTGTATT 120

TAAAAAATTA TATATTGCTT TTTCTTTTGC ATAACCTTTT TTCTTATTAG TACTAAATTT 180

TGTTTTAAAA ATGTATTCAT TATTAACTAA ATATGCCACA CTATCATAmC CACTACCGAT 240

TATTTCmATA CTATCTACTT TGAAATtATC aAAGTAATGC TCAATTAAAT ATTTCaTTGC 300

CTTAACATTT gTGGCATTAT CATCATATCT ATATTCCATT AAATAACAAT CTTCTTTTTT 360

GCCCTCGTGT AATTCATGTT CTGGCAAATC TTCAATAATT CTAAAACCAG ATTTTTGGTA 420

TGCCCTTATT GCTCTTGGAT TATTTTTATG AGGGTCTAAA ATAACTGCAT TAGCATTTCT 480

TTCTTTTTTC AAAAATTCAA AAATCAATTT AATATATCTT GTACCAATTC CTTTACTCCA 540

ATAATTTGGC TCTCCTATAA ATTGATCCAT ACCATAGACT ATCTCATCAG TTTTTGGATA 600

ATGATAATCA GTATATAACT CATCATACAT TTTATATATT TGTCCATATC CAATAGGAAC 660

ATTGTTATAT TCAATAATTA CTCTAAAAAC TTCATCTTCC CAAGGCTCTG TATAATGTTT 720

TTTTAATGAT TCTAATGTAT ATTTTTTATC TCTACCACCA TAAAATTCTA ATACTCTTTC 780

ATCAGTTAAC CATTTTAACA TCAAAGGaAA ATCATCATCT ATTAAAGTTC TTATACATAT 840

TTCATTTTCA ACTATATTCA TTTATTTATC ACCTTTTTCA TAATCATATA CATATACTAT 900

TTCATCTTTA TAATCATTTT TACCACCTAA TTTTTCATAT ACATGGCAAG CTCTAGGATT 960

ACCTTTATCA GTTATTAAAA ACATTTCAGA ACAACCAATC TCTTTAGAAT ATTCCTTAAT 1020

AAAAGATAAT AATTTTGAAC CATAACCTTT GTCTTGATAG TTAGGTAACA TTCCTATTGA 1080

GTGTAAATAA AACATTGTTT TTCCATCAGG nCTTAAAAGT GTATAGCAAT ATGCAAATCC 1140

TATAATTTTA TTATTTkCTT TAGCTATAAA CCCAAATGAA CTGGtATCAT TAAGAAATCC 1200

TTTTAAATTA TCAATATCAA AAACCATATT ATCATCAATT AAAACTTCTT CCATAAACTC 1260

AGTCAAGTCC AGACTCCTGT GTAAAATGCT ATACAATGTT TTTACCATTT CTACTTATCA 1320

AAATTGATGT ATTTTCTTGA AGAATAAATC CATTCATCAT GTAGGTCCAT AAGAACGGCT 1380

CCAATTAAGC GATTGGCTGA TGTTTGATTG GGGAAGATGC GAATAATCTT TTCTCTTCTG 1440

CGTACTTCTT GATTCAGTCG TTCAATTAGA TTGGTACTCT TTAGTCGATT GTGGGAATTT 1500

CCTTGTACGG tATATTGAAA GGCGTCTTCG AATCCATCAT CCAATGATGC GCAActTTTG 1560

AATATTTTGG kTGATCGATA TAATCATGAA TCAATCGATT TTAGCCTCAC GCGCnAAGTT 1620

AATACTGTGG ACTTAAAAAT CCCTAAnAGC GTCTCTGAAG AATTTGAATT GTTTTA 1676

(2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1635 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

ATCCCCTTAG TATAAATACA AACTCAAAGG AGAGACAAAA CATGTCAATT ATTACTGATA 60

TTTACGCACG CGAAGTCTTA GACTCACGCG GTAACCCAAC AATCGAAGTA GAAGTTTACA 120

CTGAAAGCGG AGTTTCGGCC GTGGAATGGT TCCTTCAGGA GCTTCAACTs GTGAATACGA 180

AGCAGTTGAA TTACGTGATG GCGACAAAGC TCGTTACTTA GGTAAAGGTG TTACTAAAGC 240

TGTAGATAAC GTAAACAACA TCATTGCTGA AGCAATCATC GGTTACGATG TACGCGATCA 300

AATGGCTATC GATAAAGCAA TGATCGATTT AGATGGAACT CCTAACAAAG GTAAATTAGG 360

TGCTAACGCT ATTCTTGGTG TGTCTATCGC CGTAGCTCGT GCTGCTGCTG ATTACCTAGA 420

AGTGCCTTTA TATCACTACT TAGGCGGATT CAATACAAAA GTATTACCAA CTCCAATGAT 480

GAACATCATC AACGGtGGAT CACATGCTGA CAACAGTATT GACTTCCAAG AATTCATGAT 540

TATGCCTGTA GGTGCGCCTA CATTCAAAGA gCTTTACGTA TGGGGTGCAG AAGTATTCCA 600

CGCATTAGCT yCAaTCTTAA AAGGTCGCGG TTTAGCwACT TCAgTAGGTG ACGAAGGTGG 660

TTTCGCTCCT AACTTAGGTT CAAACGAAGA AGGTTTCGAA GTAATCATCG AAGCTATCGA 720

AAAAGCTGGC TATGTTCCTG GTAAAGACGT TGTTCTTGCT ATGGATGCTG CTTCTTCAGA 780

ATTCTACGAC AAAGAAAAAG GCGTTTACGT TTTAGCTGAC TCAGGCGAAG GCGAAAAAAC 840

AACTGAAGAA ATGATCGCGT TCTACGAAGA ATTAGTTTCT AAATACCCAA TCATTTCAAT 900

CGAAGACGGC TTAGACGAAA ACGACTGGGA CGGATTCAAA AAATTAACTG AAGTATTAGG 960

CGACAAAGTT CAATTAGTTG GTGACGATTT ATTCGTAACA AATACAACTA AATTAGCTGA 1020

AGGTATCGAA AAaGGTATCG CTAACTCAAT CCTAATCAAA GTTAaCCAAA TCGGTACTTT 1080

AACTGAAACA TTTGAAGCAA TCGAAATGGC TAAAGAAGCT GGCTACACTG CAGTTGTATC 1140

TCACCGTTCT GGTGAAACAG AAGATTCAAC AATCTCTGAT ATCGCTGTTG CAACAAACGC 1200

TGGCCAAATC AAAACTGGTT CATTAAGCCG TACTGACCGT ATTGCTAAAT ACAACCAATT 1260

ATTACGTATT GAAGATCAAT TAGGCGATGT AGCTGAATAC aAAGGCTTAA AATCTTTCTA 1320

CAACTTAAAA AACAAAaTAn TTCATTAAAT GgAaTAmCGC yTAAAGGGrC mATTGGTTAA 1380

TGAmCCAATT CTCCTTATAC TCGGACGTAA AAACcGCCTT TCTGCAAAGA AAGGCGTGnT 1440

nTTTTATATT TATAAAAATA TTGAAAAAAT AGATTAGAAA TAACTTCAAC CGTACATCGC 1500

TCTATAATCA CTTGTTTAAA AATAACAAAA CATTAACAAA ACAACATTAT ATAAAAATTT 1560

AATAAAACAA AATAATTGTT ATTTTATAAT TTTAGTATTG ACTGGTTTCA GATAACGCTG 1620

TACGCTTAAA GAAAT 1635

(2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8001 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AGAGGGTGCT TTGGTCCGTG TTCAAGCCTT TGCAACTATT AATGGAGAAG ATATTACCAC 60

TAGTTTAGCG GCGGACGCTT GAAATCTCTA AAATCAGTTG GTAGTAAAAA TCAATTGTCC 120

ATTTTACAAA TTCAAGAAGA AGTATCCAAA TATTATCATG TGCCTCTTAA AGATTTAAAA 180

GGGAAAAAAC GGGTGAAAAC AATTGTGGTT CCTCGTCAAA TCTCAATGTA TCTTGCTAGA 240

GAAATGACCG ACAATTCCTT GCCAAAAATT GGTGCCGAAT TTGGCGGCAA AGATCATACA 300

ACGGTGATTC ATGCGCACGA AAAGATTCAG CAATTATTGG AAAAAGATCC AGCGATTCAA 360

AAAGAAGTCA GTGAAATTAA AAATTTATTG AACTCTTAGG ATGTGGAAAA CTAAACAAAA 420

AAGAACAAAG TTATCCACAA CTTATGCACA AGTGGaTAAC TTAGTAAAAT CAATGCTCTT 480

TTGACTTTTC CACAGAATCA ACATGCCCTA TTACTTTTAT TATTTATTTA TATATAATAT 540

ACAAAACAGT GGCGTACAAA ATTgGAmCGT ATTGAAAATA CTTAAAAAGG AGTTTACATT 600

ATGaAATTAA CGGTCnAACG AAGTGtCTTT TTAcAAGAAT TACAAACTGT TCaACGAGCA 660

ATTtCTTCTA AAACAACGAT TCCcAATCTT AACAGGTGTT AAAATTGTGT TATCAGAAGA 720

TGGCTTATCA CTTACTGGGA GTAACGCGGA TATTTCAATT GAAAGTTTTT TAAGTAAAGA 780

TGATGAAAAA GCTCAAATGA CCATTGAACG CACAGGTAGC ATCGTTTTAC AATCTCGTTT 840

CTTTGGCGAA ATTATTCGTA AATTACCAGA AGATATGTTC ACAATGGAAG TTCTAGATAA 900

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CAATCAAGTT GCAATTACTT CAGGAAAAGC TGATTTTACG GTTAATGGAT TAGATGCTGA    960
TAATTATCCG CACTTACCAG TAATTGATAC TCAAAACCAA ATGAAATTAC CTGTTCATTT   1020
ATTGACAAAA ATTATTAGTG AAACAGGTTT TGCTGTATCG ATGCACGAAA GTCGTCCAAT   1080
TTTAACTGGG GTTCACTTTA TTTTAGAAAA TCAAAAATTA CTTGCCGTTG CGACAGATTC   1140
ACATCGTTTA AGTCAACGTG TGATCCCGAC AGAACAAGCA GTAGAAGACT TTAACATTGT   1200
AATTCCAGGA AAAAGTTTAA CTGAACTTTC TCGTTCATTA ACCAATGAAG AAGAAATGGT   1260
TGAAATCAGC ATTATGGAAA ATCAAGTGCT ATTTAAAACA GAAACAATGT ACTTCTATTC   1320
TCGTTTGTTA GAAGGAAATT ATCCTGATAC CAACCGTTTA ATTCCAACTA GCCATAACAC   1380
GCAAATTGAA TTTTATGTAC CAGAATTGCT TTCAGCAATC GAACGTGCCT CTTTACTTTC   1440
TCATGAAGGA CGTAACAATA TTGTTCGCCT TTCAATTTCA CCAGATTCTG TTGTTTTATA   1500
TGGAAATTCA CCTGAAATTG GAAAAGTCGA AGAAGCTTTA AACTATGAAA ATGTTTCTGG   1560
TGAAGCGTTG GATATTTCTT TCAACCCAGA TTATATGAAA GATGCGTTGC GAGCGTTTGG   1620
CGATATGAAT ATTACCGTGA AATTCCTTTC TCCAATTCGT CCGTTTACAT TGGAGCCAAC   1680
CGAAACAGAA CTAGATTTCA TTCAACTAAT TACACCGGTT CGTACAAATT AATCATGTTT   1740
AAAAAAGACC TTCGGAAAAT CAATATGATC GCCGAAGTTC TTTTTTGTCG TCTGTTTAAA   1800
GCCGATAAAC GCTGCTAGAT AAGCTTTTTA TAACTAGAAT AGCTTTTACG CTAATATGAT   1860
TGTGAATGTT TGAACTATCG TTTGACGAAT AAATTCTGCC TTTTTTTCGT GGATAAAGAA   1920
AAAAGCCCTT TAATTTTTCG TTTAAGGGCT GTTCATTTTT TTATGAATAT TTCCTAGTGA   1980
AAGAAGTTTA CGTTGCTTAA AACGACGCTC AGACCTCTAC AAGCTACTTT TCTTCATTGC   2040
GCGCCCTCTT CGTTTGTCTT TGAGTTACCC CTAATTGTTT TTTAGTTAAA CGCTACTCGT   2100
CATTTCTGCC AAATCAGGCC CCTTTTTTCT CAAGAAAATA TCAATTTCCG TTTTAAAATG   2160
CTTTTTAAGA GTTTTTTTAT CCTAATAATA TTTTCGGTCA TTTAGAATTA AAATTGCTTA   2220
GAATGAAAAT TAGACAGATA AATTTGTTTT CTCTTATGAA AAAGGGTATA ATATATATGA   2280
GAACGTATTA GAAAAAAGAG GGATGCACAT TGAAAAAAAC GTTTGTTTTA GCAACTGAGT   2340
ATATAACGCT TGGTCAGTTT CTTAAAGAAA TCAACGTCAT TGGTAGTGGC GGCCAAGCCA   2400
AATGGTATTT GGCAGATAAT AGCGTGTTTG TTGATGGCGA GTTGGAAAAT CGTCGCGGAC   2460
GGAAACTTTA TGCGGGCATG ATGATTGAGA TACCTGAAGA AGGTACTTTT TTTATGGTGA   2520
AAAACGGAAA CGAGTCCGAC GATGCGGCTG AATGAGCTGA CACTTCAGCA TTATCGTAAT   2580
TATGAAACAG TCAGCTTAGA TTTTCCAAAA ACGTTAAATC TTTTTTTAGG CGAAAACGCC   2640
CAAGGAAAAA CCAACTTGTT AGAAAGCATT TATGTTCTAG CAATGACACG AAGTCATCGA   2700
ACCAGCAATG AAAAAGAATT AATTGGCTGG GAACAAGCAG CAGCTAAAAT TAGCGGTGTG   2760
GTTGAAAAAA AGACAGGCAC CGTGCCGTTG GAAATTTTAA TTTCCAACAA AGGACGTAAA   2820
ACCAAGGTTA ATCACATTGA GCAAAAAAGG CTCAGTGCGT ACATTGGGCA ACTGAATGTT   2880
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ATTTTATTTG CCCCAGAAGA TTTATCTTTG GTGAAAGGCT CACCTCAAGT CCGCCGGAAA 2940

TTTATTGACA TGGAACTCGG ACAAGTGAGT CCTATTTATC TTTATGATCT TGTCCAATAT 3000

CAGTCTGTTT TAAAGCAACG GAACCAATAC CTAAAACAAC TAGCTGAAAA GAAACAAACA 3060

GATACTGTTT ATCTGGATAT TTTGACAGAG CAGCTAGCTG AATTTGGCGG GAAAGTTCTA 3120

TACGCTCGGT TAGGTTTTCT TAAAAAATTA GAACACTGGG CAAACTTACT CCATCAAAAA 3180

ATTAGTCATG GACGCGAAAC GCTCACCATT GACTACGCAT CAAGCATCCC AATTGACAAC 3240

ACGGATCTTT CCTTAGAAGC ACTTCAAAAT CAATTGCTCC AACAATTAAT GAACAATCGT 3300

AAGCGTGAAT TGTTTAAAGC GAATACTTTT TTAGGCCCTC ATCGTGACGA TTTGCTGTTT 3360

ATTGTCAATG GTCAAAATGT TCAAACGTAT GGCTCACAAG GCCAACAGCG AACGACAGCT 3420

TTAAGTATTA AATTGGCAGA GATTGATTTG ATGCATTCAG AAACAGGAGA ATATCCTGTG 3480

TTATTACTAG ATGATGTCAT GAGTGAATTA GATAATGAAC GTCAAATTCA CTTGTTAGAA 3540

ACGATTGAAG GCAAAGTTCA AACGTTCTTA ACGACAACTA GTTTAGATCA CATAAAAGAC 3600

AAGCTAACAG TTGAACCAGA TATTTTCTAT GTTCAACAAG GCAAGATAGA AAGGAATTCA 3660

GCGACATGAC AGAAGAAGAA AAAAACATGA GAGAACGTGC GCAAGAATAT GACGCTAGTC 3720

AGATTCAAGT TTTGGAGGGC TTAGAAGCTG TCCGGAAACG TCCTGGTATG TACATAGGTT 3780

CTACTAGTGG CGAAGGGTTA CACCACTTAG TATGGGAAAT CGTTGACAAC TCTATCGACG 3840

AAGCCTTAGC AGGATTTGCT AAATCAATTC AAGTAATTAT CGAACCAGAC GATAGTATTA 3900

CTGTTATCGA TGATGGTCGT GGAATTCCAG TCGGGATTCA AGCCAAAACA GGTCGCCCAG 3960

CTGTGGAAAC AGTGTTTACA GTGCTACATG CCGGCGGGAA ATTTGGCGGT GGCGGCTATA 4020

AAGTATCAGG TGGCTTGCAC GGTGTTGGTT CCTCTGTTGT TAATGCTTTA TCGACCAGTT 4080

TAGATGTTCG TGTTTATAAA GATGGCAAAG TGTATTACCA AGAATATCGT CGTGGTGCGG 4140

TTGTTGATGA CCTAAAAGTT ATCGAAGAAA CGGATCGTCA CGGAACCACT GTTCACTTTA 4200

TTCCAGATCC TGAAATTTTT ACAGAAACAA CCGTTTATGA TTTTGATAAA TTAGCAACAC 4260

GGGTTCGTGA ATTAGCCTTT TTAAATCGAG GCTTACACAT TTCAATTGAA GACCGTCGTG 4320

AAGGACAAGA AGATAAAAAA GAGTATCACT ATGAAGGCGG GATTAAGAGT TATGTTGAGC 4380

ATTTAAATGC CAATAAAGAC GTTATTTTCC CAGAGCCAAT CTTCATTGAA GGAGAGCAAC 4440

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GTTTTGCCAA CAATATTCAT ACTTATGAAG GCGGAACgCA TGaATCTGGT TTTAAAACTT 4560

CTTTAACACG TGTGATTAAT GACTATGCAC GTAAACAAAA ATTGATGAAA GAAAACGATG 4620

AAAAATTAAC TGGGGAAGAT GTTCGTGAAG GCTTAACCGC AGTGGTTTCC ATCAAACATC 4680

CCGATCCTCA ATTTGAAGGA CAAACGAAAA CGAAATTAGG GAACTCAGAA GTACGGACCG 4740

TTACGGATCG TCTATTCTCA GAATACTTTA CAAAATTTTT AATGGAAAAC CCAACAGTCG 4800

GCAAACAAAT TGTCGAAAAA GGCATGTTGG CTTCAAAAGC TCGTTTAGCC GCTAAAAGAG 4860

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CCCGTGAAGT CACCCGTCGT AAAGGCGCTT TAGAAATTAG CAACTTGCCA GGGAAGCTGG    4920
CTGATTGCTC AAGTAAAGAT CCGGAAAAAT GCGAATTATT TATCGTCGAA GGAGACTCGG    4980
CCGGCGGTTC AGCAAAACAA GGACGTAGCC GTGAATTCCA AGCCATTTTG CCAATTCGTG    5040
GGAAAATCTT GAATGTTGAG AAAGCCAGCA TGGATAAAAT TTTAGCCAAT GAAGAAATTC    5100
GATCATTATT TACAGCTATG GGAACAGGCT TCGGCGAAGA TTTCGATGTT TCTAAAGCAC    5160
GCTATCACAA ACTAGTAATT ATGACCGATG CCGATGTCGA TGGTGCGCAT ATTCGAACGT    5220
TGTTATTAAC CTTGTTCTAT CGCTTCATGC GGCCAATTGT TGAAGCTGGT TATGTGTATA    5280
TTGCCCAACC ACCACTATAT GGTGTGAAAC AAGGGAAAAA CATCACCTAC GTTCAACCGG    5340
GCAAACATGC TGAAGAAGAA CTAGCAAAAG TGTTAGAAGA ATTACCTGCT TCACCAAAAC    5400
CAAGTGTTCA ACGTTACAAA GGGTTGGGTG AAATGGATGA TCACCAACTT TGGGAAACAA    5460
CAATGGACCC AGAAAAACGA TTAATGGCGC GAGTGAGTGT CGATGATGCC ATTGAAGCTG    5520
ACCAAATTTT TGAAATGCTA ATGGGCGATC GTGTGGAACC ACGTCGTGCG TTTATCGAAG    5580
AAAATGCCCA TTACGTGAAA AACTTGGATA TTTAATGTGT CGCAACGTTG TAAGAGACGC    5640
TAGAACATAT ATTTAGAGGG GAAAAAATTC ATGAGTGAAG AAATTAAAGA AAACATTCAA    5700
GACGTCAATC TGACCAGCGA AATGAAAGAA TCTTTCATTG ACTACGCAAT GAGTGTTATC    5760
GTAGCCCGCG CGTTACCTGA CGTTCGTGAC GGTTTAAAAC CTGTTCATCG CCGAATCTTA    5820
TATGGAATGA ACGAATTAGG GGTAACCCCT GATAAACCAC ACAAAAAATC AGCCCGGATT    5880
GTTGGGGATG TTATGGGTAA ATATCACCCC CATGGGGACA GTGCGATTTA CGAATCAATG    5940
GTGCGGATGG CACAACCTTT TAGTTATCGG GCTATGTTAG TTGACGGCCA CGGAAACTTC    6000
GGTTCCGTCG ATGGTGACGG CGCTGCCGCT ATGCGTTATA CCGAAGCACG TATGAGTAAA    6060
ATTGCTTTAG AAATGCTACG AGATATTAAC AAAAATACAG TCGATTTCCA AGGAAACTAT    6120
GATGATTCAG AACAAGAACC AGTAGTTTTA CCTGCTCGTT TTCCAAACTT ACTAGTTAAC    6180
GGAACAACGG GGATTGCGGT GGGGATGGCA ACAAATATTC CACCACACAA TTTAAGTGAA    6240
GTGATTGATG CAACAAGTTT ATTGATGGAC AATCCTGATG TAACGACGAA TGAATTGATG    6300
GAAGTGTTAC CTGGACCAGA TTTTCCAACA GGCGGTTTAG TGATGGGGAA ATCAGGGATT    6360
CGCCGAGCAT ATGAAACAGG GAAAGGTTCG ATTACTGTTC GTGCAAAAGT TGAATTGACT    6420
GAAATGCCGA ATGGAAAAGA ACGTATTTTA GTAACTGAAT TGCCTTATAT GGTGAATAAA    6480
GCCAAATTAA TCGAACGAAT TTCTGAATTA CACAGAGATA AACGAATTGA AGGAATTACT    6540
GATTTGCGGG ATGAATCTTC TCGTGAAGGC ATGCGGATTG TCATCGATGT TCGTCGAGAT    6600
GTGAGTGCCT CTGTTGTGTT AAACAACTTG TACAAAATGA CTGCCTTACA AACATCTTTT    6660
GGTTTTAACA TGTTAGCCAT CGAAAAAGGC GTACCGAAAA TTTTAAGCTT GAAACGTATT    6720
TTAGAAAACT ACGTCGAGCA CCAAAAAGAA GTCATTACTC GCCGGACGAT TTTTGACAAA    6780
AACAAAGCAG AAGCACGGGC GCATATTTTA GAAGGTCTAC GAATTGCCTT AGATCATATC    6840
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GATGAAATCA TTGCCATTAT CCGTGGGTCA CAATCAGATG ACGAAGCAAA AGCAACGTTA 6900

ATTGAACGCT TTGAATTTTC AGATCGTCAA GCGCAAGCGA TTTTAGATAT GCGTTTACGC 6960

CGTTTAACAG GCTTAGAACG CGACAAAATT GAAAATGAAT ATCAAGAGCT ATTGAAATTC 7020

ATTGCGGACT TAGAGGACAT TTTAGCCCGC CCAGAACGCG TCATTGAAAT CATTAAAACA 7080

GAGTTAAATG ACGTTCGCAC AAAATTTGGT GATGCACGAC GCACAGAATT ATTAGTAGGT 7140

GAAGTCCTAA GTCTTGAAGA TGAAGATTTA ATCGAAGAAG AAGAAGTCGT GATTACATTA 7200

ACCAATAACG GCTACATTAA GCGGATGGCA AACTCCGAAT TCCGGGCGCA ACGCCGCGGC 7260

GGACGTGGTG TCCAAGGCAT GGGCGTTCAT GATGATGATT TCGTGAAAAA CCTAGTTTCT 7320

TGTTCAACAC ATGACACGTT ATTATTCTTT ACGAACACTG GAAAGTTTA CCGAGCAAAA 7380

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GGTAAATACT TGTTCTTCAC AACCTTAAAA GGAACCGTCA AACGGACAGC CGTAACAGCC 7560

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TCTGTCACAT TTGATGAAAA TACTGTACGT GATATGGGCC GGACAGCATC AGGTGTTCGT 7740

GGAATCCGTC TCCGCGAAAA TGATTATGTG GTCGGCGCAG CGATTCTGGA TGAAAATAAA 7800

GAAGTCCTAG TCATTACTGA AAATGGTTAT GGTAAGCGTA CAAAAGCCTC TGAATATCCA 7860

GTTAAAGGAC GTGGCGGTAA AGGGATTAAG ACAGCAAATA TCACTGAGAA AAATGGTCCA 7920

TTAGCTGGTT TAACCACGGT CAATGGTGAT GAAGATATCT TATTGATTAC GAACAAAGGC 7980

GTCATTATCC GCTTTAACGT T 8001

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

TTTATGATTT AACGATTATC GGCGGCGGTC CTGTTGGATT ATTTGCCGCT TTTTATGCGG 60

GAATTCGTAA AGCGAAAACG AAAATCATTG ATAGCCTGCC GCAATTAGGT GGTCAGCTAA 120

CAATGCTGTA TCCCGAAAAA TATATTTATG ATATTCCTGG ATTCCCTGCT ATTAAAGCCG 180

GTGAGTTAAT TGCCAATTTG GAAAAACAGA TGCAGCCATT TCAGCACGAT GTTTGCTTGG 240

AAGAAGAGGT CACACACCTT GCACAGGAAG CAGATGGACT TTTGCGCTTA GACACAACTA 300

AAGGCACACA TTATTCTAAA ACGGTTATCT TTGCGATTGG TAACGGCGCT TTCCAACCTC 360

GACGTTTAGC TATCGAAAtG TtGaAGCCTT TGaAGGTGAG TCcAATCCAT TATTATGTGA 420

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CTGACATGAA AAAATTCGCT GGCAAAAAAG TTGCGATTGC TGGTGGCGGC GATTCCGCAA    480
TTGACTGGGC TTTAATGCTA GrAAACGTCG CAGAAGAAGT ATCTATTATC CATCGTCGCC    540
CACAATTTCG CGGCCACGAA CATAGCGTGG AACAACTGGA AAAATCTAGT GTTTCTATCA    600
GAACTCCCTA TATCATtAGT GATATTTtAA AGGAAAACGA AACGTTCACA GGCATCCAAT    660
TAACGGAGAC AAAAGGTGAC CAAACATTGG ATCTCCCTCT GGATGATTTA ATTATCAATT    720
ATGGCTTCAC TTCTTCTTTA ACACACCTCA AAGAATGGGG ATTAGACGTT TCTAGAAATG    780
CTATTAATGT TCATtCCGAT ATGTCAACTA ACATTCCTGG TGTATACGCT GTAGGGGATA    840
TCTGTTCCTA TGAGGGAAAA GTGAAATTAA TCGCTACAGG CTTTGGTGAG GCACCTACTG    900
CCGTAAATAA TGCTTTACAT TACTTACGGC CCGATGCTCG ACGTCAACCA GTTCATAGTA    960
CAAGTTTATT TGAAAACGGC GTACCTAAAT AAGGTTAGCA CTGGACTTTA GCAGTTTTTA   1020
AGCCAAGGAC AAAAATCTAA ATCGGATTTT TGTCCTTGGc TTTCTGCTTT ACTGAAAAGC   1080
CTTTCTTTTT CTCTTTTAAA TTTATTTTtG ATACAATAAA AAGTGACTnG GAGGAAGAAA   1140
GATGAACCAA CCAGTTATTT ATTTAGGTGA AGTATTCAAC GAAGAACAAC TGGAACAAGT   1200
GAAAGCTGTG GCACCCAATT ATCTAGTTAA AACATCTACC GATsATTTAT CATCTGCTGA   1260
AGAAGAGGCC ATCGAAATTA TGTTAGGCTG GCATAAAGAA ATTgGTCCGC GTTTaTTAGC   1320
ATCTGATACT AGTCACCTAA AAtGGATTCm GCTCATTTCT GCTGGTGCTG aTTATATGGA   1380
TTTTGATmAA TTAAGaGAAA AAGGCATTCT GTTGTCTAAT GGTAGCGGAA TCCATAGTGT   1440
TTCTATCTCA GAACATGTTT TAGGCGTTTT ATTAGCACAT ACCCGCGGAC TGCAAGAAAG   1500
TATCCAACAA CAAATGCaAC ACACATGGAA TCAAACAGCC CCTTCCTATC AACAACTTTC   1560
TGGGCAAAAA ATGTTAATCG TAGGCACCGG GCAAATCGGA CAACAATTAG CTAAATTTGC   1620
TAAAGGTTTA AATCTTCAAG TTTATGGCGT GAATACCTCT GGACATGTGA CGGAAGGCTT   1680
CATTGAATGC TATTCACAGA AGAATATGAG TAAAATTATC CATGAAATGT CCATTGTTGT   1740
GAACATTCTT CCTTTGACTG AAACAACAAA ACATTTATAC AATCAGGCAC TTTTTGAAAA   1800
AATGGCTCCT GAAACAATTT TCGTAAATGT TGGTCGAGGC GCCTCAGTAG CAACGAACGA   1860
TTTGATAACT GCCTTAAACA ATAAAACCAT TGCTTTTGCT GCCTTAGATG TCTTTGAAGA   1920
AGAACCTCTT CCCGAAGATA GCCCTTTATG GGAGATGCAG AATGTTTTAT TAACACCTCA   1980
TATTTCTGGC ATGACACCGA AGTTCAAATC AAAATTACTG GCGATTTTTA TTCCAAACTT   2040
AAATcAATTT GTGACGGATC AGACCCTCGT CAAAAACCAA GTTTCCTTAA AAAAAGGCTA   2100
TTAACTCAAA AAAGGCCTTC AACCATCTTT CAAGTAATTG TATGGTTGAA GGCTTTTTTT   2160
GCTATTTTTT ACCAGATAAC CTTGAAGTTA TCATTTGTCG ACGCTTGAAT GATTGGATGT   2220
TTTTTTAAAT ATTCTGCAAT CAGTTCCGTC ATATCAATTT GAATTTCTCG AATAATTTTT   2280
TCAGGTTGGA ACATTTGATA GTTTCCGCCA CCGACTGCTC GGTATTGATT TGTCACGATT   2340
TCCAAAACAT CTTCTGCTTG CACTGCTTTG CCATGATAAT TAAGTTTCGT CACTCTTTCA   2400
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CCAAACGGTT GtCTTAAATC AAGCGTATAC TCAATGCCTT CcAwACcwwA yCATAAtnAT 2460

AGTAwTGTGG TTTTGGATCG ACATATTTCG GGTTGAAAAT TGGTTGGC 2508

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 763 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

TTTAGGTTGT CTTTTCATGC CTAATTTTTA TATAGAATAC TTAGTAGAGG AGGAAGTTGA 60

TTAAATTATC AGAAAAAAAG TGTTTGGAAA AGTCGGATTG GTTGCTTAAA AATAGAAAGA 120

TATGGGGAAA AATATGATTA AAAAAATAAT AGTCGTTGTT GCTTTCATGC TTACAGGCTT 180

CTCGCTAACT GCGATGAGTG CATCTGCAGA AGAAATAACT GATTTATTTT TACAAAAAGA 240

AGTGACATAT TCTGGTGTAG AAGGAGGAAA AATTGGAGAG AATTGGAAAT ACCCTCAATT 300

TGTTGGCGAA AAAGCTGTCG ATGGCGATGA AACAACACGC TGGTCCGCTG ATAAgcAAGA 360

TGAACAATGG TTAATTGTTG ATTTGGGTGA AGTAAAAAAC ATTGGCGAAC TCGTTTTACA 420

GTTGCATGCA GAAAGTCCTG TGTATGAAAT CTTAGTTTCA ACAGATGGTG AAAGCTATCA 480

ATCTATCTTT AAAGAAGAGA ATGGGAAaGG TGGCCAACCT ACTAAAAAAT ATATTGATGG 540

CAaTAATGTm CAaGCACGTT TTGTAAAATA TCAGCAGATG AAAaTGTGsg CAACACACCA 600

AATAAGCAAT TTTACAGTTC AAGTATTATT TCGTTTGarG CATATGAnAA AAAACGACTG 660

GCCAGAAGCG ATTAAACTTT TTAACCGAGA ACCTGGACTA TTAGTGGAAA AAAGGAAAGC 720

CACCGCTAGC CTTTGGAAGT GTCCnCCAGC CGGGAGTAGG TTA 763

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

AACCCACTCT GTGGTAATGC CAAAAATCCC AGAAATCGTT TCATTCTGGC CTGCGATGGA 60

TGCAGTGATC AATGATACGT ACAAAGGCAA TATCAAACCT GCGGATTATC AAGCAAAATT 120

AGATAAATTA GTCCAAGACA CATCAAAAGA AGCAAAAGAA TAAAAAGAGT AAAGAAATGG 180

GaCGAGCTTC AATCTGCTGT CCCATTTCCT CTATCTTTTT TATTTAAGTA GAAAGTGAGT 240

GAACGAAGAT GTTCAAGAAA AAGAAAGCCC AGACGTCATT TCGAGAGGTC TTTAAAAAAG 300

GCGACTTCGC TACAAAACTA TCTTTTTTAG TTATGGGTGC TGCAAACTTC GCCAACAAGC 360

AGTGGTTAaA GGGaATCmTC tTTTTAACaG cTGrAATTGG CtTATCyaTT GGGGTAATCC 420

GTAATnGGTT CCnCGCCATT AAAnGA 446

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

AATTTTGGTT TGTTGGTGTT GAAACCAAGC ACTTTGTTCA AAAGGTGCTG ACAATGTTTG 60

TAAGTGATGC ACTTCGATCT GATTGGTTGC CTGcGGTTCT GTTGTGAAAT CATGGGCCCG 120

AATACCTATA GAATGACAAG AAATAGGAAC TTCTTGTGTA ACCATTAGTG TTTGTTGCCA 180

GCCAATCACT TGGACTCTGT GCGCATCTAT GCGTTTGACA GGCCAAATAT TTTTACAACC 240

AGTGAGTTTA GCTGCTTCAA TCGTTTGAGG TTGGTTAAAT AATTGAnTTG TTGCACCAAA 300

AAGTGTTTGG TTTTTTGTGA TTATCACTAA ACTCTGACAT AACTTATACA GTTCATCTaA 360

ACTATGACTC ACAATTAAGG CATGTTGATT TAAATTACTT AATCGCTGtT GAAGkTCaAT 420

TtGCaGCTCt TCCTTTAAGG GTGCATCTAA TGCGGAAAAT GGCTCATCTA ATAACAGGTA 480

AGCCGGCTGA GCCGCTAGCA TTCGCGCAAA AGCCACTCGC TGTCTTTGTC CTCCAGAAAG 540

TTGACTAGGA TATTGTTGTT GGACTTTAGT TAAGTGAAAA GATGCAAGCA ATTGAGTGAC 600

CAATTGTAAA TCTTTTGTCA CGCACGTCAG ATTTTCTACT ACCGACAAAT GAGGAAACAA 660

CGCATACTGT TGAAACAAAA GACCAATTTT TCGTTGTTGC GGCGACAAAT TGATCTTTTT 720

TTCAGTATCG AATAAGACTT GATCATTTAA AACAATCTGA CCTTTATCCG CAGTCTCAAC 780

ACCCGCAATA CATTTTAACA ACATACTCTT GCCACAACCA GAAGCACCTA mAATTCCTGT 840

TGTTTGAGkC TTTGTTTCAA ACTGAATTTG CAAAGTATGA CTTTTCAATT CTTTTTGAAT 900

ATCAACAATT AATCTCATTC CGATCTTCTC CAAGCGCGCT GaCTAAAAAA TTCCGTAAAA 960

AAtAAAATAA TCAGGCmAAG TAATAACATr ATTACAACAT ATTGATTGGC TAAACGCCAA 1020

TCCCCACTTG CTACAGCAGA GTAGATAGCT AAAGGAAGCG TTCTTGTTTT ACCAGCAATA 1080

TTCCCTGCTA ACATTGTCGT CGCTCCAAAT TCGCCTAACC CACGGGCAAA GGCTAACACG 1140

CCACCGGsCA AGAGACCGTT CATCGACAAA GGTAACGCAA TTTTTCTAAA ATATCGACTT 1200

TCCGAAAATC CGAGTGTCTG GGCCACAGCC AACAATTCAC TATCCATTTG TTCAAACGCC 1260

GTTAAGGCTG AACGtACtTA AAGGAAATGA AACAGCAACG GCAGCAATAA CCGTAGCTGG 1320

CCACGAAAAA ACmACTTGAa TGGCmAAAAA ATCmAGTwAA AACTGGCCCA CTGGTTGCTG 1380

AACACCmAAA aTAGTTAAGr GaAAAAAACC AAAAACAGTC GGCGGTAAAA CTAATGGCAA 1440

CGTAAATAAA CTATTCAAAA GAATTTTTAA TTTACGAT 1478

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

CCTCTTTCGT AGAACGTACA GGAATTTCTT TAAATATTAC CGATGTTGGT TGGGCACCTT 60

TGGCCACCAT CACTTGGGGA TCTCCTTACA CCCTTTACTT TCTTTTAATT ATGGTGATTG 120

TCAATGTCAT TATGTTAATT CTAAATAAAA CAAACACATT AGATGTGGAT ATTTTCGACA 180

TTTGGCATCT ATCGATTGTT GGTTTATTTG CTATTTTTTG TGGCGCAAAC TTAATAATTG 240

CAACAATCTT AGTTATTTTC ATAGGTGTTT TAAAAATTAT CAATTCTGAC TTAATGAAAC 300

CAACGTTTAA CGaTTTACTT AACGCCCCAG ATACCAATCC TATGACTACC ACACATATGA 360

ACTATATGAT GAACCCAATC ATTATGGTTT TTGATAAAAT TTTTGATAAG CTTTTTCCTT 420

GGTTAGACAA ATACGATTTT GACGCTGCCA AATTGAATAG TAAAATTGGC TTTTGGGGAT 480

CAAAATTTGC CATTGGGATT TACTTAGGGA TTTTTGTGGG TCTTTTAGCT GGCCAAACAC 540

CCACGCAAAT TTTTTCTCTA TCCTTTACGG CTGCAGTCTG TTTGGAACTA TTCTCTTTAA 600

TTGGAACTTG GTTTATCGCT GCAGTTGAGC CTTTATCCCA AGGGATCACT GATTTTGCTT 660

CGAATAAATT AAAAGGACGT ACACTTAATA TTGGTTTAGA TTGGCCTTTC TTAGCTGGTC 720

GTGCTGAAAT CtGGGCAGCA GCTAACGTAT TGGCTCCAAT TATGCTATTA GAAGCCATTG 780

TCCTACCTGG CAATAAACTT TTACCACTTG GCGGAATTAT TGCAATGGGT GTAACCCCTG 840

CTCTACTAGT AGTAACAAGA GGTAAACTCA TCCGAATGAT TATCATTGGA GCAATCGAAT 900

TACCTnTGkT CtTATGGTCT GGTACCCTAA TTGCACCGTT CGTTACCGAA ACCGCAAAAA 960

AAGTTGGCGC TTTCCCAGCG GGTCTAAATA ATAATACTTT AATTTCACAT ACTACCATGG 1020

AAGGGCCAAT GGAAAAATTC TTAGGATACT TAGTCGGCAA TGCATCACAA GGTCAACTCG 1080

AATTTATTTT ATACGCATGT CTGGCGCTAG TCGCCTATCT ACTGATTTTC ATTTGGTATG 1140

CAAAACAAAT GAAGAAGCGA AATATTATTT ATGCTCAAAA AGCTCAATAA GGGGArcTAA 1200

AAAGAAGAGG TGCATCTGCA CCTCTTCTTT TTAGTAGATC ACCCTGACAA CTTTTTCCAA 1260

TACTTTAGAT GTGTCAAATT TATCTTTATT TGTAACTACC GCTGTCACTT CTTCTAATTG 1320

ATAAAAAGAA TAAAAATCCT GTTTCTCTAC TTTAGAAGTA TCCATTAACA AATATTTTTC 1380

TATTGAGTTA TCTAATGCAA TTGCTTGTGT TTGTCCTTCT TCAATAGTGG CTGTCATAAT 1440

TTTATTATCT TTTAACGCAT TGCAACTAAA AAATGCTTTA TGGAAATGCA TTTCTTCTAA 1500

TGCTTTATTA GCGATTTCTC CAAAAAAAGA TTTAGTTAAA AGTCGCATTT CTCCACCAAC 1560

CAAATAAATG GTCAACGCAT TCTTTTTTTT ACTTAACGTT TCAAACACAG GCAAACAGTT 1620

TGTTACTACT CTTAAATGTT TAAATTCCaT TGcCTCGGCC A 1661

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

TCAGTTCCAG TTGGGTTTCG TTATGGCATC TTGAACAAAA GTAACACACC ACAAACTATC 60

CATTTAAATG CGAGAAATTA TCAAACTCAC ACGAACGTTG TCACGGATGG TTTCTATACA 120

CGTTTGAGGG ATGATCGCAC AAAaGATAAC GGTTGGAAAC TAACTGCGCA GTTATCTGAT 180

TTTAGCGATG AGACAAATTC AACGGTGTTA ACGAATTCTG GGATAGCTTT AAAAATGGAA 240

AATATGAAAA TTGAATCTAT AAAAAATCGA GATACTCCAC AAGAGAGTAT TGATCAAAAT 300

CCAACAGGAA CACCTTCAAC TGTTaGCACs AATGAAACGC TGATATCAGG ACAAGCAGCr 360

AArACATTGA TyAATGCACA GGCAAATGAr GGyCACGGTA CGTGGCAACT AAGGATTCCT 420

TTTGATAAAG TGTCCTTGAC TGTACCAGCG AATACAGGGG AAATAAATAA AAATTATACA 480

GCGACTTTGA CATGGTCGTT AGATGATACA CCATAGGAGG AGAGTTCTAT TGATACAAGT 540

ATGGATTGGA TACCTTTGTT TTCTTGCAGC AAGTTCTTTT ATAGGTTTTC TCTATTTCTT 600

TTTGAAAGAT AGTCGATTGC GTGTGGACAA CGGTAAAAAG TCAACGGAAT TACTAGTAGA 660

TTGTGGTTTG ATGTTTATTT CTTTATTATC AATAGTTGCA TCTGTTCTAT TATATCTCAA 720

CTGGCAAGAA CAGTTACAGT ATTTTCTAAA CTGATAAAAA GAAGTAACTT CAATGACGAA 780

GGAAAGATGT GTCATTTGAA GATAGTCAAC TTACAATTAT CTAATGGCAA AAAAGCTATT 840

GCATCATGGT TTCAAATTAA TCAATTAAAA GCTCTTTAAG AATTATTGAT TTAAAGGAAT 900

ATACATCTTA AAGGGGCATA TCAAGTTGAT TATCGTATAG TGTTACTTCA TAAGAGAAAC 960

TAATATTGAT CTTAATACAG AATAGTCTTT GATATTCAAA TATTTAGTAA CTGTGTTGTA 1020

TTTATAGTAA ATACTCATTA GGAGCTGCAC CAGTTGCTTA ATTAGTTGGC AATGAGGAAC 1080

TATTAAGAAT TGTTTAACGA ATTTAACTTA GTTAAAAGGG GAAAATAGTT AATGAAAAAG 1140

CGCGTAGTTA TGACTATTGC GGGGATTATG GGAGGAACCT TTACCTCGAG TGCTGTTGCA 1200

TTAGCACAAA CAAAAACAAG TGTGGAAGAA AGGGGTCCAG TACAAGAGAG TACGATTTCA 1260

ATACCAGACA GTGAGATATT GGCGGAGGAA AAGGAGGTAG CAGCAACAAT AGAGTCTACT 1320

ACCACGACGT CCACCATAAA GACAACCAGC GATAGCCTCG AAAAAGCCCT TGAGGCAACT 1380

ACCTCAGAGA CTTCTTCGAC AGAATCGGGG AGCGCAAGTC AGTCAAGCGC TTCACAACAT 1440

AGGAAAGAAA TAGAAACAGA GGAAACTTCT CTAAAAGCAC AAACTACATC AACGGTTTTA 1500

ACAGGGATGA TAGGAACGAG TCAATGGAGT TTAGATCCTA CATCTGGAGA ATTAACTATA 1560

GGCCCAGGAG TTTTTAGTGA TGATGTATCA TCTGCGTTCG ACTCCATATC AAATGTTAAA 1620

AAGGTAACAT TTTCTGGACC GGTGAAAGCA GGAAAAAGTT TAAAAAGTTT ATTCAGTAGC 1680

TGGTTTGCGC TATTGTCCAT TGAACGTCTG GATTATCTGG ACACGAGTCA AGTGACAGAT 1740

ATGAGTTATA TGTTTACTAA TTGTACTGGA TTACAAACGT TAGATGTATC AAATTTTGAT 1800

ACGAGTCAAG TGACTAATAT GAGTATGATG TTTTATAATT GTCGTGGATT ACAAACATTA 1860

GATGTATCAA ATTTTGAAAC GAGTCAAGTG ACAGATATGA GTTATATGTT TGATGCTTGT 1920

AGCGGATTAC AAACATTAGA TGTATCAAAT TTTGAAACGA GTCAAGTGAC AGATATGAGT 1980

AGTATGTTTG ATGCTTGTAG CGGATTACAA ACGTTAGATG TGTCGAATTT TGATACGAGT 2040

CAAGTGACTA ATATGAGGGG TATGTTTTTT CTTTGTACTG GATTACAAAC GTTAGATGTA 2100

TCAAATTTTG ACACCAGTCA AGTGACAGAT ATGAATAATA TGTTTGCTGG GTGTAAGGCT 2160

TTACAGACAC TAGATTTGTC TAATTTTAAT ACAAATCAAG TGACAGATAT GGCTGGGATG 2220

TTTTCGTCTT GTGATAAAAT CCAAACAGTA AATGTGTCAA ATTTTGACAC CAGTCAAGTG 2280

ACAAATATGg GGGTATGTtT TCTCATtGTt GGGAaTTACA AGCATTAGaT GTAcTAAGTT 2340

gtACATCCAA AGGAnGTTG 2359

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

CTCCACAAGA CTGACATTGG TACTGATGGA AAACTGCTTT TTTCCGTTCT ACTAAAGGCG 60

GTGCATAACG GGCACCGCCA GTCTTAGCCA ATAACTCTTT AAAGTCCTTA TCTTTATGCT 120

GATAGCCTTT GCCAGCTAAA TGTAAATGAT AGTGACATAA CTCATGCTTA ATGACTTTTT 180

CCAGTTCCTC TTGTCCATAC TTTAAAAAGA CAGTTGGATT AAAATCCAGG TGATGCGAAn 240

TAAATGATAG CGACCGCCCG TAGTTTTTAA CCGCCGATTA AATGTAGCTT GATGCAGAAA 300

AGGkTTCTGA AAAAATACGA TTGAAATTTT TTCCACTAGC GTTTGAAGCG CTTGATCTGT 360

CATCAAGACT GGTTGAGACT CTTTCATTGT TACTCTTTTC TATCAGCCCG AGGCAACATG 420

GTTAAACTAA TACGCCCCTT TTTCAAGTCA ACATCTTCTA CCCAAACTGT GACTACATCC 480

CCCACCGCAA CAACATCCGT TGGGTGCTTA ACAAATTTAG TACTTAACTT AGAAATGTGG 540

ACTAAGCCAT CTTGCTTCAC ACCAATATCG ACAAACGCAC CAAAGTCAAT TACGTTTCGA 600

ACAGTCCCTT GCATTTCCAT TCCTGGTTTC AAATCTTCCA TCGTCAACAC GTCTTTACGT 660

AAAAGTGGTG CTGACATCTC ATCGCGCATA TCACGACCTG GTTGGATTAA ACTAGCAATA 720

ATATCCGTGA GTGTTTCTGA ACCTACTTCT AACTCAGTAG CTAATTGATT CACTGGkAAC 780

TGtTTCAATT TTTCGATAGC TTCTGCTGTC CCTAATTCTT TAGAAGCAAT CTCTGCTTTT 840

TCTAAAATTG CTTGTGCTAC TGGATAACTT TCTGGGTGAA TGCCAGTGTT ATCTAACACA 900

TTTTTGCCAT TAGGAATTCG TAAAAAGCCA ATTGCTGTTC AAATGCTTTG GnCCTAAACG 960

AGTACTTTTT GACTGATTCG TGCTGTAAGA CACCATTTCA CACGATAAGG ACAAGTTGCG 1020

CGTGGTTTAT TAAGCAGAAT AGTGGTAAAG TGAGACCGCG GATCACATAC ACCACTGGGT 1080

ACGAGTTCAC ACAAATCCAT GCCGCAGCGT TGCGAACGCA GCGAATGACG 1130

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

CACTACAAAT GAAnAnGAAA GAAAAACAnG CCAATTAAAG AAAAACAAGA AGAATCTACA 60

AmAAATATCT ACGCAAAATC CAaGCGGATT ATCTACCAAG GAmACAAAAA TATGAAACCT 120

ATAACCGATT TTTTCAAGAG CGAAATAGTT TTACTAAATC AGATACAGAT GCCACATTTA 180

TGCGAATGAA AGATGATTAT ATGCGCAATA GTCAACTAAA GCCAGGCTAC AATTTACAAA 240

TCGCAACAGA AAATCAATAT GTCCTAGCGT ATGATCTGTT CCCAAATCCA ACAGATATAA 300

AAAACTTACA GACATTTTTA GACAGCTTTT TGGAACAACA CAACGAATTA CCCGAGTATA 360

TTGTAGCGGA TACCGGCTAT GGAAGTGAAG AAAATTATAC GTATATCAAC GATGTCTTAC 420

ATAAAACGCC ATTAATCACT TATGCTAGTT ATCGTAAAGA AAATAAAAAG ACCTATAGAA 480

ACAGTCCTTT TATGGTTGAT AACTGGCGCT ATTTGGAAGA AGATACATAT ATTTTTCCTA 540

CCCATCGGGC AGTTCCTTTC AAGAGATATA GTCGAGGAAA AGAGAAAGGC GGATTTGTAC 600

GTGACTTCAA AATTTATGAA TGTGaAAATT GTCGAGATTG TCCTGTTCGT AGTCAATGTA 660

CGAAaGCAAA AAGTGaGCAA AACCGACAAA TTTTAGTGAa TAtACATGAC GCTAtTTCAA 720

GCAGAATGTA AAAAGAAGCT TTTAGAGGAA AAGACAGGTT CGATTTATCG GAAACGAAAA 780

ATCAATATCG AACCAGTGTT TGGCCATCTA AAGGCTCATT TGGTGTTCCA ACATTTCCAC 840

TTACGAGGGA AACAAGGAGC CGAGATTGAC ATTGGATTGG CACTCATGGA ATTAAATTTA 900

AGGAAATTAG GGAAATAATT TCTGAGTATT GTACCGGATT AGATGCCCAT CAAAATAATG 960

TTGTGTTTTG AAAGGTCCAT TTATTCAAAT AAATAGAATG TTGGAGTATA ACTATATTGC 1020

TTATGTAATA TAATTTATTT TTATTGTATA TTTGTTCCCT TTTCGTACTT TTCAACTTTT 1080

ACTACCrGrG TwTmCTAAAa TATGCTATAT TTTTACTACA GTAGTTATAA aTTTGAGaTA 1140

AAAAAGGAGT TTTTTTTTGG ATAAAGGAGT CGCTGATATT GTAAAAATTA AGCAAGTGTT 1200

GAAACAAGAA TCAGTAAAAA GCTTAGTAGA AGGAACTGGG TTAAGCAAGA GTACTATTTC 1260

AAGTTTAAAA TCAGGTACTC GAAAAGTAGA AAAACTAAAC CTTTCTGCAG CTATTAAACT 1320

GACAGAATAT TCAGATCAAG TTTTTAGACC TATTATTGAA ATCTGGGGAG AAAAaCCGAA 1380

AAAaTAACCa CAGTTATTTT ATGAAACTAA TAGGATTAAA AATAGAAGAA CTAGAAGTTT 1440

TTTAGATGAA TGCTTGTTTA GCTCTATAAT GGATAGAACT GAAAGATAAT ATTCTTCAGT 1500

CCTACCATTA TAGAGCTATA ATTTTATTCA ATTTCAAGAA GTCTTTTTTT TACCAATAAT 1560

TTAAGATATT TCATAAGATC TTCTTCAAAT TCTATAGATT CCCTATCTTG TTGGTACAAA 1620

GATAAATAAA GAAATATTTT TTTTCGATAG AATACGTTAA AATATGAATA GATATAGATA 1680

GTAATTATAT TATCTATAAA TAGTAGAGTA TAACGATCTT TTATTTTTGG ATTTTCTATA 1740

AATTTTAAGT AGTAAGAAAA TCTTTTTCGT TCAAACTTTT CTATAATCTC TAAATTTTTA 1800

ATTTGAACAG AATTAGTTGA AATAAGCATA TAAAAATTTA ATAGTAATTG CTCCTTATCA 1860

GATTTTAGAC GTACTCTTTC AATTATATTC ATGATATATT CATCGATGGT AGAGCTTTTA 1920

TCAGCAATTT TTTCTAATTC AGAGTTTATT ATATCCAAAT TATACACAAT CACTGCCTCA 1980

TATAAATCAT GTTTTGTTTT AAAAAAGCTA TATACGGTAG TAGTGCTGGT TTTAGCTTCA 2040

TTAGCAATAT CTAAAAGTTT TGTTTTTyCA TAACCAAATT TAGaAAAgTG GTTCCATTGC 2100

GGGTAAATAT AATTTCTnCC nTTTTnAATA TC 2132

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1610 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

nTnAGGTGGA AGGCCCAACG GATTACTGGT TAGCCCTGTA CATGGTTAAT ACTAATAGAT 60

ATGCTTGATT GTAAATTTGT AGTGAAGTAC AATTTATTTT AAGAGTATAT TTGTAATATT 120

CTGTATAAGA AATTATTTAA GGAAGGAACA AATTTAATGA AGAAGAAAAA AATGATGAAG 180

AACTTAAATT TTGTAATCTT ACCTTTGTTA TTAGGGGTTT GTATTTCATT AATATGGAAT 240

ATACCATTTT TTGCkGTTTC kGGrGCTATT TACTTTGTAC TTTTAGTTTT TTTGGTTCCG 300

TCAGTTGACT TTGCCTTTAC AGATTTCAAT ACTATACGAA TAAaTCCGCA TTACAGAGGA 360

AGAAGAAAGA TAATTTTATC TAATGATACA TTGACATTAG TATTAGTTTT AATAGCACTA 420

ATAGTATCTG TGGTACTATC ATATTTTTAT TATAGATAAG AAGTATAATG GTAAGAmGGG 480

ATGAAAAAAA TCAAATATAA AACCATAAGG ATAGATAAAT ATTTATArGG TCAAAAACTT 540

TTAAGTTTTT GACCTCTTTA TTTTTTCGTG CTATACTTGG AATTATCAAG TGTCAAAAAA 600

TTATGTTCAG AAAAGGTGAG GAAATTTTGG CCATTTATGG TTATTCAAGA GTGAGTACTA 660

GTAATCAAGA TTACAAAACC CAGATTCAAA AACTAGAAAA AGCCGGAGCA GAAAAAATAT 720

TCAGTGAAAA ATATACGGGA ATAAAAAAAG AAGGAAGAAA AGAATTAGAA GAACTACTAT 780

CTATTGTAAA ACCTGGCGAT AAAGTTTTAG TGACGAAAAT TGATCGGCTA GCTAGAAGTA 840

TCGTTGATTT AAATTCGATT ATCTCTTCTT TAAATAATTC AGGAGTGACT ATCmCCTTCT 900

TAGwTAaTGC CCTAACCTTT GAcCAAATAA AaGTGATtCT ATGCAAACGT TAATGATGAA 960

TATGCTGGGT AGCTTTGCGC AATTCGAAAG AGATTTAATC GTGACGAGAA CGCAAGAAGG 1020

GAAACAGTGG CATCGAGCGA ACAATAAAAA TTATCGAGAA GGTCGTCCGA AAAGAGTTCT 1080

AAATGATAAA TACAAACATG CACTAGAGTT AATGGAAACA AACmGCmTGC gAGaAGTGGg 1140

AAAGGcAAAC AGGTATTTCT TTATCTACTC TCAAACGAAT CaAGAAACag CCAAgGAAGA 1200

ACmGTTACTT AGTGrGrAAT AATTCCAGGA GTACTTATAA TGGAAAATAG AGAGAAAATT 1260

ATTCArTTGT TCAAgAATCC TTTAGTAACA GGTTATGGGA TTGAGATAAT GTCAAACGGG 1320

CGACTTTATT CAGCAAACTT CCAAAGATAT AAGAATCGAG yAAAGAAAGA AGAGAACCCr 1380

TTGATTATTT TTGAGAGCAT GACAGAAAAA GTTGAGCAGG TATTTTTAGA ATTAGCTGAA 1440

GAAGTCATAC GAACGAACCC TAAAACAAAA CAAGAATTCA AkGAAATGAT TArAGAATAT 1500

AGTTATAAGG AGrATArCAA ATGrTAGyTC GAAAAAmATA TGATCATTTT GGTATTGAAA 1560

TTGGTATGTG GAACCGAGAC AATGTAGTAA ATAAAATAGA GTGTGATTGT 1610

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 626 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

TCAACAAATT ATTGATTATT TACAAAATGA AATTGATTCA GGGCGATTGC CTGTTGGAGC 60

GCAAGTGCCT ACCGAAAAAG AATTATCGGC TCAGTTTAAC GTCAGTAGAA TTACGTCCAA 120

ACGAGCGCTA ACTGAGTTGG AAACGCAAGG CGTAATCCAA CGTCACCAAG GAAAAGGAAG 180

TTTTGTTCAA GCACCAAAGC ATCCTCTTCA TACCTCTTTA AATAAAGTTC TTTTTTTATT 240

GCCTTTTGCA GACGATTTAT CAGTAGGAAA TTTCTATAGC GGTTTGGCCC CTACTATTCA 300

AGCAGCTGGT TTAGAAGTCT TTATGACCTC GCCTAATTTT TTGAGAGAGA AAAATGCTGC 360

GGACATTGTG AATGAGTTTG CCGGGCTTGT CTATTATGCT GCTACTAGTA ATGACTATCT 420

CGACTTACTG TTCGAGTTGG CTTkGATGAA TTTTCCAGTC GTTGyCTtGG ATAAAAAGAT 480

CCATGATTTA CCTTTTGCAA CCATTCAATC AGACAACTTT GCTGGTGGTA AAACAGCAAC 540

CGAACGCTTA ATTGGCTTAG GACATACAAA AATTGGATAT ATCCTTTCAG GAAGTCCAGC 600

CCTACAATCC GTTCGGCAAC GGTATT 626

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

ACTCAGCACG TCAAAACATG CACAAATTTA GTGGCCAATG GTCTGTGTTT GCCAaTTCTA 60

ATTTTGTTTT AGCAGmCGGA aCCAAAGTGA ATaAAGGGGm CGACATTTCG AAaCTATTCA 120

CGATGACCTT TGAACAAGGG GTAGTTAAAA TCACGGCCAG TCAAGCGTTT TTGGATGCGA 180

TGAATCTAAA AGAAAACAAA CACGTTGCGC ACTCATGGAA AGCGTTCATT GGTGTAGAAC 240

GAATTGCGGC AGGAGACGTT TACAACACAA TCGAAGAATC TTTCAACAAT GAGAAGATTA 300

AAACTAATAC GGTAGTCACA CATACGCCAG AAAAACCACA AACACCACCA GAAAAAACAG 360

TGATTGTACC ACCAACACCA AAAACACCAC AAGCACCAGT AGAGCCATTA GTGGTAGAAA 420

AAGCAAGTGT GGCACCCGAA CTACCTCATA CAGGTGAAAA AGAAAACACC CTATTATCTG 480

TACTAGGTGC CGGAATGCTA GTTGGTCTGG CTTGGTTTGG TTTGAAAAAA CGTGAAGTGA 540

AATAATGAGT AAAAAGAAAA AGCACTGTGA AAAATCAGTG CTTTTTGTTT ATTTTAGAAA 600

AAGTGTGGTG TTGTCAAGTG TGGATAATAA TTTTTGCGTT AAGTTGTATC GTAGTATCTA 660

TAATAATTGG AGCATTTGTC AGTGCAACGG TCGATGAACG ATTGGGAGAC AATATTTTTT 720

TGCTACTTCT AGTTATTTTA TTTTTTTGGT TTATTTTGAT TTTTAATTGT TAAGTATATT 780

TTTTTATATG CTATTTTAAT ATATTTAATA AGACTAGGTG AAAGTATTAT TAATTCAGAG 840

ATAGCTGCTA TTGTAGCTCC GAAATAAATA TTGGTCATAC TTTTTGAAAT AAACGACATT 900

ATTATAGAAG GTAGCATTAT AAATATTGTT GGCAAAAAGG CAAAATAATA AGTTTCTTTG 960

GTGATAGATT CGTTAAATTC TTTGATTTTT TGAAAGAAAG ATAGTTGTTT ATGATAGAAT 1020

ATCTTAATTT TCTGTATCTC GTTTAAAGAA TAAATTAAGC GCACAAATTC TTTATTTAGG 1080

TAATAAGTTA GAAGAACGGT ATCTTTGTTA ATCATTGAAA CTAAGAAAAC TTTTGTATTA 1140

CATGGGATAT CATTTAAAGA AAGTTCTTGG GACAGTACGT AAAAGTTACT ATGCTTACTT 1200

CTTGAATTAG AAGGTATTAA GGTTCTATAA ATATCAGGGA GCTTTGCTAT TGAGAAAATA 1260

AATACAATAA AATAAATGAT AAAGTAAGTT AAGTAAGCTT TACCCTCTTT AGTAAGGTTA 1320

TTTATATCTG AAACAAAATC GGTGAATGCT GTGTCTGTAG TTATTAATGC ATAAGCAAAA 1380

ATACCAGATG AAAGTAGTAA AGAGGATATT AGATTAATAA AACCTTTAAA GATTTTATAT 1440

AATCCGATTT CAGTGGGAGA GGAAAAAAGG TTTTTTTTAA ATGAATCACT TATTACGTAT 1500

CCATAGATGG AGGAATAAAT TGTGAAAAAG CCTATAACTA TAGGTAAAAG TATACCCACT 1560

GGTTTTATTA ATTGGTTAAA AAAATCAATG TTCATATAAA TAATTACTCC TTATAAACTT 1620

TTTATAATAA TTATATCAAA AGGACGTGAA TATATGTTAA TAAAATTAGG TACAGAATTG 1680

ACGAAAGAAG AATATGTTAC AAGGTATATG CGAAACTTTC AGAAATTATT GTTGCTCGGC 1740

GATCGGCCAA AAGTATTAAC GAATCGTGAA GAACAACTCT TGCAGTATGA AAAAGAATTA 1800

TGTGTGCTGT TTTATGAACA ATTTATAAAG AAACATCATA GAGCGCCTGA TGAAGCCACG 1860

CTAGACGATC AAGTTAAAGC GAATTTCATA GAGCGCTCTA AAATTTTCGC TCGATCTCCC 1920

TTAGTAATGG ACGAAGGAAA TTTTACGCAA GCACATATTG GTCAACTAAA ACGGTTGCGT 1980

GAATTGCGCA TGGAAGACTA TTTGCCAGAC AATTATACGC ATATTTTACA ACGAGAAGAA 2040

GAATTGGCAC GTAACTATTT TCGAAAACAT GATGATTATC CATTTGGGTA TGAGTGTTTA 2100

TGTATTAGTC GGTCACGAGA AGTGGTGAAC CAAGGGCTAG AAAAGCTCTT AGAGGGGTTT 2160

TATGACAGTT ATCAGGTTTA TTATCGTCGG TATCGTAAAA ATGGTTAGAA ATGGAAGTAG 2220

GAATAAAAAG CGCAGGAGGT GTAGCGAGCA ATGGCAGAAG AATCCAAATA TCCGCCAGTG 2280

AAAGAAAAAT CTGTGTTTTA TCAGCGTTAT AGTCGTGTTT CGACGATTTC TATGTTGATG 2340

GATTTAGGTT TTAGTGTGAG TGAAGCCCAG ATTGATAATG AAGATATTGT TTATATGGAA 2400

CAGTATAAAG AGTTTTTATT AAATAAAGGA ATTGTGGAAG AAAAAGTTCC TTTTAAACGA 2460

GAATTTGTAG CGGAGTATCC ATTAAGCAAA ATGCGACGAC TTTTTGTAGA AGGCTATTAT 2520

TTACGAAAAC CGAGTGGTGA AAAAATGTAT GGTAGCTACT ATTACGATTT TTATTTTAAA 2580

GAGTATTCAG GAATGGGGAT TTATTGTACG AAAGCAACAA AATCTCTTTT TTTACATGTT 2640

TTTGAACAAA GAATTAGAAA AATAAAAAAA TTAAAACATA GATTGGAAGA ATGAAAATGA 2700

AAAAAATGAT TATTATTGCC TTATTCAGTA CAAGCCTTTT AGCAGGGGGA AGCAGTGTTT 2760

CTGCTTATGC GCAAGAATCA GAAGGAAATC TTGGTGAAAC AACAGGGAGT GTTTTACCAG 2820

ATGAACCGAA TGTACCAACT GACCCAATAA CGCCAAGTGA GCCAGAGCAA CCAACAGAGC 2880

CAAGTACACC AGAGCAACCA TCGGAACCGT CAACACCAAC CGAACCTAGT GAGCCTTCAA 2940

AACCGACGGA TCCTTCGTTA CCAGACGAAC CGAGCGTACC AACAGAGCCA ACAACGCCAA 3000

GTAAGCCAGA GCAACCAACA GAGCCAACAA CGCCAAGTGT ACCAGAGCAA CCAACAGAGC 3060

CAAGTGTACC AGAAAAACCA GTAGAACCAA ATAAACCAAC CGAGCCAGAA AAGCCTGTGC 3120

CAGTTGTTCC TGAAAAACCA GTTGTACCAC AACAACCAGA GCAACCAACA GATGTGGTGG 3180

TAAAGCCAAA TGGAGAAATT GCAACAGGAG AATCTACACA ACAGCCAACT GTTCCAATTG 3240

AAACGAATAA CCTTTCAGAA GTAACACATG TCCCAACTGT GACGACACCG ATTGAAACAG 3300

CAAGCGGAGA AGCAATTGTC GCAGTGGATA AGGGCGTTCC TTTAACACAA ACGGCTGATG 3360

GATTAAAACC GATTAAAAGT GAATATAAAG TATTACCAAG TGGCAATGTA CAAGTGAAAA 3420

GTGCTGACGG AAAAATGAAA GTACTTCCTT ACACTGGTGA AAAAATGGGC ATAATTGGGT 3480

CAATCGCTGG TGTATGTTTG ACTGTTTTAT CAGGAATCTT AATTTATAAA AAACGTAAAG 3540

TGTAGTGAGT GATGTATGAA ATTTTTAAAA AAAATTCAAA CAAAGGAAAA AAGCAAAAAG 3600

AGCCCAAGAG TTCGTTTACT ATCACAAAAA AAAGCGAATC GATTAGTATT AATTGTGGGG 3660

TGTGCTCTTT TTGGATTGTC ATTGATTGGT GCTATTCGAG CAAATGTGAT GGCAGGCAAC 3720

GTGATCCGCC TCAGTCAACA ATTAGAAACA ATAAATAAAG ATGTCAAAAA AATAAAAGAA 3780

AAAAAGAGAG TGTATGATTC GTCGGCACTC TCTTTTTATG TCAGAAATTT TGTGAATGAG 3840

TATATCAATT TTAATGGAAA AGCAACAGAT GAAGAGAAAA AAGCACGTGA TGAGAAATTA 3900

GCGAGTTATT TTTCAGGAGA TTTAGCGTTA GATAAAGGAA CAGACAATGC TGCAAAAGAC 3960

TTAATTCGTA AATTATTACA AGTCTCTGTT ACTCGTGTAG AAGAATCTGA AGAGCTATTA 4020

CTTGTGCATG CGAGTATATC TTATAAAGTG CAACAAAAAG GGCAGGATTT ACTAGATACA 4080

CAAGAAATTG TTTTACCTAT TCAAGAAAAA AATGGGTTGT TTTCTATTGT TGGTCGTCCC 4140

TATTTTTTAG CAATGAATGT TCCGAAAGGA AAACAGGAAC CATTGCAATC AGTGAAAGAA 4200

CCGCTTGATG TTGAAAAAAA AGAACGACAA GGGATTGAAA AATTTTTACA ATTATTTTTT 4260

GAAAAATATG CGAAGGGGAA TACAGAAGAA TTGTCTGTTT TAATGAAAGA ACCAGTTAAA 4320

ACAAGTGGTC AAGCAACTGT GTCGTCTATT GAAGAAAAAG AACTACGTTT TTTTGAAACG 4380

AAACAAAAAG GTGTTACAGG CGTTCAGGTG TCAGTGAACT TTAAAGACAA AGCAATAAAT 4440

TTCCTTTACA CGGAAGATTT TTCGTTGTGG TTAACGAAAA CAGAAAATTC GTATTTTGTA 4500

CAAGAGTTAA AACATTATTA TACAGAAAAG GCAGGAGATA AATAGTGGAT ACAAGTAAAT 4560

TAAGTCAATT TATGAGTAGT GGATTGATTA CACTTATTGC GTTTGGTGTG ATCATTTTAA 4620

TTTTAAAGCA TTGGAAAGAA GCTGCGTGGT TAAAGATTGG TTCAGTTATT GTCATTGCAT 4680

TGATTTTAAA TGACTTTGCG ACAAATAATG GGCAGAACAT TTTCAAAGTT GTGAAGTGGG 4740

TCTTAGGATT ATTTGGGATT CAGCTGTAGA GGAGAGAAAT AATGAAACAT TTTGATTATT 4800

CGAGGGGCTT AAAAGCCCCT TACTCATTAC AAGTTATTAA GTCCCCAAAA GGGAAAATTG 4860

TTTGGTATTT TGCACAACCC TTAAGTTTAG CTTATTTAGT GATGTTATTT TTAGGGATTG 4920

TACTAACAGG CATTTTTTGG AAGTTTGTAC CATTGCCGTT AATTTTTGGT ATTAATCTTA 4980

ACCTAATGAT TATGTTGTAT TTTCCAAATA AAGTGGCTCG ATGGTATACA GAAACAGAGT 5040

TTGAAGGGAA AACAGGATTA GCTTTTTTAA AAGATGGTTT TGTTTATGTA AAAAATTATG 5100

TGTTAGACAA TAGATCAATT ATATCCTTTG AACGAGTAAA GGAAATAGAA GAATTTTCAT 5160

TTAAACGTTA GTAATAAGAA AGAGTGTATT ATGGTGAAAA CATGAAAAAA AGAAGTGTGT 5220

TGTAATAACT TCTTTTTTCA TGTTTAAATT ATGAATTTCT ATATTTTAAA TAAAGCATAA 5280

CTGCACAGAC TATTATTCCA ATAACTAAAA GTAGCACAGT AACAATACTT TCATTTTTAT 5340

CTATTTTTCT TTCAGGTCTA TAGCTAGGAT TAATTTGTTT GGCGTTAAAA TCAGTAATTC 5400

CAAAGTCTAA AGTAGGAAGT AAAAAGAGTA ATAAAATAAT ATATATAATT CCCGCTATAA 5460

GGAAAATAGG GGCGCTAGTG AAAAGTGAAA TAATGGTACC TATGATTATA GGAATTAAAA 5520

TGTATAAAAA GGATTTGATA ACAGATTCTT TTCTCATTTT AATTACCAAA TTTTGTTATT 5580

CATGTTTCCC ATATTTCCTA AAGGAACACA ATAACCACCG CTCATATTTT TCCCACCTGT 5640

AGACCAGCCA CCTTTTTTAA AATAAAAACC TCCAGGAC 5678

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1068 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

```
CCTTTTTATT GGTAACAAGG TACGTATGAT CGAAGGGTAA TTnCCACTTT ATACGGnCCA      60
ATTTTTTCAT AACTTGCCGT TGAATTTCCA CACCCAGTTC AAATTCAGAT AATTTGGATT     120
CTGTAGGCAA AnCCAAGTCG AACAAAATCT TCGGCTCTTC GCCCATGGGT AACTAAGCGG     180
ATATCATGGA CTTTTAAAGA CGCGTCAAAA GAACGAATAA TCTTTTTGAT TGTTTGATGA     240
ACAAATTGTT GTGTTGGGTC ATACAAATTC ACTGGnATCA ATATGACAAA CAAGATTAAC     300
ATCCAACTCT TCTTTAAACT TCGCTTCAAT CGCATCGATT GTCTGATGGG CTTTATTTAA     360
ATCCCAGCGA TCATCAATTT CAATGTGAAC AGACGCAAAC GTTTGGCTGG GACCATAATT     420
ATGAATCAGT AAATCGTGAT ACCCTACAAT TGTTTCCATT TTTGATAAGA CATTCTTCAT     480
TTCATCAATT TCTGTTTGGC TCGGACGCAT GCCCATCAAC TCATTAATAA ATTCGCGAAT     540
TAACTGCAAG CCACTATAAA TAATATATGC AGCAATTAAA AAACCAATAT ATCCATCAAT     600
TCGCAAACCA GTGACGCCTT CAATAAATGC AGAAATCAAA ACAGCTAATG TAGTATAAAC     660
ATCATTAAAG CTATCCTTAG CAGAAGCAAC TAATGCTTGA GAATCAATTT TTGCTGATAC     720
TTTTTTGTAA AACAGCCCTT GCCAAATTTT AATCCCAATT GATAAAGCTA AAACAGCAAA     780
TAAAATGGGT GtCAsCTTGA TTGATTCTGG ATGCAGGATG CGATCCACGG AGGTCGTTAG     840
AAACTCAAAC CCAATAAACG TAATCACTAA TGATACAAGC ATTCCACTAA TATATTCAAA     900
ACGTTCATGG CCATAGGGAT GTTCTTTATC CGCTGGCTTA CCAGCAATAT AAAAACCGAC     960
TAATGTTAAA ACTGAAGAAA TAGTATCGGA CAAGCTATTA ATGGCATCTG CCATGATTGA    1020
AACACTACCT GnAAGCAAGC CAATCATAAA TTTACTAACG GATAGAAT                 1068
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(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

```
TCGGAACGGC AATTACATAC ATCTCTTTTT CATGAATTGT TACATCACTC ATGACTTTCA      60
TTCCACTTAC AGAAATGATG CCACAAACAA CCACAAAAAC ACCGCCGATA ACTGGTGCCG     120
GAATGGCCGA AATCAAGGTG GAAAGTTTTC CAGATAAGCC AAATAAGACA AACCACGCAC     180
CTGCAGCCAC AAAAACCTTG CGACTAGCAA CTCCAGTGAT TGAAATAATC CCAGCATTTG     240
TAGAGTAACT AGTTACTGGC GTGCCGCCAA TGAATGAAGA AACTAAGCAA CCTAAGCCTT     300
CACCAATTAC GCCGCGATTA ATTTTTTCTT CGGTCAAAGG TTCAGCGACA ACATGACTCA     360
CAGCAAACCA AGTGcCTGTT GTTTCCGcCA tTAAAACCAG ATwAATaACT AACATCGTGG     420
CAATAGCTGA CCAATcAAAT TGGaAAGAAA AGTTAACTAA TGGTAACTGA GGCAAACTAA     480
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ACCAAGCCGC TTTACTAACG GCTGATAAAT CAAGtACCCC TAATAATTGT GCCGCGATGC 540

TCCCAAATAA TAATGCCAAA ATGaCAGAAG AAACGCGGAA AATCCGCCCT TTTTTCAAAG 600

CAGAACCTAA GAGCGCAAAG AAGATCAACG TACCCGCTGC TATAAATGCT AATAAAATAT 660

TTTGTCCTAA TTCCCCTTTT GCGTGGTAAA TATTATCCgA TAAAGCGACT GGCATTAACG 720

AAAGCCCCAC CACAAAAATA ATTGTTCCTC CCACAATTGG TGGAACAAAT TTAGTGATTA 780

AACGATTAAA AATACCAGTA AATCCTAATA TAATAACAAC AATTGCCCCC ACTAAACTAG 840

CACCTAAAAt GCGcCCCAGC CATTTCCTTG tTGGTTATTG GcAAAATAAA TTCCTGcAAT 900

TGCCCCGATT GGaATAAATG AAGGGcCTTG CGcAACTGGt AAtCnCCATA CCAAAAATGG 960

GGAnTGGAAT TAATCGTGGG CAAGTnCCTG CTGGC 995

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1038 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

CGnCTATCCA AGATGGCTGG AAAAATCCnG CACGTTCCAA AATTCCATGG AAGGAATTAA 60

AAnAAACCGG GAAAGnGGGC ATAAGTCGTT CCGACTTATG CCCCCCCCCT TCGTAATCTT 120

AAGATTATCa GsTAAATCaA AGTGAGTTCT TTTTAAAGAA ATACTTTTAT TTTAGCCTTT 180

TATAGATCTA AATAATTTTC TAAGTAATCT GCTAAACCAT CTTGATCATT TGTTTTTTCA 240

GTGACATCGT TGGCTACGGA TTTAATTTTA TCCGTGGCAT TGTTCATAGC AACACCCCAA 300

CCAGCATAAC TTAACATTTC TTCGTCATTA TGTTCATCGC CAAAAGCAAT GATATCAGCT 360

GGTTTGACAG ATAAAAAGTT CGCCACTTGA TCAACGCCAT GGGCCTTTTG AATTCCTTTT 420

GCGACCATTT CTAAAATaGG CaTTGGACCG CCCCAAGTGC GGACATCAAT ATAATCACCA 480

TATtGTTTtG TCAATGTATC AGCAACTTTT TcAGCTTGGT TTGGTGTGGT CCGAACCATC 540

ATTGAGGTAG GATTTGTTCG TAAATTTTTA GCAGTAAGTA AATTATCTAA GGTTGCTTTG 600

GAAGCAAAAA ATTTCGGATC GAACCCATCT AACGTATCGA TATAAAATGT TTCTTTGTTT 660

TCAGCAGCAA CAAAATCTAA TTGTAATTCT TTTTTCTGTG CCAAAATGTC AAAGACTAGG 720

TCACGCTCAA TATTGGcTTC GCTTTCCAAG TCCCATTTTT TCTCTGGAAT GTGGACTAAA 780

GCACCGTTAA AGTTAACCAT AGGGGTCGTT AGGCCAAGTT GTTGGTAAAA TTGATGACTC 840

ATTCTATAGG GACGTCCAGT GGCAATACTG ACGTAATGAC CGTTGTCAAT CGCTTTTTTT 900

AGTGTTtGTT CGGkTTTTGG aCTGATTAAA GACTGTGaTT aAtGtGTGcC GTCtAAAtCA 960

ATAGCAATTA ATTTTTGCAA GTAAAAATCC TCCTAAAATG CCTTTnACTC AnTCTAGCAT 1020

AAGACCGAAG ATTATCCn 1038

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

```
AAATATACCA TAGGCCAGTT TTATGGTTTT TTTAAGTACC CATCCCAAGT TATTTGGGAG        60

TAATTGTATT TATCCTTTAA TGCAATTGGG ATCCTACAGT AACTTCTAAT TCCCTTGGTC       120

CTGTCTTTGa ATTGAAGAAA ACAAGCAATT CCTATAGAAA CTGCTGTAAA CCCTATAATT       180

AACAATATAA CAGTCTTTTT ATTCATTCCT ACTTCACTCC TTTATCAAAG ATTCTTCCAG       240

TAATTCATAT GAAGATACTC CTTCTAATCG TTTATACACT TTTCCTTCTT TGATAATAAT       300

TACAGTAGGA GTCTGTGTTA TATTTAATTG ATCTAAAAGT AAATTACTTT CTTTATTCTT       360

CTCTTCTAgT CTACGCCATA TACTAATAAA TTTTTGTCTT TAATTACCTT ATTCAAGTCT       420

TTTTTTTGTA CATTACATGG TTGGCAACCT TTTTTAAAAA AATAGATATT CAaGTCTTTA       480

TTTTGAGAAA CCTTGTnCCT CAATACTCTC AGAAATCGGT nATTTTATAT TnCAATCTCT       540

TCTTTATTTA A                                                            551
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(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

```
nCTCTTAATG GTTTTACnTT TTCGTAAGTT TTCATACCTA TATCTGnCCT TATCTAATGT        60

TTATTTTAGT TTAACATATA TTTAAAATAG ATTTTTAAAA AAGTTTATTT CAGATGTTGA       120

CATGTTTGTT TTGGAATGAT ATACTCTGTG TATAAAGTCT GAAACAGATA ATAGACATTC       180

TGTTTTGGAT AAACGAAATT AAATAAACGA AAAAGCGTTC ACGAGAAGAA AATGAATCTC       240

CATTTCGTAA ACGCCGCATA ATAAAACCTA GACACTTTTA TTGTACGGCA TTTGACGAGA       300

TAATACAAGA GTGAAGTTTT CATTCAAGGT TATCAGTCTT TTTGTGGTGT GGTATAGTCA       360

GCCAATGAAT GACTTGCAAG GTGGCAGTAG TATCTTTAAT TAGAGCCATA TTGATGAAGA       420

TTTTAGGTGG AAGGTTTCTA GCTTTCATAC GAGGACTAGG TTCGCATACT GTGTATTTGT       480

AAAAGATTAA CAGTTAGAAC AATGGAGTAA TTTCCGCTTG GTGATTGAAG GGTGTTCATT       540

TAAAAGAATC AGATTATTTC CGATAACCAT GTCGTGATGA CACGTTAGAA ATAATTGCCG       600

AATTAGATTG AATAAAAAAA TCtATGCAAG CTCAATAAAA GGAGGAGAGC TGTACACCGT       660

ATGAGGTAAA TCTATTAATG TGCCGTAAtG TAATTTTTAT tACTAGCCGT TGAACgATAT       720

yCyATGATTT ACTTTGAATG TAAGAATCCT AAATTTTAAT GCAATtAAGG TTGTTATTTA       780
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CACGAGTGGA AAAGATTTTT TCTAAAAGAA TAACCAcCTT AACTGGAAAC GTTAAAAATA 840

GGAGCTAATT ACTTAATTCC tATTTATATA rATATTTTAG AAGTGAATAA TCTTCACTTT 900

TAAAACTTTT TCTAAAACTT TGTCGGTTGC ATATAGAAAT GCAATTGCAC AAAGTCCTAA 960

GAAAAGCAAT CTATTTACGA TTGGTCCGTA AATAAGAGTT GTCGCTAAAA CAGCAGCGAT 1020

AACAAAGATT ACTTCAAAAA GATATTTGAA GTTACGCATA GATACCACCT CCTTTTATTT 1080

AGTTATTTTA TTTTAACATA ATAAGGGAGG TTGGTACTTA TGATGTAGCG ATTGTAAGTG 1140

AAGCATAACT AGAATTCTCT GGTTGTGTTT TTTTGTGTTT AAAAAAGAAA AAATCGATAA 1200

ATAAATTACC AAGAGGAGGG AAGTCATGAT AGAAGAATTA TTACTTTTCG TTGAGAAGTT 1260

TGTTGAACGT ATGAAACGTC AGAAAAAAGC ATTCTCTATT TCAGATATAG AAAAGAGCTA 1320

TAACTTAGAA CGTAAGAAGT TAGGTAAGAG TGCAGTTAAG TTAACAAATA TGGACCGTCT 1380

AACAATTGAA AGTCAATTGT TAAAATATCA GATTTTACAG CGGACATATA AAATGACAGG 1440

TTATCATAAA CCTTGTCAAG TTGTGTTTTT TAGTTAGTAA TAAGAATTGC ATAAAGAGAG 1500

AAAGGCAGTT AGTTGTTGAC TGTtTATTTT TGtATAAAAA TTAAGTgAAA GAAGGAAATT 1560

ATTTgGCmAA TAGAATTCAG GAAATTGCAT TACCAGAAAA AATCTAGGAG TAAATTAAAG 1620

CTATTTGTAn AnCAGA 1636

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

TGGTATGATT ATGACAACTC CAGACCTTGG TGGAGCCACT GAATATTGGA ATATTTTTGG 60

ATACCATGTT GCACAAACAA ACTATGCCTA CCAAGTAATT CCGGTATTAG CTTCCGTATA 120

TCTTTTGTCA ATATTGGAAA AATATTTTCA TAAAAAACTT CCTTCATCTA TTGATTTTAC 180

ATTCACACCA TTATTATCCG TAATAATTAC TGGATTCTTA ACTTTCACAG TTATTGGTCC 240

CACAATGTTA TTACTATCTA ATGGAATCAC AGATGCTATT GTTTGGTTAT ATAATGCAAC 300

TGGGkTCATA GGAATGGGGA TCTTTGGTGG AACATATTCA CTCATTGTTA TGACTGGTCT 360

TCATCAGTCA TTTCCTGCAA TCGAAACACA GTTACTTTCA rCAtGGaCmA ATGGTATCGG 420

ACATGGGGGT TTwayCTTgT AGTTGCTTCC ATGGGCAAAT GTAGCnCAAG GTGG 474

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1094 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

TGTGTGACTT CTTTGCTTTA TGAACGTATC CgTCCAGAGT TTCATCtTGC ACGCTGGATA 60
TATTACGAAA AAGCACGATA TGAGTTAAAA GGGGTAGAAC TTGAAAGTGC AAAAATATTT 120
TTCAACGGGC TAAAGAACCT ATCCGAATCA GATAAAAAGA TTTTAATTGA TGTTTATTAT 180
CGCTCAAAAG ACTATTATAA ATTTAACCGA CAAACAGGAT TATATCAGTC TGTCAGACCA 240
ATTTCCGACG ATGCAATAGC AGAACAATAC GGAATTACTA AAAAAGAAGT AACGAAAGTA 300
AGACGGCAAG CGATAGATCA TTTAGCGGAA GAAATGCGGA AAATTATATT AGCTATAAGT 360
ACAGCCTTTC ATTTGAAGAT AGGTAAAGAC TTATATCTAG TTAGGCTTAT AAACGAAGGA 420
ACATACAAAG AACAGTTTGT TCTTGGAAAT AAAAGAGAAG CTAAAGTGTT TAGCGCAGAA 480
AAGGAAGACA CAATTAGAAA GTTTATGCAG CTAGGTTTTG AAAGAGAGCC AGCATGaATA 540
AGGCTTAACC TTGAGAGGTA TTCTTATGAC AAAAAATAAG TTATTTCATT TAACAGATAA 600
GTCCAATATC AATAGCATTA GAAAACACGG TTTAGTAGGA GTAAAAAAAG CAAAGGATCT 660
TTTAAGAAGA GAGACAGGAA CAGACCATAC GCTCTTTAAT CAGCAAACCT ATTCTATTCT 720
AAATACTTAC GGGTGGAAAG GCTACGATCT TAGATGTGCT ACTTTTATGT TTGAAGAAGA 780
TAGTTGTCTT GGCTATGAAT TGCTGCAGCT AATGAATGAC GATCCATATA TTTTAGAAAT 840
AGAGATAGAC CGTTTAAATA AAGATAAATT ATTTGTGTTT AATACGGAAA TTGCTAGCCA 900
TTTGCTAAAT TATTCGAAAC AAGATCAACA CAGGcTAGCT AAGTTTTATT GGAATACAGC 960
AATTCCATAC AACACTTATG TACCAAAACC AAGGACAAAG TTAAATGGAC GCTTTTCAAT 1020
TTAGGCAATT ATCCAGGTAA TCnAAGCAGG AATAAGGTnn AATTTCGGTG GAnATTTCCA 1080
CCCAAAATTA TTAT 1094

(2) INFORMATION FOR SEQ ID NO: 641:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

ACAACAAAAA AAGCATAGAA CAATCCCGTT AAACATGTTG CGTAACCATT GTACACCACA 60
TTGTATTACG AAATTCTTCC ATGCCTAGTA TTATCTAGTC ACATGAAAAC GCTATTCATT 120
TGTTAACAGT GCTTATTCTA ACGAGTATCA TTATTTTTGT CAACCTTTTT CAATTATTTT 180
TTTATTAATT GTTGACTATT AACAAAAAAG AAGCTCTTAT CGGAAAAAAA GTACCTTCAG 240
CTAAAGGTAC TTTTGTTCAC TAATTTATTC TTTATAGGCA TACTTATATG TGCTCGTTGC 300
ACCGAAGTTA TGATACTGAA TACCTTTGAC ACCTGGTCGT ACAAGCTGAC TACGGGCCTC 360
TTGGTATAAA GGAATTAAAG CGGCATCTTC TTCCACCAAT ACTTTTTCAG CTTTAATTAA 420

TGTTTGCCAA CGAGTTTCAG GCTCATTTGC GTATTTAGTT GTTGCTTCTT CAATTAGTTG 480

ATCAAACGTT GGGCTAGAAT AGTTCATACG GTTACCACTA ACTGAGCTTT CTAAGAAAGT 540

CATTGGATCC TGATAATCGG GTCCCCACAT GCCAACAGAC AATTCATAAT CCCCTTTTCT 600

CATTAATTCA ATtGCATTAT TTAAAGGAcT GTTTTGACAT TAATAGTGAG ACCAGGCACG 660

TTCTTGTACT GGCCTGGATA ATnCAnCACT TT 692

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

AGTACAACCA TATGGCAGAT GGCTGAAGGT ATTATTAATC ATTGTTAATC TTGGCGCTTT 60

GTTTAGTATT CTGCGTCTAT TTATTCATTT GTTGATTTGA AGGGGTCGAA AGGTGAGAAA 120

ATGAGAAAGT TAATTTTAGT TTTTGTGGGT TGTGCCATGG CCTTTTGTTT ATGGCCTAAT 180

CAAGCGGCGG CTGTAGCTGG TGGCTATGGC GGCGGGCGTG TAGAAAGTCC TAGCGGAGGT 240

AATCCCTCGA ATGGTTTTTC GCCAAGCGGT GATGGATCAA GAAGTTATGT TCATCATAAC 300

GAGACCGGGA CCAGCAACAC AACGCCACTG GAAGGCTTAA TTTCAACAGT GTTTTTTGTT 360

CTTTTTGGGG GCACGATGAT TTGGCAAAGA CGCCGTAGAA ATCAACCAGT CGATGAAGGA 420

GCTTTTCAAG AAATGTGGGC AkCATTACCT GGAACATCAA AAGAAAAAAA GGCACTCTTA 480

AAAGAAATAC AACAAACGTT TTTAGAAATA CAACAAGCGT GGGATCAAGA AAACTTGTCT 540

GTGGTCAAAG ATAACTATAC AGAAAAACTT TATCAAAAAC ATCTTGCAGT ATTACAAGCA 600

AATCAACAAG TGGGCATCAG AAATCATGTG AAAAAAGTGA AAGTAGCGCC AGCTTCGAAT 660

TATCATCATA TTAGTGAAAC GAGTTTTTCA CTGATGCTTC ATTTkTCTTG TATTGACTAC 720

GAGGAAGATA CTCAAAGCGG TCGTGTTTTA TCGGGATACA AGCATCAAAA ACAATATTTT 780

TCACAACTTT GGTATTTTGA TTACAATCCA TCTCTTGGAA AATGGCAAGC AGACTTCATT 840

CAACCTAAAG GATAGTGCTA AAAAGCGCTT GGGGTTTAAA TCCCAAGCGC TTTTTTATTC 900

TTCGATGcGT TTTACAAGCT GTATTTTTTT ATTTAATACG TAAATCAGGA TACCGCCGAC 960

GGTCATTGAA AGAAGTTCAC CAAGTCCAAC GGTCAACCAT GTGTACCAAA AAGGTAACTG 1020

ATAAAAGAAC GTTAAGGGTC CGGCGACAGT GAACATGGAC AAAGCAAAAA gAATGGCCGT 1080

CAGCATTAGT TTAATCAATA AATTTTGCTG ATTTTTTGTC GCAAAATAGG CAATCCATAA 1140

GACTGCGCAC GTTCCAGCAC TACCGATGAC TATATCGATG ATACCAAGAG GCGAAGCGGT 1200

GTTGGCAATC GCAACCCCTA ACGTAATGGA CCAGATATAT CGCTTGTTAA AAACGCCTAA 1260

ATAATTAAAT AATTCGGCAA GACGAAGCTG TATCGGACCA AAACTAAGCG GAGCGAGAAG 1320

TACAGTGACA ACGACATACA AAGCGGTAAC CAGCGCCATT TTAGCCAACG CCGTAGCTGA 1380

CCACGTACTG GTTTGTGGAT TTGATGAATG ATTCATTTAA GATTCTCCTT TATAAAACAA 1440

CGACGTGTTT TAGTGATAAC CATAACCAAA GGAAGGGCAG TAAAG 1485

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 951 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

AGAAATATCA TTTCAAGTTC TTTTTAAAAA TATTTTTAAA TGAAATTACA TTTCTTATAT 60

AATTTTTGTG CTATACTAAA AGAAAACGGT TTAGGAGTGA TTATGTGcGG GTTTTGCTGA 120

TTTATTTCAT AACTATTTTT CTATCCAATA CAGTTGGGGC GCTCTCTGGG ATGGGTGGAG 180

GCGTCATTAT TAAGCCTGTT TTGGATTTTC TTGGGTTCCA TTCGTTAAAT AGTATTGCGT 240

TCTATTCAAG TGTCGCTGTT TTTGTCATGT CCATTTCTTC GACTTATAAA CAGTATCAAA 300

ATGGTGTCCA AATTGAATGG AAAAAAGCCG CGAGTATTTC GTTTGGTTCC TTAGTCGGCG 360

GCATGTTAGG TGATTTACTT CTTAATCAGG CGATTGCACT AGCGCCAAAT GAAGAAAAAG 420

TACAACTAAT CCAATATATC ATCATGTTGC TGACCTTGGT TTTGGTTCTT CTCTACAATC 480

AATTTTCCAA CTGGCACTTA CACCTCAACG GATTGAGCAT TTTTCTGATT GTCGGATTAG 540

GCTTAGGGAT TCTATCAACC TTTTTAGGCA TCGGTGGCGG TCCCATTAAT GTAGCTTGCC 600

TTATTCTCTT TTTTGGAATG GATATCAAAT CAGCAACTGT CTATTCCATC ATTACTATTT 660

TTTTCTCCCA ACTCGCCAAA CTTGGCAATA TCGGCTTGAC CACAGGGTTT GCGGTTTTTG 720

ATTTGACAAT GCTTTGGGCT ATTATTCCTG CCGCTTTATT CGGTGGTTAT GTCGGAGGTC 780

TTTTCAGTAA AAAATTATCC CAACAACGGG TCGCCCAAAT TTATAGTTTA GTTGTTTTTT 840

TAGTTATTTT GTTAAATATG TATAATTTGT GGACTGTnAT CnAAAAAAGA AGCGCTTTGw 900

CGTATAGACA AAACGCTTCT TTTTTAATTA AATCACTGTn AATTGAACAT C 951

(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 647 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

TCCAGAGAGT TGCCCTCCAG CTGAGGCTAT CCCATTTGAT GGAGTTTTTT TCAGACTATG 60

TAAGGGTGAA AACTTTTGCs AAGAAGATTT TCTTACTCAT TTTGAAGCTG GGAAAAGTTT 120

CCCAGATAAA AAACTGTGTG AAGCTATGGC ATTATCATTT TTTGATAGCT ATGATCATGC 180

AGAAAAAATTA AAAAAAAGAT TTAGAAAAAA ATTnGCAACA TGTTCTATCA AACCTGTTGC 240

AATTATTGAA GATTATGGAG TAGGAATTTT TGAAGAGAAT TCAGGGCATC TTAATTTATG 300

GGAGCACAGG AACGTTGATA TTTTTGCTGA TTTAATGAAG GAGGATAAAG GAAAAGATGA 360

ATAATCTAAT ATTTTCAGAC ATGGgAATAT ATTTTCGkTT TTGACTATTA TGaTACTCCt 420

TTATTTTTCa TTtCTCGAAG TCGGAAAAAT AATAATTACy AaTTAwTCTA CTCTATAAAT 480

GATGACGTTT ATTTTTACAG TGAGCTATCT GCTTCGGATA TTAATTACTT ATTTAGTAAT 540

CCAAATGGAT ACGACATTCT TCATTACCTT AAAAAGAAGT CTAAATTAAA TTTTGTTATG 600

GTAAATAATA ATTCTTTTGA TATCTATAGC TTAGCGGAAT ATACAAA 647

(2) INFORMATION FOR SEQ ID NO: 645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

GACGAATGGC CCAACAGGGC ACTTACAGAA ACAATATCTG AAGTACTCTC TAAGCAACGT 60

GTCGCAAAAG TGTGTCGTAA TTGATGGAAG TGTACTTTGT CCAATTGGAC TTTATCGCGT 120

AATTTGTGGA AGTAATACGT AAGTAAGCGA GGCTCACAAG GCTTATTATT ACGAGAAAAA 180

ACAAATTTTC CTTGGCTGTG TTCTTTTTGA CACTTCAATG CATTTTTTAC TGTATTACTC 240

ATAGGAATTA TTCGCTCAGA ATTTATCGTT TTTGTACAAT CGTAGTAAAG TTGAGTAGAT 300

TCTCCGAACG AGCTTACAGA TACTCTTTGA AAAGTATGCT TTACATGAAT AGTATCCTTC 360

TTAAAGTTGA TGTCCTCCCA TCTGAGCGCA GTAATTCTCC TATACGTAAG CCGGTATGTA 420

AAGCGmCAAT AACTGaTAAT CCyTGTTGCT GAGGATTTTt ATAGGCAACA TTCtCCaATT 480

tCTTTkGcyC TTCAATATCT AGTGCACGAA TATGTCGACG CTTTGGTTTA GGAAGCGAAA 540

TAGTTGAACA GGGATTGCTT TTCAAATGCT TTGCTTTTAC TGCATGATTC AAGGCTCTTG 600

AAAGGATACC GAATATGACA CAAATCGTAC TTTTACTCAA TCCTTGTGCG ATCAAGTCCT 660

CTACTAATTT ATTCAATCTC AAATCATCTA TTTCATTTAA TGCAGAGTCT CCCATTGTTT 720

TTAAGACATA GTTGCTTAAC TTGTAACTAT AACTAGCGAA AGTAGAAAGT TTTACTTCCT 780

TCTTTACGAT GACTAACCAC TGTTCTATCC ATTCATTAAG TGTAAAAGCG CCTTGACCTC 840

GAGATTGATA GATAGTTTGT TGATTTGCTT TTGCCACATA GAGTTTTTGT CGTACCTCTT 900

GATAAGTAGA ACCATAGATA TATCCATACT TTAATTTTCC ATCTATCTTC CTTCCTCGTG 960

GGAAGCGACC TTCCCATCGT CCATCTTTTC TTTTATATAT ATTTTCGCCA CGTTTACTCA 1020

TTTCAATTCC TCCGTTTAAC TACTATGTTC TGACGGCTAT ATTGACGGCT TATAGAAAGG 1080

CTTATTTATA GCTTTAAAGA ACATTAGTTA TAATATAAAT CGTTATTATT GCTAAAAAAT 1140

ATCATTATTT TACTTTTTGT TGACACATAT TTTGGAAGTA GATTATAATT CTnCTGTACG 1200

GGGATGAATG ATGnCCTACA TTGGTCTATA TATGAnTCCC CACAGGGGTT TCAATAAC 1258

(2) INFORMATION FOR SEQ ID NO: 646:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

ACTGTAACAC TTGACGGCCA AGACCGCGAC CTCGTTGCGT TTTTGTCACA ACAAAGCCAT 60

AAATCCCCCA TTCGTycTTC AAAATGATCC AAACGTAGCG TGGCTAAAAG TTGATTGTTT 120

TCTTTATAAA TAAGTGTTCG TTGAAGGTCC TCCGGCAAAG GCGTACCTTC GAGTAACCTA 180

GCCAAGGAAT CCAAATCAGC CACTTGTGGT CGGAGAAGTG TCAGCTTCGC CAACGCCTGT 240

GAGTAAGTTT CTCTTTGAAA AACCAGATAC TGTTCTGAAA AAGCTGGCAC AATTCCTTGT 300

CTATTAAAAT AATTCAGGCC AACAGATTGC TTGTCGTCCA TCACGAGAAA GACTTCTTTC 360

ATTCCCCACA AAGCTGCTTG CTTTTCGAGT TCTTGAACAA GTTCTTCAAA AAATGGTCCT 420

ACATTTGGCG CAACAATCGT CGCTTCCAAG GTTTCCCCAT CAAAACAATA CCCTACGATA 480

TATGCTTGAA TGGTTgTTCC TTCCTGtATA AACCATAATA AGTATAAGCT GATtCCTCAn 540

GAAATGTTGT CCAAT 555

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

AAGGCAAGCG TCGATTTTCG ACAATATCCA ATAATGCATG GCTTTGTCCG TCCATCATGA 60

TAAAACTCAT TGCACTGGTC ACATGTCGAA CCGATTTGAA TTCATCAAAG CATAAGACCT 120

TTGGCAAAGT CTGTTTGAAA GGATTCAATG GGCGGTAAAA TCTCTTCATG ACACGATAGA 180

CCGAAGAAGT GGAGATATTT TTCTGACGGG CGATTTCCGT CATGGAAGTA TTCTCTTTTA 240

AGCGAGCAAT AACAGACCAA CGAACTTTTT GACTAATGAA ACAGTATTTT TCAGCGACAG 300

AGGTATCCGC TACGAATGTT CTTTGGCAAG ACTTACATTT AAATCGTTGT TTCTTCAACT 360

CCAGATAAGT GCGATACTCA TATATTCTTT TTCAATCAGC CAATCTTCAT CAAAAAATAA 420

ATGTTTATCT GTTAATCCGA GTAATTTTCT AGTATGATTA TCCATAGAGC GACTCCTTTG 480

AtaggGTGAT GTTTTGGtCG ACTAAATTTT ACCAAAAGTG AGTCTCTTTT TGAGTTGAAA 540

CGAAGaAAAA GGGTGTTGGa AAATCGCCTT CGATTTTCCA ACaACACAAA ATATTATAGA 600

ACCCTTTATT CTAAAGGaTT TCAAGGTGTC TGTTTGcaTT tATTAAAAAA AAgAAAAAGT 660

ATTGGCAACc AGAAGGCGTC ACCaACaCTA GATATTATAG AGCCcATAAT ATGCTGTATA 720

AtATCTAGTG TATAGGCTTA AGTGGAGGTA TATATGAAAA TATTnACTGT TGAAGATGAT 780

AATATGATAA GAGAGGGAAT AAGTGAATAT CTTTCAGAAT TTGGATATAC TGTTATTCAA 840

GCTAAAGATG GAAGAGAAGC CTTGTCAAAA TTTAATAGCG ATATAAATTT GGTTATCTTA 900

GACATTCAGA TACCTTTTAT AAATGGTTTA GAAGTGTTGA AAGAAATTAG AAAGAAAAGC 960

AATTTACCAA TTCTAATCTT GACTGCATTT AGTGATGAAG AATATAAAAT TGATGCATTT 1020

ACTAATTTAG 1030

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1023 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

AAATATTTCT TCTnTCTTTT ACATAATAAG TAGCTCCTTA GTTTGACAAT TGGTTGTACC 60

CAAGGGTAGG CTTTCTTTTT GCAAGCGGAG CAACATGGTA CCATGTTGCG ATATTTTGAA 120

TGACCCCTAC CAAAAATACT GGTAGGAGTC GTTCAAATTT TTGGGGTTCC CCCAATCCCC 180

ATCGCTACAC TTTGACATTT ATTGACGTTT CGACTTACCA TTTTTGACCT TTATTTTTTC 240

TTTCTTATTG ATAAGGAGCT AATAACTCAT CCAGAAAGAC TAAATACGCG TCATTTCCTT 300

TCAACTTTCG TAAATAAGTA GCTGCTTCTT CGTAAGGAAA TAAATCAATT TCTAATTCTT 360

TTTCTTTAAA ATCATGAATC AACGTATCCA GTTCTTTTAG CACCGTTCCT TTTGATTTTT 420

CTTTCTTTTT CTGGTGGACT CTTGGTTGTT CACTAAGCGG GTCTGCCAAG AAAAATTGTG 480

TCAGAATAAA TTTACTTTCG TCCGTTAATT GGTCCATTTT GTTTTCTCCT TTTCTCTTAT 540

TATTTGTTTT TAAAATCGAG TGGGATTtGC TATTTGAGCA GAAATTTTTG GTTCATTTTG 600

GTGCCTTTTT TGCTCGTTAG CTTGGGACTT TCCCACTTCA GTTTCTTTTT TCTnCGCATT 660

CAATAAACGT TCTTCAAATT TATTTTGGGG gAAGTtGAAT GCCcTTTTTC TATGGATAAA 720

GCATGGTCGG CTTTTTCAAT TAGCGTGCGC GCCcTCTTTC GTGATCGTTT CTAACGATtG 780

CGTAAaTtCT tCTAACTkTT CTCCTTGCTT CGTCCAAGAA GAAAGATAAC CAAAAGAATA 840

CGAGGACGTA TCCAGCCCTA AGTGACGGGA GACAATATAG GCAACTGATT CCGCTTCAAA 900

TTCTTGTCGA GAATAAACGT CATCTCCAAA TATCGCTTGC GAATCTGGGT GAAGCATGGC 960

ATGCGTCATT TCATGAAGTA AGACTTTTAA AGTCATCACT TCTCCTAAAT GTTGTTGGAG 1020

GAC 1023

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

TATTTTCGAT TCATTCTTTG GCGGCGGCGG TGGCCGTTCT GTTGATCCAA ATGCACCAAG 60
ACAAGGCGCC GATTTACAAT ATACAATTCA ATTGAAATTT GAAGAAGcTA TTTTCGGTGT 120
CGAAAAAGAG rTTAAGTACA ATCGAGAAGr TACTTGTGCm ACCTGTGGcG GTAATgGCGC 180
CAAACCAGGC ACACACCCAG AAACTTGTCA TAAATGTCAT GGTCTGGAAC AATCCATGTT 240
GACGTCAAAC GCCATTAGGT CGTATGATGA GTCGTCAAAC TTGTGATGTG TGTCATGGCA 300
CAGGGAAAGA AATCAAAGAA CCATGTCCAA CTTGTCATGG CACAGGTCAT GAGAAAAAAG 360
CACATACTGT CAAAGTAAAT GTGCCTGCTG GAGTAGAAGA CGGTCAACAA ATGCGCTTAG 420
CTAACCAAGG AGAAGCGGGT ACCAATGGTG GACCTTATGG TGATTTATAT GTAGTCTTTC 480
GTGTTGAAGA TAGTGATATT TTCGATCGAG ATGGCGCAGA AATCTACTAT GATTTACCAG 540
TAAGTTTCGT CCAAGCGGCT CTAGGGGACG AAtAACTGTC CCAACTGTTC ATGGTGACGT 600
GAAATTAAAA ATTCCGGCTG GAACACAAAC TGGcACAAAC TTCCGCTTAA GAGGCAAAGG 660
TGCGccACGT TTaCGTGGTG GGGGCAATGG TGATCAACAC GTGAAAGTGa AATTAATAAC 720
ACCAAAAAAT CtTAATGaAG aACaAAAGGa TGCCstACgA gCnTTTTGCC AAAAAGCTGG 780
GCCGGGACCn AAAAATGGTT AACCTnGGAA CCCCAACCCA AGGGAAGGA 829

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

TGACACTGTC GGTAATTTCT TAGAATCAAT GCCCAGCTTG GTTAnCTGAT GGTATGGCTA 60
TCGGTGGTGG TATGGTCGTT GCCGTAGttA TGCATTAGTA ATCAACATGA TGGCAACAAA 120
AGAAGTATGG CCATTCTTCA TTATCGGTTT CGTAGTCGCA GCGATTTCTC AATTAACATT 180
AATCGCATTa GGTGCTTTAG GTGTCGCTTT AGCTCTTATk TACTTGAACT TATCTAAAAT 240
GGGCGGTTCT TCTAACTCAA ATGGCGGAGG CAACTCTGGC GACCCATTAG GCGATATTTT 300
AAACGACTAC TAaTTCTGAA GGAGGAGCAA AGAAAATGGC AGAAAAAATT CAATTAACTA 360
AAAAAGATCG TTTAGCTGTA GCTTGGCGTT CAACATTTAT CCaAGGTTCT TGGAACTATG 420
AACGTATGCA AAACGGCGGC TGGGCATTCT CAATGATTCC AGCAATCAAA AAATTATATA 480
AAACGAAAGA AGAACGTTCA GCGGCgTTaA AACGTCACTT AGAGTTCTTT AATACACACC 540
CATACATTGC CtCACCAATT CTTGGTGTAA CATTAGCTTT GGAAGAAGAA CGTGCCAATG 600
GCGCACCAGT TGATGACGTA GCGATTCAAG GGGTTAAAGT TGGGATGATG GGTCCTTTAG 660

CCGGTGTCGG TGACCCAGTT TTCTGGTTTA CTGTTCGTCC AATGTTAGGC GCTTTAGGTG 720

CTTCCTTAGC AATGGGTGGT AACATCTTAG GCCCAATCTT ATTCTTCGTT GCTTGGAACT 780

TAATTCGtTG GTCATTCATG TGGTATACAC AAGAGTTTGG TTACAAAGCA GGTTCTAAAA 840

TTACTGATGA CtTTCAGGTG GTTTACTACA AGATATTACA AAAGGTGCTT CTATTTTAGG 900

GATGTTCGTA CTGGCCGCAT TAGTTCAACG TTGGGTATCG ATTAAGTTCT TACCAATTGT 960

CTCACAAGTT AAGTTAGACA AAGGTGCTTA TATCGAGTGG GATAAACTTC CTGCTGGCGG 1020

TGAAGGAATG CATAAAGCCT TTGAACAAGT GAACCAAGGC TTGGCGCTTT CACCAACGAA 1080

AGTTACTACT TTACAAGATA ACTTAGATCA ATTGATTCCA GGTCTAGCAC CATTACTACT 1140

TACATTCTTA TGTATGTGGT TATTGAAGAA AAAAGTTAGC CCAATCGTTA TCATTCTTGG 1200

TTTATTCGTA GTCGGCGTTG TCGGCCACTT AATCGGCTTA TTATAAGAAT GACGAGGTAA 1260

GTTTATTACT TCTAATCAAA AAAAGCGGAA GAGAAGTCGA GAAACTTTTC TTCCGCTTTT 1320

TTAAACAAAG ATGTAATTTT GTTTGTTTCG ATCAGGAAAG AAACGTATAA TAAA 1374

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

GGAAAAATTC CTGGCGCCTT CATTAAACGT GAAGGTCGTC CAAGTGAaCG TGCGACATTA 60

mCCGCTCGTT TAATCGaCCG TCCTATTCGT CCAATGTTCT CAGAaGGCTt CCGTAmCGAA 120

GTCCAAATCA CGAmCATCGT TATGAGTGTG GAGCAAGACT GTACACCAGA AATGGCTGCA 180

ATGTTTGGGT CTTCCTTAGC GTTAgCAATT TCAGATATTC CGTTTGATGG ACCAATTGCT 240

GGTGTTGACG TTGGTCGTAT TAATGGCGAA TATGTTTTAA ATCCAACGGT AGAACAAGCG 300

GAACAAACAG ATATTGAATT AACTGTTGCT GGAACAAAAG AAGCCATCAA TATGGTTGAA 360

AGTGGTGCCA AAGAAGTATC AGAAGAAGAT ATGTTAGGTG CCTTACTTTT CGGTTTTGAT 420

GCCATTAAAG AACTAGTGGC GTTCCAAGAA GAAATCGTTG CCGCTGTAGG TAAACCAAAG 480

ATGGACGTGG ACTTATTACA AGTGGACGCT GATCTTAAAA AAGAAATTTT TGATGCGTAC 540

TACAATACAA TGAAAACAGC CGTAATGACG GAAGAAAAAT TAGCACGTGA AGTTGAAATT 600

GACAAAGTAA AAGATACAGT CAAAGAAGTT TACGCTGAAA AATTTTCGGA ACACGAAGAA 660

GAAGCACAAT TACTAAAAGA AGTGAAACAA ATTGCGGAAG ATCTTGAAAA AGATGTCGTA 720

CGTGAGTTAA TCACGATCGA TAAGATTCGC CCGGATGGCC GTAAATTAGA CGAAATTCGT 780

CATTTATCAT CAGAAGTAAG TATTTTACCA CGTGTGCATG GTTCTGGCTT ATTTACTCGG 840

GGTCAAACAC AAGCTTTATC CGTTTGTACA TTAGCGCCTT TAGGGGAACA TCAAATTATC 900

GATGGGTTGG GTGTCCAAGA TAGCAAACGT TTCATCCATC ATTATAACTT CCCGCAATTC 960

TCTGTTGGTT CAACAGGACG CGCGGGCTCA CCAGGTCGTC GTGAAATCGG TCACGGTGCG 1020

TTAGGTGAAC GTGCCTTAGC ACAAATTATT CCATCAGAAG AAGACTTCCC TTACACAATC 1080

CGCTTAGTAG CAGAAGTGTT AGAATCAAAT GGTTCTTCTT CACAAGCAAG TATTTGCGCG 1140

GGAACATTAG CATTAATGGA TGCGGGTGTG CCAATTAAAG CGCCAGTTGC AGGTATTGCA 1200

ATGGGTCTTG TTAGTGATGG CGAAAACTAT ACAATCTTAA CAGATATTCA AGGTTTAGAA 1260

GACCACCTTG GCGATATGGA CTTTAAAGTA GCAGGAACGA AAGACGGAAT CACTGCTTTA 1320

CAAATGGACA TCAAAATCCA AGGAATTACA GAACAAATTT TAACGGAAGC ATTAGACCAA 1380

GCGAAGAAAG CACGGATGGA AATTCTAGAA GAATTAACAA CAACGATTGC TGCTCCTCGT 1440

GAAGAATTAA GTCAATATGC ACCGAAAATT GAAATGATTC AAATTAAACC AGCGAAAATT 1500

AAAGATGTCA TTGGTAAAGG TGGCGAAACA ATCAACAGCA TTATTGATGA AACCGGCGTT 1560

AAGATTGATA TCGATCAAGA CGGTAACGTA AGTATTGCTT CATCAGATGC TGAAATGATT 1620

AAAAAAGCCA TCAAGATTAT TGAAGAATTA ACCAAAGAAG TTGAAGTCGG TCAAGTTTAC 1680

TTAGCAAAAG TTGTCCGCAT TGAAAAATTT GGTGCGTTTG TTAACCTAAT TAAAGGCAAA 1740

GATGGCTTGA TCCATATTTC TCAATTAGCA AACGAACGTG TGAACAACGT TGAAGATGTC 1800

GTGAAATTAG GCGACGAAGT CCTTGTCAAA GTAACTGAAA TTGACAAACA AGGCCGTGTC 1860

AACGTGTCAA GAAAAGCGTT ATTAAACGAA GAAAACAAAG AAAAATAATT TCTTTTTAAA 1920

CCAACGAAAA CCAAGGAAGC TTCCTTTCTT TTCGTTGGTT TTTTCGTTGA AAACAAGCCC 1980

TAAAAAAGAA ATGATAAAAA AAGCTAAAGA CGATCGCCAA CTCTTTTGTT TATAGTCAAT 2040

TAGTGGTAAA ATTAATACTA TCAGTCTGAA GAATATCTGG GGTGTCTTTG TGAAAAAATT 2100

TAATCCAAAT AAAAATATAA TCATTACCTT AATTTAGTC ATTATTTTAG TAACCATTAT 2160

TAGTTTAACT GctGCGCAAC GTTCTGAAAA AGGCAAAACC AATGTCGTTC AAGGTGGCGT 2220

CAATAATAGC GTTAGTATGG TGGATCGTGT GATTTCTTTT CCAGCTCGTG TGGTGGAAAA 2280

CGGCTTGTCT TCAATGGGCA ATTTAATTAA CACGTTTAAA GAAAACGAAC GTCTAAAAGA 2340

AAAAATTGAT AGCTATAATG AATTAGCTGT CCAAAACAAT AACTATAAAC GTGAAATTGA 2400

TAGTTTAAAA CAAGAATTGA ATCTGAACGA AACGTTAGCC AACTATGAAA AAGTAACTGC 2460

GAATGTCATT ACGCGTTCGC CGGATACTTG GCAAGACTTA TTAATTATCG ATAAAGGAAC 2520

CAATGACGGC ATTGAAGCGG GCATGGCGGT CATGGCGCAA AAAGGGtTAG TGGGGCGTGT 2580

TATTGAAGTC AATGCAACGA CTGCAAAAGT GGAACTACTA ACGTCTAAAA ATGTTAACTC 2640

GAACCATTTC CCTGTGCGAG TAACTTCCGC AAATGGCGAA TCGTTTGGTT TACTTAAAAA 2700

TTACGACAAT AAGACGAATG CATTAATTGT GTCACAATTA ACTGGCGATG CCACTCTGAA 2760

AGAAGGCGAT GTCGTTCAGA CTTCTGGCTT AGGTGGTAAT TCCCCAGCCG ATTTAGCGGT 2820

AGGGACAGTT ATTAAAGTGA AACCAGATAG TTTTGGTTTA GATCGTGAAG TGTATGTGAA 2880

ACCTTATGCG GATGTCTATG GTATCTCCGT TGTGACGGTC GTGAAAAGAT CGGCAGGGGA 2940

AAGCGAATGA TTCGGAAAGA GTATTTAAAA TACGTCACAC CTATTCTCTT GTTTTTCTTA 3000

ATGTTAATTG ATGCTCATTT AACAAAGTCT TTTGAAACGT GGACAAGCAA TGTTTACTTC 3060

GCCAGTTCTC ATCTGTTATT ACTTGCGTTT ATGTTTGCCG TTCCTAATTT TTCTAAACGT 3120

TATTTATTAA TTACTTCGTT AATTTTAGGC TTTATTTGCG ATAGCTACTA CATTGGTATT 3180

ATCGGGATTT ATACAGTTGC ACTGACGATT TCGGTTATGT TGATGTATAC ATTTAAAGAA 3240

GTAATTCAAA CAAATTTACT AACTGGTTTT TTTGGGATCG TCATTTTTAC CACGTTGTAT 3300

GAACTGATTG CGGTACTGAT TCAAGTGGCC TTTCATTTAG CAGATGTCAG CCCGATTTTA 3360

TTTATTACGC GTGTGTTGGG CCCTACATTG CTATTGAACA TGGTGTGGTA TGTTATTTTA 3420

TCTTATCCAC TGAAAAAACT GTTTTCCGTA AAATAAAAAT TGAAAATTTT GTTCGTTTGC 3480

GAAAAATGCT CATTTGTTAG CATTTTTCGC TtTTTTTATT TTCTTTAAAT AACAAAACAA 3540

TGAGAAGCTT ACCCTGGAGA CTTGAAGAAA GTTGTGAAAA AAGTGAAGCT TTTTTTTGTC 3600

ATTTACAAGA AGAAAATTGA AATATTACTG TAACATCCAT ATTATCTCAG TGACATACAG 3660

CTATGCTACA ATTGCTCTAT CGTTGAAAAA GAGAAATTTA TTCAAATTTT AATAAATAAT 3720

AAAAAAGCTT AACAAAAAAG GATTTTCGGA GGACAACAGA TTGAAGAAAA GTGTATTATC 3780

GGCTCTAATG GTATGTTCCA TTACATTAAC AAGCGTAscG TTGCCATCCG CAGCATTTGC 3840

AGATGAATAC GATACAAAGA TTCAACAACA AGATCAAAAA ATTAATGCGT TAACTAGCCA 3900

AATGTCAGAT GCAGAAGCAA AAGTTGCCGC GATTGAAAAT GATATGGTTG AAACGGCCAA 3960

ACAAATCGAT ACATTAACAG CTAAAAAGAA CAAGCTATCA TCAGAAGTAT CTAAATTATA 4020

TAGTGAAATT TCTGATTTGA ATGTCCGTAT TCAAAAACGT GAAGTACAAA TGACAAAACA 4080

AGCACGCGAT GTCCAAGTGA ATGGTCAAAG TGATTCAATT ATTGATGCTG TCTTAGATGC 4140

AGATTCAGTA GCAGATGCAA TTGGTCGCGT TCAAGCGGTC TCAACAATGA TGAGCGCCAA 4200

TAATGAATTA CTAGAACAAC AAAAAGAAGA CAAAGCGACT GTTGAAAAGA AACAAAGAA 4260

TGTTGAAAAA CAAATTGCTG AATTAGAAGC AGCAACAAAA GAATTAAATG ATAAAACAGA 4320

ATCATTAAAA ACATTGAAGA TTCAACAAGA AGTGGCTAAA AATGATTTAG AAGCACAACG 4380

TTCTGAAGAA CAAGGGAAAA AAGACGGCTT CATTAAACAG AAAAAAGAAG CGGAAAAACG 4440

TTTAGCAGAA GAACAAGCAC GTCAACGTGC AGCTGCTAAA AAAGCAGAAG AACAAGCGGC 4500

AGCGCaAGCA CAAGCCGCAG CACAAAAAGC GGCAGCAGAG CAAGCGAAAG CAACAAAAGC 4560

AGCCAATGAG GCAGCAGCAT CCGCCGCTGA AGAAAAAGCC GCAACACCAG TAGTAGAATC 4620

ATCAACAACT ACTGAAAGTA CCACAACGCA AGAAACAACA ACTTCAAGTA CTGAAACAGA 4680

AAGTGTTGTA ACAACACCTG TGGCAGCAGC ACCTGAAAAA GAAAAAGAAG TTCCTGTAAC 4740

TAACCCAACG ACTCCTGAAA AAGGCAATGA AGCAAAACCA GGGAATGGTG GCGTGACTTC 4800

AGGAAAACAA GCCGCAATTA ATGCAGCTTT AGCAGATGTT GGTAATTCTT ATGCAACAGG 4860

TTGGAATCAA CCAGGCGAAT GTTTAGTATC TGTTCGTCGC TGGTTAGCGG CAGGCGGTAT 4920

TAACTTCGGT TATGGTGGTC CAAACAGTGG CTATGTTGCT TCTGGCGCAA CACAAGTTAG 4980

CTGGAGTAAC GTGCAACCAG GCGATGTTGT TCAATATGAA AGTGCCTATA GTCCAGATAG 5040

CTGGATTGGT GGCGTGCATA CTGTCTTGGT TACAGGTGTA AGTGGTGGAA GTGTTCAAAT 5100

CGTTGAAGCG AACAACCCAG GAGGTTCTGG TTATGTTTCT TCTAACTCTA ACTGGTCACC 5160

AGCACCACCA GCAGGATTCC GCGCTGTTGT ATGGCGTTTT CCAGGCTAAA TAGTCATCTA 5220

TTAATAATTG ATAACAAGGA GTGGTAACTA ACAAAAATCG TTAGTTGCCG CTTTTTTTAT 5280

TCATTTAATT TTAAATATAT GCATAAAATG TATCTGAAAA TATTGTAATC TGGCCGTTTT 5340

TTTGCAATTA TAGAGGTATA TACATATTAG GAGCGGAGGA ATCAGCATGA GCGGAACGCA 5400

CGATACAAAA CAAGCAATCG CTTCAGCTTT AATAGAATTA TGTGAACAAA AGGATTTTCG 5460

TAAAATAAGT GTCCAAGATA TTACCAAAAA AGTGGGCTTG AATCGTCAAA CATTTTATTA 5520

TCACTTTACA GATAAATATG ATTTATTACG TTGGATTTAT CGTCACGATG CATTGATTTA 5580

CTTAGAAACA GATATTTGTT TGGAAAACTG GGAGGAACAA GCCCtGAAGT TATTAAAAGC 5640

GATTAAAGAG AAGAGTCATT TTTACTATAC AACGGTGACC TCAGATTCAG AAGTTCTTCT 5700

TAATGTTTTT TCCGCTTCGA CCAATCGCTT ATTTATTTCA TTATTTGAAC AAGTCGATGT 5760

TGAGAACCAT TTAACAGATA AAGACAAACA ATTTTATGCG AATTTCTTTT CCTATGGATG 5820

TAGCGGCGTC TTAACGAAAT GGATTCTTGA GGAATATCCT CAAACTCCTT TGGAAATGGC 5880

GACGCAATTA TTCCGTTTAG CGAAAGATAC AGAATTTATG GCTTATCATT TGTATGAACA 5940

AGAAGCCAAT GAGTAATGTG TGAAGGATAA AAAGTTTTAT GAAGGAGTGA AACGtTGTGG 6000

TAACTGTGTT ATTTGTTTGT TTAGGCAATA TTTGTCGCTC GCCAATGGCA GAAGCGATTT 6060

TTCGTCAGAA AGTCCAACAA GCCGGTTTAG AATCGACTAT TCAAGTGTTT TCAGCAGCTA 6120

CTAGCCACTG GGAAGTTGGC AGTCAGCCAC ATAAGGGAAC CAGAAAAATT TTGGAGCAAC 6180

AAGGAATTTC CTATCAAGGA ATGCGGGCGA CACAAATCCA GCCAAGTGAT TTTAAAAAAT 6240

ATGACTATAT CATTGGGATG GATACGAATA ATGTGGCCGA TTTAAAAGCA TTAGCTCCTC 6300

AAGAAGAGCA ACCGCGGATT CATTTATTTA TGGAAGTTGT GGCTGGTAAA GAAACCATGG 6360

ACGTACCTGA TCCTTATTAT ACTGGAGATT TTGAGGAAAC TTACCGCTTA GTGGAAGCAG 6420

GTACCTCAGA ATGGTTGAAA AAAATAAAAG CACAGCTGAA AGATTAGGAC TATAGTCCGA 6480

TAGTACTTTC TGTTTCCCCT TGGTACAATA GTGTTAACAA ATTGTTCAGG GAAAAAGAGA 6540

CGGGAGGGAA GTAAGATGAA CAGTAGTTAT TTATCCTATG TTTTTGAATT GAGTTTGTAT 6600

TATTTATTGT TGATAATGAG TCTGCCGCTA GTGTATGCTG TCACGTATCA TTTATCTTTT 6660

AGTAGTATGT ATACAAGTGA ATGGTTAATA ATCTCTGTTT TCTTATCTCC GTTAGTTTTA 6720

TTATTTGCAG GTATTCGTTA TGGTTTTGCT CGTTTGAAAC AGCAAGAACG CCAAGTGATG 6780

AAATAAAGCA AAAAATCCTT GAAAAGTGTC AAAACTTTTC AAGGATTTTT TTATTAAGCC 6840

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ACCCAATCGG CTAAAGTTTT TTGCTCCAAT TGGAAAGCCT TCAACATATC GTCGTTGGCG    6900
TCTTTAATAG GCGTCGTTGC TGCTAATGTT CCTTGAACAG CAATTCGCGT CGTTGCTTGT    6960
AAATCGCCAC AGGTAATTAA GGTAATCATA TTTTGACCAG GAACGTCATC AATTAACTCA    7020
ACACGGGTTG GTTCGATTTT TTCTACAGAA GTTATTTTGT ATGTATAAAC AGTAGATAAA    7080
TCAGTGATAT AAATGAGTTC GTCTTTTTTG GTTCTTTCTA AAGGTGAAAA TAAGGAAACG    7140
CCATCTTCCG TTCGATGACT AGCCAAGGCA TAATTGTTTT TCCCCATGAC TTGATCTTCT    7200
TTCATGGTCC CGGCACCAGT TAATAAAGCG ACATTGGACA ATCCTTTAAA AATGGGcAAA    7260
TTAATTTCGA CACTTGGTAT CGCAATGGCA CCAATCACAG GTAAGTTTTT GTTTTCAAAT    7320
TGGGCTTTCA TCACCGCTTC TGTGCTCAAG GACTCAACTG AATCAAAGTC AAACGTTGTT    7380
TCACGAGCCA TATTTTTCTT CACATCAGCT GGTTTCAACT TGCTAACGGC GTACGAGCGG    7440
CTATTTTGTT GAACCACCCA ACTACGTATC TGATTGTTAA AAATTAAGGC TAAGCCAATG    7500
ATAAATAGTA AAACTAATAA ACTGTTGATT AACCAATTTT TTCCTCTTTT TTTCTCTTTT    7560
GGGCGCATAT TTTCCCTCCT TTTAATGTAT CAAGTTTACC ACAATTTATT TGAAAAACCT    7620
ATTTATTTTC TTTGGGGAAT AGGTAAGCTG GCCGGACCTT AATTTAATAA AAAACAACTG    7680
AATCGATTGA TTTTTCAAAA AAATCCTCAT TTTGTAATGG AATTTTAAAG TAAAAGAAAC    7740
AAGCTTTTCT TTTGAAAATA TTGTAAAATG GTAAGGAGGC TAGTAGAGGG GAGATGGGAA    7800
TTTGCTTGAT TTAATTTATG TACATATAGA TGTAACCAGC AACGCGGTTT TATCTAAAGG    7860
AATTACCCAT TCCGATTTTG TTCGTTCAAT TGTGCATCAT CCACAGAACT TACTATTATT    7920
AGATCCTTCT GCCGAAGCTG GCGAATACGA TATGCATTCA GGCTTGAAAA TTATTCGTGG    7980
AGAAGAAAGC GTCAATCGCT ATTTTCAATC GCTACAACGT CGTTGGATGA CTGAAGAGAT    8040
TAAATGGATT GACTTTTCCG ATGTGACGAT GCTAAAAGAG CTAACGCCAT TAGAAATTTC    8100
GGAACTTCTT TATTTTGGAC ACATGAAGAA TAGTTTGCAT TCGCCTTTCT TTTATAAGCT    8160
ACAAAATGAT TTTGTCTTTT TTGAATTTGC AGATCAGATG ACGCGTGTCT ATTATCGTTA    8220
TATTGATGAA TTTTATCGAA TCTTTGCTGA TAAAATTACA CGTGTTGTTT TAGAGAAAGT    8280
CAACCAGAAA AAGGCCTTCT TTAAACGAAA TACGCCTGTC GAAAAATTAA GTCCTGAATT    8340
ACTTAAAAAT ATGAAAGGTA TCTTGCAAGA AGGTGTTATT TTTTGCTTCC AACAAACGGA    8400
AGTGGATAAA GAAGAATATC GGATTCCTAT TTACTTGGTG GAAGATTCAC TTAGCAAGAT    8460
GAAAAATACC TCTTACCAAA AAGAAGAAAT TTTGGCAACG CTTGTCTATA ATAGTGAAAA    8520
ACGCATTTGG CACATTGAAC AAGAGAATGA TTTCGGTGAA ATTTTTATGT TGGCCCATGA    8580
AGGCTGAGAG AGCTCTAACT TTATCAACTA AAGTAGGGCT CTTTTTGTAG CTATGATTTG    8640
AATGAGAAAT CAAGTATAAT AAAATGATAA AAAGGAAAGA AGGTTGTTTA ATGAAAAAAA    8700
TACTCTATGG CGCTCTGACT GGTTTTGCCC TCTTTTTGGT AGCTGGCTGT ACACCCAAAA    8760
CGCCTACTGC TGTTTCATCA ACAAATGAAC AAAAAGAAAC aGCAATATCm ACTAGTGAAA    8820
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CmAGTTCATC CGTACAACaA GAaGCAaCGA cGACATCAGA GAGCCAGTGC GTAnTGGTCC 8880

CTTAGAAAAA GTACGCAGCT TTGGGAAAAT T 8911

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

AGTACGCCAT GAGCAGCCAC GTGAAAAAGG CATACAACCA CTGATACCTT TTAAAACTTT 60

TACTTCGGTT ACTTGACCCG AGCCATCCTC GCTAGCCCGA AGCCAAGCAT AAAGCCCTGT 120

AATGTCCATA ATAATATAGA AGCTTTGTAA AAGAACTTCC GCATATACCC GTGTCACTAA 180

CCCAAAATAG CCAATAATCA CTGCACTGAT TAACCCAAAA ATGTAATTGC TGACTTTTCC 240

TTGGGCAATT AAATTCACAC AAATGATGCC GGCTAAACCA CCTACTAACG TAATCCAATT 300

CGATGGATTG ATAGCGAACG CAACCAACTG TACCCCCACC ATCAAAGCTA AAAACAAGTA 360

ACTTCTCGTT TCCCAACCTT TAAAATCATT CACCAAAAAA TTCTTATTCA CGACAAATTT 420

CCGACCTTCC TAAAACCAAA CTTTTCTCTG TTGACGTCTC AATAAGAGTA CTCCGTTTTA 480

AAAAACAAGT CAATCAGATT TCGGAATAAA AAGAAGATTT TAATACTATA TATTGATTCG 540

AAAAATATCr AAACACTACA TATAGTTATT AAGCAAGCTT TCTGATATCC TTTATTGCCA 600

CAATATTTTC TTCATCTTGT TTTAATCTTC TATGTATTCA TGGATTTGTT TCCATCTAAT 660

AATTCCTGCA GCAGAACCCT TTACGACGGT AGCGCTTCAA ATTAATATTG CGAAAGCGGA 720

AGCAACCGCA CATATTTATA CkTCAAACAC AGCCATCGTT CACTCTTTTT ATTGAAATGC 780

TTAAAAATTG aTGGCCTTAT TTCTCGAATC TGGCCACTTA TTAACTTATT ACATGAAAAC 840

ATTCGCCTAA AAAAGCAAAA AAAAACGACT CACCTAAATA AtCGACCTAC AAACAATTCC 900

TkTCATTTGT AGGTCGATTA TCTTTATTAG GTTTGATACG GATGTTTCGC CATTCCTAGT 960

TTCCCTTTAC TGCTCATCTC TATTTATTTT TTTACTGTTT GCCAACAGCT CGTTGTCTGA 1020

AAGTACTATC CGTCCTTTTG TACTTtGTTC AAAGCTGTAA GCTkGCkCAA ATAACGTTTG 1080

cwCTTtATTG GcAGTTTGTG TAAAAGTCAG CCCATAAGGT TGTCCTTCAC TGTTTTTCGC 1140

CAAAGGAACA GTCAATTCAG GATATCCTGC CACAGCACTT AAACCCGTAC CTTCAGAATC 1200

AATAAAGGCA TATCCGTCTA ATtGTTGTTT TTTtAGCAAC GCATCAAACG TTTGCTGTGC 1260

TTTTTTAATG GTTGTTTGAa TGATTtCTTT ATCTGGTTGT TTCTTTTTAA CATCTGCTTC 1320

TAATAAATCT TGCCCATACT gGCACGAACC TTTTTATCTT GTTGATTATA CGCAATTAGT 1380

TCCTCCAGTG TTTTAAATGG TAAGTCATAA CGTTTCGCAA ATTCTTCCAT GCAAACTTAA 1440

ATTCATTGGA AATAACTTTC CCACCATCAA TCCCTTCCAT GTCTGGCGTT ACCGGAATCA 1500

CTTCTGCTCC TGCTTTTTGG AGGGCCTTTT TAGCAGCCGT AAATTCTTCT TCAGCACTTG 1560

GCATTTCTAG CAACCCAATG CGTTGACCTT GTAAGTTATT TTTAGTAAAT TTCGTTGAAT 1620

CAATGtCTCG GAACCGTGTC TTTCTTAAAC GCATTATAGC CTTgCGCAGC ATCAACGACA 1680

CTTCGGGCAA TCGGGCCAAC TGTATCTAAT GACGGTGCCA ATGGCAAAAC ACCTTCGCCA 1740

CTTACTGAAC TGTGGGTCGG TTTAAAACCA ACCACTGATT GATGAGAAGC GGGGGAAACA 1800

ATCGATCCCA TCGTCTCAGT GCCTAAAGAG AAGGCGCCGA TATTCATCGT CACACTAGCC 1860

CCACTCCCAG AACTTGAACC TGAAGGTGTT ATTTTGAGCG GCCCATAAGG ATTAAGTGTT 1920

TGTCCATGCT TGGAACTATA GCCACTTGGT GCTTTCATTG ACATATAATT CGCTAGTTCA 1980

GATAAGTTTA CTTTTCCTAA AATCAAAGCT TGCGCCTCTG TTAACTTCTT AACTACTTCC 2040

GCATCTTCCT TAGGCTTGAA CGTGCGTAAG GCATAAGCTC CTGCACTCGA AATCATGTTG 2100

GTCGTATTTA TATtTTCnTT CAAAGTCACA GGAATACCAT ACAAAGGCTT CTTCGGTGTT 2160

TGAGAGGCTT GCTGGTcAAA TGCCTTGGCT TCCTTAATTG CTTGCGGATT GATTTCAGAG 2220

ATGCTGTTCA TGCCaTTATC TATTTGATCG AACTGTAAAA TACGGTCCAA ATAAAACGCC 2280

GTAAGTTCTT CATAGGTCAA TGTTCCGTTG GCAATCGCTT GCTGTAATTC AGTGATATTT 2340

TTTTCAATAA TCAACGGTGC TTTGGTCCGA GCTTTTTGTA CATCTGTTTC TTTTAATTGG 2400

TCTTCAATCG TTTTAACGAT TCTCTCTTGA TTGTACATTG CTGGGGTTTC TGCCTCAGGA 2460

GTGAACTTTT TGAGTATAAA CCAATACGCT GCAGCGCCTA TTATGACTAA CAAAACAGCA 2520

ATTATTCCGA TTA 2533

(2) INFORMATION FOR SEQ ID NO: 653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

AAACACTGTG GGTGAAAAAT GGCCATCACG TGTTCTGGGT ACTTTTAATT CTAGCGTGCC 60

TACACGTGTC GTAAAGCTGC GCTCATAATA GCCATTTCGT TGACTTTGTC GGTTTTCTGT 120

TCGTTCATAT TCTTTTGCTT GAATATATTC TGTTCGTTGA TTTTCCATTA GTTGATTAAA 180

TACCGTTGTT AAAATATTTT TAGAAACGTC ATCCTTTACm GAATATTCAA TAATGCTTTG 240

AATCTCTTCG CTTTTCAGTG TAAAATGTAc TTGGGTCATG TAAAAGTCCT CCTGGGTATG 300

TTTTTGTCGT TAAAAACATT GTACCGTAAA AGGACTGTTA TATGGCCTTT TTACTTTtAC 360

ACAATTATAC GGACTTTATC AATATTTGCC TAATATAAAT ATTTAAGTTC GCTCTAAACA 420

CTAATTCTCC AGTTGATCTA TTACTAAAAT ACATTAGTGG CATACTAAAA AGTTTATCAA 480

TATAAGAAAA CATTAATTTA AAAtCAAaTT CATACTGAAa TTCTGCTACT ACAGAGCTTT 540

TTAAGTATTG AACTACATAT AAAACAGAAA AAAAACTAGT TAATATTAAT AACAGAACAT 600

AGGTAGGAAT TTCTTGAAAA GATCTAATAT TATCTATCGA ATACTTTGTT GCAATAGGAA 660

TTAAGAGTAA TAAAAGTTGT GAAACAAATG ATAATATTAT TAAACTAAAG AAATATCTTT 720

TGAATTTTGT AAAAATAAAT GACTTTAAAA AAAACTGTTT CCTTTTGCCT TCTTTTTTAG 780

TCTTTTTCTT ATGTGCGTAT ATTAATATAT TTGAAAAATT TTTTTTGAAT TCTGAAATAT 840

CAATCCAGCG TTTATTACTT GCAGGATCTA AGATTAATAC TTTCTTCTTT TTTATTTTCT 900

CTATGACCAC AAAATGTTGA TTATTCCAAT AACTTATTAC AGGAGTCGGA AGATCTAAAT 960

AATTTGAAAA ACTTGATTTA AATGTCGATA CATCAAATCC ATATTCGTCA AAGACAGTAC 1020

GAATATTCTT GATAGTTAGT CCTCCTTTGG GCACCCCATA TTTTTCCCTT AGTTCTACTA 1080

GTGTACTTTG ATTACCATAA TAATTAAGTA GCATAGTGAT ACATGCCAAA GCACATTCAC 1140

TATGCTCTCC TTGCGCAACG TACTTCAATC TTTTCATAAT TACACCTCTT ATAACTCAAA 1200

AAGTAATGCA TTCGGAATTT CAGAATCTAG GTTTCTCAAT AATTCATAAC CCACACCACT 1260

GATTCCTACA AAGAATCCTA GTGATTCTAA ATACTCACTT cCGGCAACCT TTAGTGTATT 1320

AtTTTTTTCa AAATCaTTTA gCATATAGCT AATAAGTTTA TTTTTTTTAT ACTGATAAGT 1380

TTCAGGATCT TTTTTAGCTA ATTGAATTAG CCCTTCTAAA GTACCTGCAT TTCCATGGCA 1440

CAGACAA 1447

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

TATGAAACAC GAACATTATA TCGAnTATAT ATATAATAGT TAATATTTTG TTGTAAAAAG 60

ATAGCGATTC TCTTATAATC AAGAGTATTA TTCGAAAACT GGATTTTAAG GGAGAGAAGT 120

GCAATTATGA ATACGTTTTT CAAATTAAaG GAAAACAaGA CAACGGTATC AACTGAAATA 180

ATGGCGGGGG TCACGACCTT TTTTGCAATG AGTTATATTT TATTTGTTAA TCCGTCCATT 240

CTTTCAGAAA CAGGGATGCC TTTTCAGGCT GTTTTTTTAG CGACCATTAT TGCTTCAATC 300

ATCGGTACAT TAATCATGGG GCTGTTTGCT AATGTACCTT ACGCTCAAGC ACCAGGGATG 360

GGACTCAATG CTTTCTTCAC GTTTACGGTC GTTTTTGGGA TGGGGTATAC ATGGCAACAA 420

GCATTAGCAA TGGTTTTTAT TTGTGGTTTG ATTAATATTT TGATTACAGT GACAAAAATT 480

CGCAAAATGA TTATTAAAGC AATTCCAGAG AGTTTACAAC ATGCTATTGG TGGTGGGATT 540

GGAATTTTTG TCnCTTATGT AGGGTTGAAA AATGCTGGCT T 581

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

TTTTATCATA GATCGGAGGT TATGAGGATG AAGTTAGATA TGGTCGGTAT TATCGTCAAC 60

GATATGACAC AAGCACTCTC TTTTTACCAA ACGCTAGGTT TTAACGTGCT GGAAGAAGCT 120

TCGCCTGATT ACACAGAATT ACAAAACAAT GGCGTCAGGA TTTCTTTAAA TTCACTACAA 180

ATGATTACTG GTGTCTATGG GTTTGCGCCT AGCCAGCAAG GCGATAAAAT CGAACTTGCT 240

TTTCTTTGTG AAcGGCCGCA GAAGTTGATA ACACCGTGAA AAAAATGAGC CAAGCTGGTT 300

ACATTGTTTT TAAAGAACCT TGGAATGCAC CTTGGGGCCA ACGATACGCA ATCATTAAAG 360

ACGTGGATGC AAATTTAATT TCACTCTTTG CCCCTCTATA ATATTACTAA nAmATGCGCC 420

ACTTTCGTTT CTTTTACTCT CTTTCGgAAA GATTAGTGCA GAATGGGtCT TAAGTAGGaT 480

GTCyTTTCtG tCyCtTTTTT TTGGTATAAT GAACCTTATC CAATGGATGG GGn 533

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1061 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

GCACAAGCAA ATGACATTTG AAGAAGTATT GCCACAGATT AAAGCAGGAA AAAAAGCCGT 60

ACGTAAAGGC TGGAGCGGTT TTGAACTTTT TATTGAATTA CGTGATGAAA TTGGCACCTC 120

CGAAnGTGAA TTTTTACAAG TTACCCCGTA TTTTTTAATC AAAACTTCTG ATGAAGGCTA 180

CAGCATGTTT TCACCAACAC CCTGTGATGT CTTAGCAGAA GATTGGGTGA TTGTTGAAGC 240

ATAACTACAC GCATAAGGTC TGGCAGATTA CGGCGATTGC TCGTTCTTCC AGACCTTAAT 300

TTTATAAATG TTTAAAGGAG TTTTTCTTAT GCCAAAAGAA TTTGAAACAA AACGGGTGCT 360

TGTAACCGGT GCAGCTTCAG GGaTTGGCCA AGCACAAGCA ATTGCCTTTG CTGAGCAAGG 420

TGCTGAAGTT ATTGGCATCG ACCTAGACGA AACGGGGTTA AAGCAGACAG CCGCACTGGT 480

TGACCCAGAT TCTGCTAAGT CGTTTACTTA TTTTGTCGGT GATGTGTCTT CTCCCTCATT 540

TGTGCAAGCC ACGATGAAAC AAATTGTGAA AAACAACGGC CAAATTGATA TTTTATTAAA 600

TACGGCAGGT ATTTTAGATG ATTATCGCCC TTCTCTAGAA ACTTCAGAAG CTTTATGGGA 660

TCAAATTTTA GCAACCAATT TAAAAAGTGT CTTTTTAGTG ACCAATGCCA TATTACCTTA 720

TTTCCTCCAA CAAAAAAAAG GAGTAATCGT TAATATGGCA TCTATCGCTG GCTTAGTAGC 780

TGGGGGCGGC GGCGCAsGTA gcACTGCCTC CAAACACGCA ATCaTCGGGT ATACAAAACA 840

ACTTTCCTAC GATTATGCCA AATTAGGCAT TCGAGCAAAT GCGATTGCGC CAGGTGCCAT 900

CCArAcACCC ATGAACGCAG CTGATTTTGg CAGGAGAAGG TGAAATGGCT GCyTGGGtAG 960

CACGTGaAcA CCCGCGGGCC GTTGGGCACA GCCACAAGAG GTAGCnAAAC TTTCnTTATT 1020

TCTAGCTAGT GnTGACGCTG ATTATATCCA TGGCACAGTT A 1061

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

GAACAGCCGC AATGTGTCAA GACACATAAA AGAACTTTCT GTTATTTCTC ATAAATAACA 60

GAAAGTTCTT TTTTATACTG GTTTATTTTT TTCTAAAGCA TTACTTAAAC GAGCGAATTC 120

TTCTAAAGAC AATGTTTCAC CACGTCTAGA AGGATCAATT TCTGCTTCAG CTAGGCTCTC 180

TTTTAGCCAA GCCACCGTTT GTTCATCTTT CCCATAAAAA TGCGTTAAGT TATTCCACAA 240

TGTTTTACGT CTTAATTGGA AACTGGCTTT GGTTAATTTG AAAAATTCTT TTTCATTGGT 300

CACTGTCACT GCTGGTGTAG CACGGCGCGT CAATTTAATA ATCGCCGAGT CAACATTGGG 360

cTGCGGCACA AAAACTGTTT TTGgGCACAA TAAAGGCGAC ACTTGcTTCC ATAAAATATT 420

GGACAGCAAT TGaTAATGAG CCATAAGCTT TCGTTCCTGG TTtAGCAGCA ATTCGATCAG 480

CGACCTCT 488

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

TAAAGGnGTT ATTTTAACGG ATACTTTTTA CAATTATTCG GAGCAAGTGT AGCCAATATT 60

CCnGGAAGGC TTTCAACAAA TGnCnCTGTC ATTACCAGAT ACCGTCTTGG CCTTTTTGCC 120

CAGCTTTGAT TGTTTGGTCT ACCTTTAAAG CATTTAATGC GACGCCTGTA ATCGGGATTG 180

TTATTGGTTT AATGATGGTA TCACCCATTT TACCAAACGC TTATGCAGTT GCAACACCAG 240

ATTCTGGCGT GAAAGCTATT ATGGCTTTTG GTTTTATCCC AGTTGTCGGT GCACAAGGGT 300

CCGTTTTAAG TGCAATTGCT GCTGGTATAA TTGGCGCAAA GATTGAACTT TTTTTCCGAA 360

AAAAGATGCC GAATATTCTT GATCAAATTT TTACACCCTT TATGACTATG TTAATTACTT 420

TTTTAATCAT GATTCTCGGA ATTGGCCCAA TTTTGCATAC CGTTGAGTTA GGCATGGTAG 480

ATGTTGTCCA ATGGTTGATT GGGTTGCCCT TAGGATTAGG TGGTTTCGTG ATTGGTGCCT 540

CATATCCTTT AATGGTTTTG ATTGGTATTC ATCATACACT AACTATGGTA GAAACATCAT 600

TATTAGCAAA TACAGGATTT AATGCATTGA TTACAATATG TGCCATGTAt GGGTTTGCCA 660

ACGTTGGCAG TTGTTTAGCC TTTGCGAAAA AAgCGCAAGA TAGCAAAGTG AAGTCGACAG 720

CCATTGGTTC TATGTTGTCT CAATTATTTG GAGTTAGTGA GCCTGTGTTA TTTGGATTAC 780

TTATTCGTTG GAACTTAAAA CCGCTGCTAT GTGTCTTGTT TACATCAGGT TTAGGCGGAG 840

CAATTTTAgC TATTTTTCAT ATTCAATCAA ATTCTTAkGG CTTAGCCGTT ATTCCTTCTk 900

TCTTAATGTA TmTCTATAGT GCACATCAAT TAGTGATCTA TTTATTAGTC GCACTTTTAT 960

CTGTCGGTGT ATGTTATGCA TTAACCAGTC TATTTGCAAT TCCGCAAGAA GTTTTGATTT 1020

CAGATaAAGT AATCGAAGAG GAAGAACGCG AAGTCTTTGA AATGCAACAC AATACCTTAG 1080

ATGAACAACT TTTTTCTCCG GTAACTGGTT ACGCCATGAA TCTTACTGCT GTTAATGACC 1140

CAGTATTTTC AAGCGAGATG ATGGGCAAAG GTTTAGCAAT CATGCCAACA GCGAACAAGG 1200

TTTACGCGCC TGCAGATGGT TTATTAAACT TGGTTGCAGA AACTGGGCAC GCTTATGGTA 1260

TCCAAACGGA CGCAGGAGCT GAAGTATTAA TTCATATAGG AATTGATACT GTCACATTGG 1320

GACAGGAGGT CTTTCAGACA CAAGTAACCC AAGGTCATCG TGtTAAAAAA GGAGATCTTT 1380

TAGGAACGTT CGATCGAAAA gCCATTAAAG AAGCTGGGCT TGACTCAACT GTCATGGTTA 1440

TCATTACAAA TACTTCAAGT TATTTAAGCG TAGAGCCAAT GATGTCAGAT CATAATGAAA 1500

TTACGCCGGA ACAAATCATT TTAAATCTAA ATACACCTAA CTAAACAAAA GArCAGCAAG 1560

AAGTAGTTAT CACTTCTTGC TGTTCTTTTT CTTAATAAAA AACCAATGAT TTTCGGTTGT 1620

ATTTGTCTAT CCGTTTGTAG TATGATTGAG TCAGTTTTAA AGGAAACATG CCAAGTATGG 1680

AAGACCATAC TTGACACGCA TTGACTAATT AAACATGGGG AACGTTGCCA TAAGTTGATG 1740

TTCCAGTCAA TAATGCAAGT AAATCmAACc ATAGCATGTA CCTCCTTTAA TTGATAATCA 1800

AAGTATAACC ATTTTGnAAT GGAATTTACC ATAGATAATA CCAAGTGGAG GTCTGTnCGT 1860

GGAAGGAGnC AGGAGGCCAG AAATTAAACC AAGCCGGGGA AAnCTT 1906

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

GGCTGAAAAG GGGTGGCTTC AnCCCAAAAA CTTTTTTGGG CTTCCGCnAA CGACCGCTGG 60

TGGGTCAAGT CACnGCTGGT GGACTTGayC CAAgCACCTT GtTTtGAtCG ACCACTGCTt 120

GgTTGGTCTT tAAaCAGATt GgAtCAATGG TGtCTTTTtC TTTTTTCGCA GTGTCAGCAA 180

CTTGTTGTTT TTGATCGACA ATTGCTTGTT TCTCTGTTAC TTGTTGCTGT TTTTCAGTAA 240

TGGCTTGCTC CGTTGTTTCT GTAGCTTTCA CTGCTGGTTG TTCTGTAGAA CTGTTTTCAG 300

GTGTTTTTGG TTGCGCTTGT TCTGCTgCCt GTACTTCATT TCCCCCAATA CCTGCTACCC 360

CCGTTGCGAC TAAAATACTT AACCCTGCAC TTGCGATCTT TTTCATTTTA TTTTCCTCAC 420

TTCCGATTAT TTTTGTTGTA AATGGGATAC CCATtGTCTT TACGCCATtG TTGTAACGCT 480

GTAGTTGTTA TATGGAACTC TTCCGCTATT TCTTTAAACT GTAAGCCCAT TTTTTGATAG 540

GCTTCAAATC TTTCCTTGCT AATATGCGAA GAAAATTGTC TGGTGTTTGC TGTTTCTATC 600

TTTCTTGCAA GTTCTTGTAT TCGTTTAAAA CGCTCGGTAT CTTCATTCCT ATACCAGTCT 660

GCGTCTTCAT TCATTAATGC CAACATTTCT TTACGCCATA TTTTTATTAA TTTTTTAGTC 720

ATACCCCTTT CACCTCAAAT TAACAATAAC AAAATAATAT TTATTATGAA AATAGTAACC 780

TTTTAGAGAA AATAAAAAAT GTCTTTTACA TGACAATTAT TAAATGCCAT AAACAACATT 840

ATCTTTAATT TCAAATTCAA ACCATTCTGA AAAATCTTGT TTAAATCCAT TGACGCTATA 900

TTTTTCTTGT AAAACTACTT CTTCCGCATT CGCAGGGTCT AAATAGGTCG GTTTATCTTT 960

TGGACGCGCA TAAACACCTA CCCAACTTGT AAAATCCCCC TCAAAAGCAC CATCAATTTC 1020

ATAACCAACT TCTTCTAGCT TCTGACGAAC TTGTTTCTTT ATATCAATAA TATCTTTAGG 1080

aATATAATTT TGaTACTTTT CTTGAAATTC CTTAAAAGCT AATACTTCTt TACCATAGAA 1140

CCTTTTTATn 1150

(2) INFORMATION FOR SEQ ID NO: 660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

TCnGATTnTC TTATTATTAA CGTAGTGGCT TATTCTAnTA TCCCCAAAAT CCCCACTGTG 60

TATTTAATCT AATCTtAAAC TGATTTTCCC ACGAAAGTTT TATAAaCCCA AATATTAATG 120

ACTCTGGTCT AcTTTATTAA ATAATCCAAA AGCTAAATGA CCTAACTCAT GTACAAAGAT 180

AGACAATAAT AAGGCAAAGT ATGCTATAGA TACTAAATTT AATTCAAAAA CAAGAGTAAA 240

GATTACGAGA AGTAACGTAA AGATCATCGG AGATATAAAT TTCATCTATT TTATTCTCAC 300

CTCTTTGTAT TTAAGCATGC TATTTTTATC TATAAAAGAA ACAGCATTTT ACAATATTTC 360

TATATGATCT AGTTTCAACT TCTATATTTG TTTCTAATGC TGTAAAACCA ATCCCAATCA 420

TGCCTCAAAT AACTAAACTT TTAACTAACT TCTTTTTCAT TAGTATTCAT CTCGAAAATA 480

AAAATTAGAA AACGTCTTCC ACGCAAGAAT TGTAGCTCCA TTGATCTAGT TTTGTAAACA 540

TTGAGACAAA GGTTTCTATC TAACAATTTT GTAAGTTGGT GCCCTTCGAA TTTGATTAAA 600

TTAGATTTTA TTCCGTTTTA TTTCAAGGTA AGTATTAATA CAAGTTTTAA TTTTTATAAA 660

AAAATGAATC TTACCATAGA GATTTACTAA CTAATTATTT ATACTTTTTA TAATAGATTG 720

GAGGTTACTA TATGAGGGAA AAGTTATTAA TAGGGAGTTT TTGGTTATCA TTCTTTAATA 780

TTGTTTGTAA AATTCTCGGA TTCATTTATC TAATACCTtG GCTAAAATTT ATGGGrACTA 840

TCCACAATCA ACAAACTGCT CAAGCTATTT ATAATGTTGC ATACTTACCT TATGCTTTAT 900

TCTTATCACT TGGTACAGCT GGATTTCCTA GTGGCATTGC TAAAAAAATT GCTGAATTAA 960

ATATTAATGG AAATAAAAAC CAAATAAAAG AATTGTTCAA AAGTGGCTTG ATAGTTATGG 1020

AAATAATAGG GATTCTCTCT GCTTTAnTAA TGTTTATTTT TGCTCCTACA TTAAGTAAAA 1080

TAAGTCCAAT AGTTGATCAT ACTGCGGGTA TCACAGCAAT CCGTAGCCTT TGTTTTTCTn 1140

TATTAATTAT TCCTAnACTT AGCGCACTAA GAGGG 1175

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 965 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

TAGTCCAAAC CCCCTTTTAT ATAGGGCCAG GCGCCTTAGG CTATCCACTA ACnAnAAAAT 60

CGGATnTCTG CCCCCTTAAT CATTGGTTTT CCCCCCCGTC AAAGCTACTA ACTGTTGATT 120

AATTTTnTTA ATCTTTTGCT CCTCCCATTT GAATTAAATG TCGCGATTGA TCTCGTTTTC 180

TTAACAAAAT AGTTTCCaAA AAAGAAGCAT CCTTAAGTTT TCTCAAAGTT TCCGCCATCT 240

CTTCAACTTT AAACCCTGAA TCTCTTAACA GTAAAATTTG TTTCAATAAA GGAATTTGAT 300

GTGCGCTATA ATAGCGATAT CCTGTTTTTT TATCAATTTC ATTTGGAACA AAAATTCCTG 360

CTTTTTCATA ATGACGCAGC ATCCGTGGGG AAATATCCAT TAACTTGGCA AATTGCCCAA 420

TTTGATACAT AGAGTCTCCT TTTCATTCAA TTGATATTCT TATCATAAAC CTTGACACCA 480

TGTGAAAGTC AATGAAAAAG TTTCTATTCA TACATTTCTA TTTTATTTGA ATATTCCCGT 540

GATCTTTCTC TAGTTATTCA GAAGTATATT GAGGGGTGAA ATTTTGGAAT TAAAAAAAAC 600

GATTTCCAAC AAAATAATGA TTATTTTAAT TGCAATTATC GTTGCAATCT TTGCAATGGG 660

ATGGATTCTA CCTATTGGCA TCGATAAAGT AACTAGGTTA AGTTACCGAG AATACTTATT 720

TAGTACATAT ACTGTATTTA CACAATTTGG CTTTCTAATG TTTTCGTTTC TAGTCTCTTT 780

CTTTATTAAT AAAGAGTACT CAGGAAAAAC AATTTTATTT TATCGTATGA TGAATACCAA 840

TAGCCTTACT TTTTATATAA AAAAAGTTTT GACACTTACG GTAGAGACCC TAGGCAGTAT 900

TCTAGTTCTG TTATTTATCG TTTCCTTTAT TTTTATGGAT TTTTCTGTAA TcTGCAAATG 960

TTTTT 965

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1610 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

ATGTAACAGT TTACAACGAA GAATAAGAAG ACTATnATTA TGTTAACTAT TTTTAGGTGT 60

GCCTAAAAGT GAAATGTGTG AACAAGATAG ATTGAGGGAT GTTGGATGAA AGAACAGAAA 120

ACGGaAAAAA TGCTTAATTA TGCAAATGGA CCTAGTTTAG AAGAGATAAA TAATACCGTC 180

GAGGTACCTA AAAACGCAAG CTTTTGGCGA ACTTTGTTAG CCTATAGCGG ACCTGGCGCT 240

TTAGTGGCTG TTGGTTATAT GGATCCAGGA AATTGGATTA CGTCAATTGC TGGCGGAgCG 300

GAATATAAGT ACACGTTACT TAGTGTGATT TTGCTTTCTA GTTTAGTTnC CnGGGGAnTA 360

CAAAGTATGG CTGCGCGCTT AGGAATCGTG ACAGGAATGG ATTTAGCTCA AGCGACTAGA 420

GAGCATACAA GTAAACGAAC GGGCGTTGCC TTGTGGGTGG TGACGGAGTT AGCCATAATG 480

GCTACAGATA TCGCTGAGGT AATTGGTGGT GCCGTTGCTT TGCAATTATT ATTTGGTTTT 540

CCATTATTAA TTGGTGTGTT GATAACAACG TTTGATGTTT TATTACTGnT GCTACTGACA 600

AAGTTAgGCT TTCsCaAAAT CGAAGCAAwT GtTTCTTGTT TAATTGCAGT CATCTTTTTT 660

GTTTTTGCTT ATGAAGTGGC ATTAGCAGAT CCAAATGTTG GTGAAGTATT ACGAGGTTTT 720

ATTCCAGACA CAAAAATAGC GACAGATAAA TCCATGTTAT TTTTAGCCTT GGGGATCGTT 780

GGAGCGACAG TCATGCCCCA TAACTTATAT TTGCATTCTT CCATTGCGCA ACACGGAAAa 840

TTTGATCGTA ACGATGATGT TGAGAAAGCC AAAGCAATTC GTTTCACTAC TTGGGATTCA 900

AATATTCAAT TAACTGTTGC TTTCGTCGTA AATTGTTTGT TGTTAATTTT AGGAGGAGCA 960

TTATTTTATG GAACCAACAG TGAATTAGGT AAATTTGTTG ATTTATTTGA TGCTCTGAAA 1020

AATCCAGATA TTGTTGGTAA TATTGCTAGC CCAGTGTTAA GTATTCTTTT TGCAATTGCT 1080

TTACTGGCTT CGGGTCAAAA TTCAACGATT ACAGGTACGC TGTCAGGACA AATTGTAATG 1140

GAAGGCTTtA TCCATTTAAA AATGCCGTTG TGGGCACGAC GAGTGTTAAC TCGTTTGTTA 1200

GCAATTGTGC CAGTCATTAT CTGTGTCATT ATTTATGGCG GTAGCGAAAC GGCTGTTGAA 1260

GACtTGTTAC TTTATACGCA AGTTTTCCTA AGTATTGCTT TgCCAGTGTC GATTATTCCT 1320

TTAACGATGT ATACAAGTGA TAAAAAATTA ATGGGCCAAT TTGCGAATCC AGCGTGGGTG 1380

AAATTTTTAG CTTGGATTAT TGCTATTGCC TTGACGTTAT TGAATTTATT TTTAATTTAT 1440

GGCACATTAA CTGGTTTAAC GAATTAATAA AAACAAAGgC TGACTAGAAA AGTTAGCCTT 1500

TgTTTTTTCA TAGAATTTGC GCGTAAGAAA TGGTAGAATA GGAAAGATGA AATACAAGGA 1560

AGAGAGGCTT TCACGTGACA GATTATTTAA ATGTAGGAAA AATTGTGAAC 1610

(2) INFORMATION FOR SEQ ID NO: 663:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

AAATTTAGGT GGTGGCGGTC ACTTTACTAA TGCGGCAGaC AATTATCAAA CGTAmCAGTA 60

GCAGAAGTAA AAGAGCAACT ACTTGATGTA ATTCGTCAAA ATATTAATGA AATGTATGAA 120

CAGGAGTGAA GGAAATGAAA GTCATTTTTT TACAAGACGT TAAAGGAAAA GGAAAAAAAG 180

GGGACGTAAA AGAAGTGCCA ACTGGTTACG CCCAAAACTT TTTAATTAAA AATGGTTATG 240

CGAAAGAAGC CAATAAAGGG AGCATGAGTG CGTTAgcGGG TCAAAAGAAA GCCCAAGAAA 300

AACATGAAGC AGAAGTTTTA GCACAAGCAA AAGAAATGCA AGCCTTTTTA GAAGATGAAA 360

AGACTGTTGT AGAAATCAAG GCAAAAGCTG GAGAAGACAG CCGTTTATTT GGCTCAATTC 420

CTTCAAAACA AATTGCAGAA GCCTTAAACA AACAATACAA TGTAAAATTG GATAAACGCA 480

AAATCGAATT AGCCAACCCA ATTCGTTCTC TAGGTTACAC TAACGTACCA GTCAAACTAC 540

ATCATGAAGT TACAGCGAAA ATTAAGGTTC ATGTCGTAGC GGAATAATAC AATCGATAAA 600

AAAGAAGCCG ATTTCTCCGG CTTCTTTTTT ATGCAAAATA AATTACTAGA ATTATTTTTT 660

ATAATATTTA AAAATCAAAT ATACAACAAT TTAAATTAAC GAAAGTATTA TATTTTTATT 720

AATTGTATAT TTTTAAAAAT TGGAAAGTGA ACTAAAAATA GAGAAATCAG CAGAGAAAAA 780

ATGTACTTTT TTAATGAAAT TGTGTTAAAA TGGATAGACT AAACGAACCA GAAAGTAAGA 840

CATCGTGGGA GAGAaCAAAA TGAATGAATT ATTGCAAGAT AGGGTACCGC CACAAAATAT 900

TGAAGCGGAA CAAGCCGTTT TAGGTTCTAT TTTCTTAGAT GCAGATGTGC TAATAGAAGC 960

GATGGAATAT GTGGAACCTA AAGATTTCTA TCGTCGTAGT CATCAGTTGA TTTTCCAAAC 1020

GATGATGAC 1029

(2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

CTTTCTCAGA AAGAGAAATA TGATAAAAGG AGTTGTTCAT ATGGACTATG CTAAACTAGC 60

TTCCGACATA ATTCTAGCAG TTGGAAAAGA TAATCTTATC GCTGCTGCAC ACTGTGCAAC 120

ACGTCTTCGT CTCGTACTAA AGGATAATAC AAAAGTTAAT CAAAAAGCTT TGGATGAAAA 180

CCCAAATGTA AAAGGTACCT TTAAAATTGA TGGTCAGTAT CAGGTTATTA TTGGTGCTGG 240

TGACGTTAAT TTTGTCTATG ATGAACTTAT AAAAAAAACT GGCCTTTCAG AGCTTTCAAC 300

AGACGACTTG AAACAAATAG TTGATAAAAA TAAAAAATTC AATCCAATTA TGGcATTAAT 360

TAAACTACTA TCAGAAATTT TCGTACCAAT TATTCCTGcA CTTGTTGCaG GTGGtTTATT 420

AAkGGCTCTA CGAAATTTTT TAACTGCCGC GGGtCTTTTk GGACCAAAAT CaATCGrAGa 480

AAgTATCCTG cAATTAAAGG AATTTCCTCT ATGATTCAGC TTATGTCAGC TGCACCATTT 540

ATGGTTTTTA CCATTCTAGT TGGTATT 567

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

TTTCCGTTTT CTGCAGTGAT GAAGCCAAAG CCTTTGTCTG AGTTAAACCA TTTTaCTGTA 60

CCTGTTTCCA TAATAAATAT CCTCCTAGAT GTGTGTTATA ACACATTCAT ATTTTGCAAT 120

TACTTGAAAG GTGAAAAATG TGGAAGATGT TTATTTGAAA CAGCTACCCA TATTACCGAA 180

CAAAAACTAC ATCTATTACT ATAGCATACT AACTGGTTTT TGTATAGCGA TAACCTTATT 240

TTCTTTTTTA TCGGATGTTT TTTAAAAACT AGAAAGTGAA GATAAGGCTG TTATAGTGCT 300

GTTTCAATAA GGCTCAGAAA AAAAGCCCAT TGTAAGGCGC TTTCTTACAA TGGGCTTTTT 360

GCCTGTTTTT AATAACGGAG GATAGCCGCT AAAGATTTTT CATCTGGTGC AGCTTTTTGG 420

TCTAAAACAA AAACTTGACC GCCGTTTTGA ATGACTTGGT AAGCAATGGT GTTTAAAAGT 480

TTGCGACGAT CATACTCTTC AGATGACATT TCATTGTTTT CAGTAACAAA GAGTGACGTT 540

GCAATAAAAA GATGGGAAAT TTTGCCGTCA GCTGCCGCTG GCGAAATATC TGTAAATTGA 600

TCTAAGAATT TACGATCTAG TAATTTGTTA TAAGAAGCTG TTTCTTTTTC TGTTAACTCT 660

GCAGCTATTT TTTCACTAGC GCtGCGGATA TCTkGAATGG TTGCTTGTGC AGGTGAAGCA 720

GCAACTGAAA TTGAGCAATC ATAATAAGGA TTTTTAGCAA TCTTTTTAAA GAGTGTTTGG 780

TTTTCTGGTA AAgCATAAAG ATAAAGCGGT AATTTTTCAG GATTATCCAG TTGATCTTTT 840

AAGAAAGTAT CGACTGCTTG ATAGTAGTTC ACCCAATCAA TTTCAACTTC TTTATCTTTA 900

GTATTGATGC TATGATAAGC GACACCTTCT TTAGAACCGT TAGAACTACC TTGAGTTGAA 960

AAGTTTAAAT TACCACCCGT TAATTCATCA CCTAAAGCTG TGACCACGTC TGTTGGCGCG 1020

TCTTTAGGCA ATTCAACAGG AGTCACAGTC GTATGATCAA CCTTGTAAAG TTTCATTGAA 1080

TCGCGATTTA GAGCAAGTAG GTAATAATGG TAGTTAAATT GTTTGTCTTT GACTAGTCCA 1140

AGTAAATAAG GAATCGTGTC CACGTAATAT TGATCGTCAA CGGGCACATC TAATCGTTGA 1200

ACAAAGGTGT TTTCTGGAGA TAAGATGATT GAAACACTTG CTGTGCCGTT GCGCCAGAAG 1260

GAAGCATCAG CTAGAAGTGC GTCAATTTTT TCTTGGAAAA CAGACCATTT TTCCTCAGGA 1320

AATTTTTTTT CAAAGCGTGT TTTTGCCGCT TTTGCAAAAT TTTTCAAAAC AAGCGAATCT 1380

TTTTCTACGT TTTgATGAGC GACATGGGTG TTAAACAAGA AAGTAACAAA CGGTCCATGA 1440

aCTTCTTCAG AAAATAATGT TGATAAGCTA TCTTTTTTTT GATTTGCCAT AATAAAATCC 1500

CCCTTCTAAA AGTAAGTGTA GCACAGGAAA TCGAATGTTT AAAACAATAT GTTCAATAAA 1560

AGArAACGCT TTAAATAATC TAAATAAAGG ACTGTTAATG GTGTTCTAAT AAAAGTTTTA 1620

TAAAAAATAT AGCTGAAACT CATGATAAAA AAGGCACAAA CCACTATAtT ACGTTATGCC 1680

AATTATCCCG AATTGGTTTT TTCATACTTA CTCCTACCAA GAGTAAATAA CAACCTTCAT 1740

TTCCACCACA GACGACGGTC GTGGTGGTTT TTTTTGTTTA GGTGCTAGTT TTTTTGCTAT 1800

CAATTGACTA GGAGAAGTGA ACGTTCTTTA AGAATTTGTC ATTTCAAATT TACGGAACCG 1860

CAAGAAACGA TTTGCTTCTT CCTCTAACTG AGTAATTTCT TCTTCTGTTA ACTCTTCCGT 1920

AGTAATGTGA ATATGTAACT CTTTTTGTGT GCTTTTCATA GGTGCCTGAT GATTAATCTC 1980

TGTTTGTTGG GTGCGGCCCA TTAAATAGTC CAAGGAGACA GAAAAATAGT CTGCTATTTT 2040

TAAAAGATTC TCTACTTTAG GCGAAGAGGT ATCCCAACGA CGAATTTGTC CATTGGAAAT 2100

GCCGACGTTT CTTTCTAATT GGGCGAGGGT TAGTGCTTTG ACTGAGCTAA TTGTTTAATG 2160

CGAGAAATTA AGGTCATTTC AAGTCCTCCT TGTGTTTTCC GTTTGCTAAT TTTAAATTAG 2220

CGTAAAAGCG AATGnTTGTC AATTGCGAGC GTGTAATAAG AAGGTGAACA TCTCATGAGT 2280

GATTTTTTAG AAAATTTCCG ATGAAAAAAA GAAGAAATAG AGTTATTATT AGTAAGTAAA 2340

CTGTTTTGGA GCGAGAGGGG ATGAATCAAT GGAGAAAATT AAAAGTTACC AAGAGGATTC 2400

TGAAGTGCAG AAAAATCGTT GGTGGATCTT AGTTTCTGTG GC 2442

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

CCAATTCGGn CCAGCCTnTT CGACCAATGT TGCACCAAAn ATAAGTCnTT TAGACAATTA 60

TTCATCTGCC GAGGGAAaGC CTAGCACGAG TGATCGGGAT TCATTTTTTG TAAGAGGAAC 120

GTCGAGCGCA ACAATTCGCG CACCAAAATC TGTTGCTTTT AAAGTCACAC CATTTTTATT 180

CGTCAGTGTG TAAAGAAGCA TTCCTTGTCC AAATGATTCA GTTGAAATAG TCAAAATAAT 240

CAATCCTTCC TTTAAGTAAA TATTTAGTAA ATTTAACTTT GTTGTTTAGA TTATTTAAAT 300

AGTCAAAAAG AAATGCtAAG AAAATAAATC TTTATTTAAT TGTATTGTAC ACGTTTTCAA 360

TTGAAATGAC AATTAAGAAA ATATTAAGTA AACATTTGCA AAAGTTTAGT AAATATTGTA 420

CAATTTGTTT ACTAGTGAAA GGAGCGATTA GTGATGGAAG AACTGTTAAT GAATCGATTT 480

GTAGAAATAT TTGGTGAGAA AGGGACAGCC TGTTATTTTG CCCCTGGAAG AATTAATTTG 540

ATTGGTGAAC ATACAGATTA CAATGGCGGT CATGTTTTCC CAGCGGCTAT TACTTTAGGG 600

ACATTTGGTG TGGCAAGAAA AAGAGACGAC CAAAAAATTC GGATGTTTTC TGATAATTTT 660

AAAGAGGTTG GTCTCATCGA ATTTTCATTA GAAGATTTAA CCTATTCAGA TTCAGATGAT 720

TGGGCAAATT ATCCTAAAGG CGTTTTAAAT TACTTGATTG AAAGCGGACA CAATATTGAT 780

TCTGGcTtAG ATGTGctCTT CTACGGTACG ATTCCTAATG GTGCTGGCTT GTCTTCTTCT 840

GCTTCTATTG AACTTTTAAT GGGAACGATC TGTAATGATT TATATGCTTT ACACTGTCCA 900

ATGCTTGAAT TGGTGCAAAT CGGTAAAAAA GTGGAGAATG AATTTATTGG CGTTAATTCA 960

GGAATTATGG ACCAATTTGC CGTAGGGATG GGAGAAAAAG ATCAAGCTAT TCTACTAGAT 1020

ACCAATAATA TGCACTATGA AATGGTTCCC GCCAAATTAG GTGAGTATAC GATTGTCATT 1080

ATGAATACTA ACAAACGCCG TGAATTAGCA GATTCAAAAT ATAATGAACG TCGTGCAGAA 1140

TGCGAAGAAG CCGTTCGTTT GCTTCAAAAA GAGTTATCTA TTGAATTTTT AGGTGAATTA 1200

GACAGCGAGA CATTTGAACA ATATCAAGCA TTGATTGGAG ATCCAGCGTT GATTAAACGA 1260

GCGCGTCATG CCGTCACAGA AAATGAACGA ACTTTATTGG CAAAACAAGC GCTAACTGAA 1320

GGGGATTTGG AAGAATTTGG CTTATTATTA AATGCCTCAC ATCGTTCGCT AAAAGAAGAT 1380

TACGAAGTAA CTGGCATTGA GTTGGATACC TTAGTGGCTT GTGCGCAAGA ACAACCAGGC 1440

GTTTTGGGCG CACGGATGAC TGGTGCAGGG TTTGGCGGTT GTAGTATTGC TTTGGTACCA 1500

AAGCAAAATA TAGATGCATT TATTGAAGCT GTTGGCCAGA GTTATCAAGA TAAAATTGGC 1560

TATGCTGCTG ATTTTTATCC TGCATCAATT GATGATGGTG CCAGAAAGTT ATTTTAGAAA 1620

GGAAGGCTTT AAATGTCTAT TTTAGTATTA GGTGGCGCAG GCTACATCGG CTCACATGCC 1680

GTCGATCAAT TAATTTCAAA AGGCTATGCC GTTGTTGTTG TTGATAATTT ATTAACGGGG 1740

CATCGTTCAG CAGTTCATGA ACAAGCGACT TTCTATGAAG GCGATATTCG TGATAAAGCT 1800

TTTTTACGTA GTGTCTTTGA AAAGGAATCA ATTGAAGGGG TGTTGCACTT TGCGGCCAAT 1860

TCTTTAGTAG GAGAATCCGT GGAGAAACCG TTAATGTATT TCAATAACAA TGTTCACGGC 1920

ACTCAAATTG CGTTGGAAGT CATGCAAGAA TTCGGGGTGA AACACATTGT TTTTTCTTCC 1980

ACAGCGGCCA CTTATGGCGA ACCAAAAGCA ATGCCTATTA CAGAAGAAAC CCCAACGAAT 2040

CCTAAAAATC CGTATGGGGA AAGTAAATTA ATGATGGAAA AAATCATGAA ATGGTGCGAC 2100

AACGCTTATG AAATGAAATA TGTTGCTTTG CGTTAtTTTA ATGTtGCAGG AGCaAAAAAA 2160

GATGCCTCaA TTGGTGAGGA TCACACGCCA GAAACGCATA TTGTGcCAAT TATTTtACaA 2220

GTGGcATTAG GCCAACGAGC AGAGCTAAGT ATTTTtGGGG rTGATtATGA TACACCAGAT 2280

GGCACGTGCA wTCGAGATtA TGTTTACATT GAAGACTTGA TTGCAGCACA TATTTTGGCT 2340

TTAGAATACT TGAAAAATGG TGGCGAAAGT GACGTCTTTA ACCTGGGTAG CAACAACGGC 2400

TATTCTGTTA AAG 2413

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 548 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

```
GCCGnACCCT TAAATCCGGC CAAATGGTAT AATTGGTCCn CTGGrTTmCC CAatArCCcT      60
cTTCtCyTCt GTCaCAGtGC TTCCgGCTCC aCTTGGgCAT cgCTTaGCTA ATTTTTTCCC     120
aTAAGCAGTT TGACTTTTAG CATTTTTCTT TGCGGCATTC AAACGGGAAC GCGAACGTAA     180
ATCTAACGCA TCTTCGCCAA AACGTTCTAA GTCTGGTTTG ATTTGTTGAT ATTGTCGTCT     240
AGTTAAAGGA ATCTCAGGTT CTGAGGTTGG AATATTAAAT TTCCGCACCG TTGGATCTTC     300
TTCCGTATCT TTCACTTGAA AAGCCGTTGG TTCATCATCA AGAATGACAT ATGAACGACG     360
ATCTTTTTTC ATTGCTTTTA GCAACTCTTC TTCAGTAAAA CTAGGTTCCT GTTCCTCAGG     420
AATCACAGAA GCCGGGaTAT ATTTAGGaAC AAAATAAGAA GGtGtCGTTT TTTGCACTAA     480
TGGTGATGCG GCAGGtCTAC TTGGTTTCGC TaCGaCTTCt TTTtTTTTAt AcGTTTTGGT     540
GGTCCCAG                                                              548
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(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

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TATGATGTGT GGACTTAGTG GTGGGTATGC TTCGGTAGAA GCCAAAATTG ACTTTTkGAG      60
AATaCGATTT AAGACATTrG ATGTTCGGAC AGTTGTTGAA AAGTTGTTGC ATATGGATAT     120
GAACTGGTTT ACTTATGaAC CTAGAGGGTT TTATCATTAT ACTGAAACAT TTTCGTATAG     180
CTCTATTCGG ATTTTTCGGA ATCCaGAAAA CGTGAATATG GGAATTATGT TGGACTTGTC     240
TGGCGAAGGT TGTCGTCAAT TAGAAAAAAT TTTTGAAGAA GACAACAAGC GATCGTGGAC     300
AGAATTTTTT CGCTCACTCT ATGATGATGA TATTTTCGGG CAAGGTGTTT TAGTTGATAC     360
AAAAATAACT CGAATTGATA TTGCTCTTGA TGAATTGATT GTGAAAGAAC AAGAAAATTT     420
TGATTTATAT GTTTTGAAAG AAAAAATGGA ACAAGGGCTT GTGGATACCA CTTTTAAGAA     480
TTTTGATTTT AGCGGGGGCT TTGCTTATGA AAATAAAAAA ATGGTAAATA AAGGTTTGTC     540
TCTTTATTTT GGTAGTCGTC AATCGCCATT GTATTTTAAC TTTTACCAAA AAGATTATGA     600
GTTAGCACGA AAAGAAAGTA TAAGTGTTGA GGAAGCAAGA GAAAAACATG AAATTAAAAA     660
TCGGTACGAA ATTCGCCTTT CTGATGAAAA GGCGTTTTTG TTTGTAGAAT ATTTTCTTTC     720
TAGTGGTGAA ACGTTGGATT GGCTAGTCAA GGAAATTATT AATCAATCTT TGACTGTCTA     780
TGACATTGAA GATGATATGA AAGTCTATTG CAAAGCTTGG TATGATGTTG TTGATAAATT     840
GGAAGGTTTA AAATTGTCTG TTCAAGGTGA AAAACCGTCT ATTGAGAAAA CACTTCGGTG     900
GTTATCAAAT TATTTAGCCC CTTCATTAAA GATGATTAAA GAAATTGATC ATTTGTTAGG     960
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AACAAATGAG CTGATGGAAC GTATCGATTT AGCAGAATTA AAAGAGAAAC ATGAAGAAAT 1020

AATTGAAATG GTCTGTGTTG ATGCGAAAGA TTTATTGTTT ACCACTAATC AAAATAGCAG 1080

TGTTCGATCT TATATGGAAC AAGAATTTGA TTTGGAGGAA GTATATCCAT TTTAAAGATT 1140

AAGGGGGATA TGTATACACT TGATTCGTTA TTTTAAATAG ATATGAGTTT AGTTGAAAGG 1200

AATGTATGAA TTATGAGTAG AGAATTTATT GAACGCAATA CTAAAGTAGC AATTTCTATT 1260

ACTGAAAAAA TGAAAAAAGG TAAAAATGAT TTACAAAAAA CAAAAGAAAA AATTGTTCAA 1320

TTAGATGAAC AAGGGGAATT GaCTaTTcCt TATTTAAAGA TTACTTTTGA AAAGTTTTCA 1380

GAATCAAATG AAGAGCTTTT AAAAGAAATT TCAAGATATG AATATACTTA TGTGGTTCAT 1440

GAAGCAGAAA TGGCGGTTAA AGAGAAAGCA ATTTGGGAAG AATTTTTCAG TATAAAAAAA 1500

TTGTATGATA AAGAGCTTTC AGAATTTGCC AGTTTTAAAG AGAAGTATAA ATATTTTGAG 1560

CCTAAAAATA GTGAAGAATT AAAAAAACAA GCTCGAGTGT TGCTAGAAAA GAAAGGGTAT 1620

ATTGTTGACA GTCCATTTGA AGGAGATTTT GAmaGATGGA TTGGCGTTTA TGCTAGACCT 1680

AAAGATAAAC CAACTTATTT AGATCCAACG GATGGAGAAG AAGCTGGATT ACAAGAATTG 1740

TACAGTGTAG ATGGATTTAA GCAAGACTTT GCAGAATGGT TTGAGTTTGA AGTTGTGGAA 1800

GGGaAATTAA AGGAGGACAT TTTGTAGTGA AAAAGATTTG GCAATTGGTA TGTTTAGAAA 1860

ATAATTATGA TTCACACAGC TCTTATTTTC GGGrTATGGT AAGATATTTT TCCTATACAC 1920

TGTTAGCACT ACTTTTATyC yTTTtAGGTT kGwATTTtAm CATAGGTTGG GTAAGTGGTT 1980

TCTGTTTTGT AGGTTTGATA CTTTTACCAT ATATGGGCTT TTTATCTCGT GATAATTATA 2040

GAGAATTTGC ACCGAGAGTA TGGAAAATAA GAGATGTTCG AGAGTTAGAA GAATTGTAAT 2100

CCTGTAGTTG TTGATAGAG 2119

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

AAAGATTGAC ATGTGCAACA ACCAATTGTA ATTGTTCTTT TTCTGCCACC TGTTCCATTA 60

CGTCAAAAGG GCCATGGAGT CTACACCACC AGAAACGGCG ACCACGATTG TTTGATGCGG 120

TTGCCAAAAT CcTTGTTCTk TTCCTCGTTT ATAAAACTGC CAAAACATTG TTCGCCCTTC 180

TTTCTTCCTT AGAATAAAAG AGGAACCGAG AAATAACCCA TTCGTTATCC CCAGTCCCCC 240

TATTTGTTTG TGCTTAGCCG CGACGTCCGC CACGTCCGCC ACGTTTGCCT TCAGTATTAC 300

GTTTTAATGA AGATAAACGG TCATCACTAT CTTTCAAGAA AGAGCTCATC AATGAGTCAA 360

AATCTTGTTT ATTGTTATTG TTATTTGCTT GTGGTTTAtT GAAAGGCTTT TTGCCCCCTG 420

CGCGTGGAnT ACGGTCACGA TTCTCATAAT TGTTTTCACG ACGTTGAAAT TCACGTTTTG 480

GTTGTTGCCC TTCTGCTGGC TCTTGTGCTT TACGGATCGA TAAGCCAATT TTGCCGTCGT 540

CACCAACTGA GGTTACTTTC ACTGTtAmTT CGTCACCTAC TGTTAATACA TCATGAATAT 600

CTTTAACGAA TCCATTAGAC ACTTCACTGA TGTGTACTAA CCCAGTTTTT CCTTCTCCTA 660

AATCAATAAA TGCACCAAAG TTAGTAATCC CTGACACTTT TCCTGGCAAT TTAGCTCCTA 720

CTTCGATTGA CATAAAAAAA TTGTTCCTCC TATTTTTTCC CTAATTATAA TTGCAGTTTA 780

TTCAGCTGAA GACTTAGTTG TTTCAGTTGA AGACTGTGAT TGACTATTTT TTTCTGAACT 840

GCTCTTGCTT TCTTCCGCTC CAGAAGTCTG TGTTTTTTTC ATTTGTTCTG GTGTGGGATA 900

AATCTGTTCG CCTTCTTTTG AGAGAAGGAA ACGGCTACGT GCTAATTTTG CCACATAATC 960

ATCATCTTTT AACAAAGCAA CGTCTTTTTT TAGATCCTTG ACCTTCTTAT CAACTGCTAC 1020

GGATTCAGCA ATTGCATCTG CTCGTTCTTG TTTGAAAGCA CCTAAGCGAT GATAATCTTT 1080

CATCAATTGG ATGCCAGAAA AGGCAAAAAT AATGAAGGCC ACGAGAAAAA TCGCTGCCAA 1140

GCGCTGATGA ATCCCCTAAT GATTTTTATC AAAATCATTA AGTTAAGGTA GATACACATC 1200

TTGTCATATG ATCAAATGGT TTCGCCAAAA ATCAATAATC AGACAACAAA ATGTGCGAAC 1260

TCGATATTTT ACACGACTCT CTTTACCAAT TCTGCCCCGA ATTACACTTA AAACGACTCA 1320

ACAGCTTAAC GTTGGCTTGC CACGCmTTAC TTGACTGTAA AACTCTCACT CTTACCGAAC 1380

TTGGCCGTAA CCTGCCAACC AAAGCGAGAA CAAAACATAA CATCAAACGA ATCGACCGAT 1440

TGTTAGGTAA TCGTCACCTC CACAAAGAGC GACTCGCTGT ATACCGTTGG CATGCTAGCT 1500

TTATCTGTTC GGGCAATACG ATGCcCATTG TACTgTTGAC TGGnCTGAAA TTCGTGAGCA 1560

AAAACGACTT AAGGTATTGC GAGCTCn 1587

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

CAATATGATA ATCATACAAA AGAAGaACTT AGTGAAATGA ATACAGAAGT CAGCGTTGCt 60

GgACGTATGA TGACAAAACG TGGTAAAGGA AAAGCTGGTT TCGCCCATTT GCAAGACCGT 120

GAAkGCCAAA TTCAAATTTA TGTTCGGAAG GACCAAGTTG GAGACGAAGC CTATGAACTA 180

TTTAAACATG CTGACTTAGG CGACTTCTTT GGTGTGACAG GTCAAGTAAT GAAAACCAAT 240

ACGGGGGAAG TTACTGTTAA AGCTCAAACA ATTACGTTAT TAACTAAAGC TTTGCGTCCA 300

TTGCCAGATA AATACCATGG ATTAACGAAT GTGGAACAAC GCTATCGTCA ACGCTATTTG 360

GATTTAATCA GTAACAAAGA AAGCTTTGAT CGTTTCATGA AACGCAGTCA AATTATTAGC 420

GAAATCCGTC GTTATCTAGa TGGCAATGGC TATGTCGAAG TAGAAACGCC TGTCTTGCAT 480

AACGAAGCAG GAGGAGCTGC TGCTCGtCCA TTTATCACAC ACCATAATGC GTTAGATATG 540

GACTTATACT TACGCATTGC CCTAGAGTTA CATTTAAAAC GkTTAATTGT CGGtGGCATG 600

GrAAAAGtAT ATGAAATnGG 620

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

CTCTCTCGTC ACTGCGTCTn TTGGATCGAA TAAGTCGTGC GTGTATTTCG TGCGAGCTCC 60

CnGnCATTCT CACACTAACG CCGTAGTACT GTGTAAGTGT ATGATGACGA GCGCCGATTC 120

TCCTCTGTAG GAGATCTACC GAATCCACTT AGGCTTCATC GTCTGGTGAA CAAGGTTCAA 180

AATAGTCATT TTTCAATAAT AAATAATTAA TCAAAAGATT CACCCCGAAT CAACATTTTT 240

TGTTCTAAAT CCATTATAAT AGAAGTATGA CACAATACGA GAAGAAAAGC TTATAAAAAA 300

CATTCAAAAA TAAGTGGCCG CGATAGGTGA GGCCTCGTTT TGAAAATGGT TTGATAAGTA 360

ATCCGTTTTT TATATGAAAA AGCAAGCAAA AAGGGCTTTT AGCACATATA TTTAAACGAA 420

ATGAAACATC TGTGTACGTT GATGAAGTAT AGTTATAGCA GGTGGAATGA AAGGATTTGT 480

TGAGAGAATG GTGTCGTTTT CGGCAATAAT GTTATTTTGG TATATTTTTC CGGTAATTGT 540

GCTCTTTGCG TGCAATTTTC TCGTGTCCAC TTTTTCCCTA ACGGAACTTG GGAAAATAAA 600

AGCACCGGAT TTGGCCATTC CGTTTTTATT CATAGGGATC CATGAGTTAT CCAAAGATAG 660

TTATGATGAA TCGATTATGC CGTATTTTGT GATTTCTATT TTGTTATTAG GAGTCGCTGT 720

TGCCCTGTTT CAAGCTTATT ATTATGGAGA GATTTTATAT AGACGATATT TCCAGAAGTT 780

TTGGCGGTGA CGTTTTTACn AACGTTTGGG TGGAAGGGGT GCCAACCTGC CAAAAACAGn 840

A 841

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

ACnAAATGTC TTAAAAAAAT GCTTTTTTCn TAAAAAAATT ATTACAAAAA AAAaCAAGAA 60

GTCAGCCAAG TATTGGCTGA CTTCTTGTTT TTTTTATTTA ATTATTCAGC TAAACTAGCT 120

TTTAACGCTT CAACTTTATC TGTTTGTTCC CAAGGTAAAT CAATATCTGT TCGACCAAAA 180

TGACCATAAG CCGCAGTTTG TTTATAAATT GGGCGACGTA AATCTAGCAT TTCAATAATG 240

CCTGCTGGAC GTAAATCAAA GTTTTTACGA ACTGCTTCGA TTAATTTACT TTCTGGAAGA 300

TCACTCGTAC CAAACGTATT AATAGAAATA GACACTGGTT GCGCCACACC AATTGCATAA 360

GCTAATTGGA CTTCTACTTT TTTCGCCAAA CCAGCAGcAA CAaTGtTTTT CGCGaTATAA 420

CGCGCAnATT AACTAGCAGA GCGGtCAACT TTGGTTGCAT CTTTTCCAGA AAAAGCACCG 480

CCGCCATGAC GAGCATAACC GCCATAAGTA TCAACGATAA TTTTACGACC AGTTAAGCCG 540

GCATCTCCTT GAGGGCCACC GATTACAAAG CGACCAGTTG GGTTGATAAA GTATTTTGTT 600

TCATCATCTA AAAGTTCATG AGGAATCACC TCATTGATTA CTTGTTCTTT AATATCTTTT 660

TCGATTTGTT CTAAGGTTGT TTCATCATCA TGTTGTGTAC TGATGACGAT CGTATCCACA 720

CGTTGTGGTT GACCTTGATC ATCATATTCC ACTGTTACTT GAGATTTTGC ATCAGGACGT 780

AAGTAAGGTA AGACTTTTTC CTTCCGCAAT TCTGCTAAAC GGCGAACCAA ACGATGACTT 840

AACGCGATCG GTAATGGCAT TAATTCCGGT GTTTCGTCAA CAGCAAAACC AAACATTAAG 900

CCTTGGTCAC CAGCGCCAAT ATCGTCTTTT TCATCTTGAT CACGCACTTC TAAGGCTGCG 960

TCAACCCCTT GAGCGATATC AGGTGATgCT CATCGATtGC TACAAGAACT GCgACAGTCT 1020

CTCCATCAAA TCCATATTTT GCTCGTGTAT AACCAATATC TTTCACAGTT TGACGAACAA 1080

TTTTTTGGAT ATCTACATAA GCTGTTGTAG AAATTTCTCC AAATACTAGG ACTAAACCAG 1140

TTGTTACGGa TGTTtCACAT GCCACGCGGG CCATCGGATC TTTCTCCAAA ATCGCATCTA 1200

AAATTGCATC ACTGACTTGG TCAGCTACCT TATCTGGATG TCCTTCTGAA ACGGATTCTG 1260

ATGTAAAtAA ATGTCTnTCT GTCATAATGT TATTCCCCCT AAATAGTTTC GGTTACAAGG 1320

CATCTTTAGT AAGTAACGAC AATTACTTGC TAAATCCTTT CGGGAACTTG TAACAAA 1377

(2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 536 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

TGTTAACGTG aACTATTATT CATCGTTTTA AAACGTGTTT CCATTAACTC CACTGTATTT 60

TCCAAGCATT GaGTAATATC TTTTTTTCCA GTATGAACTT TTCCTGCAAA TAGCGGTAAC 120

TTGCCTAAAG CCATCAAGTC AGAATTTTTC GGGTCACAGA TTyCmAsmTs ACCcACTCGA 180

CAAAGCGCAT AGATCAGAGA CAAAATTGTA AAAGTTTTAC CTCCACCaGT GCCTCCACCT 240

AATAACAAAT GTGGATCTTT ATCaAAGTGC CAATACAACC CTTTCATCAA CTGAACTTTG 300

CCTtCGTCTG CTTGCATATC CTTAATCCAA ATACGCTTAT TGTACACATC TGTTGCTAAT 360

TCATAGGTAA CAAAACCTTT TTCATCAATC TTATTTAAAT TATCTGCATG AAACGkTGkT 420

TCCAAAAAAC CACCAATGGT TTCAAATTTT TCCTGAAATT TATTACCCGC TGTTTCAAAT 480

GAAACAAAAA TACTATTTTT TGCAGACTTA TAATAAATTT TTGGAAACTT GATTTT 536

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1079 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

CGATTGACTT TCTAACACTA CTTCCATTAT AATTAGCTTT GTTGTGTTAC AACTATTGTC 60

ATAGTAGCTC AGCAGGATAG AGCATCCGCC TTCTAAGCGG ACGGTCGGGG GTTCGAATCC 120

CTCCTGTGAC GTAACGATAA CAAAAGCGCC TCTTAGAAAC CTTGGTTTCT AAGAGGCGCT 180

TTTGTTATCC CAAGTTCATC CTAACCTAGT TTAACTTTCT ACCAACTTGA AGTACCTCCA 240

CCTCCGCCAA AACTCCCACC TCCGAAACTG TCACCGGAGC CATCATCAGA AGAACCCTCG 300

TTGCTTGTAA CCCACCAATC ATGACGATTC GCATACATAC TGGTCTTTTT TAGTTGCCTG 360

TCAGAACGTG AACTTGCTAG AAATTTAGCA ATAGACACAT TTCCATAAGC AAAACGCATA 420

TCATAGTATT CAGGATACGT AnTCTTAATA AATCTTATCG GGTAGAAGGA TTTTGAAGCT 480

TTTTTGTTGG TAATCTTTTT TtCTCTAATT TTTTtCCGCA AtAATTTTTT TTCAATTTwA 540

TATkGCtGGT TGTCtAAATC GTTTGCyAAT TGTTTtAATG ATTTTGATTT TTCTGAACTT 600

ACTTGCTGGA TTTCTTTTAA AAACCTACGG ATCATAGAAT CCAGGTGCAA TCTATTTTGT 660

AAGCCAACAC CTATTGATTT TATATAACCA AATAAGAAAA AGACCGGAAT CAAAAAATAG 720

ACCAGACTAA CCATGGGTAC TAAAGAGTCT TCGTCTTCTA AAAATGTCAG AATCTCTGTG 780

ATTAGTGTGA AAACTGTCGA AGGaAACGAC TGCyCTGATA AACTAACTTG AACATAAATA 840

ATCAGAGTCA CGGATACCAA AAAAGGATGT TTTAATAAAA TCGAAAGAGG AAACAAAATA 900

ATTTTTAGGT AAGCAGATAT TAAGTTATCA TTAATTCCAC TAATCCGACA CGCGGGCAGT 960

TTCTTTTCTG GGAACTTTTT CCCAATATAC TTCACCTATC CAAAAACGCG GGTAAGTAGG 1020

ATCCATGGGT TnGATTCACC CTTCCCAAAA AnnAGGCACA CATAGAAGAG GCTTCnTTA 1079

(2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

GTATGAATTG GAAGACTTAA TGAAACGGAT TCCACCAATG TATGAAGAAT TAAATGAAAC 60

TTTCCCAGAT CAATTAAAAG AAATCGAAGA AGGCTACAAC CAATTATTAG CTGACGATTA 120

TGTGTTCCCT GAACAAAACT TTGCTGAAGA AATTCAACAT GCGAAAAAAC GTGTCGAGAA 180

TTCAATGGCT GATTTAGAGA AAACAGAGAT TGCTGCAGTA GAGGTCGCAA ATCGCGACAC 240

AGCAACGGCG ATTGATGCAT TATATGAAGT GATGGAACGT GAAATTGAAG CGAAGAAATA 300

TGTCGTGACC AaTCAAAAAA TTATTGACGA TTATATTTCT CATTCCTTAA AAAATAACCG 360

TCAATTAATG ATTGAATTGG aCCATGTATC ACAAAGCTAC ACCTTAAACA ACAACGAGCT 420

AGGACGTAGT CGTGGCTTCC AAACGGAAAT TGAAGAAATT ATCCGCCGTC AAAAAGACTT 480

GGAACCTCGA ATGAAAGAAC ATACCGTTCC TTACTCTGAA ATTCAAGCGT TCTATAAAGA 540

ATGCTATAAG ATTTTAGATG ATATTGAAAA TCAACAATTA GAAATTGATG CTTCATTGAA 600

AGAACTAAGA AAAGGCGAAA AGGTCGCCCA AGAAAAAGTC GACGAATACG AATTCCGTTT 660

ACGGAGTATC AAACGATATG TTGAAAAGCA ACGATTACCA GGTTTGTCTG CTGATTACTT 720

AGAATTTTTC TATGTGGCAA CGGATCGAAT TGAAGATTTA AGCCGAGCCT TAAATAAAAT 780

GCGCATTAAC ATGGATGAAA TCAATCGTTT GTGTGACTTA TGCGAAGATG ATTTAGAGTT 840

ATTAGATAAG AAAACAAAAG ATTTAGTCmA TGCAGCAGCT CTGACAGAAC AAATGATGCA 900

ATATGCAAAC CGCTmtCGTC ATACTCACGA GAACATCCGA GCGGCTTTAG ATAAAAGCAT 960

GTATTTATTC TCGACAGrAT TCCGTTATCA AGATGCATTA GATGAAATTG GAACGGCATT 1020

GGAAGCTGTT GAGCCAGGGG CGTTCAAACG AATCGAAGaT TTTTATTTTA AAAATAnCAA 1080

TAACCCTAAT 1090

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

TATCTTCTTT TTCCGTTATT GAAATAATTA ATAGCGTTAA TAAAAATAAA GGAATAAAGA 60

GGAAGTGCAT AACCATTTGA GTAACAACTA TCGATACAGT AATCGTGTGC TTGTCAAATA 120

GCTGAACTAG TATTGGATTA AACCAAACAA TGGCGACTAT TACTAACGAA AAATATTTAG 180

TCACGCTTTC CAGCCTTATT ACATACAACA AGCCAAAGAA AATTAGTAAA CTAATAATGA 240

TATCTTTATA AGTAAAAAAA TGTTCATAAT TCATAATTTC TTTCGTTTCA TCTCCACTCA 300

ACTTGCTTAA CTATTCAAGG TTTAGGTAAA TCACGTTTCC CATTTTCTCA CATGATCGTT 360

CAAAGAAACA GAACGTTGTT TGGTGTTTTA AAACGTAAAA GTTGAGCAAC ATATCCTGTC 420

TAAACATTTA CTTGGCAGTT TATTTATAGA AAAATTGTTA CTTTCCAAAT TTTTGTATGC 480

TTTTTAGAAA TGAAACCAAG CTTATGTTTT AATGCTTCTT ATGCAAA 527

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

ACACGGATnA TTTATTGATC CCTAGGTCAT TnGGCGGGAT TCAAATTCCT TCGCATAAGC 60

CAGGCCaTTA AAtTmCTCGt GGtCaTAwGa cyCCtTaCaA TATwCyTTTA AAAAaGcTTT 120

TATCaTCTGG TGTCATAATk GTGtTATTTC atATCTCGAC TTAATAGkTT CtCAAAgCAG 180

ATCGCTCTTC aTCAGTGACA CTAATATTgG TCTTAAAACA GTAGTATTAT TACGATTTGA 240

CATATTACCA ACATTGATtC TTTTTATCTC TAAATCATTT TCAATAAATG GTAATAAATC 300

TACGGGTGAT TTGACAATCA TCAGAACATT TTGTCCTTCA TATTTGCCAT TTTTAATATT 360

ACTAATAGCT GTTTCTTCAG TTATGATAGA CGAAGAAATT CCAGCAGGAA CTGCCATTCT 420

TAAAACCTGC TTTTGTAAAT CATTTTTAGC AACGTTGTCG TTCACTACCA TTAAACGTGT 480

TACTCCCAAT TTATTACTCC ACATTGTAGC TACTTGACCA TGGATCAAGC GATCATCAAT 540

TCTAATATTG TTAATACCTT TCATTTCCAT CGAAAATGCC TCCCATAAAT TATTTTATTT 600

TAAAATACCT AGAGCCGCTA AAACAATTGA CAATACCATA ACACCAAGAA TTAAGTAAAT 660

AGGTTTAACG TTCTTCTTTA ATGCCCAGAA AACTAAACCA ACTAATAATG CAGGCAATAA 720

TCCAGGCATT ATTTGATCCA AAATATCTtG ACCTTTCATT GAAAAATTAC CCTGTTTAAA 780

GTTTAAAGTA ATATTAGCTT TAACGACTGA AGGTATTAAT GCCCCCACGA CCATTAATCC 840

TAAAATCGAa GTTGACTCAG TTAATAATTT CAAACTTTTT TCTATAGTAG CAATTAATTT 900

TGTTCCTGAG GCATATCCTG CATTAAATAA TGGAATACTA ACTAATTTTa GCGCTACACT 960

TACAACAATC CATAACAAAA TTCCAACTGG ACTACCATCA ATGGCCATAT TTGCTGCAAT 1020

AGCACCAAAT ATAGTCCaAG GAATAACTAC AAATAAACTA TCACCCAAAC CAGCTACCGG 1080

GCCCATAAGG CCTGTCTTAA TAGATGTTAC AGCCTCTTCT GTGTTTTCGT CAGCATTCTC 1140

TTCCATAGCT ACATTAATAC CTAAAATGTA AGGTGCCACC CAAGGATTAG TATTAAAAAA 1200

TTGTAAATGA TTTAATACCG CTTTTTGTAA TGCTTCTGGT TTATTTTTAT ATGCTATTTT 1260

TAAAAATGGT AATACTGCAT AACAATATGC TAGCGCTTGC ATCTTTTCAT AATTAGAAGA 1320

AACTGAGCTT GTAAAAAACC ATCTCCACAA AaCACTTCGT TTAGTTTTTG TATCAATGCG 1380

TAATTTTAAT TGTTCGATAT TATTCATCGT CATCCATCCC CCCTGCTATA TTAATCACAG 1440

TATTCTTTAC TAAATCTTGA CTATTTTTTT TATAAATTAT TAATGCAATA GCT 1493

(2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

CCAATGGATA ATCCTCCTTT AATTTATATA AACTTATTTT TCATTTCCTG TTAGTAGGTC 60

TATCATATCT CTTTTGTACC AAAAAAGCAA GAAAAAACCG AACAAACATT CGCATATTTA 120

TTTTTTATTA ATGATTCGGC GCCGCAAAAG ATCTAATCCT CGCATAACCG CACTCTGTCT 180

AATATAATTT CGGTCACGGT TAAAATGGAA ACATTCTGCA ACGGTTGGTT GGCCTTCTTC 240

CGCCAGCCCA ATCCAAACAG TGCCTGTCGG TTGACCTTCG AGTGGGTCAC CAGCGACCCC 300

AGTAAATGAT AAACCATAGT TAGATTTAGC TAACTGACGC GCTTTCTCTG CCATTTCTTT 360

GGCACACGCT TCACTTACCG TGCCATGTTC TTCTAAAAGT TCATGAGAAA TTCCTAAAAA 420

GTTCTCTTTT GTTTCTTGCG AATACGTCAC GAAGCCTCCC TTAAAAATCT TCGAAGCACC 480

CGCAATTTCC CCCAGTGTAC TTTGGGAtAG GCCAGCGGTG AGGCTCTCAG CAGCCGTAAC 540

GGGTTTGnCC CGTTTTGGTA nTAACAAATC nACGGTAAAC nT 582

(2) INFORMATION FOR SEQ ID NO: 679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

CTGGTTCGCC ATCTTTCATT GTCATAGTGG CACCAATTCC TTCAAAATCA CCAGATAAGC 60

TTTCGTTTAA ATCATTGGCA GCAGATTCAT TTAGATAAGT TGAGTATGGG TCTCCAATGG 120

CTTCAGACAT GCCTTTTAAG GCGCCTTCAA CTAATTCATT TTTATCTACT TCACCTACAT 180

AATTGGTACT AATTTCATTA TATAAATCCT GCACTTTGCT TAAATCAGCA TTGGTAATTG 240

CCCCTTCTTG ACTCATCTTT TTAACACGAT GATCAAAATA AATATAACtA CTTCCTCCAG 300

CTAAAAATGC GACACAGAGG AGCGAAATAA TATATTGATA AAAAGGAACA GTTCGTTTGT 360

TCTTCATAGa TTTCATCTCA TTTCTAACAA ATTCGTCACT ACTTTTGTTT ACTATAACAT 420

GAATGAAAAA AGAGGAAAAG CTTTGTTTGC TTTTCCTCTG GATTTATTTA TTGTTTTCAA 480

GGTACTTTTC CCATAACTCA TCAAAGATGT CCATGTTGCT TAAATAGTCA GCATTCATTT 540

CTAAATAAGA AGAAAGTTCA TGATAATCCT CGGTTTGTTT TGGAAACTGA ATATCTTTGG 600

CCGCTTCATT GGCAAAATCA GTTTCAGAAT CTTTAGCCGG ACCTTTTAAT GTCATTAAGT 660

AATGGTAAAA GCTTCGTCTC ATGTAAATTA ATCACTCCAT TTTTCTTCAA TAAATTCACT 720

TCTACGTTGA TGGGACAATC CATAACGCAA AGCGTCTTTT TTATAAAAGT CTTGATGGTA 780

TTCTTCAGCA GGATAAAATG GTGCTGCTGG TTCGATGGTG GTAACAATTG GTTCTGTAAA 840

ACGGCCGCTA TTAGCTAGAC GTTCTTTACT TTTCTCAGCA ATTTCTTTTT GTTCTTGAGA 900

ACGATAAAAA ATAACTGGCC GATAATTATC GCCGCGGTCT TGAAACTGGC CGAAAGCATC 960

AGTAGGATCC GTTTGTTGCC AATAmATATC CACTAATTGT TCGTAAGAAA TAATCGCTGG 1020

ATCAAAAGTG ATTTCTACTG CTTCCGTATG GCCTGTTGTG TGTGTTAGAA CCTGTTCATA 1080

TGTTGGATTA GGCACGTGCC CACCTGTATA ACCCGAAACA ACTGAGATAA TCCCTGGTTG 1140

TGTATCAAAA GGCTGCACCA TACACCAGAA ACAGCCGCCT GCAAAAATTG CT 1192

(2) INFORMATION FOR SEQ ID NO: 680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

GTTATCCACG AGCGCCTTAA AATATGTCCn GGGAATGTGC CCGATTCCCT AGGCATTACA 60

AAAACCAAGC CTGGGAAATG TGCTTTAGCT GCTTATTCCC AAACAGTTTC CTGGAAGGAC 120

TTGTATACGG CGATTATAAA CTGTTTTTTT AAACtAACGG TACATTAGGG ATCGTTGAAT 180

GGTTTTAAAA CAAAGGAGCT ATATTATGAG AAAAAGTATT TTATTCATGT TGGGAATATC 240

TTTGTTCTCA ATGACTGCTT GTTCTAATGG GGATAAAAAA GAAGTAAAAT CAAAAGCATC 300

CTCsTCTACT GTTATCTCTG TCAACAAAGA ATCATCTGGT AaTACGAAGA AAAATGAATC 360

AAATTCAATA ACTAAAACGT CTAACGTTGT TTCTTCTACA TCTGTGGAAA AAACACgtGG 420

AAGTAAGTTT AGCgATTTTA TkGGTtGGGG TATtCmAAGT GGAAaCCTTT TTTTATTAAT 480

GAAGATGGGA CATATTCAAA TGGTCAAGTA GACCATTCTT CATTAATTGc CTTAAATTTA 540

GTATTTTAGC AGAcGGAAGA AAATCAATGA GCTCAAATTT AGGAACTCTA ATTAAAGAAT 600

CTGATGGCAC CTTAACAGAT GGTGAACTAG TCTTTCAACC ACTTGAGTTT AGTAACAAAG 660

AAGATTTCCT TGCAGATAAA CAAAAAGAAT ACAAAAATTC TCCCGAAACT AATGCACCTG 720

AGAACGAaGT TGAAATTACT AATACTATAG rAGATATCAC TAACGGAAGT ATCTCTACTG 780

ACACAAATAC GCTCACAGGA TTCTTAAATG TGTATGGTAT GAGTCCTGCA GCTTATAAAG 840

TTACTATTGA AGGAATGAGT GAAGAAGAAG CTTTAAGAAA CACACCTAAA GAAATGAAAA 900

CTTCTGCTGA AATACAATTA GGTATCTCTA AATATGGTAT TCAATAATTT GTCTACGATT 960

TATAATTAAC ATTAGCCATA AAAAATACAC ATAGGAsrCT AAAAAATGAG TGCATTTTTA 1020

GGTCTATCAT CTTTATTAGG ATTATTCGTA ACTTCTGTAT ATTTTGTTTA CTGTATTTTT 1080

AAGAAGAGAA ATAATTTATC CTATTTTGTA TGGATTTATA TGATTCTTAT TGGATTATTT 1140

TTCmCTGCGT TAGAGTTATT TATTCCAGGT ACTATTTTTC TTACTATTTC ATTGTATAAA 1200

ATATTAAAAG AkCCAAAAAC AAAGGaATTG cTACATGaGC aAGaAATAAA AcgAACmGaA 1260

AAAAtAATAG aAAAACAAAA CCCTATTCAA GAATTCACAG AAAGTAATTC AAACGAAAAA 1320

GATCTAAATC AGAAAGTTGC TTCAACATAT TCTAACGATT ATTATCCCTC GGATAAAAAA 1380

GcTGGGCTAT TCCATCTTGG CGTCTATTGT CCTTATTGTA GAAGCCTTAA CGTCCAATAT 1440

AT 1442

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

TTGCTTTACG CGCCGGCATG GACGGGCGGC TTGCTCCGTG CGGAAGCnAG CGACGACTTT 60

TCCGGCGTGG CCGCAATCTA TATTGACGGC GAGAAATACn ACCGATTTTA ACCAACGGCA 120

CACTGGACAT ACCGCTGCGG GATTTGCCGG ATGATTACGA ACAGCTTTCC GTGCAGGCGG 180

TGGACGCTGC GGGAAATAAA TCAAAAATCG TGCAGGTCAA GAACCCCAAC TATCAGGCGG 240

AGGATAACAA GCAGAAGCCC TCCACCGGCC AGACACAGCC CCCGGCGACC ACCGCGCCGG 300

TTACATCCAC CACGCCTGCG CCAACGACAC CGGCCACCAG CGCAACCACA CCCCCGACTA 360

CACCGACCAC CAATCCGGCA ACAACGACTG CCACAAAACC GGCTGCCGGC ACGGGCAGCG 420

CAAAGCCCTC CGCTTCGGCA AGCGCAgCCC gGACGAAGAA ACGGACACCA CGCCCCGCGA 480

TCCGATCCCT TTGACCCCGG ACGGCCAGGC TACCGTTCTG GACAACGCCA CCGGTGAGGA 540

CGGTAAGGAG TTTTATACCA TCCAGACACC GGATGAAAAC GTATTCTACC TGATTATCGA 600

CAACCAGCGC GATACGGAAA ACGTGTATTT CCTCAATGCT GTCACCGAAG CCGACCTGAT 660

GGCTCTTGCA GTAAAAGAGG ACGATACGCC GCAGACAGAC GCAATCCCTG ACCCGGAGCC 720

GGCCTGCATC TGTACGGAAC AGTGCGCCGC CGGCGAGGTC AACACCGCCT GCCCGGTCTG 780

CACCCTGACC CGGAAAGACT GTACCGGAAA AGCCCCCGTG ACCGACACGG AAACCGAACC 840

CGACGAAAAG CCGGAAAAAA CGAAAAGCGG CGGTTCCGGC ACACTGATTT TAGTGCTGCT 900

TGTGGCGCTG GCGGCTGGCG GCGCTGGCTA CTACTTCAAA ATTTACAAGC CCAAAAAGGA 960

TTTGGACGAT GCAGAGGACT TTGACGAACT GACCGGCGGG GACGAGGAGG AAACGGTCAA 1020

CGAGGACGAG GATGTGGACG CGCAGGAAGA AACCCGGCAG ACGGGCGATG AGGAACCGGC 1080

AGCCTATGAC GAGCCGGAGG AACCGGACTA TCCTGAAAAC TATGGCGGGG AGGACGACTG 1140

ATGCGCTTTA CGGACAGCCC TTTTGAGCGG ATGATGACCC AAAGGCCGGC CCCCAGCCGC 1200

GCCGCGCCTG CCTCCCCCGT CCATCCGCCC GGACACCCTT GCCACCGCTG TCCcTACGGG 1260

CTAAATGCGC CCTGCGTGGG GATATGCTAC AAAAATCTGA AAAAGGAGCG TGAGAAAAAT 1320

GCAGTTAGTG ATCGCGGAAA AACCGTCGGT CGGAATGGCG CTGTCTAAGG TATTAGGCGC 1380

GAAAAGCCGT GGCGATGGTT ACATGGAGGG CGGCGGCTGG CTGGTAAGCT GGTGCATCGG 1440

GCATCTGGTG GAACTTGCCC CCGCCGATGC CTATGACCCC CGCTATTCCA AATGGAACTA 1500

TGCCGACCTG CCGATTTTAC CAAAACCTTG GCAGTTCCAG GTGCTGCCGG ACACCAAAAA 1560

ACAGTTTGAA GTCTTAAAAA CCCTGATACA CCGGGCCGAT GTCACCGCCT TAATCTGTGC 1620

AACAGACGCA GGACGCGAGG GGGAACTCAT TTTCCGCCTG ACTTACCATC TGTGCGGCTG 1680

CACCAAACCC GTCAAGCGGC TGTGGATTTC CTCAATGGAG GAAGCCGCAA TCCAGAAAGG 1740

CTTCGACAAC CTGCTGGACG GGAAGAACTA CGACAATCTC TACGCCGCCG CTCTCTGCCG 1800

CGCCAAGGCG GACTGGCTGA TCGGCATCAA CGGTACGCGC CTGTTTACCA CACTGTACCA 1860

GGGCAAGTCC CTGAACGTGG GCCGGGTGCA GACCCCGACG CTGGCACTGC TGGCAGAACG 1920

GGAAGCCGCT ATTTCCGGCT TTCAGAAAGA GAAATTTTAC ACGGTGGAGT TGGAACTGGA 1980

GGGCTTTCGC GCCGCCAGTG AACGCTTTGC ATCCAAAACG GACGCAGGCA GGCTGCGTAC 2040

CGGCTGTGTG GGCAAGCCTG CAACGGTACA GACGGTTTCC CAAAAGGAGA AAACCGAGCG 2100

CCCGCCCAAG CTGTACGATT TGACTACCCT CCAACGGGAG GCCAACCGGC TGTTTGACTA 2160

CACCGCCCAG CAGACGCTTG ATTATCTGCA AGCCCTCTAT GAAAAGCGGC TGGCGACCTA 2220

CCCCCGCACG GACAGCCGGT ACTTGACCGA GGATATGGCG GCGGGGCTTC CCGCGCTGTG 2280

CCAGTCCGTC GCTGCGGCGC TGCCCTTTGC GGCAGATTTG TCCTTGCCGG TAAATGCCGC 2340

GCAGGTaATC GACAACAGCA AAGTCACCGA CCATCATGCC ATCCTGCCCA CGACAGAAGC 2400

GGCAAAAACC GACCTGTCCG CGCTGCCCTC CGGGGAGAAA AACATCCTCT TTCTGGTTGC 2460

CGCCCGTCTG CTGTGCGCGG TAGGCGAACC CCATACCTAT GCGGAAACCG CTGTCACACT 2520

GGAATGTGGC GGCGCTGTCT TTTCCGCAAA AGGCAAAACG GAAACCGCCG CAGGCTGGAC 2580

GGCTATGGAG CAGGCTTTCC ATGCCACACT GAAAAAGAAA CCGAAGCAGC CCGAACCCTC 2640

CCCGCCACTT CCTGCACTCA CCAAGGGCCA GAAGCTGACC GCCGGGGGTG CATCCATCAA 2700

AGAGGGCGCG ACCTCCCCAC CGGCCCATTT TACCGAGGAC ACGCTTCTCT CCGCAATGGA 2760

ACACGCCAGT GCAAAGGAGT TTGCGAAACT GGAAGATGTG GAACACAAAG GACTTGGCAC 2820

TCCGGCCAcC CGTGCCGGCG TGATTGAAAA GCTGGTGCGC TCCGGCTTTG TGGAACGGAA 2880

GAAAAAGCAG CTTTTCCCCA CGGAAAAAGG CACGGAACTT ATCAAGGTAA TGCCTGATAC 2940

GCTGAAATCC GTCAAGCTGA CCGCTGAATG GGAGGAACGG CTGGGCGCGG TGGAGCGCGG 3000

GGAACTCTCC CCGGAGGACT TTATGGCGGG CATTACCGCC ATGCTCACCG AACTGGTAAA 3060

AAGCTATCAG GGCGTGACCG TGGCATCTGC CGCCCTGTCT GCATCCGGGC GCACGGTAAT 3120

TGGTATCTGC CCCCGCTGCG GCAAAAACGT GGTGGAGGGC AAAAAGAGCT TTTTCTGCGA 3180

GGGCTGGaAC gTGCGCCCGC CTGCGACTTT GCCCTGTGGA AGAACGACCG CTTTTTTACC 3240

AGCaAGCACA AGGAACTGAC CCGcAAgGCT GCCGCCGCCC TGCTGAAAAA AGGGCGCGTT 3300

GCCATGACCG GCCTGTTTTC CGAGAAAAA GGCGTCCTCT ATGATGCAAT TGTTGTGATG 3360

GAGGACACCG GAGAGAAATT TGTTCGCTTT AAGCTGGAAT TTGACAATAA CACACCTAAA 3420

AAGAAAGGAA ACTGACGCTT ATGGAAAAGA ACATGAACGC ATTTAACCGC AACCTGCACA 3480

ACCTCCTGAC CATCAGCGGC ACGGATGCCG CTGAACTGGC GCAGACCCTT AACGTGGAAC 3540

TGCCGGAGAT CAACCGCTGG CTgmAacsTC CGCCGCGCCG GATGTGTACC AGCTTCAGGA 3600

AATCGCCAAG CGGTTCGGGA TGCCCTACTC CTACTTTTTT GAGAGTGAGC AGAGCCTGCC 3660

CAATGTGCCG AAAGTAGCGG CATGGCTGGG CTTGTCGGAG GAAACGGTGG AAACCCTGCT 3720

GGCAATGGCC GATACCGAGC CGGAGGATGT CATGGACGCG CTGGACGATG CCATTTATGC 3780

AATGGCTACC GCTGTCAGTG CTGCGGGGGA GGTGGATACG GAATGAAAAA AGAAGAAGCG 3840

AAAGACATCC CTATCGGCGG AGAAATCGCT GTCCGGCAAA CTGGCGTCCC CTATGGCTGG 3900

CTCTACCGGC GCACGGAAC 3919

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

GGTCCGTCCT TGATATTGAA CGGTTAACGC TTGTAACAGC TAAGTTAAAG CTTTTTCTCA 60

TGAAATTCCT CCTTTTTTAG GTTTGCCTTA AAATCAGTAT AAGGGATAGT TTAAGAAAAT 120

GCAAATAATT TTTAGGCGCA CCTAAATACA AGCGCTTTTT TCACAAAGAA AACCGTTTCT 180

TTCAATAAAT TAAGGAGGAT CCCATGATTT TTATGACAAA AAATGGTAGA ATATGCATGA 240

AAACGACTAT TATTTTATAT TGACGGAGGA TATCATGACC GAAAACTATC AAGATGGACA 300

CCTTACGCAT CTTCAGTTTA AATGCAAATC GACCACTTGG CTGAAAAAAA TCGCGnCATC 360

AGTAGGaACA GAATTAGGAA AAAGCACCGT GcGCCaATTT AGTGaTGGcG AAaTTCaAAT 420

TAAtATTGAA GAAAGTATTC GTGGCGATCA TGTCTACATC ATCCAAGCAA CGAATGCTCC 480

TGTAAATGAT CATTTGATGG AATTGCTTAT TTTAATTGAT GCATTAAAAC GTGCTAGCGC 540

AAAAACAGTT AATGTTATTT TGCCTTACTA TGGTTATGCT CGCCAAGACC GCACAGCGAA 600

ACCAAGAGAA CCCATTACTG CGAAATTAGT TGCTAATATG TTGGTAGAGG CAGGCGCAAC 660

ACGTTTGTTG ACATTAGACT TGCATACTGT TCAAGTCCAA GGATTTTTTG ATATCCCAGT 720

AGATAATTTA TTTACAATGC CTTTGTTTGC TCATTATTAT CGTCAACAAG CATTAGTAGG 780

GGAAGAAATT GTGATTGTTT CGCCTAAAAA CAGTGGCGTT CAACGCGCAC GTAGTTTATC 840

GGAGTACTTA GATGCGACCT TAGCAATTGT CGACCATGAA GAGATCGATG GGGTGCGCCA 900

AGAAGGTTAC GTTATTGGGA ATGTCGCTGG GAAAAAATGT ATTCTTGTTG ATGACATTTT 960

GAATACTGGT CAAACGTTAG CCACAGCGGC GGAAGTTTTA ATGAAAAATG GTGCGCAAGA 1020

AGTGTATGCT TGCGCCTCGC ATGGTTTGTT ATCAGAAGGC GCAAAAGCAA CCTTAGAAAA 1080

TGCGCCAATT AAGGAAATTA GTATTACTGA CTCTGTTTAT ACGACAGCAs ACCGCCAACC 1140

AGCAACCTTG AATATTATTT CTTGCGCTGA GTTAATGGGG GAAGCGTTAC TTCGTATCCA 1200

TGAAAATAAA CCAATGAGTC CATTATTCCG TTTAGAACCA AAAGGAGAAT AAGTGATTCC 1260

TTAAACTAGA AATAGGTCTA ACAACTTTAA TAGTGTTGGG CCTATTTTTC TTATCTCTTT 1320

ATAAATnGAA GAGAAAGT 1338

(2) INFORMATION FOR SEQ ID NO: 683:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

TTCAATGAAT AGAAGGCTGC ACCTAATGTG TAAGACACAC CCCCTGCGAC CAATAACGCT 60

GTTCCTGTAA ACCCAAGAGA TTCATATAAC GGACGAGCAG CTATGATACA GAGCCAACCT 120

AAAACAATAT AAATAATCGT TGAAATGTTT TTCACTGTTT CTTGTTTATG CAACGTGAGG 180

GATTTATAGA CAATACCGAC GATGGCGATT AACCAGACTA AACTAAATAA GGTCCAACCT 240

AACCAACCGC CAATACTAAT TAAGCAAAAC GGCGTATAGC TGCCAGCAAT CAATAAGAAA 300

ATAGAACTAT GATCGAAGAC CTGAAAGACC TTTTTGGCTC TTGTAAAAAT TAAACTATGA 360

AATAACGTTG AAGATAAAAA AAGTAGAATC AACATGGAGC CATAAATAGC ATAAGATACC 420

ACGTGAATCG GTGAGCCTAA ACGAGCTCCT TTAACAAGTA AAATGACTAA GCCAGCAATA 480

CTTAAACCTG CGCCTATGCC ATGTGTAACT GCATTCAAGA CTTCGTTCAC GATTAGGTAT 540

TTTTTTGAGA AaTGCGTTTT TTCCAATAAA TTCACTTCCT TTATTTTAAT TTGATGAAAA 600

ATtCGGCAGT GTCTGTTATA CTATAACTAG ATAATTAACC GTTTAATGGT ATTCTACCAT 660

GAAAACAGGT TCCTTTTAAA GAAAGAGTGT AAATTTATGA CAAACGTAAA ATCGTACGGT 720

TCTCATGACG TGGAAAAAGC TAGGGTGATT AATATCATAT GTGCTTATCA TTATGGTGTG 780

GGTGTTATCA GTGTGTCATT GCAGCGAAAT TATGGCAGTG GCAATGGAGG CTACCCAACG 840

nGCACCCCAT TGGGATGnGA TAnTGTCCTG GGAGTGCGGA GATTCGTCCA GCAA 894

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

GTAACGATCG TATTGACAAT TGACCTTAAT TACAGCCATT AGCACCGCTG CCCCAAAAAC 60

TTGAGAAGCC AAAGTTCATT TCCCCCACAA AAaACGAGGT CATTTGTAAA ATCGCTGCAT 120

TGACAACAAA GCTAAATAGA CCAAACGTTA ATAAAGTAAA TGGGAGCGAC AAGATTGTTA 180

AGACTGGTTT CACCAACATA TTTAGGATTG AGAGAACAAA GGCGGCAATA ATTGCAGGCA 240

TTATGCCTCT CACATGAATC ATGCCAGGAA AAACAACTGA TAAAGAAATG AATGTCAGTG 300

TATTAACAAC CAATCGCTGA AAATATGTCA TTAAAAGTCA CTCCATTCGT CATCATCAAT 360

TTTTTCCGCT TCTTTACGTT GCTTTTTATT GGCAGCATAA GGATTTTCAT TGCGAACATT 420

TCTATTATAA GGATTTTGAT GGCCGTAGCC GCGATCGCTT CCTGTTCTTC CAGAAGGGAT 480

CAAGACTGCT AAAGCAATGT ATAAGAGAAT GCCTGGAAAT CCTGcTGAGA AAAAGCTGAG 540

CmAGACATAA ACGACACGAA TAATTGTTGG GGTCAATTCC TAGCCAnTCA GCAATCCCAG 600

CTAAGCTTCC TGnTAAAACC ACGTTATTCG GAGATTTTGG TAGT 644

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

GCATTTnnTA GTGTCCGATT CGnCTTAGAA gTATTTTcAA TcGTAAaGCT AATAAAaTTt 60

CGTtGGCTTt CCGTTtAAaG GTCGTTyCAT CAGTTAAAaT CTGkTGcTtG rCCAATTGCk 120

GAGTCAaTGT TGAmCCmCCr GAgAcCGCsG ATACCTGTCG CATCAGAAtC AACGCTCGAA 180

CTAGCGCTTT TGGTACCACC CaTGATGTTC yTCmAAATAT caTCTTCTGT GGAAATAATG 240

GCTTTTTTTA GCAtGGAGAC ATTTGATCGC CATTAATTCG TGTCCGAATT AAATCTGATT 300

TGATGTTAGC AATCGGAGTA CCATCTGCGT AAGTCATTTT TGACACTTCG GTAATATCAC 360

TGATTTCTTT TTGCAATTCT TCCTTCGTTG GGGGCTGTGT ATCTTCAACT AGAAAAGCAA 420

AaTAGCCCAT TCCAATACCT AAGCCAAGAG AGCCACCTAA GACAATCAGA tAAcCCCAAA 480

ACCACTAATG CTGAAAACGC G 501

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

CTTTGTAATT GATGTACGCC AAAATCCTGG TGGACTGCTA GATCAAGCAG AGCGAATGGC 60

CAkTATGTTT TTAAAAAATG GCGAAACAAT TGTTCAATTT GAAGACAAAA AAGGACGTAC 120

GATGAAAGAA GTTGCTTCCA AAGAATTAGA CGGCGGCTTT aAAGTAAAAG AACCTGTTGC 180

AGTTATCATT GATGGCAATA GTGCCAGTGC ATCCGAAATT TTTGCTGCAG CACTGCATGA 240

ATCTGCGAAT GTCCCATTAA TTGGAACGAA AACATTTGGC AAAGGAACGG TCCAAACGGT 300

GAAAGATTTA AATGACCAAA CCGAAATAAA ATTGACTGTT TTAAaATGGT TAACACCAAA 360

AGGCGAATGG ATCArCGAAA AAGGAATTGA ACCAACCATC AAAGCTGATT ACCCCGAGTA 420

TGCCTATTTA AAATTGATTC CTCGCGATAA AACGCTAAAA GAAGGAGATC AATCTGAAGA 480

TATTCAGAAC TTAAATGCTA TTTTAGCTGT ATTAGCGTAT CCTGTTGATG AAAACAATGC 540

AAACTACACC GCAGAAACAA AAGCAGCGGT wAGCGATCTT CAACaGAAAA ATGGCTTGCC 600

TGTAACTGGA GAAATCGACA ATGAAACAGC CACAAAAATT GAAGCCACTT TAGGTAAATT 660

AATTCTTGAA AATGACGCTG CTTACGATAC AGCAGTCAAA GAAATTCAAA AAAACTAGAA 720

AAArGTGGCA CGAaGTTGAA GaAGAAcGTG ATTATGTTGG gTATTtAATG kACTTyCTGA 780

AAATnTTAGt ACCAGCAtCg TAgCCGTTTT tATTTtAAGr GGtTTTCCC 829

(2) INFORMATION FOR SEQ ID NO: 687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

TAGATTCTAT AATGGTGACA GGGCTAGTAC CATATTTAGC GATGAAAGAT AAGTCAGATT 60

CGAAGGATGA AGGGGTTAAC CTTAGTGCGT TAAACTTTAA AGAGCAAAGC GTACCGTTCA 120

AGATATTAAA AATTAAAAAT ACATTTACTG ATGAAATGCG TTTTGAATAT CAAACACACA 180

TTATGGATAC TGCAAAAAAT ACTCCAATTA TGAATAATGA AAAAATTAGT TTTATCAGCT 240

ATGAAAAATA TATAGTTACT GGTATGAAAA GTATTTTAAT GAAAGCAAAG GATTCTAAGA 300

AAAAAATATT GGCATATATT AATAATAATT TACAAAATCT TATAGTTAGA AATGTAATCA 360

GACCAACTCA AAGATATGCT GATATGTTGG AATTTTCATA CCATCCTAAT TGCTTTTCTA 420

ATGCAATAGA GAGAGAAAAA GTACTTCATA ATAkGTGGGG CCTATCCCTT ATAAGGAnTA 480

AAAAG 485

(2) INFORMATION FOR SEQ ID NO: 688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 970 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

CTATACGCCA CAAACAATCT CCAACATGAG TAAATTGGTG GCTGAAGATG TTTTAGCTTT 60

TAAAGAmAGA ACGTTAGAAG CCAATTATTC CGTTATATTT ATGGATGCGA CGyaTATCCC 120

TGTGAAGCGA CAGACTGTTT CGAAGGAAGC AGTGTATATT ACGATTGGTA TTCGTTTGGA 180

TGGAACCAAA GAAGTTCTTG GGTTTACTAT TGCCCCAACT GAGTCTGCTT ATATTTGGAA 240

AGAAGTTCTT CAAGATCTTA GAAAACGTGG GTTAGAAGAA GTTTTATTAG TAGTGACAGA 300

CGGATTAAGC GGTATTGAAG AAAGTATCCA TAGTGTGTAT CCGAATGCCC AATTTCAACA 360

ATGTTGTGTG CATGTATCTA GAAATATCGC TCATAAAGTT CGTGTTCGAG ATCGAAAAGA 420

AATTTGTGAG GATTTCAAAT TGGTTTACCA AGCGAATTCA AAAGAAGAGG CATTGGATCA 480

CATCGACTTT ATGATTAGGA AATGGAAAAA GCAGTATCCA AGAGTCGTCA ATTTACTCTT 540

GAATCCTGCC CTATTAACCT TTTATAATTT CCCTCACGCC ATCAGACGAA CAATTTATTC 600

GACGAACCTG ATTGAAGGCT TTAATAAGCA GCTAAAACGA TATACTCGAA GAAAAGAACA 660

ATTCCCTAAT GAAGAATCTC TAGAGAGATT CTTCATTTCT CAATTTAATC AATATAACCA 720

AAAATTTTTA GGTAGAATTC ACAAGGGATT TAAAGAAATT CAGGATACAT TAGAGTCGAT 780

GATTTAACTG TAATTAACAG AATGGATTTT CCATTTACAC ATAATTCTTG ACGCTACCAT 840

AATCTAAATA ACCATCATAT TCATCTACTA CTTATATAAT TGAGTTTTAT TAAACTTTTT 900

AAGTTTCTAT TCTATCAAAT ATTTAAACAA TCTCTGCATC CGAAAAGACT ACCTCGTATA 960

GTTTTACTAA 970

(2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

ATAAACATAT TGGTAAAAAT TATGTCTCTT CAAAAAATCC ATCTGkTTTT GAAAATTTTC 60

TTTATCCGTT ATATCCATAT TAGCATCTCC cTTTTTTAAC GATTACTATT GCTTATTCTA 120

TCGACTTTTT CCCTATTATT TACTTTGAAT AAATCCTCTT TTTATTAGTG TTGTTAATAT 180

AGACGAAGCA CACCGCAAAA CAGCGCTTTC ATAAAGGACA ACTATAATAA GAAATAATAG 240

TTAGTTTTAT TAAATCATAA ATACAGCTAA AATAAATCAT ACAAAAGTCC TAAATCAAGT 300

TTTATTTTAA GTkTCTAACT TTGATTGCkT TAGTTAAAAA TGACACmACC aTCTTATATC 360

nTATTCCATA CCATTTTCnT AAT 383

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 850 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

GnCTATGTTG AGAAnAAAGT CGGTAAATTA GAnAGATATT TCCAGCGATT CACCTGAAGC 60

AACGGTTCAC GTGAATTTGA AAGTGTACAC TGAAAAaAaC AGCCAAAGTC GAGGTTACTA 120

TTCCTCTTCC TTATCTAGTT TTACGAGCTG AAGAAACGTC ACCTGATTTA TACGCAAGTA 180

TTGATTTGGT TGTCGATAAA TTAGAACGAC wAATTCGTAA ATTTAAAACA AAAATCAACA 240

GAAAAtCTCG TGAAACAGGA CGTAACAATA CAAAAGCCGC TGTCTTCTTA GTTGGTGAAG 300

AAACAGAAGA AACACCTTCA GAATTAGACA TCGTTCGTAC AAAACGTCTA TCATTAAAAC 360

CGATGGACAG TGAAGAAGCT GTTTTACAAA TGAACATGTT AGGACACAAC TTCTTCATTT 420

TTGAAGATGC TGAAACAAAT GGAACAAGCA TTGTTTACCG TCGTAAAGAT GGCAAATATG 480

GCTTGATTGA AACAGACTAA AGCTTAAAAT ArGAGCTGAA ATGCCTTCGT GCATTTCAGC 540

TCTTTAAACA TCTTTAAAGC ACGGAGTAAA GAAAAAATAA AGAAATACAT AAAATAACTT 600

TAAAAGTTCC TCTTTTAAAG GAAAATGTCT GTAAAATAGA GAGAAATGGT TTTCTTTCTC 660

GTCAAGTAAT GATAAAATAA AACGGATAGA TTGTGCTTCT TGTACAAAAA GGATACAAAA 720

ATAAAAAGAG GTAATTGAAA GGACACAGTA CCATGGCAAT TTTTTGAAAA AATGTCGAAA 780

CGTAAAAAGA TTAGCGTTGA AAAACGCGTA ATGTCCTGCA GGCATGACAC TACGTGACAT 840

TCGGAAACGT 850

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

ATACTCACCT ACATCTTAAT TCCAACTAAA CTTAATACCC ATTTAACAAC TGCAAAAaTA 60

TTTTTTCCTT GATTCGTCGC AAAGTCCTGT AAAATTAAGG CAATGACAAT TACTGAACCA 120

ATTTTTGCCC ATTCGGCACC TTTCCAATGT TTTAAAATCA AGATAATCGC ACCAGCCGCT 180

AAAATTGTAA TAAAACCTGT ACTTAAAAAA CTACTCAAAT TGCCTGTATT CATTAGTCAT 240

TTCCTTCTTT CTCTGTAAAG TAATGTTTCA TCGTATTAAT AAAATAAGAA TTCTCCGTTT 300

TAGATAACCA AAGCGAAAAA TCCTCAGTAT GCGTTAATTT TGTTGTTTTA TCTGAAAAAG 360

TGACCGATAC TTGAACCCCT GTTACACCTT TCTGCTTTGT ATCAAAAAAT TTCATATCAC 420

CAGAATCTAT TGAAACAAAT GAGTCTTGAC CTGCTGTCGT TGTTGGATTT TTCATTAACA 480

ACATTAATTC TTGTTTGTTC CCAACTGAAT ATTTTGTAAA AAACATCTTT AAAAATTTCT 540

CTATAGATTG TTTTTCTTTC CCATCAACAT CTATTGAATT TTCTGTCTGT TTTAGAGATA 600

CTGTTTTTCC TTGTGGTAAA CTACTTGCTA CAAAATAAGG ACGTCCTACA ATTGAAAACA 660

AATTATCTTT TACTTGAATT GGTAAAACCA TATTCTGTGT CACATTTTCA GTCTTTTTAT 720

CTTTCTCCAA TTCATAATTC ACATTTAGAT AAACCAAATA ACAATCTTCC ATTTTCTCTA 780

TACGTGATAA AGACGTATTT TTAAACGTAC GTAAGACATT CCCTTGTAGA TTTTCTGTTT 840

CATCAACATC TTTTACATCT AGTGATAAAT ATTTAGATAA TCGATCAATA CGAGCCTTTT 900

TAGCTTCATC ACTTGCTTTA GAGTTGTAAT TTAAATACTC TTTCGCAAAA TTTTCGACAT 960

AAAAAGAGAG GGCTGAATAA TCAAACTCCT CTCTTACGAC GTTATTCTTT TTTGATTGTT 1020

CGCTTAATGT ATCCACTTTT GAATATAAAC TATCTACATT ACTTGCCATC ACATTGGCCC 1080

GAATCGCACC AACTCCTGAC ATCACCAGTA AAACACTAGC GCCAATTAAC ACAACCCGAT 1140

TCGCTTTCTT TTGAGAAAAT GTCTTAACCT TTGGTGTTTT TTCTTTTTTC TCTTTCTTTT 1200

TAATTTTCTT TAAATTCATA TTCCCCTCCT GCAATCAATA AACCTAAACA ACTTTCAAAT 1260

GATTTTAAAA AGGTAGATTT AATAACTTTT TCAACATAAA CTCTTTCTTT AACACGACCT 1320

TTATATGTTt GAAAGCCTtC TTTATACAAA TAAAAATAAT ATGAATTGTA CATTTTATCT 1380

CCATTAGGTT TTCTCAAGTA TTGACCTTCT GCTATTAAAC TAGTTA 1426

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

AATAAAGAAA ATGAAATtCT AGGAAaTAAG rAAATTACTA CTAAGcAGAC CAsATGTTGA 60

GGGGAAAGAT GATATTTCAn ATAGTCGATT TGCTCTTTGG CAAAGTGCGA TnGATTTAAT 120

GAAATTAAAT CCTATATTTG GCACnTCTCC AAAAGGTTTT GCAGATATAG CTAAAGATAA 180

ATTGCCTCAA TCTCATATTG CTAAGACAGC TCAAACACCG CATAGTTTTT TCTTCTATTT 240

ATTAGCAGCT ACAGGGATTT CAGGTACAAT TGTATTTCTA ATTTTCTTGC TATCTAAAAT 300

GTTTAACTCT GCTAAATTGC TGTTTAGCGT TCGAATTAAA AATTATATGG ATTTTGTGTT 360

AGATAACCAA ATTGTGTTAG TCATTTTAAT TTCTGGATTA CTGATAACTG AAGTCATTTT 420

AACAAGACGT TTTGCAACAG TTATCTTTTG GTTATACTTA GGTAAAATTC AGTATCGCAC 480

TGACATGGAA AATGATTTGA TTAGAGGAAA TGAGCaATGA TGCTCATTTT tTCTACTATA 540

(2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

GAAAAACAAA AAGGTGTCAT GACATCTTTA GGAGGCAGTT TTAATGAAAA CAAACTCAGT 60

AAAACGTTTA ACAATTTCAG CACTTTTAAT TGCAATGGGG ATTATCATTC CAATGGTTAT 120

GCCAAGAATT ACCATTGGTC CAGCCAGTTT TACATTAGCA AGTCACGTCC CAGTTTTTAT 180

TGCCATGTTT ATTTCTCCAG TGGTGGCAAT TGCGGTTAGT CTAGGAACAG GTTTTGGTTT 240

TTTCTTATCC GCAACACCGA TTATTGCTTT GCGGGCCTTA TCTCATTTGA TTTTTGCAGT 300

CATTGGCGCA tGaTTTTACA AAAGCATCCA GAAATTTTAA TTAATAAAGA GGGGAAATTC 360

ACTTTATTAA ATGGAAAATT ACAGTTGTTT AACGTGGGAA TTGGAGTGAT TCATTCCGCt 420

GCCGAGCTAG TGGTTGTTct GTaTTtACAC AATGGGCAAC TTGcCAGGAA CCTATnATAC 480

AGC 483

(2) INFORMATION FOR SEQ ID NO: 694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

AAATGAAAAA TTGTCTGACG GGGAACCAGC TCAATTTGAT GCAAAAGAAG AAACGTTTTG 60

GAAAAAAATT TCGCAAAAAG TTATTTTATA AAAGTAATAC ATACGAATAA GAGCGTACAC 120

ATAGAAAGAA GCGTAAgCAG TTTAACACTG CTTACGTTTC TTTTTTAATG AATAGGAATA 180

ACTGTTTCAC GCTTAATTAA TTTGTGAGGA ATAACGAGAC GGACACCATT TGTCAATTCT 240

TCGTGGATTA ATTCATATAA TTTTTTCATC GCCATTCGAC CTAATTCTGA CGTGTCGATG 300

TCAATGCTTG TTAGATAAGG ATGTGTCAAT GTTGgAAAAG ATTGAGTtGT TAAAACTAAT 360

AATGGATAAC GTTTCCrGGr ACyTGaTAAC CAwAnGATTT GCGCaAGTTg CATCgG 416

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

GCCTGATACA TACATTTCCA ACATTGAAGC CATGAGGGCT TTTTCGTTtC GTTGATAACG 60

TTCAAACACT GTGGGTGAAA AATGGCCATC ACGTGTTCTG GGTACTTTTA ATTCTAGCGT 120

GCCTACACGT GTCGTAAAGc TGCGCTCATA ATAGCCATTT CGTTGACTTT GTCGGTTTTC 180

TGTTCGTTCA TATTCTTTTG CTTGAATATA TTCTGTTCGT TGATTTTCCA TTAGTTGATT 240

AAATACCGTT GTTAAAATAT TTTTAGAAAC GTCATCCTTT ACAGAATATT CAATAATGCT 300

TTGAATCTCT TCGCTTTTCA GTGTAAAATG TACTTGGGTC ATGTAAAAGT CCTCCTGGGT 360

ATGTTTTTGT CGTTAAAAAC ATTGTACCGT AAAAGGACTG TTATATGGCC TTTTTACTTT 420

TACACAATTA TACGGACTTT ATCATAATTT AAGTAATACT AATCAATGAA ATTTGAATTT 480

TGAAATAGTT ATTTATTTTC ATTTTAAATA CGTCTTTTAA TTAACATTAA CCTATGATTG 540

ACTATAATAA AAAATAGGCT CTCTTTGTAT AGAAAGTCTA TTAAATTTTA ATAATTTATT 600

TAGTTGACAA TAAGAATATA CCTTCAGCAA TTTTATTTTT AGTAATAGGA ATTACTTCTG 660

AATAACCTTT AGAGTTTGTT ATAATAACCA TTATTGTATC ATAAAGGCCT GAATTTTTGA 720

TCATTGGGTT GTCCAATGTT CCAAGAACCT CCCCCTTTTT ACTTTTTGAT TAGCAACAAA 780

TTTTTTAGCG AATCATTTAC TACTTAATGA TACTGTATCA ATACCAATAT TAATCAGTAA 840

CATGTCCAGT TTCAAATAGA ACTTGAACAA TACCACATCT ACTGGAGAAT AAATAGTGTT 900

TCTATTTGGC TTAATAGGAA CTATTTTCTT ATTGTTGATC CGTCTTGTGT TTGTATTGAA 960

AAAGAAGAAA TAATGAGGGA TTTAAAATTA GCAAAAAAAT TGGTAAAATG AACTAAGGTA 1020

ACGATCGCAC CCTCAATATA ATAGTGTCAT GAATTTAAAC CTCGATTTTT TTGCGGTTGT 1080

TACCTTTTTA TTTTAGGGTG GAAAATAAAT GTcTCTTTAT TTCTTTTTGT TATTTCGCAA 1140

GTGATAAACT CCTGTTAAGA TAGTGGCTAT ATAAAAAAGG CAGATACTTA AGAAGAGTAT 1200

ATTCATGATT TCCTCCTAGT TTAAATGAAA GTCATGAATG ATTGTACCAA GATTTTTTAG 1260

AGAAGTTAAG ATTGAATAGA AAAGTAAATA CGATArAATT TTTATAGACT GTTACGTTGA 1320

AATGTTCTTC AGAGACTATT TCTTCCAATA CCnCCTACTA GATAGGTGGT TTTAATCATT 1380

ATTTTCGGAG GTTGTGTTTT GGCCAAAAAG TAAAGATTTA ATGGATGTAG GTTCATTTGT 1440

GA 1442

(2) INFORMATION FOR SEQ ID NO: 696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

CTATGATTGG CTTGGAGAGC tTTCGTTAAT TGATTTCTTA CGTGATGTTG GAAAAAACTT 60

TACAATTAAC TATATGATGA GTAAAGAAAG TGTGAAACGT CGAATCGAAA CAGGAATTTC 120

TTATACTGAA TTTGCGTATC AATTATTACA AGCGTATGAT TTCTTGAAAT TGTACGAAAC 180

AGAAGGTTGT TTATTGCAAT TAGGCGGCAG TGATCAATGG GGAAACATTA CTTCAGGGAT 240

TGAATTATTA CGCCGAGAAC AAGAAGTTCA AGGATTTGGC TTAACTATGC CTTTAATTAC 300

AAAAGCAGAT GGTACCAAAT TTGGTAAAAC AGAAGGAAAC GCAtTTGGCT AGATGCGGAA 360

AAAACTTCGC CATATGAATT TTATCAATTC TGGATTAACA CAGATGATCG TGATGTCGTG 420

AAATTCTTGA AATACTTTAC TwTCTTAACA TTGGATGnAA TTGCAACAAT TGrAGaAGAA 480

TTTACAGCGA ACCCAGGTCA ACGTGCTGCG CAAAAAGCGT TACCAAAGAA GTGACTACTT 540

TAGTCCACGG TGAAGCAGCC TATCATCAAG CGGTTAAAAT TTCAGAAGCT TTATTCAGCG 600

GGGATATCCA AAGCTTAACA GCAGAAGAAA TTAAACAAGG CTTTAAAGAT GTACCGACGT 660

ATGAGGTGCA ACCAGAGGAT CAATTAAGTT TAGTCGACTT ATTAGTTACC TCArAAATAG 720

AcCATCCAAA CGTCAAGCCC GTGAaGATGT TCAAAATGGA GCGATTtACG TCAaTGGAGA 780

aCGTaGACAA GATTTAGCAG CTGAATTGAC AGAAACTGAT AAAaTCGAAG GACAATTTAC 840

TGTGATTCGT CGCGGTAAGA AAAAATATTT CTTGTTAAAA TACTArAAAA ATGaAAGCTT 900

GGGACGaAGG TCGTTTaGAC AACAGGTTCC AAGCTTTCGC TTTTAAAAAA gATAAATTGG 960

GaTTAATTCT GTTACAAAAA ACTCTTTTTT aCTATTGGGc mTATTCaATT aCAGATAACT 1020

TGTGCTATGC TAGAATAAAA AGTGCAGTCG CTATAAGGAG TAGGTTATGA AATCAATTGT 1080

CGAAAAGTTA AACTTAACGA AGTATCAGCA ACTAGTTATT TTAAATAGAC CACAGGGAGA 1140

GTATCTATCT GAATTTGCTT CAGCCGCGCA GCAATTACCC TCAGAACCAG TTGAGCTGAT 1200

TTTTGCATTT GTGAAAACAA TGGCGGAATT TCAAGAGATT GTTTCAATGG TGATTGAAGG 1260

TCAACATTTA GTAGAAAATG GGTTGTTATA TGTGGCTTAT CCGAAAAAAG GCAATAAAAT 1320

GTATCCAACC TTTGTCCACC GAGATGAAAT TTTTCCAACA TTACAAGTAA ACGAGGCAGA 1380

TGGGTATATT AAAGGCTCAA CCTTAAAATT TAATCGCATG GTTAGTTTAG ATGAGACTTT 1440

TACGGTTGTC GGCATGAAGA ATGTTCTTAA AAAGCTAGCG AAGAATCAGA CCAGTTCTGC 1500

TGTTGGGGAT ATGTTCATAT TTACCGGAAA TTGAAGCGTG GGACAACAGA CCACTGCTGC 1560

AGCGACATCG TGCATACGCn GGTATCCAAA GATGGCCCGn ATGTTTAGGC AACGACGnGC 1620

CCGnAAC 1627

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

TCAAACGTTT ATCATAAATA AATGTAAATT ATAATATTCT TTTGATTTAA ATAGATTTAT 60

ATATGTnATA CGTTTGACTT TTTTCTGATT TGTTTATACT ATTAGACTAA CTACTATTTT 120

CTAATAAAGG AGACATTACT TATGTCAAGC ATCATGAACC AATGGACGGA TGAATTACGT 180

TATGCGCCTT ATTCTTCTTG GACATCTGCT CACCTCGAAA ATCTAACTTC TATTATCGCG 240

CAATCTAGTT GGCGTTTTAA GTATCATATT CAACCACAGA CAGGACTACT AAATGATCCC 300

AACGGTTTTT CGTATTTCAA TAACCAGTGG CATTTATTTT ATCAAGCGTT TCCTTTcGGG 360

AGTGTTCACG GACTAAAAAG TTGGGCCCAC TTAACTTCCT CCGACTTAAT TCACTGGGAT 420

TATGAAGGAA TTGCCCTTTA TCCCGACTCT GAATATGATT CTCATGGCGT CTATTCAGGC 480

TCAGCTTTAA CAATAGATAA CCAACTATGT TTATTTTATA CAGGAAATGT TCGTGATCAA 540

ACTTGGCAAC GATTTGCATA TCAAAATATT GCATGGCTGA ATTCTTTAGG TGCGATCACA 600

AAGGArTCAA CACCATTCCT ACCTATTGAC CCCAATTATT CTTCCCATTT TCGTGATCCG 660

ATGGTATTTC CTTATCAAGA AGGACTTGTT TtATTAATTG GTGCTAGTGA TTTAAATGGA 720

CAAGGAAAAA TTGTGGTCTA TTTTTCTAAA GATCGAAATG TACACAATTT TCATCAACTT 780

GGCGAATTGA CGTTCACCAA CCAAGAATTA GGCTACATGG TTGAATGCCC CAATTTGGTA 840

TTTATTGATG GCCAGCCTGT CTTATTATT 869

(2) INFORMATION FOR SEQ ID NO: 698:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

TGTCAGATTG CTCGTTTATC GTTTCAATGC AGCATTAAGG AGTAACGAAA TGCGATTCGC 60

TACTCCTCAA AGACTGATTT CTATTCTTTT TCTGAACCTT CTGTTGCATG ATAGTTCACG 120

CTATTTGAGG TACCTTTTTT AGAAAAGTTT TCAATTAGCT CTTTCACGTC GAGGCCCGTT 180

GTTTCTTTTA GTGTTTCTTG TGTACCAGCC AACAAATTTG TTGCATAATT TGTAATACGG 240

TTGGCGCCAG AATTTTCGCC ACCTGCGCCT GTATCTACCA CTGAAATCTT GTCGATGTTG 300

CCCAATGGTT GTGCTGCTTC TTTCATTAAT TGTGGCAACA TTTCCATCAC CATACTTAAC 360

ACAGCTGCTT CACCATATTC TTTGAAGGCA TCAGCAATCT TTTGTTTGGC TTCGGCTTCC 420

GCTGCACCAC GAGCTAAAAT AGCTTCGGCT TGCGCTTGAC CTGTTAAACG CGTTTTGTTG 480

GCTTCCGCTT CGGCTAATGC TTCAACTTTG AAGCGTTCTG CTTCGGCTTC TGsCACTTCG 540

CGTGcCTTTT GAGCAAGAGC TTCTTGTTCG CGTGCGTAAC GATCTGCATC GGCTTTTTTC 600

TTCACTTCTG AGTCGTATTG TTTTTCACGA CGCGTAATTT CTTTTTCTTC TAACTCAATT 660

TGTTTTTGAC GTTCAACGAC TTTGACTTCC ATTTCTTGTT CCACCACGTG TTGTTGTGCA 720

CGCGCGCTTT CCAAGtTATA GGCTTGGTCT GCTTTGGCTt TGGCAATATC TTGT 774

(2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 992 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

ATCTGTAAAA ATAATCAGCn TCTCGTTCTT GTGCGTGTTC AATTTGTGTC AAAATTTCAT 60

CATTGATAGC AGACCCAATC GTTTCAATCG TATCCGCTGC AACTACCTCT TGAATGCGGC 120

GTGTGTCGTC TTTTCCTTCA ACGACAATGA TTTCTGCAAC TTTCATTTTT TCTTTCATTT 180

ATCTATCCGA AACAAGCGAT GAGCGkTGAC TCTCGTTTGT TCTGCCACTT CTTCAAAGGT 240

TAGTTGTCGT aATTCAGCAA TTTTTTCCAC TACGTATCGT GTATAGCCTG GTTCATTCCG 300

TTTACCACGA TAAGGAACAG GGGCTAaATA GGGTGCATCT GTTTcCACCA ACATTcTTTs 360

tAGTGGTACC GCCATCGCCG CTTCTTGAAC ATCCAAtGCC TTTTTAAACG TTACGACTCC 420

ACTAAAaGaa TATaCmAACC TAAATCTAAA AATTTCTTCA TCCACTCGGC ATCACCACTG 480

AAACTATGCA TGATTCCACC AATATCTGAA ATTTTTTCAT CTTTTAAAAT TCGATAGGTA 540

TCTTCTAATG CCTCTCTCGT ATGCACACTA AACGGTAAAT TCATTTCCCG AGCAATCGCA 600

ATTTGACGGC GAAAGACTTT TTCTTGCACC TCTTTAGGAT CCTCCATCCA GTAATAATCA 660

AGrCCGATTT CACCTAaTGC TACAATTTTT GGCAACGTTA ATtGTTCTTG TAAtCGTCGT 720

TCAACCTCTG GCGTATAGCT ACCCGyTTCT GTTGGATGCC AACCAATGAT ACTATAAATA 780

TTGGCATATT CCTGACTAAG TAAAAGAGAT TTTTCAATCG TTGGTTCATC AAAACCGACC 840

ACGGCCATCT CTGTAACACC CAATTCTTGG GCATGTGCAA TCGTTTCTGG AATATCATCA 900

TTAAATTGTT CTGCATTCAA ATGTGTATGT GTATCAAAAA TCATTATGAT TGCCTCCTTT 960

ATCTCCTCTC TACTTTATCA TATTTCTTGA AA 992

(2) INFORMATION FOR SEQ ID NO: 700:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

GCCAGATTAT GAATTGTTAA TTAAAATCCT TAAAAACGAT TCTAACTATC AATTACTTTC 60

TTTTGAAACA nGAACATTTT CGTTAnCTTT TGCAArGTtA GTkGAyCCTA aTACTGTAGC 120

TCATTCCAAA CAATATTTTG GTGGAGAAGA TAAGGACTTA GGAGTTTTTG TAGATATTTT 180

TCCAATTGAT GGTATCCCTG ATACTCAAAA GGAGAGAAAT GAACTAAGAA AGATAACGGA 240

ACAGTATCGG TTAAACTTAA TGGATACTTT AGGTTTAAGC TATGCACGAA gTTTTCATCT 300

TAGTAAGGCA TTAATAAAAT TAATAACTCG TTATCCTAAT CATTTTAAAG TGAAAAAAGT 360

AGGaAACAAT CAATATTGGC GTGATTTATA TCAAACAGAG GCAAAAAAAA CCCCATTTGG 420

AGCAACAAAA CATTGTGGTT ATCTAGAATG GATTCATATA GATTGGGGTG TATTTCCTAA 480

TGAATGGTTT TTGGAATATG AGGATGTAGA GTTTGAAGGA CATAAATTTA TGGCCATTAA 540

AAACCGAAAa CAATTTTTAA CTTTACGTTA TGGAGATTAT ATGGaAATGC CTCCAGTAGA 600

AGAAAGAaTC ACTCATCATC CCwAwGAwww wtACCAAAAA TAmAGATTAT TTATAGGTTT 660

TTTAGAAAGA AGGCGTACTT AAATGAAGCA GCAATATACA GCAACTGTTG TTATGGCTAC 720

CTATAATGGA GAAAAAAATA TCTTAGAA 748

(2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

TGGTGCCGAC TTTCGTCATC GCAnCGCACG ACCnTTTCGA AAnGATATGG GTTCCATGAC 60

GTTGTCTTTG nGCTGGTAAG TTTGTGTTAA CTCCCATTCG ACTCTAGGTA TTCCAAGTTA 120

ATCACCATAT TCGGTTTGAT TGACGAAGTA AGAACCGTTT CTCGAATTAC CTGATTAAAA 180

CCAGTGCGAT CATATTTTTC GTAATCTAAA AAGCCGTTAA TTCAGTCCGT AGGAGTGTGT 240

TTACGCTTTT TCTAAGTGCG AACGGAATAA TTCATTTAAA TCGCCTTTAG TGACTAGAGT 300

TTGCACAATT TCkGTAGTAA AATCATTCAT AGGGAAGTCC TCTTTTCTGT GAATTGGTTG 360

TCGTTAACTT TATTCTACAG AAGCGACTTC CTTTTTTGTA TGGATTTTTT CATyTACACA 420

AAATATTTTA CACTCTCAAG TTAwCGTACG ATAACTTTAA wwCATATGTT GTACAAGTTT 480

TTTTGTTAAT TGTTTTTAGT TATATTATCA TTAAATTAAG TGAACTGAGA CAGTTTTATT 540

GGCTTwAAAA TCTATATTAA ATAAAACAAC AAAGACCTTA AGTTGGAGTT TAAGGTCTTT 600

GTTGTTTTAT TTAAGATTCA TAATCACAAT GCCGACAATA ATAACCACAG CACCAATAAG 660

GGCATTCGTT GTGATTGTCT CTTTTAGAAT AAGATTTGAA GCAATTAAAA TAGCGATGTT 720

TGTACAGGCA ACGCCTAAAG GAACAATGTA AGAAACATCG GAACGACTwA TAATTAACAT 780

CCATAAAATA AAACTAATTA AATAACAAAA TAAACCTAAT AAAGATATAA GTGAGATATT 840

CATTGaAAAG ATTGTTTGTT GGaGTTGGAT GTTCmAACTG CTAGAACCTA GTTTAAATAA 900

GACCmGACCA GCmGAAGACm GAAATACGTA AwTAATAAAA rGAaCCmTAA TTTCCCTTCT 960

CTCAAAAATA ATTTCCGTGC AAAAAAATGC AAGACCTCCA TT 1002

(2) INFORMATION FOR SEQ ID NO: 702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 855 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

CTTGAATAAA CGAAATCAAC TTGTCATTGA GAAAATGCTT GTAAGGAAAT CTTTGATTAG 60

TGCATAAAAA ATGCTCACTC TTATCTGGGA GCAAGACTyT CGTTAATGAC TGTTTAATTC 120

TGATAAAAAT AAAAGACCGT AGCTTATAGT AGGCTAGGGT CTTAAATACG TTATTGAGTA 180

AAAGAATTTA ATGTATACTT TATTTTCGTT TCGTTGGTAT CGATATCAGT AATTTGCTCT 240

TTAGTAATAT AAGCATGAAT ACTTTTTGAA ATCGTAATTT GTACTTCAGA GGTCTTTATT 300

TGTTTAAATA GCGTTCTTTC AAATGTACCT GaGATATCTC CATGTGCTAA AGACCTAATC 360

TTAAAATAGT TCTTACTTTT ATTTGCAGCC AAGACCTCTC CTTCTATCTC TATTTCTTcA 420

GTTAACACGt TTCnTTCATT TATTtGATCA TTCACACTAG ACAACATAAC ATCTAAATTT 480

CTTTTGATCT TTTCTGATTT TtTTATATTA CTCAACTTAA CTTGATTGGA AATTAAATCA 540

ATTGATAAAT gCATTTTCTT CAATAACTTT ATACAGCTTA GCAGTTTCTT CAATGAGCTT 600

TCTTTCATTA AACAGTTCTT CTTCATCGTA CATTGGTATA TAGGCTAAAT TATCTACGAA 660

GnCAACAGAA AAAGAGGCCT CATCAGTAAA TAATCCCGTT TGnCGATCCT TTTCTAATTC 720

GAAATCAAGT TTTAGCGACC CTCTTGAAGG TGCGGACATC AAAAGTTTCT TCTGAGTTCC 780

TAATTCTGCA TGCCTTTGAC TTAAATCTTG CCATGTACTT CTTATAAATT CTAAAGCACT 840

ATAAACAATA TCAAT 855

(2) INFORMATION FOR SEQ ID NO: 703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

ACAGAAACAG TTGATGTTTC ATCAATGATT GATGAATTAG CAACAAAAGC GAATGTCGCT 60

TTAAAAGCAA TGGAAGATTT TACACAAGAA CAAGTAGATC ACATTGTCCA TCAAATGGCG 120

ATGGCGGCGT TAkACCAACA TATGCCTTTA GCAAAAATGG CTGTCGAAGA AACTGGCCGT 180

GGaATCTAkG mmGATAAAGC AATCAAAAAT ATGTATGCAT CTGAATACAT TkGGAATAAT 240

ATTAAACATG ATAAAACAGT GGGTGTAATT AACAAAGACG AACAAACCGG CTTAATGGAA 300

ATTGCTGAGC CAGTTGGCGT GGTATGTGGG GTCACACCAA CAACGAACCC AACGTCAACA 360

ACTATTTTTA AAyCcTAATT GCCTTAAAAA CmAGaAATCC mATTGTTTTg CTTTCCATCC 420

TAGCGcACCA AAAATGTTCG GCAGAaGCGG cACGTATTGT ACGGGATGCG GCGATTGCAG 480

CAGGTGCACC AGAAAATTGT ATTCAATGGA TTGAACAACC ATCGATTGAT GCAACATCTG 540

CTTTGATGAA TCATCCAGGG ATTGn 565

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

ACGTATGTTC GCTATAGATn ATATGTATTA TTAATAAAAG GAGAaCTACA TATGATTACA 60

aAAAmaGAAA ATGGTTACTT TGTTGACGTT AGCTTGGGGA TTGATCCAAT ATCaGGCAAA 120

CAACGTAGAA AGAGACTTAC AGTTTCAACT AAAAAAGAAG CTCAACAAAT TGAATCAAAG 180

TATTTAAGGT TATACCACGA AAATAAATTA ACAACTAATT CAGACTTAAC TTTAAAAGAT 240

ATTTACGAaG TTTACGAAGA AAAATACACG CAAAACCTTA AGCCATCTTA CAAGCAAACA 300

CAAGAAAGAA TTTTTAAAAA CTATATAGAA CCTTATTTTA AAAATACTCA AATCAAACTA 360

ATAAAAAAAC AACAAATCTA TGATTTCCAA CAGTTTCTAT TAACTAGTAA ACCTAAGAGA 420

AAAGAGACTT TATCAAATAA GACAATCAAT ATGATTATTA TTCATCTACA GAAATTATTT 480

AACGTAGCTA TGAAAGAAGG ATTATCCTAC GAAAATCCTT GTAACCAAAT AGACAAGTTA 540

AAAGTGCAAA AAAAAGAAAT TGATTTTTGG ACATTAGACG AATTTACAAC CTTTATTTCT 600

CATATTGATA AAAATAAACC ATTTTTAAAA GTATTCTACC AGTTTGCGTT TTTTACAGGA 660

ATGCGTGCGG AGA 673

(2) INFORMATION FOR SEQ ID NO: 705:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

ACTGnCGAAT TGCTTATCAG CAAGTATTAG ATGTCGTTTC GCAAAATTTG CCAGCAGGAT 60

TTGAATTAAC AATGCAATAT GGCATGCCAA CCTTTGTTGT GCCGCTTTCA GTATTTCCAG 120

AAGGCTATCT TAACCGTGGT GATGAACCGT TACCATTTAT CAGCTTAGGC GCTACTAAAA 180

GGCAAGTAGC TTTATATCAC ATGGGATTAA TGGGAAATGA AGCCGTCCGA AGTTGGTTTC 240

AAGAAGCCTA TCAGGAACAA GTGTCAACAA AGCTAAACAT GGGGAAAAGT TGTCTTCGCT 300

TCACTAATCC TAAGCGAATA CCCTATGAAC TAATTGGCGA ATTAGTAACA AAAATCACGC 360

TAGAAGAATG GCTGCAACAG TATCAACACT ACCAAAAGAA AAAGAAGAAT TATTAGGAGG 420

AACCACATGT TATTAGGATC aCACGTTAGT ATGAGTGGCA AGAAAATGCT ATTAGGCTCT 480

GCCGAGGAAG CGGCTAGTTA TGGCTCAACA ACCTTTATGA TTTATACAGG TGCGCCACAA 540

AACACGCGTC GGAAACCGAT TGAAGAAATG AATATTGAAG CTGGGCAAGC TTTTATGAAG 600

GAACACAATT TAAGTAATAT CGTCGTTCAT GCCCCGTATA TTATTAATTT AGGTAATACA 660

ATTAAAACGG AAAATTTCGG TTTTGCCGTA GACTTTTTGC GTCAAGAAAT TGAGCGAGCA 720

CAAGCGTTGG GAGCAACGCA AATCACGTTA CACCCAGGTG CGCATGTTGG TGCAGGTCCA 780

GAAGCCGGCA TTAAACAAAT TGTTAAAGGT CTAA 814

(2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

TATAAATAGC GAAAATTTTT GACCAATAAA ATCTTTTTCT CTATAAAAAA ACACCTTTGT 60

CGAACTCGTA TAAAAATAAG TCCAACAAAG ATGTCAATAT ATATATTTAA CCTTTCAAAT 120

ATTCTCTTTA CTTTAATAAT CAATAAGGTT GTTTATTGGC GGATAGCTTA ACCCACTTTT 180

GCTACATACC ACTTATTAGC AGTTAAATAC CCTTGTTTCG TCTTTAACCT TGGTATACCA 240

TTGTTTGTAT ATTCGATTGC TTCAACTTCA ACAATCGTAT TCTTCTTAAC AGCCTGTCCT 300

TTTTTAGTAA ACTCAGTATT ATTGTAGAAA CAATCATCAA TTAAGAGCTT AACTTTTTTT 360

GGATTAGTGA TAAAGTAATT GTTATTGGTA TTTCCAGCAG CTGTCACATA GTTTTTATTT 420

GcAGTAAGAT ATCCTCCTTC TGtCTTCAAG CGAGGaACAC CTTTAGAGGA ATACyCaATG 480

CCCTTAAaCT GGaACmACaG TCCCaGATGa TAAGGTTCTG CTACCATTAC GGAAACTCCA 540

ACATCnGTAT AAAAGTTTAT CCnGGACACC CGCCAnAAAA ATTTGGGnGG 590

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

CCCTAnTGTA AAAATATTAT CCCTAAAAAT AGTCCCAAAC ATCCAAAAAT CAAAGGATAT 60

TTaTaTTTkG ATATGAATTC TaCCaTTGkt TTCTCCtATA AAACTTTTGA TTTAGTCTTT 120

GTATTTTTTT CATGATAATC CTTAAAAATT ATTTCGGTTA ATATTATTTG CTCTGCACCA 180

AATAATTCAT TTAAATTAGT ATTTACCTTT CTTATAAAGG CTGTTTGTCG CTCTCCCGtT 240

TGaAAAGCTT TGCGTAtTTT TCCTTGTATA TAGATTTTGA TTTTCTTTTT CTTAATTACA 300

GATTTTACTG TTGGATCAAC AATAAAAGGT TCTTCTTTTG CAGCAATTAA TACAAAGTTT 360

TCAATTGCTT TTTTTTGGAC TGCTATTTTT CCACTATCAG TCTTTTTTTC TATACAATTA 420

TGTGCTTTAG GATAAAACAA TACAATAATT AGAATAATAA ACAATAATGT TAGCAAACAT 480

CCACTAATCC AAAACAAAAA CTGTGCCATA CTATTACCAA TGTACGGATA GTTTGTAAAT 540

GGAAGTAGGT AAAATGGTAA ACTAACAACA CCTTGCATTG TTATTAATGT GTGTGCTAAA 600

GGAAAAAATA AAAAAAATAA AACAAGGATT AATAATAATT TTAATCTTTT TCGCATAATA 660

CACCTCTTTG TCTACGTTGT GAATATATTC AATTATCTAG TCATTCCTTG AAAATTCACA 720

ATTCAAATAA AATATATACT ATTAAAAATT TCTAAAGATT TTGTCACTTT GACTyCTwTA 780

wCyTTCTCTC CTTTCAACTG TATAACTTAT TTAGGTGAAC TGATAAAATA AATTTTATCA 840

GTTACTATTT CTAAAATTCT TAAAGTAATC AGACCTCaTT TCAGAAAAAT AATGAATGTT 900

TATTTTATAA AATAAAATAT TTGATGAAAC AATATTAACA AGAAAAATCT ACTAAGTCAA 960

ACAAAATGAA CGATCATATT TTTAGGGAAG AAAAATAATT TAAATTTTAC AATGAATGTA 1020

TGAGcAAATT TGTTGAGCTA ATATTTGGAT ATTTTTATAA TAAGTTTAGG GGTATCCCAA 1080

TATCACTCTC TAGGGGTGAC TCAGAGcAGG GGAAGGAGTT ACCCCTAAAA AGTATGTTAG 1140

AATGATTTTA TCGCATCATA TCCTTTTTTA TGTAATTAGT TGATAAAATC TAtCTGTACT 1200

TATATTTAAC GACyGaAATC GGTCACTTAC TGAAAAAACA TCTAAGGTAG AAATGAATCT 1260

CACCTAAGAT GTTTTTTGAT TnT 1283

(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

GGCCCCTGGG TTTCCAATCC AACCCCAnGG ACAATCCCCT AAnTTTTTTT TTAAACnTCC 60

TCTTTTCCGG TAAACTGGGG CTAGGCTTCC TTGGGTGGGA ATTctTTCtC tAtTCtTCtC 120

aTGgAAACtC aCTCCCaATT AATGgaATTT AtCtTTTTCt AGtAATCGtT TCAAtTCaCT 180

TTcAAAtTCt TCAGCTGaAA AAACATGCAA TCGATCAAAC ACTTCTTkGT ACTCGTCCCC 240

TTCTTTGTCA ATAAAATATT CTTTAAACAT ATCAAGTTCT TCTTTAATGA TTGAACTAGG 300

TGTTACATAA ATTAAGCGTG CATCTTCATA ATTTTTTAAA TGTTTAATGT ATTTTGGAAA 360

CACACCCTGA CTATAACGTC GTTTTGTCTT TAGTGTTAAT TCTATTTCAA ATTGCCACTC 420

TACTTCTCGT CCAATACTAT CCAAAAACAT AAAAATGAAG TCAGGAACAA AGTATTTTAC 480

GCCTTTTTGA TTTTTCTTCT CGTCTTTTAC TTCATATACT TTACGGCGTT CTGATACTAC 540

CGCTTTAAGG TGCGGGTGGT TATTACAAAG TTCCAACATT TTTATCAGAT AATCATTAAT 600

TTGTAAGTGG TGTTGTAAAT TGTATTCAGG AACTTTTGGC AAGGTGTAGT ACCCACCAAT 660

GTAATTATGG CCTTCTTTTG TTAGGTAATA AAATTTTGTT AATCCGATTT GGGAACATTC 720

CACTAGATTT TTTTCCTTCA GTTTTTTTAG ATTACCGTAT ACACTACTTT TTTTTGCCAT 780

ATTATCAAAT TGACAAAAGT CAATAAGTTG TTTTACCGAT ACAACTCTCA ATTCATGTAG 840

TAAACACAAA AGAATCAAGT GTATCTTATC TTCTTTTGAA TAATCAATAA AGTAATTGTA 900

AAGTAATGGT TTCAAAGTAT CACCGCATTT CTATAAAATG TACAAATAGG CAAAGCCTAT 960

TTGTTTCATT GAAAAAGAGT TTCGGAACAA CGTGTAGAAA TACTTTTTCA GCTTTTAAGT 1020

CCTCCAAGTT TTGGTGGAGG ATTTAGGAGG TTGTTGCTTT GGGCGATAGT CCCTTCAAGG 1080

TTTGGTGAAG GGGCGTCTAT CGCAAGGGGT AGTTGTTAAT CTTTTGAACT TTATCTTTTG 1140

AACTTTTTTC TTTAATTTTT ATTACTTCTA TCACCTTACT CATTCTATTT TTTTACTCTA 1200

TTCTGTTtGT CCTCGGCGCT TGGTATTTTT TTCGTAGTkG CAAAATTCCT GACCATTTTC 1260

GCTTAATGGG GGTTTTAACC CACGTTGAGC GAAAATGGTC AGGAATTTTG CAGGCGGAGA 1320

AAGCCTTTTA TACCAAGCGC CGAGGACACG CCACTACAAT TTATAATTCC ACACAATTTC 1380

CAGTGGTTTT CCTAAGTATT TCCATGATGT TTCCAAAATT TGACACACTA TATTAATCTA 1440

TTTTGAATTA CTTTTTTGTA ACCATTCGAG TGCGTTTCGC ACATAAACTT TTTGTGGTGG 1500

GAGGTTTACA TTTTCTGCTG TACGATAAAT AATAAACTCC CCTGTACGCA ATTCTTTTAT 1560

CTTGTTTGGA CTAATTTTGA AGCGATCTAC ATTACGTTTG GTTCCTCTAT CTCCTGACCA 1620

ATCAGATTTT CCAACATCTG AATAACCATC TTCTTGTTCC GTAACTGAAG TTACATCAAT 1680

GTCTTGATAC GTTCCCATTG TTTCACTCCA ATACTCGGCT TCACCTTTTT CGTTGGTCTT 1740

TCCAATGAAC AAAGTATTCA CATTTCCGAC AAGTTGTTCC ATTAATTTAT CGCCTAATTT 1800

TGCAATATCT GCCATCGTTT GAGGGGTGAA AATACCGTAA ACACCTGCAC CTCTACCTTT 1860

ATTTACCATA TCAATAAACG TTTCATTTAG ATAAGAAGCA GGTTCATCAA AAATCACAAG 1920

GACTTCACGT TTAACATTTT TTCGATACAT TTCAGAAGCA AAATAATTTA CGTCTCCGAC 1980

TAACATTTGC GCTAAAGTGC GGATATATTC TTTGTAAATC AATCCATTGA ACGATACGTA 2040

AACTAACTTT CGTTGATTGA CAATTTCTTG CACATCGAGA ACATTTTTTG CGTTTTTAGT 2100

ATCAAATAAT TTTCCTAACT CACTGTCTAA TAACATGTTA ATGTTTGTCT GTAATGCTTC 2160

TGATGTGGCA TACAAATAAA ACGGTGAATC TTTATGTTCa TAACGAATAA ATAATCGTTC 2220

GAACAATTTT TGTTTGATAT TTTCTCCTGT TTCTTTGTCT GTTGGCAAAT ATCTTAGGTT 2280

TCGTTTGAGT AATAAATAGT ACGAGTCTAA ATCTAATGTT TCTGGATTAA GGACAATCGT 2340

TTCCGTTTCT TTTTGTGCTA TTCCTAGTTG GGAAATGTTT CTAAATTTAC TGTTCTTAAT 2400

TTGTGAATCT TCCTCTTTTT CTTCTTTATC AAGGTCTGAA TCAGGCAGTA TCTCGCTTCC 2460

TTCTTTCACT GATTTTTTCT TAGGTTTTTG TATTTTCTTT TCTACTTCAA TCTCAAATAG 2520

TTTGGGATTG TtTGGTAAAA TTGCATCCGC AAATAAGTGT AAAACATTTC TCGGAAGTAA 2580

AAATCGTTGA ACAAATGGTA GACTTCGTTC AACGGTTTCT GTCGTACGAG TGTCTCCAGA 2640

TAAAGTAACC TTGGCTCCTT TAAACTCGTC TAACAATTGA ATTGTTACTT GCAAAAGAGC 2700

TTTnCGctGC GCCTGAATAA AAGACACTTT CTGTTTCGGC TAAAGACACT AACTTATCCC 2760

GAATAGATAT GTCATTTCCA TGCTCTACTG GGTTGTATCT CATATCGCCA TCATCCGTAA 2820

AAGCATGCAC TTCTTTGTCA TAAAATTTGG CAATTTCTCG CATACTTTCT AATGTATCTC 2880

GAGCGCCTTT TCCATCAATC AATATCACCG GAAAATTAAA TTTGACTGCG TGTTGGACGA 2940

GTAATTGAAG TAACGTTGTT TTCCCTGAAC CTGTCGTTGC GGGAACAAGA ACATGCTGAT 3000

TGAACTCTGA AAAGTTGATG ATATATGACA ACCCGAACTC ACTCATACCA AGTAATAATT 3060

GGTTGGATAG TTCTTTATAC TTGTCAATAT CAACACTTTC TACTGCTTCT TGGTATTCTT 3120

TTTCTTGTTC ATCAGTAAAG CGTTGTGACT CTTCAAACTT ATTTTTTTGC CTATTTTTGT 3180

ATTCTTTAGA TTCCGTCACT TTCTTCCGTT CGTCTTCCTT TGAAATAACT TTTCGTTTTG 3240

CCACAAATGA AGAAAATGCC AAAAAAATGG CCCCCATTCC ACTTGATCCA ATAAGCAAAG 3300

CGACTATTGT CTCCCAATTA AAACGAAGTG CTGTATGAAG AAGATTTAAG GGGAAAAGAA 3360

GATACGCAGA CAGATACCCT CTGGGAATCC AGAGGATAAA TGCAAAGACA TTTATTACAA 3420

ATAACACAGC TGAAAAACTA AGAAAGACAA TACTATTTCG TTTCAAAAAA CTCTCATAAT 3480

CCATATCAAA TACATTTGCA GCCTTGTCTC TTTTATCAAC CGCTAGACCA ATTAGTAATG 3540

GAATACTGCC TAAAATCGCA AAAGGATATA AAAGAACTCC GACTAATCCA AAGACTAGTC 3600

GGAGTTGGTG GTAGCGAGTC ATTTTTTGTT GTTCTTGCCC TATTGGCGGT TTCTTTGGTT 3660

GTAGCAACCC ATTGTTAAAC AAATTATTTC CTTGCACGAG GTTGTCTCAC TCCTTTAGGT 3720

TTGTTTGTTA TCTTCTGT 3738

(2) INFORMATION FOR SEQ ID NO: 709:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

GCGAGCTTTT ATTCAAATTG TTTTACCCAA TGTGTCTTCA GGAATTTTTG CAGCCTTTAT 60

GTTAGCATTT GTCAATTCGT TTAACAATGT TCCTGTATCG ATGTTTTTAT CAGGTCCCGG 120

TGTGACGATG CTGCCTACTT CTTTATTAAG TTATATGGAA TmCaATTATG aTCCaACTGT 180

TTCmGcAATT TCTGTATTGT kGATGCTACT AACaATGGGC TTAATGTTTT TAATTGAAAA 240

AACGTTGGGA CTAGCTTCCA TTGCCTAAAA CATGGAAGAA GCACGAGATA GAAAGAGGAG 300

AAAATTTTGA CTTTTGTGGA TTTAAAAGAT ATTCGCGTCA cTATGACGGA AAACAAGATA 360

TTTTAAAAGA TTTAAATATT TCAAgGAAAA AGGAGAATTA GTTtCTTTAT TAGGACCGAG 420

TGGTTGTGGT AAAACGACTA CGCTAAGAGT GATTGCTGGa TTAATTawGC CAAaCGACGG 480

ACAGTTTytC GTTGACCAAG AAGAACTAAC AAAGGTTCCT GTCCAnAAAA GAAACTTCGG 540

GATGGTTTTT CAAAG 555

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

TAAACCAAAC TTTTTTAATT TTATCTAATC ATACTAnAAA CATTCAATTT GGAGTCACTA 60

ATCCnGGTTn CTCTTTTGGT TCATCATAAT ACTCTTttCA aCCCcTCTCt ATACTCTtCT 120

CGAaTCTCAA CCaTTGATTT tGGTtCTTGT ACATTGCCTT tCTCTATAAA TATAACGTCA 180

TCAAGAAaTG TTTCCATATC TCTCAATATA TGACTACTAA TTATCAACAC TCTATTTTCG 240

GACAAGGTCT TAACATTCTC AATAAATAAC TCTACACCAT CAGGATCTAA ACCGTTAAAT 300

GGCTCATCTA ATAATACTAA TGAAGGGTTG TGAGCTGTAG CAAGACCTAG CAAAAACCTT 360

TGTTTCATTC CTAAAGACAT CGTATTAAAC TTTCTTTTTT TATTTACATT TAGACCAACA 420

TCCATTAATA GAGTCTCTAT CATTAACAAA TTTTTTAACT TGTAATAAAA AGCATGGTCA 480

TTGTATATAT CTTCAAGCAT AAATCCATTT AAACTATCTG AGTTAACAAA GTTAGTACCC 540

ACCTGcAATA ATATTTTAGG GTCTGCTATT TCTACTTGCC GATTGTCTAT TTTAAGTATT 600

CCACTATCAG GTCTAAnGCA AACTACATAG ACATTTCCAT CAAAGTTGGT TTTTACCTGC 660

ACCATTCGGA CCCAACTAAT CCCATAAAAT TTTnCCCTAC 700

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:

CGTAnATTGG GTGGnGCGGA GCTGTATTCC AAATGACATt CaCGTATTTC AAACTTTTTC 60

AAaGCTAAAT ATAACCTAAT CATACACTCT TGATAACAAT CTTCATCAAA ACTCCCATTT 120

CTACAAGATT CCTTAATTAG TAACGGTTaA ATTkGTyCAC AATCTGAGCG AACGCTTCTy 180

CATCATCCTT TTGAACTAAA ATAACAAGTt CTACCAATGA TTTCATTTCG TATTTCCTCC 240

AAACACTTAT CACTTTTTTT CAGTGAAAGC TCTGGTGGAT CACGATTCTT ATATATTTTT 300

TTAACTAACG TAgTAAACGT TCTCGTATTT TCTTTAGAAT ACGTTGACGC TTTTTTGTTA 360

CACCTTGTCT ACTTAACGAT AATTGAATTG AAATTTCATA ATCCGAATAT CCAAGAATAT 420

ATTTTCGCAT TAAAAAGGAT TTCTCTTCCC TATTTAATTT TTCAAATTCA GTAGCTAAAT 480

CTAAATTGTC GAATTCAAAT GATAAATTAT CTGtTTCAAC yCTGATCATT TCyTTTACmA 540

AGrAAGTCtT ATCTTCAATT AAGAAATCAA GAAACTTTTG TCCAGAAATA ACCTCTGCTT 600

CTTCTATTCT GGAATTTTTT ACAAAGTAAT TTATCGCaGT ATTATGAACG GTTTttTTAA 660

TATAATTTAT AATTTGAGCA TCATATTTTG TAACATCAAA GTTCTGTTTC ATCGCAGCCA 720

CTTCTTCCTT TGGAAATTCG AAAGGAAAAA GATATACGGA CAAGTTAGGG TGTGTTTCTA 780

TACTGCCAAT ATCCTCTCAT TGCACGCTCC ACAGAGATTG AATCATCTCG ATTTATTTTT 840

GGAAGAATAT TATTCACGAA ATTTCTATAA TCGGGAAGAA TATCATTATT TTTAGCTAAT 900

TCCtGATATA TTTGTTTACC TGACAAAGGT TTTCCTGACT CTTTTAAAAT CGATGCAATA 960

ATAAACCCAT AATCTTTGTA ATTTCGTTGA TGAGTGCCAA TCATTTTTCG CTGAATTAAA 1020

TAATCCTGAA GCACTTTTTC ACTTTTGAAA TTTGnAAATT nAGTTTCTTG AGATAGTTCA 1080

TCACTAGAAT CCGAAACAAT CTTGTCTTCT TCTAAATGAA TCAAGTACTC TTTTAAATCA 1140

TAATACTGTC TTGAAAGTTC CCTCCTTTCC TCCATTAACA GTTTCAGCTG TTCATACACA 1200

TGACATTTTT CATCAGGAAT ATCCAG 1226

(2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

AGTTGTTCAA TTTTCTACAG AAAATTTTTG GTTTCGCTTT GTTAGTGGAT TAGTGGCTGT 60

TGGACTTGGT GCCTATTTCG TCTATCTATT TGTTGCTTTT TTGAAAAAGA AAAAGCTCAT 120

AATTTGGACT TTTTTAGGAA TCAAAGAAAC CTTGCCAGTG GTCTTGTTAG GTTTGGTGAT 180

AATCTTTTGT GTGGGAATAT TTGGTGATTT CTTATTACGT CTGGAAGGAT TAGAGACGAC 240

CTCTAACCAA CAAAGTGTTG AAGAAATTGT CCAATCTATT CCTAAAGGGC TTATACTTAT 300

TTTTGCAGGT GTGATTGGGC CAATTTTCGA AGAGGGAATT TTTCGTGTCG GGATTCAAGC 360

GTTTTTCAAG CCAGCTTCAA AAATAGGCAT ACTCGTTTCT TCwAwTTTAt TTGCACTTGn 420

GCACACGCCG ACAGATATAG GkAgTTTtGT tATTnATgGG GCAnGGGnTT AGCTTaAGTT 480

GGGnCyAwCw ACGCACGGGC GCT 503

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

AGTCAAAGAA TTACAAGCAT TGGCGGCAGC AAAAAATCTG CGCCTGATGG TTGGCTTCAA 60

TCGTCGTTTT GCCCCTTATA CGGAAGTATT GAAAAATATT CCTGAAAAAC AAACAATTTT 120

TATTwAAAAG rACCGCATCm ATaCAACGAG AGAAACAAGT TTTATGATGT ATGATTTATT 180

TTTACATGTC GTTGATACCG CAGTTTATTT AGCGGAAGGA CCGCTCCACG TGGTGCAGTC 240

AAAATTAGTG GAAGAAAACG GTCATTTAAA ACGAGCAATT TTACAATTAG AAACCGAACA 300

GACAACGATT GTTTGTTCCA TGGATTTACA CTCTGGGGCC AATACAGAAA CTTTTGAAGT 360

CACCAGCCCC ACAGGTACTT ATCGCTTGGA AAATTTAACG CATTTGACCA TCCAAACAGA 420

AGAAGAATAC CAAGTAAAAG AGATGGGAGA TTGGACGCCA ACATTGGAAA AAAGAGGTTT 480

TTACCAAATG GTTACTGCTT TCATTCAGGC CATTCAAAAA CCGCAAGAGC AAGAGTTAAA 540

GCAAGAAAAA GTCTATGAAA GTCATGCGTT ATGTGAAGAA ATGCTACGCC AACAACAACG 600

GCATGTTCTT TAAAGGGGAC TAGCAACTTT CTTTCTATCA TGCTAGGGAG GTGCGACAAG 660

TCCCTGnTAT GnGTCATGTT TGTCATCTGG AGCCATAGnA CAGGGTnCAT CATG 714

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

TTAACTTTTC CCGGTnGCCC CAAAnAcCAg GCyTACACCa ACTAATACTG ATGCAACACC 60

CACACTTAAT TtTTTTATGC TATACTTTAA TACTCTTTTT CTcCCTTTTT TTAAAATCAT 120

ATGCTTATTG TTTTTTCCAA ACAAACTAAA TTTGCTCCCT TCCTTATTTA AATTTAAAAT 180

TACATTTTTA TTATAAATAA TACAAAATAG GAATTCTTGT AAATATCACA AATATTTGTA 240

AAAAAATCAA AAAAATAAAA TATTATAAAA AAAACCGACC TTTACGGGGT CACTGGAACA 300

TCCCTAGAAA TCAAGTAAAA AAAATCCAGA GGATTTTCTC CTCTGGATTs ACTATTACTC 360

TACATTTTTT AGTTATTTTA TTATTCAATT ATTCTCATTA AAAATTTTTC TTTCTATATT 420

ACTTAACACG AGATTCCGTT AATTCTTTTG CTTTAGAACT TCCTTTAGAA GCTAGcTCTT 480

TTGcTTTCTC TGTTTGCTCA CTGGcAAAAT TACTTACTGA TTCTGTTGCC TCACCAACCT 540

TATCTTGTAA ACTAACGGAA TCTTCTTCAT GCTGTTCTTC TGTCTTAATA TCAACAACAT 600

TTACATTTAC TTCAATAACT TCTAACCCAG TCATATTTTT TACTTCTTTT GTAATAATTT 660

CTTTCATTTC ATTGTAAATT TTATAAATAT CTTTTCCATA TTCTGCAACA ATATCTAAAT 720

CTACTGCTAC CTGTTTTTCT CCTACTTCAA CCACTACACC TGATGTAACA TCATCGGTAT 780

TCACTAACTT ACCAGCTAAA TTTGAGAAAA ATCCACCATC AACCGTAAGC AATCCTTCTA 840

CTTTTTCTAA AGAAATGCCA ATAATTTTTT GAATCACTTT ATCTTCATAC GTTAATTTTC 900

CTTGTACATT TTCCTTCTTT GTTTCTTCCT TTACACTTAC TTTTGTTTTC TCCATTTGTA 960

TCCACTCCTA AATATTCTTT ATTTTATTTA TTTTGGAAAA ATTTTCCAAA TAAATCCTCA 1020

TTTTTAATAT AACTCCCTAT AAATACACCA ATCCCAACCA TAACTAATAA GAGAATTGTT 1080

TTAAAAAAAC CAATAGTGAA AAAGAAAAGT GCTAATACCA ATCCTATTAG TCCTCCAATA 1140

ATTGGATACT TATATTCTAG GAACAATTCT TTCATATTCT CCCCTCTTTC 1190

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

TTTAAAACAG ATACAGGATC GATTCTGATT AAACGTGTGA TTGGTTTACC AGGAGAAGCT 60

GTGCGTTACG AAAACGATCA ATTATATGTC AATAATCAGC CAATCGCTGA ACCGTATTTA 120

ACTAAAAACA GAAAAAAAGA TCATGAAACG ATGCCTTACA CTACGAATTT TGATTCAAAA 180

GAATTGTTAA TGCAAGAAAA ATTACCTAAA GATAGCTATT TTGTGCTTGG TGATAATCGC 240

CGTATGTCCA AAGACAGCCG TTCTTTTGGT GCAATACATG CAGATCAAAt CTTAGGGAAA 300

GCACAATTTG TTTATTACCC ACTCACTCAT ATGAAGATCA TTCCTAAATA AGTAAGACCA 360 mTAGTTCGTT TATTtAAATA ACGACTAGTG GtCTTTCtAA TCTGaAAAAT TGTyCTCTTA 420

GCTGnAAAAT GGTAAGGGTA AAGTAATGGT AGATGTAGGA GGnCATGCCA ATGATTAGAA 480

AAACAATTTT n 491

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

TAGTACTAGT AATCGTTATT ATTGCTGCGG TGCTATACTT AATTGGTTAT TTTATGCGCA 60

AAAAAAATCA AGAACAATTA GATGAATTAG AAGTTCGTAA AGAAGCCCTG TTTGACTTGC 120

CAGTCTTTGA AGAAATCGAT GACATTAAAA AmATGCATCT AGTTGGACAG AGTCAAAATA 180

GTTTCCGTGA ATGGAATCAA CGTTGGGTAG AACTATCGAC GCGTTCTTTC GCCGAACTAG 240

AGAGTCAAAT TTATGAAGTC GAAAATCAAA ATGAAATTTT CCGTTTCATG AAAGCGAAGA 300

AAGCGGTCGT GGAAGCGAAT GAAACGATGA CCGAAaATGGA AGCCGAAGTG GAAGTCaTcG 360

TAATGGCTTG AaAGAATtAC GTGaAAGTGA AGAGCGCaAT TCATTAGAAG TTCAAAAAGC 420

TTnGGAGGnC ATGA 434

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

AGTGCAGAGA TTGCATTATT TTTTATCGCG AAAAAAGAAC CACCTGGATG TGTGGAACTA 60

GAAGCGAATA AGGAAGGAGG AGAACAAGGA ATGCCTACAA TTAACCAATT AGTACGTAAA 120

CCTCGTAAAT CTAAAGTAGA AAAATCTGAT TCACCAGCCT TAAACAAAGG ATATAACAGT 180

TTTAAGAAAA CTCAAACAAA CGTTAACTCT CCGCAAAAAC GTGGAGTTTG TACACGTGTG 240

GGTACGATGA CACCTAAAAA ACCGAACTCA GCTTTACGTA AATATGCCCG TGTTCGTTTG 300

TCAAACTTAA TCGAAGTTAC AGCTTATATC CCAGGTATCG GTCACAACTT ACAAGAACAC 360

AGCGTGGTAT TATTACGTGG TGGACGTGTA AAAGACTTAC CAGGGGTACG TTACCATATC 420

GTTCGTGGTG CGCTTGATAC TGCCGGTGTT AACGACCGTA AACAAAGCCG CTCTAAATAC 480

GGTACAAAAC GTCCTAAAGC TTAATTATAA TAAGACAATA ACAACTTGAA AAATCATATT 540

TCGGAAGGAG GAGTTACGGA TGCCTCGTAA AGGTCCTGTT GCAAAACGTG ATGTTTTACC 600

AGATCCAATT TATAACTCAA AATTAGTAAC TCGCTTAATC AACCGTGTAA TGGTTGACGG 660

TAAACGCGGG ATTGCTGCTA ACATTATCTA TAATyCATTT GATATCATCA AAGAATCTAC 720

AGGTAACGAT CCATTGGAAG TTTTTGAACA AGCAATGaAA AACGTTATGC CTGTTCTTGA 780

AGTTAAAGCA CGTCGTGTTG GGGGTtCTAA CTACCAAGTA CCAGTTGAAG TTCGTCCAGA 840

ACGTCGTACA ACTTTAGGTT TACGTTGGGT AGTTAACTAC GCACGTCTAC GTGGTGAACA 900

CACAATGGAA GAACGTCTAG CGAAAGAAAT CATGGATGCT GCTAACAACA CTGGCGCTTC 960

TGTTAAAAAA CGCGAaGACA CACACAAAAT GGCAGACGCA AACCGCGCAT TTGCTCATTa 1020

TCGTTGGTAA GATCCTCTCT GTCTGTCGCG TAAAGTGGCA GCAGAAaGTC AATTTACmAT 1080

CGATTTaAAT AAAGAGAGGA GTAAACATAC AAAATGGCAA GAGAATTTTC ACTTGAAAAA 1140

ACTCGTAACA TTGGTATCAT GGCCCACGTT GATGCTGGTA AAACAACAAC AACTGAGCGT 1200

ATCTTGTACT ACACTGGTAA AATCCATAAA ATCGGTGAAC CCATGAAGGT GCTTCACAAA 1260

TGGACTGGAT GGACAAGA 1278

(2) INFORMATION FOR SEQ ID NO: 718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

CGTTnCCACC AGGAACAACC ATTAACnGAT GTTACnTCCT GGTGGTACAA TCGATACTAA 60

TACACCAGGT AATTACGAAG GTGTCATTGA AGTAACGTAT CCAGATGGTA CAAAAGATAC 120

AGTAAAAGTT CCaGTAGAAG TAACAGACAA TCGCTCTGAC GCTGATAAAT ATACACCTAA 180

AGGTCAAAAA GTAACTACTG AATTAAATAA AGAACCAGAA GCATCTGATG GAATTAAAAA 240

TAAATCGGAT CTACCAAAAG GAACTATGTA TTTTTGGAAA GAAAAAGTAG ATGTGGGTAT 300

ACCTGGAAAT AAAAAAGCTA CTGTTGTAGT AATATATCCA GATGGATCTA AAGAAGAGGT 360

AGAGGTTGTT ATTTCTGTAG TAGATAAAAA AGCGCCGAAT AAACCTCaAG TTGATCCTAT 420

TACAGATGGT GACAAAATTG TTACTGGTAA AACTGaACCm AATGCaGATG TaACaGTwAC 480

GTTACCTGAT GGAAGTCAAT ACCATGGCmC AGCTGATAAG AGTGGTTACT TTAAAGTTAA 540

CGTTCCTAAA TTAGAGGCAG GGACAAAAGT AAAAGTAACT TCAACTGATG AATCTGGCAA 600

TACTAGTGAA CCTACTGATG TAGTTGTTTC GTCAAATGAA TTAAACGGTG GAAAAGGTAA 660

TGGAACAGAC AGTAAGACTA ACAACAATCA AGATAAAAAA CAATTCTTGA AAACTTATCC 720

TAAAAcAGGA gAgGTTgAtA GTAATATTTA TACTATTGCT GGTGGTTTAA TATTGTTAGG 780

AACTTTAGGG TTATTAGGGT ATGAAAAATG GAAAAAAGAG GATGAATAGA AGTTTAAATT 840

ATTAAATATT CTCTGAAAAG AGGAAGAAGT CTCTTCCTCT TTTTGTTTTA tTGTTGTTTA 900

tTTAAATAAT AtTGTGGATT TTATTATtTT TTATTAAAAT AATGTTGATA TTAAAATGAG 960

TAAATAATTA CTAGATAATA TTTATTTACT TATAGTAAAA GTTCATATTT AAGTAAAGGA 1020

GTTTTTTTTT TGAATACGGA TAAAGAAGTT TTATTAAAGT CATTACATGT ATGCTTAGGG 1080

ATACCTATAT TAGTATTTAA TGAAGATTAC ACTCTTGTAG AAGAATATAG ATCTGATAGG 1140

ACTATATCAT TATTTTATGA TTTCCCAACT TTTTTAAAAA AAGTTGGGAA AGACAAGCTT 1200

AAATTTGATT ATATAACTGG TAATTATAAT GAGTTGTTTT TATTGTACGC ATACAATAAA 1260

AAACTGTTTT TGTTTGGTCC ATTCAGATGT AATACCATAG AAAAAGATAA ATTCTATTCT 1320

ATGGGATAAA GTCCGTATAA TTGTGTAAAA GTAAAArGGC CATATAACAG TCCTTTTACG 1380

GTACAATGTT TTTAACGACA AAAACATACC CAGGAGGACT TTaCmTGACC CAAGTACATT 1440

TTTACACGGG AAAGCGAnGA GGA 1463

(2) INFORMATION FOR SEQ ID NO: 719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1064 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

CTAGAGTATT GAACCCGCAA GATAAGCAGG TGGGTTCCTC GATCGCAGTA TTGAACTACC 60

AAAAGAAAAG GCATGTTACC AACTTTGATA CAAGCAGGAT CCCTAGATAT CAATAAAAAT 120

GTTCGGTCAA CACAGTGAAA GGACAACGCG TACATCACAG ATTTACCATC TTTATAATAG 180

CATACTCTCT CArAATCGGC AACGAGATTG TTTCTTTTTT TGAAAGCGTA TTATTTTGTT 240

ATTTTTTCTG TTTCCATTCT TGGATACGCT TGAGTTGCTG ATGTAAGGCT TGTTCATATT 300

TACCAATATC AATCGGTTCG TAATAACGTG CCTCTTTTAA TTTGTCAGGT AAGTATTGCT 360

GATTGACCCA ACCGTTTTCA AAATTATGTG GGTATTGATA ACCAATGCCA CGGTTTAATT 420

CTTTGGCTCC AGCATAGTGG GCATCACGTA AATGATCAGG AACATCTCCC ACAGAGCCTT 480

GTCGAATATC TGCCAAAGCA GCATCAATCG CTGTGACTGC AGAATTTGAT TTTGGCGATA 540

AACAkAAATC AtGACGACAC TAGCTAGAGG AaTCCTAGCT TCTGGAAACC CTAGCTTTTC 600

GGCGGCTTGA ACAGCGGTGA CCGTCCGAGC GGCGGCCGCA GGATTCCCAA GACCGATATC 660

CTCGTAAGCA ATGACCATTA AACGACGACA AATAATCGGT AAATCACCTG CTTCAACTAA 720

GCGACCCAAA TAATGAAGTG CAGCATCTAC ATCGCTTCCT CGAATCGACT TTTGGAAAGC 780

GGAAATCACG TCATAATGGG CATCGCCATC TTTATCATGC GTTAAGGCTT TTCGTTGCAC 840

GCACTCTTCA ATAATCGGTA AGGTGATCTT AATTTCGCCT TGTTCATTTT TGGGtGTTGA 900

TTTAACAGCT AATTCTAGTC CATTTArCGC ACTACGTAAG TCACCGTTCg TTGCGCGkGT 960

CAAATGTgTA ATGCTTTTTC TTCTAAGTGG ACAGGATAAT CGCCTAAGCC ACGTGTGCTA 1020

AACGGnTAAn GCTCTTGnAT CGCTTGCTGA ATGCTGTTCC GAAA 1064

(2) INFORMATION FOR SEQ ID NO: 720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

GCTATTAnAA TTATATTTTA ATTCnAAAAT GnATAAAAAA GTTAATTCAG AAATATrCAT 60

TGAAgCAAAA TAAAATAATT ATTTCTGAGA cTGCTACATC TATAGTTTTA AAAGAAAATA 120

ACAATATTAA TAAACACGCA TATATAAAAA AATACATTGA GTGTTTAGTT GAATTGTATA 180

AAGATGACAA CTATAAAAAT ATTTCAAATA AAATAAGATT TTATCATGAT TCAATAAATA 240

AATTGTATGA AGATAATTTT GAATATTGGA TGTCACATGA GCAATCAGAA TTAGAGAAAA 300

TTAAGAACAC ACCACCAGAA AAATTAGAAG GTGAAGATTA TGATTATGTG GCTGCAGAGA 360

AGAATATTGA GCATTATCAA AGAAAAATAA AAGATATAGA AGTTAGTTTA ACAAACTATC 420

ATAAAGCTAT TGATTTCTTT ACAACAGTTA TATCCTTATA TTTAAAAATA GArTGGGATA 480

AAGCCAAAGA AGGCCAGTAA CAGTATTGTA AaTTACTCAA TTTAATTAGG CATTTATAGG 540

ATAGTTGAAA GCAGTTAAGC TAATATATGG TACTGTAAGT TAAATTAAAG TTTGCTGAGA 600

TACTTTTTTT TCGATTTGTC ATACGCTATA CTTAAATTCA TAACGTTGAT TTTAATAACC 660

AAATTTATGA ACGGAGATGT CGTT 684

(2) INFORMATION FOR SEQ ID NO: 721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

TGTCTATTCT ACTCCCATTA TAGAACAGCA AATCAAGCTA AACAATATAT AAACACTAAC 60

CCATTGCTTA ACTTTATTTC CTGAAACAAC CTATTAAATT GTTACTACCG CTTCTAATAA 120

TAGCTTTACT TGTTGTATAT CTTCACTATT TTTTTCACTA GGTGTCTCAA TCATAAGATC 180

TAGTTTACCA ATCGCTTCTT CAATATTATC CGAACCAATA CAAACTTTTC GTTCAAAATC 240

TTCATGTATT TTACACGCAT AAGACCTTAC AAGTTGTTCT AAAAATCCTT CAAATAACTT 300

TACTACTGCT TCTTCATTTT CAAAAAATAT ATTATCCAAT AATAAAAATT GAACTAAATA 360

TTCACTCGTT TCTTCATATA AATTCAAATA CAATTGATGA TAATATGGAA AACTGCACCA 420

ACAACGATAG GCACTAAATT TACCATTTAA AAAACGTCTA TACTTTTGTC GTTTTAATTC 480

TAATtCTTCT GATAACATTC TTCTTTTAAT ACACCTCCTT CGTTTGAAAT TTCCTTCAAA 540

TTACCACTTC CTTTATGAAG AAAAACAATA CTGCTCTTCA ATCTTCTCTC AACTAGCCAA 600

TTTAATGGAT TCAATCTACG ACTTTCCAAT AATTCTTTTT CTTTTCTAAC TGGACGTTTC 660

TCTTGTTTCA TTCCAATCAC TCCCATTTTT TTATTAACTT TACCCACTCT TTTTGAACTC 720

ACTCAAAATA CTTTGAACTA AATCACTACT AATAAAACCA GCAAAATATA GTTGCATTAA 780

GTATCTCCGA GCATAGTCAT ACCTGCTCAT TGGGAAAAAT GGGTTCGTTT CAAAAGTAAC 840

AAATAATTCC CTTAATGAAT CAATCGCTTC ATTtGATAAG TtGAATTTTT TtGGATtCTT 900

AATTAATTCC TCTAATCGAT tCATCkTTtA ACTAACCACC TCATTTTTTA TTATTAATGT 960

CTATTAACAA ACCTTGTTGA CACAAATTAA TAATAAAAAG GGCACTCGTT AGAATGCCCT 1020

TTACAGCTGT TAAACGGCGC TACCGTTCGT CCGAATACAA TATTTATTTA CTTCTATTGT 1080

TTATTTTCTT GTTTTTCCTT TGGTTGAGGT GCCTGTGTTT 1120

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

AAnGAnCCTC TACATACAGT AGGCCCATCT AACATGTCTG GTnCTTTTCC TAACATCTTA 60

GCTAGTAGCC TTAGGTnTCT TTCACACTTC TCTTTCCCTA AGTATTTCTT TGTAACCGTC 120

ATGGAAAAAA GTAATCTCGC TTTCAACGTT AAAAATTGGA TCTAATCCTT TGTTGTTCCT 180

CAACTCTTCA TGTATTAGAC CATAATACTT AATTTTATTA TTGTTTCTAA ATAATCGACT 240

TTGGCCATGT GTGATAACAT TATCTAATTG ATATATTGCA CAACTAACTC TTAATGAATC 300

TTTAAATTTA AACCTGTCTA ACATATCTAT TAAGAGCCTT AATTTGGTAA GCTCATCTGA 360

AGATACATAT TCATCTGCAT CAATAATTAA TATCCATTCT TTACTTGCTT TTTGTATTGA 420

ATAATTTCTC GCATCTGAAA AATCATCTTG CCAAGTATAA TCAAATATTT TTACTTTTTC 480

GCTGCnATTT CTTTTACTAT TTTTTTTGTC AAATCAATGG ATCCTGTATC AATAAATAG 539

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

CAGTTGAAAC AATTGCTACT GCCAATTTAT GGCTACGAAC AGCAGATCGG ATTAAAATCG 60

TCGTTGGCGA ATTTAACGCC TATAGTTTTG ATGAATTATT TGAAAAAGTT AAAGCACTTC 120

CTTGGGAAGA TTATTTGCCT TTAGATGCAG AATTTCCAGT TGCAGGTAAA TCAATTAAGT 180

CAAAATTGTA TAGTGTTCCT GATTGCCAAG CCATCACCAA AAAAGCCATT GTTAACCGTT 240

TAAGAGAAGT TTACCATCGT CCAGCGACGG TGCCTTTAAC CGAAACAGGA GCTTTGTTTA 300

AATTAGAAGT GGCTCTTCTA AAAGATAAAG TGACGTTGAC GTTGGACACG ACTGGACCAA 360

GTTTATTTAA ACGAGGCTAT CGCATTGAAA AGGGGGGCGC ACCTCTTAAG GAAAaCATGG 420

CAGCTGCTTT AGTGAwGtTG ACCAATTGGC GCAAAGaTCG TCCTTTTtAT GATCCAGTTT 480

GTGGTTCTGG AACAATTTGT ATTGAAGCAG CATTAATTGG GCCATAACAT TGCCCCTGGC 540

TTTAATCGTA GTTTCACTTG TGAAACATGG GATTGGGTTG ATCCAGCAAT TTTTGAAAAA 600

GTACGTAACG AAGCCGAGGC AAAGGCAGAC TAC 633

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

ATAGTTTTAC TCAGAAAATA AAAAGAAATA AGGTATGAAA TGATTGTTGT TATAGTTGGA 60

TATAATTTTG AGAAACCGTC TGAAGATTTT AAAAATGCAC TGCCTATTAC TTCACTGACT 120

ATkGCTAwTA mCAAaTATAA ATATGGCATA GAAATtGCtC CTTTATTAaG TGATATTTAT 180

ATTTTAcmyT TTAGGTGGCT AATTCaATAA TAAATAGACT TGTATTTTTC TAGTGATTTG 240

CGAGGTATTG ATTTTTGTGA TTTCAAAAAT TTTAGGTAGG TTCTGAAACG AGTTGAAAAC 300

GAGTTTCTTC TTGTCTTGAT AATATAGGTA ATTATTCAAT AATATAGGTA ATTATTCACG 360

GCGAGTTATA TCTACGCTAA ACCGTTGATA TTATTGGTTT AAAACACAAA AAAAGTTGCT 420

TTTTTCAGCA TACTATTTTA TGATTAAGGT GTCGAATCAA AATCAAAAAT AGAGAGGAGA 480

AAAAGCAACT GTTTTTTGCT ATAAAAAACT CTTAAGTTGT TTGGTTCTGT TGCAAAGTTT 540

TAAATCTACT ATCAAATAAG GTAGAATAAT AGAAAAAGAT AGCAGGAGGA ATGACGATGA 600

ATCATTTTAA AGGAAAGCAA TTTCAGCAGG ATGTGATTAT TGTAGCCGTG GGCTACTATC 660

TcGTTATACC TT 672

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 599 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

GGTAAACCAG GATGTCCTGA GTTCGCTTTT TGTACGGCTT CAATACTTAA TGTCCGGATT 60

GTATTAACGC CCAATTGATC TGTCTTGTCA AACAAAAAAA TCATCTCCTA ATTTAGGTTT 120

TTTTTACCTT TATTCATAGT GTAGCTTATT TCGACAATGA AAGCAATTAC TTTCTGTTGT 180

GAAGTCCTTT TTCACGCTGA ATTTTTTTTA GTTTTTCAGG AGTCACATCG GTCCCTTCTT 240

GATCCACGAC CTTCATTCCT TCGATATGGT GACGCATCCC TCCACGAAAT GCTTCTAAAT 300

ACTCTTTACG TAATTCTTGT TGTTCGACTT TTTCTTTCGC ACTAAGTTCT cCACTTTTGC 360

TTaTTCGCTA ATTCATTtAT ACGGGCAATT TTTtCTTtCG ATAACATCAA AATCCCTCCT 420

TACTCTCACt GTCTAwATtA TAAGAAcTGC CTtAAAAAAA CAaCtATATt CTGATATTtA 480

TAAAaCaCGA aCGCTtGTTt GATTcGTcGC ATTTATGGTA CACTAnTTTT nTTAnGGAAA 540

GAGGTGCGGG TTTGGCGAAC GACAGAACAA GCAATAGAAG ACTAAATATA TATACGACA 599

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

TTTATATCCT CAGGCACGAT CTAGATGTAG CTCTTAGTAA ATCTTTTTTA AAGAAAAATT 60

GTCGCTTTTC TATTTCAAAT TTTGAGTATC TATTTTTATC ACACCATTCT GAAAAATTAA 120

GATATCCAAA AGCGCCGTAT TGTTCTCCTA AAATnAAAGC AACCCATGTT TTCAACGCAA 180

CCTCAATTTT CTCTATTGCA TGTAACAAAT GAATTCTTAA ATTTTTATCT TGATAGTATC 240

TTTTCAAAAC ATCGGAAAAA TATATTCCTT TGTAATCATA TACAGTATTT TCATTAACAA 300

TTTTCTTATT AGCTAAAGGC GCAGCAAACT GCTTAATTCG ATAATATCCT ATAACTTTTA 360

ATTTTTCTAC ATCTTTTGAG GTCATCTGCA TACCTCTTTC TTCAAAAAGT GCCATTTGTT 420

CATCAAACGA TAATGATAGT GGTTCCTTCA TATTTTTCCT CCAAAATAAA AAAACCCCCA 480

TGTCAGTACG TGACTGTCCT AAAAAGGGAT GGGGGGATTG TCTTCTTTTT TAAAGAATAA 540

TATACTTTTA AAATATTGTC AATAGCTTTT ACTTATTTGA ATGGACCATA CAGGACTCGA 600

ACCTGTGACC GAACGGTTAT GAGCCGTTTG CTCTAACCAG CTGAGCTAAT GGTACAAGTA 660

AGAACCACCT TATTGAGGAT AAAATAGTTC TTAC 694

(2) INFORMATION FOR SEQ ID NO: 727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

TATCCAAGGA GTGATAGGAC ATTAATCGAT CCATAATTTT ATCTGGTGCT GGCCCCCGGT 60

CATAGATATC CCCAATAACA TGTAGGTGAT CGATAATCAG ACGTTGGATT AGATAAGCTA 120

ATTCTGTTAC GAAACGTTTG GCTTCACCTA GTAAAATAAT TTTTTCAATA ATTTGTTGAT 180

AGTAACCGTT TTTGGTTGTT GTTTCATCAT ATTGATAAAT CAATTCTTCG AGAATATACC 240

CATAGGTTTC AGGAAGGGCT TTGCGAACTT TAGAACGTGT GTACTTCATC GAAGAAGAAC 300

GGACGATTTC AACCAGACGG CGAATCGTTA ATAGCCACCA TTCATnAGaG AGGGCGCTTT 360

CATTTTCTAA AAGTGTTAAT TtTTCTTCTG GaTAGTAGAT AATAAAACmA AGCTCGTCCa 420

TCTGATGGGC ATTTAATyCT kGTTTAAATA AAAATkGAAC TTTTTCTCGG aTtCGCCCAG 480

AACCaTTTCt TAAAATATGG TCAAAAGCTt CAAaTTCACC ATGTAAATCA CTGACAAAAT 540

GTTCTGTTCC TTTCGGTAAA TTCAAAATTG CTTCCAAATT AATAATTTCT TCAATTTGTT 600

GATCGCGGTT CAGTGTAGCC AAGTCATCTG CCTTCTTTCT TTTTCGTATA TACCAATTTT 660

AATTTAAAAG ATTAAAGTCT TGATAATAAA GGTTTTTTAT TCGTATGCCA ATTATTGTAG 720

GCTAATTGGC GAAAAAAAGC nACCGGAGAA AGTCAGAGGA AAATGGGGGA AATTATAnGG 780

AGCnACCGGG GTTTAAGCCA AGAATTTTAA TTAAACCAAA TGGAAGGGCC GGGAAACCAT 840

GTAATTGGGA CAGCCAAAAT GGATCCGGGA AATCCATTAG GAAATCGGnG GTTGGGACAC 900

CGTAAAGTTG GCGCCAAAAA TCCGGGAC 928

(2) INFORMATION FOR SEQ ID NO: 728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

GCCTGGAGCA GAGCATGCGA GAACTTnATA ATAAAAACCC AGAAAAATAT AAGGAAACAG 60

TAGCTGCTTT TCTAGATAAA TATATAAAAT AACAAATTTA TTCTTTACTA ATAGTAGCAA 120

CAACAAAAGA CTTGTTCTTA AGTTAACGAC TTAGTGAACA AGTCTTTTGT TGTCAGTTGA 180

TTTTTTTTAA TAAGTTGGAA TTTACCCATG CAATCTAGGG CATAATCTGA TAGGATAGTA 240

CTAGAAATGA GGGAAGGATA ATGGAAGAAC AATTAGTCGA TTATTTACAC TATTTACCAA 300

TAGAGCGGGG cTTATCaATA ACACACGGCG GArTTACGAA CGAGAtTtwA AAAAAtACGT 360

rGCCCTTTTT ACCAGGACCA AGGCnGCATT CTTGGGCCGA ATTGGACCGT TACCnGGnTT 420

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

GATGGGAGGC AAAAAAATGA ACATTGTCCT GAACAATCCA TTGGAAACAG AAGCAATTGC 60

TAAAATCATT GGACAAAAGG CACAAGCTGG TGATGTAATT GTCCTGACTG GTGATTTAGG 120

GGCCGGTAAG ACGACAATGA CGAAAGGGAT TGCTTTAGGA TTAGGCATTT CCCAAATGAT 180

TAAAAGTCCC ACCTATACGA TTATACGCGA ATATCCACAA GGACGACTTC CGTTATACCA 240

TATGGATGTC TACCGTGTTG AAGAGGGTGC GGATGAATTA GGGTTAGATG aGTATTTTGA 300

AgGAGATGGG CTATCCGTTG TAGAATGGGG CAGCTTGGAT TGAAGAAGAA TTGCCAGAA 359

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

TCCACTTATT TTTTCATTtT CCATTGACAG AATAGTTGTa ATTGTcCAGA wAATTGTATA 60

TAATAAAGAA AGTTATTTTC ATATTATTTT TTTTCAATTA AAGGAGAATC CTATGAGTGA 120

AACACAACAA ACAACCTTAA AAAAACAATT AAGTCGCGCC ACATTACGAT GTTAGCCTTA 180

GGGGGAGCGA TTGGCGCAGG TCTTTTTAAA GGAAGTGGCG AAGCAATTGG TATTGCTGGT 240

CCTTCTGTTT TAATCGCCTT TCTAATTGGC GGTGCTGTTC TCTTCATCGT CATGAGTGGT 300

TTAGGAAAAC TTGTTTTAGA TGGCGGArAC ACACATCATG GTTTGTCTGG CTTGGTTCGA 360

CCATTTTTAG GTGCACATTC TGCTGATTTT ATTGATTGGG TTTATTATTC CATGTGGACA 420

ATTAATATTA TCGCAGAAGC GGTTGCCGCA GCTTCCTTTT TACAACTTTG GTTTCCTAAT 480

ATTCCTGCTT GGTTTTTTGT TTTTATTTTA rCTATTTTAA CGACGCTCAT TwaTCTTTAC 540

TCGtTCGTTT ATTTGCAGAA AcArAAtATT GGTTGGCGTT TGCTAAAATT AGTGTCATCA 600

TTTTGTTAAT TATTTTTGGT GTTTATCTGG TGGGACAACA AATGCTAGGC AGTGGTGTCT 660

TCCCTACTTT ACAAAGTATC ACCGATCAGG TGGCTTCGCC CCACAGGCAT GAAAGGTATA 720

GTTAATTCTT ATTAGTAGTT ATTTATCCTA GGCGGTTCAG AATAATCGCG ATTACTGTCA 780

GTGAAGCAGA TGATCCTAAA AAAGCCATCC TAAAGCGATC GTGGTGTGAT 830

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

TATTAAAAAA AATAGTTGnA AGAGTACTTT sAAATTTGTA AAsAsTAGAA ATGATTTTTA 60

AyATTAGTAA GsTTAAAATA GTCATTACTA TAGTTGAATA AACTAATCTT GAATAATACT 120

TTCTGTTATA TTTTATTGGA TTAATATCAA ATTTTCTACT TAGAAATCTA TAAGCTAtGA 180

TGGTTGTAAA CATCGTACAT ATAATTGTAG CAATCGATAA TCCATACCCT TTAAATAGAT 240

ATATACATGG AATTTGAATA ATAAGTTTTA ATAAAAGAGT TATTGAAGTG ATTTGCATAG 300

CTTTCTTATG AAAACTTAGT GCTTGTAAAA TAGATAATAC TATTGTAAAA ATCCCTAATA 360

GAGATGTGCT AATAATTGTT GCTGATAAAT ATCTACTTCC ATCTAAATTA AATCCAAAGA 420

ATAATGTATT AAGAGGATTG CATAATATTA TCATTCCTAT CGAAGTAGGT AGTAAAAATG 480

TAAAGGCTAA TCGTAGTATT TGTGAGGTAC CTTGTAATAA CTCAGGTTTT GATTTTACAG 540

TACTTATTAA AGGTAGAGCT GAAATAGTAA TTGATCCAAT AATACCTAGT AGTACTGGAG 600

CTAATTTATT AGGATTTGCA GAGGCTAATG TATACAATGT TTGAAGTTCg CTTAAACTAC 660

TTTGAGGAAA AAACAAAGAA TACAAAACCT TTAAAGAAAA TTGATCAATT AATTGTAAAA 720

TAGAAATAGC CGATCCTACA TATACAAACG GCAATGATTC CTTGATTATA TCTATAGCAA 780

GACCTTTCAT GTGAGATATA GATTTTaAAG GTAAGAAGTA AAAATCTTTA AGTTGAAACA 840

AATTTCTTTT TTTTCCGATA A 861

(2) INFORMATION FOR SEQ ID NO: 732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

TACGACCTAC TAACAAGCGG ACGTCAATCG TAATTTTTTC CAACGGTCGC TGTTGTAGCT 60

CGGCTTTAAC TTCTTGAGAA ACTtGCCACT CTAATGGCGA CATTTCTAAT AAATCCAACC 120

GTCTTTCCTC GGGAATGTCA AAGCAATAAG TTATTCGTTC ATCTACTTCC ACAGCTAATT 180

CCTCGGCAAA ACGTTGGACT ACTTTTgATT GGAATAACTT TGTTTCTTTT CGTCATTGGG 240

ATAAAAAGCC GCTCGTAATT CCTTTAAGTA ATTCTCTTCA GGAATAATTT TAATCACAGT 300

CCCGTCAGCT TTTAGTACTC GCCGAAATTC TTGATAATGT GAAGGGGAAA AAATATTTAA 360

AATCGTATCA AGCCCTTCAT TCGCAAATGG CAAATTCGTT AAATCCGCCA CACACCAAAA 420

CGCATCAATT GGCTGATTAC TTGCTAAATA GATTCCTTCC TTTGATAAAT CAAACCCGAT 480

TTTCAGTCCA GATAAGCCTG CTTGACTTAA CTCAGCAAGA AAACTCCCTT CACCACAACC 540

AACATCGACT ACTGTTTTAT TTTGAGGAAG ATAGTGCATA ATTTTGTTTA ArACAGGCGC 600

GTACATGCCA CTTTGAATCA TTTTTCCTCG AGAAGTAAAC ATTTTnTnAT nATATnCTGT 660

CT 662

(2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

AGAATCGATA TCTGTAATTT TCATTCTTAG CAGTACCTCA GGGTCAACCT CATATCCTGT 60

AAAATCTTGC TTCATAGAAG CCACTAGACT AGCTCCTAGA TAAAGTAATT CGAAAGCATT 120

AAATTCATCT GATGTAGACG GTCTTTTATA ATTATATTGT TGAAAAAGAG AGCCAATATA 180

AACTGTTCTC GCTGAACCAT ACATCATTAA TTCCTTAATC ATCTTATTTA AAACAGCTGG 240

CTTCAAATTT TCAATTTTTT CAGTATCCGC TATCATATCC ATCCAACGAG AGAAAAGGTC 300

TTCTATTTTT TTACCTGAAA TTGAACGATA ATAGTTATCA ACTTGCAATT CCCTAGTTGT 360

TTGATGTTCC TTGTCTTGCA TTATATTACT ATTTTCATTT CTTATCTCTT CTAGTTTTTT 420

TTCATGTAGC CTTTGTGGCA ATTCAGATAA GCCATTTTCG ATAGCCTTTT TTATCCCTTT 480

ATAGCCAGGA TAAATAAAAA TTAAAATAAG TAACTCAAAC CAATTATTTT TTAACAATTC 540

AAACATTTTT TCCTCTCCTT ATAATTAATG GTAAATTTCC TGTAACATTA ATTATAAAAA 600

ATAAACGAAA AATAAGCTAG TTTGTATTAT CTCTTATTTT TAATATATTG ATTTCCATTC 660

CAATTTACCA ATGATTTATT GGATGTTTTA ATATTAATTA CATTTTTTAA ATTATCTGCA 720

ACTTCTCTAT CAATAGTTGG ATATAAATGT GGGTACGTTT CCTAATGTTA TTTGTATATC 780

AGAGTGTCCA AGCCTTTTTT GAACTGCTAA AGGATTAGCA TTCAACTCAT TAATCAATAA 840

ACTTGCATGG CTATGTCTTA ATCCTTTTGA TAGTGACTAT TAATAAAATT CATCAATTAA 900

AAGGAAGCGA TTTCAACATG TCAAAAGAAA CTTTTCTTAA GTATGGTTTT GTTGTCCTCT 960

TCATAGGAAT TTTTTTACTT CGTGCCCAAA AATTTATTTC TGAGCCCCTT TCGTACCTTT 1020

TTTCGGGTAT TCTTTTGCTT GTTGTTGCGT ATTTAATACT CGTGAAA 1067

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

ACTTAAAGGA GGGAAAATAT GTTCGCAGAA AGATTGAAAT TATTAAGAAA ATCAAAGCCA 60

AATTTGACTC AACAAGATAT GGCAAATATk TTAGGCGTTG CCAAAACCAC ATACGCATCG 120

TATGAGCAGG GAAAACGAAC TCCTGACGCA GAATTACAAA ATAAAATTGC TGATTACTTk 180

GAkGTATCGT TAGACTACCT ACATGGAAGA GACGTTATTA ATAACTCAAA TCTAGATAAA 240

AATATGAATA GAAACAACGA GCTTTCTCCT GAACAATTAA CAGTAGCCGC ACATATAGAT 300

GATGATGTTT CTGAAGAAGA AATGAAGGAA ATACTATCTT TCATTGATTA TATAAAGAAA 360

CGCGATCACT ATAAGTAGGT GTAtTTGATG rATAAATTGG GAAAGCyTGA TGGcyAAwTa 420

TCCkGAACtA AACTACCnGA TTAGGA 446

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

AATTCTTCAG CGTATACATC ATCAACTGTT TGTGTTGGGT CGATAACAAT GTATAAGTTT 60

TTAGTTTTTT CGCTGACTTT TGTAGATTGA TAGATGTTAT CCAAGCCCTC ATCTGTTTTA 120

TCTTTGTAAG GGAAATAAAC TAAATCTGGT GTGCCATTTT TGTAAAGAAT TTCCATACGT 180

TCGATATCTT CATATTTTAA AGCACGAGAG AACATCCCTA ATTCTAAGCC ACCTAAGTTA 240

ATATCGTGGG TTTGAACATG ATCTCCTTCT TGGAAAATTT CAATTTTGAA CCCTTCACAT 300

GGATGAATTT CAACAAATTC ACTACCATGG ATACGGCCAA AACTTGTTGT AATATGTTTG 360

ATCCATAAAT CACCAATArA ACGACGATCA ATCGTCCaAG TTTCACCATT TCTGAAATAr 420

AATTTAAGTC CTGTCAkTTC TCTAGCCATA GCACAArTCT CCyTACTTAA AAATAATTTC 480

TTACATTATT AGTTTACCAT ACTTTTGATA AACGGTCACA AACTTTCGCT GTAGATTCnT 540

AAATCTTTTG TnATACTTTT TAAAAAAGGA ATCCAATCnC AACTACCTGC ACGTTGGTGG 600

AGACCCTTTG GCAATTnGCC GTCC 624

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

GTCTTGAAAA AAGAGGAGTT ATTAAGCTTT ATAAAGCTGT AGGTAACAGT GTTGAAAAGT 60

GGTCAGAAGT AGGAAATCTT GATTTTTGTA GTAGTGGTTC AGAATACATG ATAGAGTGCC 120

CTAATCTTTT ATTTGTAAAT GATACACCAA TTCTGATTTA TTGTCCTCAG GGTCTTGATA 180

AATCAGAACT TAGTTATGAT AATATTTATC CGAATACTTA TAAAATTTGT CAAAGTTTTG 240

ATGAAAGAAC TGCGAAACTT GTGGGTTCTT CTAAAATTAA AAATCTTGAT TATGGGTTTG 300

ATGTTTATGC AACACAAGGA TTTAATTCTC CTGATGGACG TACTTTAATT GTTAGTTGGA 360

TTGGGCTTCC TGATGTTGAA TATCCAACAG ATAAGTATGA TTATCAAGGC GCAATGAGTC 420

TTGTTAAGGA GCTTTCTATC AATAATGGAA AACTTTATCA ATACCCTGTA GATGCTATTA 480

AAACACTGCG AACTAGTTGT GAAGATTTTA CGTCAAAAAT AGAAACAAGT AATACTTATG 540

AACTGGAAGT GACTTTTCCG GCTAATCAGA AATCAGAATT ACTTCTTTTT GCTGATGATA 600

AAGGGAATGG ACTCAGCTTA ATAGTTGrTA CTAAAgAAGG AAAAgTTATT TtAGATCGGA 660

GtAAAGCAGG aATTCaATAT GCaTTGaTTT GGtAwGaCtC GTGatGCtTA ATAGATCnGG 720

AGAACCAATG CTAATATnTT GGAGAAATCC ATCATGAGAT TTATAATAAG GGAGAAGTAT 780

TACnGCGGnA TTCCGAGAGG 800

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

TGTTGTGACA ACTTCTATAT CTTATCATTA TCTCAGTTGT TTGTCAACAA CTTTTTAAAA 60

CTTTTTTGTT ATTTTATAAC AAGTTTTTTT GATCAAACGA TTGATTTAAA AGCAATCTCT 120

TTAACGACTT TGTTATTCTA ACATGTTATT TATCTTTTCG TCAAGAAAAA TTTTTAACTT 180

TTTAAAACTT TTTTCTTAAC GAACTGTTTG TCAGAACAGA TATTAATATA CCAAGGATTT 240

TTCTAAAACG CAACTATTAT TTTGCAGAAA AATAACATTT TTTTCAATTT CGAACGATGA 300

ATATTTTCTG cAAAGaAAAC ATTCGTTTCT TatCTTATAA TCCCTTTTCT CTTACTTAAA 360

TGTTCGTTAA TCATTCGTAA AAAAAGCAAC GTACTTTATT GTACGTTGCT CTCTTCTTTT 420

ATTCCAGCGA TTGGGAATAA AAATTCCAAA GATCGTTCCT GGATGCAATA CGCTTTCTGC 480

ATCAATACGT CCTTATAGTT 500

(2) INFORMATION FOR SEQ ID NO: 738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

AGTAGAATCC GTCTTGATTT TATGCATCAC TCGTCGCAAA CATTTGTCTA TTTCTTCTTG 60

ATAATCTTCA CCAATTAGAA CGAGATTGTA TTCTTTTTCT ACTTTAGTTT TAGCACGAAT 120

AATTGTTCCT ACTTGCTCAT GAGCTTCTTG AATAGTATTA GAGAAGGCmG CAATAAATTT 180

TAAGCTATCT TTGTTTAGGA AAGTGTTCTC TTGAACTTCT GAAAACTGaT CGAGCAATAA 240

TTGTTGTTGC AATCGTTCTT TTTCAGTATC TATTGTATCT ATTGTATCTG TATTTAGATT 300

ATTAAATACT GTACTGaTTT TCATACCCTC TGaTTTATCA ACGTTTTGGc AGGGTATGAT 360

TTtCATACCC TCTTGATTAC CAAGGGATtC AGCGTTTGTT TTTCTTTGGG GGGTGGGTAT 420

GATTtTCATA CGCTCTGATT TATCAACGTT TTCTTGCATA GTATCATCGA ATGTTTGCAA 480

TTGATAAATA TCGTTTtCtG TTACTtCAaG TTCCGCTAGA TAAAGTCTAT TAGGATTGTT 540

CTTACCTAGT GTTTTATTAA AA 562

(2) INFORMATION FOR SEQ ID NO: 739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

GCATTATTTT TTCGTTTTAA AATAGTATAA ATAATCCTTG TAATCAAAAG AAGGCTACCT 60

AAGAAAAGAA ACGCGTTTTC TTTTGTTTCT CCTGTTTTTG GCAATTCCTT ATTACGAATC 120

GCCTGTTTTT CAATGGTTAT TGAAGTAGTT TCTGTGGTTG AATTCGTGGT AGTATCTGTT 180

GTCCCACTCG TTGGTGGTGT GGTACTTTCT ATAGGTTTTT CTGGCGTATA GTGATTAGTA 240

AATACTTGAC CTCCATCATA CTGAGTAGTT GCTACAAGAT TTCCTAAAAG CGCCTCGACG 300

GTTACTTGAA CTTGAAGGTt GTGCGTAtCG TAGGAAAcAC CTGTCTGTTG CGTGkTTAcT 360

kCCCGAATGG TGTATTGATA GTTTCCAGGA GTTCAAAGGT TAATGGTGAA AATTGAATTT 420

TCCCTAAAGT ATCGTTA 437

(2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

TCATTTAAGA AAAATGAGCG TGGGACAAAA ATCACTTTGG ATTTTTGCTC CACCCTCAAA 60

AACTGATAAA CGGCGGGAAC AGAACCAACT CCTTCGGAAA TAAGCCGAAA TTCTCCAAAA 120

ATTAAAGAGC AATTTTCGGA AATTTCTTCT TATTTCTCGG AGCTAAACGG TTCTGTCCCG 180

ACCTCATTAT TTCTTATTTT GCTGATTCTT AATGGTATAA GTCGAAACGA CCTTTAGCCA 240

TCATTTCTTT GGTACCACCT GTTTCAAAGA GCGCTTTGTT CATGATAATT TTTTTCATGA 300

ATGAAGCTGG GTATCCTTTA ATGTCTGTTT TACCAACGAT TCCTAAAGCA CGTGTATTTC 360

CGACAGAACA AACAGAACCT TGTGATTTAA AGCTGAAAGG TTTAGTTGCT TCCCCTTTCA 420

ATTGTGCTTG AATATTTTTA GCAGCATGAG CGCCCATCTT CAAGGCGATT TGTGCTGTTG 480

TtGGGTAgGT CGAwTGGGTT CnG 503

(2) INFORMATION FOR SEQ ID NO: 741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

TATTGACAAT TAAAAATAGC GGTGGTATAC TTTTTTTAAG TTATCAAAAG TATACTAAGG 60

AGGAGTTGTC AATGGGAAAA GTATATGTTA TTGGAAATTT TAAAGGtGGG GTTGGTAAAA 120

CTAAAACAGT AACCATGCTT GCATATGAAA GTGCACTACA ATTAGGACGA AAAACGTTAG 180

TAATTGATCT AGACCCTCAA GGAAACGCTA CTAGAGTATT AGCTAAGACG GGAGATTTAG 240

CCGAAATCAC TTATACTGTT ACTGAAGCTT TTCAAGAAGG TAGTCTTGAA CCAGCAATCA 300

CCAATATCTC AGAAAACCTT GATCTCATTC CAGCTAACAC TGCTTTTAGA AATCTCACCA 360

AAATTTTAAT GACAAAATTT CCGTCTAACG AATTTGACCA AATAAATTAC TTAAATACAT 420

TATTAAAACC CCTTAAAGAG AAATATGACG CAATTTATAT TGACGkTCCA CCAACTATTt 480

CAGATTTtAr TGrTAATGCm ATGCyTGCmG CAGATTACTG tAwTAwTGkT CyTCaAACmC 540

mAGAGTATCT TTAGACGGTG CTCAAACATA TATCGCCTAT ATGCAATACT TAGCTGACAC 600

ATACGATAAT GGATTTACAn GGCCCTAGGG AAnAATTCCC TGGTATGTTG CGGnCCCGGG 660

GGTAnGGGAA GCC 673

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

TTGGTAGGCT GGTAAAGTTn GnGGTTTAAA CTCmCCaTTA CGAtCtCTAG GTATtTCCCA 60

AkGTTAATTC CmCCATATTC GGTTTTGaTT GaTCGaAAGT AAGAACCGTT TCTCGAATTA 120

CCTGAATTAA AACCAGTGCG ATCATATTTT TCGtAATCTA AAAAAGCCGT TAATTCAGTC 180

CGTAGGAGTG TGTTTATCGC TTTTTCTAAG TGCGAACGGA ATAATTCATT TAAATCGCCT 240

TTAGTGACTA GAGTTTGCAC AATTTCTGTA GTAAAATCAT TCATAGGGAA GTCCTCTTTT 300

CTGTGAATTG GTTGTCGTTA ACTTTATTCT ACAGAAGCGA CTTCCTTTTT TGTATGGATT 360

TTTTCATTTA CACAAAATAT TTTACACTCT CCAAAAGAAA TACCATTTAA AATATTTTTT 420

TCAAAAACAG ATATAGTATA GTAAACATTA TTAACCCTAT AAATAAACTC TTCTTTTCCA 480

ACATTTCCTT TTTTATTATT AAAATCATTT TTTTCTTCAT AAGTTAAAAC TTCAGATAAT 540

TTTTGAAAAT ATACATTTAA TAGTAGAAAG TCATTATAAG AGGAAACCAA ACTTAGAATT 600

GGCTTCATAA CCATTGTTAC TATAGAAACA AAACCAATTA GTGATCCTAA TGACAAAGAA 660

TTGTTGATTA TTAATTTAAT ACCTATTATT AAAAATAGAG CTGGCATTAC ACTTTGTATG 720

ATTTCTGGTA ATATTCCAAA AATAGCTATA TATCTATTTT TATTTTTTGT AATTAATAGT 780

TGAGACGTAA ACATGTTTTT CCAATTTAAC AAAAAACTCT TTTCTGCATT AGCAGATTTA 840

ATGGTTTCAA TkcCTTCAAT TGCTTCTGTA ATAATTCTCT GGACGTTTCC TTGTTCCATT 900

ATTTCTTTAT CTACAAATCT TTTTATTGTA TGCGAATTTA TAATACTTAA AAAAGCTATT 960

AAAGAGATTA GAACAAGAGC TATTATTGTC AGTAAAATAG AATAGTTAAC CATTAAAAAC 1020

AAATATATCC CTAAAAAAAG ACTATCTATT AAAGTTGTTA TTACCTTTTG AGACAATATT 1080

TGAGTCAAGT CCAGACTCCT GTGTAAAATG CTATACAATG TTTTTACCAT TTCTACTTAT 1140

CAAAATTGAT GTATTTTCTT GAAGAATAAA TCCATTCATC ATGTAGGTCC ATAAGAACGG 1200

CTCCAATTAA GCGATTGGCT GATGTTTGAT TGGGGAAGAT GCGAATAATC TTTTCTCTTC 1260

TGCGTACTTC TTGAkTCAGT CGTTCAATTA GATTGGTACT CTTTAGTCGA TTGTGGGAAT 1320

TTCCTTGTAC GGTATATTGA AAGGCGTCTT CGAATCCATC ATCCAATGAT GCGCAAGCkT 1380

TTGAATATTT TGGTTGATCG ATATAATCAT GAATCAATCG ATTTTTAGCC TCACGCGCTA 1440

AGTTAATATC TGTGAACTTA AAAATTCCTT TAACAG 1476

(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

CCTGAACTGG AATTGTTGAA GTAATATCTC ATGCTGGTAA AGTAACGTTT ATTGAACAaA 60

AAATTAAAGa AAAATTTTAA TATAGTCTGA CTAGACATAC TAGAAGACAT CTGACCAATT 120

GTGTTTTTAC ACATTGGTTA GGTGTCTTTT TGTATTTTTA TTAGAAGGAG CGATTCGCCG 180

ATGTTAGACC AACACGGAAG AAAGATTTTG ATTCAGGAAT ATAAGTCTGA TTTAAAAGAC 240

GCAAGTCGTC AGCATCGACG AATTGCAAAG AAGAAGTATC AAATTGAAAA AAATGGCAGA 300

TTAGAAACAA TTGATGACCG CACTGCAGAA GATATAAAGG AACAGTCCAT TTATGCTGAA 360

ATTATTTCAT CTACCAAATA TGCGTTATAT TGGCTTGAAC ATGGAATTGA GCGACCTCTT 420

GATGAGGAGG CAGCAAAAAA AATACCTAAA TATCGCAGAG ATAAACATAT TACAAATATG 480

GATAAGATAT CATACGAAAT TTATTGTAAC CAGTATGAAT CTGCACGTAA TTACCCTATT 540

ACTGAAGAGA AACAAGAGAT GTTGATTCAA CTTAAAGAGT TGTTATCAAC GTTCaGCGAG 600

AGAGAACGTG ATTTGTTTGA TTATATCCAT AATCAGCAAC TTACTTATGC AGAAGCTGCT 660

GAAAAAATGG ATATTAAAGT AGGGACTGCT AAATCCATGT CACAACGAAT TAGGAATAAA 720

ATTGATGCTT ATTTCGAATA TGGACATCAG ATTTCATTAT TTTAAATTTC ATTTTTTTGT 780

AAACCATTCC CACCTATAGG TGAGAGGTAA AATTCTCCTA TTCTAAGTTG GTAGAGTAGC 840

TTAATAATAT TTACTTGTAA AArAATACAA GAGAGGAGGT GTTCCTCCTC CTCTAAATTT 900

CTACAAATTA CGAGTAAATT AGGTAGACGT GTAGCTCAAT AGGTAGAGCA ATTGATTTTT 960

AATCAATGGT GCGTGATTGC TTGTGCCAGG TTCGACTCCT GTCACGTCAA TAAGTGGGAA 1020

ACCACTTAAA TAAAAAATCG GTATATGTCA ATAAATGTTT CTACTACTGT GACACACGAT 1080

T 1081

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

TTCGAGGAGA AAGTATGATT AACGCAGGGT TGTCCTGGAT AAAACACAGA TGTATCAATC 60

CCAGGATTTA ACGCTAAAAT TTGTTCTAAT GTCATTCCGT TACGTTCGGC AACTTGACGT 120

GCCCCTTCGC CACTTTGAAC GGTATCATAA ACAGGTTGTT GGTTCTGCGC TTGTTGCTGT 180

TGTTGATTTT GAGCTTCTTG TTGTTGTTGC TGCTCTTGTT GTTGCTGTTG CTGTTGTTGT 240

GCTTGTTGGT CCTGTTGTTG CTGTGCAGCA GCATCTGAAC TTGAAGGTGT TGTATTTTCA 300

GCTGGTTGGC TGCTTGCTGG TTCTGAGCTT TCCACTGATT TTGACGTACT TTCTTTTTTC 360

TTCTCTTTTG ATGATGATTG GACTAATGAA GAAGATGGCT GGCTATTTTG CTAGCACTTT 420

CGTTCGGTTC CTGGCCTGCA TCATCCATAA GAAAGTCCCA ATTGGAAnGC nATAATTAAT 480

AATAGC 486

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

AGTGAATTTA CCnAATAAAT TAaCAGTTTT AAGAATATTT ATGATTCCGA TTTTTATTAT 60

TATTGTGTCG GTGCCAATGG ACTGGGGAAC GATTAGTTTT GGCGACACAA CGTTAGCCGT 120

TACCCAATTA GTGGGCGCGA TTATTTTTGC AGTTGCTAGT TTTACAGACT GGTTGGATGG 180

CAAAATTGCC CGTGCACAAG GCTTsGTGAC GAACTTCGGA AAATTTGCGG ACCCaTTAGC 240

GGACAAAATG CTAGTGATGA CCgCTTTwAT CGTCyTAGTk GGTCAAGGca AAGTACCtGC 300

tTGGATTGTA GCaATwATTG TTTGTCGTGa ATTGGCaGTA ACTGGkTTAC gGTTGTTAwT 360

AgyCGAmCAT GGCGAAkTAA TGGCAGCAGC TTGGCCAGGA AAAGTAAAAm CAGCyACCCm 420

AATGGTgCaA TATTtACyGk TCaTTAmCAA CATyCCATTT yCAGaCTcyA CCACTAGATC 480

AAATCATGCC ATATGCCTGC TTGAATTTTC ACCATTTACT CTGGGAG 527

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 772 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

ACGTATCCAG ATAAAAACCG GTTGAATCAA ACGTCATnTA ATGGTATTnT AGACGAGTTG 60

TTATCCTTTT ATGAACAAGC AGGGGAAAAA GTGGATCAAT TTGGCCGAGT TTTTGAAGCG 120

GCCTTTGCTA CAACCGAAAA TGGCCATTTG TTATCAGGTC CCATGAAACG ATTATTGGGA 180

TTGTTGTTAC AAGTTTTATG GAGCCAGCAA GTCAATCACT TTGACTTTCA ATTTAAAAAT 240

TTTATCATTT GGTTTATTCG CTTAGGTTTT CCGGTGGCGT TTCCAAAAGA AATTTTAAGT 300

GCTGATTACG CAGAACAAGT TTTGCTTCAC ACAGAAACAC TAGGTCCTCC TATGGTGTTG 360

GAAAAAATCG GTCAACTAGG AGCAGCTTTA AAGCCAACGC CCGATCAACT GTTAACAACG 420

ATTGAAAGAT ACCAAGAAAT TTTAAAAGAG ATTTGAGGGG AAATTATGTC ATATAGTGaA 480

AAAATGGTTC AAGCATTACA AGCTGaAAAT TTaGCaGAAG CACAGTTAAT GTTTGaAGAA 540

GCaTTAAAGa AAGATGaTGa AAATACCTTA GCTGATTTAG GGGAAACGTT ATTATCTTTA 600

GGTTTTCTAG AAGAAGCCAA ACAAATTTTC CAACAGTTGT TGGAACAATT TCCCGATGCA 660

GATGGCTTAA ACATTCCATT AGCAGAAATC GCCATTGAAA ATAATGAAAT AGATGACGCA 720

TTCATCTATT TAGAAAAAAT TCCAGAAACT AGTGACAGTT ATGTCCAAAG TC 772

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

GCCCTTTTAA AATTTGTAAC CATAATTCTG TTACATCTTT ATTCTCTTGG TTCGTTAAAG 60

TATACTTATT TTTATTAAAT ACCTCTACAT TAAaCCAGtC ATtAGTAATA AAaTTTyCrG 120

AaTaCATTAt CTCTtCACCT CATTACTTtC TATTAGAGAT AGTTAtGCAa TTaATTTtGk 180

GTAaCACTCT GGGTTATCTG TTAAGCATAA TATGTAATCt ACGCTTGTAG AATACAAAgT 240

GATAGCTTAA CTAAAATATC TACTGGTACC ATTGTTGCAC CACTCTCATA TCTGGAATAC 300

GCAGATTGAG AACAATGTAT ATAGTTACTG ACAAAAGATT GAGTATAATT ATTTTTAATT 360

CTCAAAAATA GCAACCTAGA TTCCATAATT TTTCCCTCTC CTGTATGCTA TCTTTGTTTG 420

TTAATAACAG TCAATATATT ATTCGGATTC TGCATAATTC TAAAATTTTT ATTATTTATC 480

AATCACGAGA AAATAAAATA TGTCTATACC TTTATAAAAG GTAAAAATTT GTATTTCTTT 540

ATTATTTGTT TTATAATATA AGTATCCATT GAGCAAAAAC GCTCAAAATA GGCTGATCGA 600

GTTAATCGAT CAGCCTATTT TctTTAGATT TATATTATTT ACTAAAACTA TACTGTCACG 660

AAAAACAACA TATATAATAT TATGTTGTTT TATTCAAACT ATAAATGATA aTATAyyTAA 720

ATATATAATA GAGACTGTCT CTTGGGGGAG ACAGTCTCTA AGGTTATAAC TTATTTTAGC 780

CTTTCATTTC TAACAAATAA TCATTCATAG AACTGAACGA TCAATTCATT CAGTCTGAAA 840

GAAAATAGTT AAATCTGAAA TAGCTATTTT TATTTTACAG TAtCTGCCTT GGCCTTTCAA 900

TTTCCTTGAT ATTACTTTTA TTTCAGGATT ATTTAACATA AACAAATACT TCTGAATCTT 960

TTACATAAAT GTCATGGTAA TAATTAGATT TCATTAATTC ACTTTCTTCT TTACTCAACG 1020

CGTTAATATC AAAGATCTCC ATGTTCACGT TTAAACCAGT GTACGTTCTA AATAAAAACT 1080

GATTTGGCCA ATAAAGGGCT TCATTTGGTG GA 1112

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

GGGCTTCCAT TTCnGGnTAT GCnGATGGCG CATCAAAACT TGCACGTAGG TAGTCTCCCG 60

AAAGAGGaGT AAtGcTAAAA AAaTATGGtC GCmCTTtCGG AAAaGCTTCa CTTGGTACAT 120

TTkGATTGGC GTGATgTTcA TTATGTAGgC TTTAGCAATT TATTTTTTTC AACAGTTGTT 180

AGATCATTAT CAAAAAgTTT CCaACTAGGG TTGTTAGTAG CGTATGGAAC GACAATTATT 240

TTAATTCCTC TATTGTCTTA CTGTGAACAG AAACCGAAAG CTTaCTTaAC TAATGGCATC 300

TATTTCTATT TGAAGAAATT AAGTTTAATA AAAATGAGCA AGATTTCCTA TGAAGAATAT 360

CTAAAACTGG GAGCGGGGGC TTTACTACAA AAAGTAGAAG TTGGTGCAGC AGCTGGGAGA 420

AATATCCACT TGAATTTTTA TGGGCGCTTA TTTCGAGAGT TAATTCCAGA GACGTTATTT 480

AATTTATTTT TCATAGCATT GATTGATAAA AAATTATTAC CAGCAATTCT AATTGGTTAT 540

GTGATTGTAT TTATTTTAAC CAAAATACTT TTGAAAACGC TACAAAAAAT GAAAGAAAAA 600

ACACTTATTT CTGAAGAAGC AATGAATGCT ACTTTGATAC GAGGGATGAC CGAACTAGTA 660

ACTTTTAGAA TTAATCGAAA ATATAAAAnA GAGATTGAnA ATTACGCGTT AATGGCAGAG 720

GGAAAATAGT CAAAATATAA CAAAAATGGA CTATGGATCC ATGGAATTTT TCTTTGGGCT 780

TTTTTGGCCT TGTTAGTTGG CACTTATCCA AGTAAGTATT GTCCGTACTT AGGTTTTACC 840

TAACGnCGnG GCGCCCAGTT TAGG 864

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

ACCAACCTTC AAGATAAGTT TTAAGTCTGT GCCCTTACAC GAGATTTTTT TACGGCAAAA 60

ATAATCCTTT GGTAGTTCAT CCAGCACAAG CACATTTTTA TATAACTGAT TAATTTGGTG 120

GAATTATAGT TATATCTATA TTGATTAnTA GCTGATCTTG CTAAGCATGG ATTTAATAAG 180

AATATTTTTG TTAAAAAATC ATATAnCCTT ACGTGTAGTG CTGCAGCACT CATTTCAAAT 240

TCTTCGCAAA TTTGACGGAA AGACATTTGC TTTTTTAAAC ATTCTTTCAA TGCTTCATTG 300

TTTATTAAAG CAAGGGATGC AAATATATTA GCTCTTATTT CTTTTGGTTC ATCTtCGCTA 360

GTGtATCCTT TTCCAGTAAT TAAATCTGAA AAACTTTGAG ACTTGCATTC CTTATTCATA 420

TCAAAAAAAT AATGTGcAGA TTCATGAAGT ATTGAGAAAT TTTGCcTTCC TTTAACCATT 480

GtTGGATTAT AGGaAATTCC GCATTTATCG TGAAATTTTA TTATGTTTCC TGaAAATATT 540

TTTcTkGAAA CATCACCGAA ACTATAGGGA ATTATGTCAA CATTTTCTAC GTCAATCATA 600

TAATCTTTGT AGTGTTTCCA TCTTAACTCT TTTAGTTCAA TTCCATAGTA ATTAGCAACT 660

TTTTCAATAA TAATATATGT CTGGTCATGA TATTCAAAAT AAGTATCGTA GTCTAAATAC 720

ATAGGGGTCA TCCAATCATT TATTTTTAAG TCTTGATTTC ATGAATTCTA AGTACTCTTT 780

TAATTCTTCT CTGAGCTGAT CTTTTTCGGA TTCGGTkAAa TCTtCTGTAT TTACACGGAA 840

GAAAGTTGTA ATTTCATCTy CTTCTAAGTT ATTAGAATTT GGATTATCAG TTCGTCCAAG 900

TAAATAAkCT ACAGATATAT TGAAGTAGTC CGCAACTTTT TTTAATTTAT CAGAACCAGG 960

AGTATTCTTA CGCCATCTAT TAATTACCCC GTTtCCAaAT CCCAATGTTT CTTCTAATTG 1020

TCTTATTGAC ATTTTCTTTT CGCTAGCAnG TAATTTTATT TTnTTCGTAT AAATCCACTT 1080

ATATCAACCT TTCTAGAAAT ACAAAGAAAA TATGTATACA AAAAATCTAC AAAATGGTTG 1140

ACAATGTAGA AnAAATGTAT ATAATAATTC TTGTAAGTTA ATTGGATAGA AAAAAAGCAA 1200

ACTAAAAACA TACCTTACAG CATTAAGTTT GGCGACCGAG TGCATAATAA AGGTTTTGTT 1260

ATAGGCTTAT TTAACTATGT TCTGATTGTA GAATATTTGT ATACATAAGT CAATAGTTTT 1320

ATAAATTCTA TCTAATTAAT TTACAAAAAA TACTAAAGAA AGGAGAAACT AATATG 1376

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

TTTTGTAAAT GTTGTCATTC CATTTTATTT GCAGGATGCA CGCAAACTAA GTGCTAGTTA 60

TGCTGGTCTA TTAATGATGG TATTTCCGTT ATTAATGGTG GTTGGGGCTC CTCTGAGTGG 120

CTATTTGACG GATAAAATTG GCCCAGGTAT TTTAACATTT GGCGGATTGT TGCTCTTGTG 180

CTGTACGTCG TTAATGTATA TGTTTTTAGA TATGAATTCG CCTATCTGGT ATTATGTGAT 240

TGCAACGGCC ATTATGGGCT TGGGAAATGC ACTTTTCCAG TCTCCAAACA ATACAATGGT 300

TATGAGCAGT GTTGAAAAGC AAGATTTAGG TGTAGCAGGA AgTATGaATt CTTTTGCTAg 360

AAAnCTtAGG aAkGGyCATk GGGATTGCGT tGTCaACGAC CATTTTAtAt CGTGGCATGA 420

GCGAACCTAA TGGTGAACgA GTAACCaCGT AtCTGGctAA tCgCCCaGAt ATAtTTATTG 480

TGGGAATGCG TGAAcCTTTT TTGTCGCCTT TCTATTATGT GTGGCGGCCT TTATATTAAC 540

GATTTTACGT TTTCGGAAAA CAACCAAATA AGTAAAAAGA AACAGACGAG AAAGATTCAT 600

GATTTTTCTC GTCTGTTTCT TTACTAGCTA AGAAaATAAG CaATGCGATT GTATATTTCT 660

GATCCCnGn 669

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751:

AAAATAATTA AAAACAGGAG TGATAAACGT GAACGTATTA GAATTCGGCG GTACTCGCTA 60

GCATCAGCAC CACAGTTACA GAAAGTCTTA CAAATCGTCA AGGAAGAGCC GCGCCGAACG 120

TTTGTCGTTG TATCCGCTCC TGGAAAGCGA ACCCCGCAAG ATATTAAAGT GACTGATTTA 180

TTGATTCAAT ACTATCAGCG CTACTTAAAT AATGAGGAAA TTGAATCGAC AATCTCTGCC 240

ATCATTCGTC GTTATGAAGA TCTTTTTGAT GAATTACACT TGGATAAAGC AGTTTTAGCT 300

GATATTGCTA TTTCGATTCG CCAATTAGCC ACTTTACCAA AGAAAACAAT GCTTTTTTAT 360

TTGACTATTT TTTAGCTAGC GGTGAGGACA ATAATGCCAA GTTGTTGCCA GTTTTTCAAG 420

CAAATGGCTT AGATGCTCGC TACATTAGTC CAAAGAATAG GnCTCCTAGT GAnCCTGAGC 480

CAGCATGCCG CATTTTACCA 500

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

TGAGTTTTAC AACGAGTTGC TTAATGAAGA AATAACTAGT GCTCAAAAAA GAAAAATGAG 60

CAATGATATT AAATTCTTAG CGAGTATTTT AACTAATATT TCTTGCTACA GATACTCAAT 120

TACTTTAAAT GATGTTTTTT TTAGAGGTAA GAATAAACTT GGCTATTtGA TAGGGGAATT 180

TGGTGTtAAA ATAGTAAAAT CATATtCGAA CTTTATATTC TCATGTTTAT CAGGAGGCGA 240

GTCTATATAT AATGTGGTTT TAACATCCAA AAAAGGAAGT AAGTTAAAAG TGaTAGAtTT 300

TAATTCTGAT GaATATGAGA TGTCTTtATTG GTGTTAGACC nGATAC 346

(2) INFORMATION FOR SEQ ID NO: 753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

GTCGATTGGT TAGTACTTAC CaAAGGAATG AATCGATAAA AAAAATAGCA GTGATGGCGA 60

TAACCGCTTT GACTTCTGCG GTCGGTTTGA ATTTCTTTyT GATTCCGGCA AAAGTTTTTT 120

CGGCAGGGAT GAACGGAATT GCGCAAATCA TTGCTACATT ATTATATACA AATTTAGGAA 180

TCCATATTAA TACAGGGATT TTCATTTTAT TTTTAAACAT TCCCGTCTTC ATTCTAGGGT 240

TTGTAAAATT AGGGAAACAA TCAACGATTc TTAGTTTCAT CAATGTTATT GGTATTTCCG 300

TTGTCACTAT GTTTGTGCCA ATCGTAACAG TCACAACGAA TCCTTkGATG AACGCAATaT 360

GGGTGGTGTC TaGTCGGCGT TGGCGCAGGc TTcATgAAAA TGGGCTTtAA CACTGGCGGC 420

ATGGACATTA TTTCACTGAT TCTtCAAAAA CAACAGGGaA AACAGTTGGT AATTTtATGT 480

TCTTATTAAA TGGtAwTATT GTGCTGTTGG CTGGTTTTGT ATTTAACTGG GAAAGTGCGT 540

TGTATACTAT TATTTCTATn TACTGTTTGA GTCAGGTGGT CGACATGATT CATACCAGTC 600

ACCAAAAAGT CACAGCAATG ATTGTCACCA CGAGACCAGA AGCCGTTGCC TTAGAAGTTC 660

TCAACAAATC GCTCGTGGCA TGAnC 685

(2) INFORMATION FOR SEQ ID NO: 754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 682 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

GGTGAATGTT TTACCGTCGC TAAGATTCTC TTCCAGATTA TAAACAAGCT GTGGCAACTC 60

TGCGCCGGTC GTTTGTTCTA CATCAAAGAC AGGCGTTAAA AAATAGCGCG TCTCTTTGAC 120

AATTTCTCCA TTTTCATCCG TGACTTTTTT CCCATTCTTA TCGACTTTAT CTTTAAAATA 180

AGGGGCATAC ACATACAGTG CTTTGCTGCC TTTTTTTACT TGACGATCTA ACTTTTTCCA 240

CGCATTGTAA CCAGCTACAC GACGTATGTT TGGATTTTGT GCCAACAACA AACGAATATT 300

TTTTGACGAA TATTTATGAA ATTTTGAAGC AAAATCTAAA TAGTTTTTAA ACGTATCACT 360

TGTTAAATAC TCTTTGaTCC CGTCGTTCAA AkGCTGCGAT AATTTTTGaT AAtCTTTCTT 420

TTTAATTATC TCTTCCAAGG kGATTtCkGG TtGGCyTTTT tGCTTCATTt GTGTTTTTTC 480

AGACATTyCT TwATtCCTTt CTCTGGATCG TTTTTTTGCT TCTTGACGCT TTAATTTTGC 540

TTCTtTTyTC TTTGTTTCAT TCTTTGTTTT CTTTAAAATA TCGTTCCAAT CTGTkTTACT 600

TTTTCCTTCA ATTAGTTTAG GkTGGTCAAG AGTAATnGGG ACACCAGTGA ATTGGAAAAT 660

GGTGGGAATA AATTTCCTTC CC 682

(2) INFORMATION FOR SEQ ID NO: 755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

TTGAGGGCTT GTCCCTCTAC TCATCGGAGA TTAGAGAGGT CAAAAATTGA CGAGGTAGAG 60

AAAATATTTG AaAATATTTT TTAATAGGCA TGAGTAACGG CAACATCCGT CAGATTGGAT 120

GTTGCCGTTG cTCTTaCCTA CTAAGGAAAT ATATACGAAT CTGCTTAAAT GCTCTTTGAA 180

GCAGGCGAGT TACCGCCGAC GGGTCACATC CGAGGaTAAC TGCAATCTCC TTGTATTGaT 240

ACCCTTGCCA GAAGTGaAGT TCaATCACTC GcCGCTGCCG GTCtGTCAGA CGGCTTAgAG 300

CAGCCgATaA ATGCTCATTC TGAACAGAGT CCATAAAATC CTGCT 345

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

ACGTTTTATA TATCTTTTTC ATTAGTCAAA AAGCGCTTTT TGACTAACGA TGCTACTCAC 60

TATAATACGT TTTAAATCGT TTAsCAAGTC TTTTTATTAG AGAATGTTCA TCTTAGATAA 120

GAAACCCACC TATTTTGAAA AAAGGAAAAT CAAAAATAAG TGGGGCAGCA GTCGAAACGA 180

CTGCTGCCCa CTtGcTaACT ATTAAGATAA TTCCCTGAAc AAAAGTAGCT CCTTTTATTC 240

CTGTTrAATT TAAATCACTT CTTCTTCCTC TTCGACTTCA GAGAAATGGA ACTTAATCAT 300

TTCAyTGACG AAAATTGGcA CAAAGGATAG GAAAATTGCT AACATCCAAT GATTTAAACT 360

AATATGCACT AATCCAAATA GTTCTTGTGT GAAtGGTAAT AAAGcAAkGG TtGTGGTAAT 420

TAGTAATGGC TAAAACGACC ATTTCAAAGA GCGACTTGTT GCTGATAATT TTACACGGAA 480

AACAGAGTTC GCACTACGAA CATTAAAGAC ATGTAAGATA GAGGAATAAG CTAAGATTAA 540

AAATGCCACT GTTTGTCCAA CTTCATAnCG TTTGAnAnAT AGGCTGAAAC ACCGGTACAA 600

GGCACCTA 608

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

GATTCTCCCT CATAATCTAA CTCAGCTTGT CAACTTTAGC TCTAGnATTT TnCCTTTTAA 60

CATGGAACTn TCATTATTAT AGCCCCCTAT TGTAATTCAA ATGTAAAATT ATCTATTAAT 120

CTTGTTTTTC CTATAAATAC TGCTATTGCA ACTAAAACTG ATTTTTCAAT ATAATTTACT 180

CTTTGTAATG ATAAAGAATC AACAACTTCT ACATAATCAA TCTTTGCCAA ATTACAAGTA 240

TTTATATTTT TACTTATTAT CTCmATTATT TTTrAGcTAT CTCTCTCTCC aTTATTTAAG 300

GCTTCCTTrG CTAAAGTTAA rGATTTATTT AAAAtAGTAG CTGAAGATCT TTCCTCTAAA 360

CTTAAGTATG TGTTTCTAGA ACTTTTAGCT AGTCCATCCT CTTCCCTTAT AATTGGACAC 420

CCTACAACGT CTATATCAAT ATTAAGGTCC CTAACCATTC TTTtAATTAC AGCTAACTGT 480

TGTGCATCCT TTTCTCCAAA ATAAGCTCTA TCTGCTGGTA TTATGTTAAA TAAyTtACTT 540

ACAACAGTGC AAACCCCTCT AAAATGTATT GGCCTACTAG CTCCACATAA ACCTTCTGTT 600

AATCCAGTTA TATTAACAAA AGTACTTGCA TTGTCACAAT ACATCTCTTC AACTTCAGGA 660

TTAAATATTG CTGTTGCTCT ACCTCTTGTG CATACTTCTA TATCTCTTTC TAAGTCTCTT 720

GGATAACTAC CTAAATCTTC ATTTTTCCCA AACTGAGTTG GaTTTACAAA GATACTtACA 780

ACAACTTTAT CATTnTCTTT TGATGCTTTT CTAATTAAAC TTTCATGACC TTCATGTAAA 840

TATCCCATAG TAGGAACTAA TCCTACCTTT AAGCCTTGTT TTTTCCACTC TTTTACTTGA 900

CTTCTAACAT CATTTACTGT TTTAAATATA ACCATATTTC TTGACCCTTT TAATATAATT 960

TTTCTAAAAC ATCATCACTT ATTTTAAACC CATGTTCTGG ACCTGGAAAA ACTCCATCTT 1020

TTACTnCCTC TATATATTTT GTAAATGCTT TATTCATCTC TTCTGATAAA TTAGCATATT 1080

TCTTCACAAA TTTAGGGGTA AAATCACTAT ACATCCCCAA CATATCTTGA TATACAAGAA 1140

TTTGTCCATC ACACCCTGCA CCTGCTCCAA TACCAATkGT AGGTATTGAT ATCTCTTTAG 1200

AAATTAACTC TGCAAGCTTA GTTGGAACAC ATTCTAACAC TACAGCGAAT GCTCCTGCTT 1260

TTTCTACAGC TTTAGCAGCT CTTATTAATT CTTTAGCAGC TTCCTTGTCC TTTCCTTGTA 1320

CCTTAAATCC TCCAAATGCA TTAACAGATT GAGGTGTTAA ACCTATATGC GCCATAACAG 1380

GTATAGAAGC CTTTACTATA GCCTCTATTT TATCGCATAC TTCTATCCCT CCTTCTAATT 1440

TAACAACCTG AGCTCGTCCT TCTTTTATTA ATCTTCCTGC ATTAACTACT GAATCATATA 1500

CTGAAGTTTG ATAAGACATA AATGGCATAT CTGCAACAAC TAAAGTGTTC TTAGCTCCTC 1560

TTGTAACTGC TCTAGTATGA TGGAATCATG TCTTCCATTG GTACTGAAGT GTATCTTCCA 1620

TGTCCTAGAC ATACCATACC AAGAGGnATC TCCTACTAAG TATnCCATTT AT 1672

(2) INFORMATION FOR SEQ ID NO: 758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

TTCTCACACA GATAATACCA GTTGAAATTT TATTCGTCAA CTCAATAAAT GTAACTTTTA 60

CATTTTGATG AAGAAAAGCC TATTCTATCA ACAAAAATTT TTTATTAAAG GAGATTTTAT 120

ATGTTTTTAC AAAATAAGAA TGTCGTCGTA ATGGGTGTTG CCAACAAAAA AAGTATTGCT 180

TGGGGCTGTG CAAAAGCATT AAAAGATCAA GGGGCCAATG TTATTTATAC GTATCAAAAT 240

GAACGCATGA AAAAGCAAGT GGTTAAATTA GCAGATGAAA ATGATTTGTT GGTGGAATGC 300

GATGTTGCTT CTGATGCGTC CATTCAAGCA GCCTTTGAAA CAATTAAAAA TGAAGTGGGC 360

ACGATCGATG GACTAGTCCA TGCGATTGCT TTTGCCAAAA AAGAAGAATT GTCTGGAAAC 420

GTTAGTGrCC ATCACTCGTG ATGGTTTcCT ATTAGCACAA GATATTAGTA GCTACTCTCT 480

TTTAGCAGTC ACTCATTATG CGAAACCTTT GtTAAATCCT GGTTCAGGaA TTGTCACATT 540

GACGTATTTA GGtTCCGAAC GTGCGATTCC TAACTACAAT ATGATGGGGA TTGCTAAAGC 600

TTCTTTAGAA ACTGCCGTGA AaTATTtAGC yTTTGAATaG CtGCmGAaAA tcGTGTCAAC 660

GGAATCTCCG CAGGnCGGAT TAAAACATTG GCTGTGACGG TGTAAAAGAC TACGATCAAT 720

TGATTAGTAT TCnG 734

(2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

ATTATTCAAC AGACGGAGAA GTAGATGAGT ATCTTACGCA ACTTATTTTG AAAGCTCGTC 60

AAGCAGGTAT TTTCTTTATT GTTGCAATGC AACGTCCAGA TGGAGAATTT TTAAAAACAG 120

CATTACGTGA CCAATTTATG TTTCGCATGT CTGTTGGACG TCTATCTGAA ACAGGTATTT 180

TGATGATTTT CGGTGATGAA AATAAAAATA AAAAGTTTAA ATATGTTGAA AAAATTGACG 240

GTCAGAAAGT CTATGGTCGT GGATATGTGG CTCAAGGAGG AGGAACTGCA CGTGAATTTT 300

ATAGTCCTCA AGTACCACAA GACTTTGACT TCATTGAAGA ATTTATCAAA ATTTCTAAAG 360

AGTTAGGTTA TGAAGATGTT CCAAAAGAAG TACAAGAAGA AGTATCTCAA AAAATATCTA 420

AACATATTGA TAAAGAAGCA CTGGCAGAAA TTGATGAAGA ATTTCAAGCA GAAAAAAATC 480

AGTTATCAGA GTTAAGTGAG AAATATTCTG CTTAAAAAGA AGTCACATAA ATTAGTTGGA 540

AAAGGAAGGT TTTTATGGAT TCTAATGAAA TAATTAAACG TGTCAGAGAA CGAGTATATA 600

GAGAAGTAAA GAAAAAATAT ACTAGAGACG ATTTGGATAC TCGTATTCAA GATGTATTAT 660

ATTATCGTTC AGAAACATAT ATGAAATTAG TTAGCTTTGC AAATGGTAAA AGAATTAAGA 720

AGTTAGCTGA TCCTAGAAAA TTTGAAAAGT TTATGGATAC AAAAGGAGTA AAGATTGTTG 780

CAGAAGTACT TGATGGATTG AATAATCAAC CAAAAATGCA AGCTATGGrA TACGAACAAA 840

AGGTACTTAC TAAAGTACGT CAATGGTATC AGAAAAAGAA TCACCCTGAG CTTGTAGATT 900

TGGAAGAAGA AGCATTTGAA CAACTTGTAG AAAAAAATAT CATCTATAAA AAAATGAAGA 960

AAAGGTTGTA TGAAGAACAG GATAATCAAG GTTTTGTTTA TTCGGATAAT TTTGATATGC 1020

AATTGATTCG TGATTCATGT GATATTGAAG AGGCTCTATA CTTAGATATC ACGTTGGGGG 1080

ATTACTAAGT GAAAGGAGTA AAAAGAAAGT GAAATTTAAA TCTCGAGTAC AAATGTTAAA 1140

CTATGTGATT GGGAAGAAAC CAGACATCAT GAAAACAGTG ATCGGAGAGC AGAAAAAGAG 1200

GGGGGTACAG ATGATAATAG GTTACTTGAT TATAAATTAT TAGTAATTTC nGnTTTAGGT 1260

GC 1262

(2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 776 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

CACnGACTTA AAACTTATCT GGAAGTTTGT TGATAAnACT ACCACCAAAA ATGGAGGnAT 60

TATAGTATGT TTTTATTTGG AAATAAAGAA GAAAnAAAGG TAAAGAAAGC AGAAGAAAAG 120

CAAATAAAAG AATATTTTAA AAATAATCAT GATATTGTAA TAGGCGGTAT TTATTTTAAT 180

GATTCAGACA AAAAAATATT TATCCCAAAA AGTATTTCTG AATCAAGAAA ACAACAAGTT 240

ATCAACTATG ATGATTTGAT TAGTTACACA GATATTTTTG TTGGTGGCAA TATAAAAAAA 300

CATCACGGAA TAACTCGTGC AGTTGTTGGT GGCGTTTTAG CTGGTCCTGT TGGGGCTTTA 360

GTTGGTGCTG GAACAGGTGG AAAAGAATTT ACTTCCATTA AGCAATTAGG AGTTATGTTA 420

CATCTTCCTA ATAATCAGAC AGTAAAATAT ATGTTAATCA CAACTGAAAC AAAAACTGAT 480

TCTATGATTG GTAAAGGTTT AATGGATAAA TACAACGAAT TAATTGCAAA ACTGGaCCAA 540

ATACTAAAAA CTAATTCAAG TAATAAAGAT AACACTGTAT TATCTTCTGC AGACGAGATA 600

AGAAAATTTA AAgCCTTGTT AGATGATGGc ATTATTACmA AACaAGAATT TGAAATAAAA 660

AAACGTGAAw TGtTACmATA aAAATaACGC ACCCTCTCCG GCTAAGAAGT TAGtGCGTTA 720

AAAATaGAAC CaAAATAGGC TwATTTkGTT ACGCCTATTT TACCACAAAG AAAAGG 776

(2) INFORMATION FOR SEQ ID NO: 761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

ATTGCTTTTT CAATTTGGTC CTGAGGATTC CCAGACCCTC CGTGTAATAC TAGAGGTACA 60

TCAGAACCGA CAGCTTCAGC AATCGCTTGT AAGTGATCAA ATGCTAAACC TTTCCAGTTT 120

TCTGGATATT GACCATGGAT GTTACCGATA CCACATGCTA AGTAGTCAAT ACCTGTAGCA 180

ACCATTTGTT TACATTCTTC GATATCAGCT AATtCGCCAG TACCGATGAT TCCGTCTTCT 240

TCACCACCGA TTGAACCAAC TTCACATTCG ACAGAAATAC CTTTAGCGTG CGCTTTTTCA 300

ACTACATCTT TCGCTAATTT TAAGTTTTCT TCGAATGGTA AGTGAGAACC ATCAAACATG 360

ATTGAAGTAT AGCCAACTTC GATACATTCT AAAGCAGCTT CGTAGTCACC GTGGTCTAAG 420

TGAATTGCTA CTGGAACTGT GATATTCATT GAGTCTACTA AATTAGTAAT CATGTCTTTA 480

GCTACTTTGT AGCCGCCCAT GTATTTAGCA GCGCCCATTG ATGTTTGGAT TAGAACTGGT 540

GCTTTTTTAG CTTCTGCTGC TTCTAAAATC GCTTGTGTCC ATTCTAAGTT ATTTGTGTTA 600

TAGCCACCTA CTGCATACCC GCCTTTACGT GCTGCTTTTA AGAATTCTGC TCCTGATACT 660

ACTGGCATAA AAAATTCCTC CTAAGTTTTT AAAAACTTTA TTTGTTAGGT GTTCCCTAAC 720

CAACGGTTCT ATTTTAGCAG AATTCCTGAC ACTTTTCTAG TAAAATTCCC TTTTTCAGAA 780

AATTTTTGTC TATTCTTTCA CATAACCTTC ATTTTTATAA AAAAACCTCC AGTTTTCCCG 840

TTAAGACTTT GGGACCTGAn GGCCGACTTG CTATTTTAAT TnGTCTTGGT GGATAACGTT 900

CACCTTGTAG GATGAAGCnC AGGAAAT 927

(2) INFORMATION FOR SEQ ID NO: 762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

AATTACCAAA CCACTGAATT AGAAACAAGA CAAGCAAAAG AACGGGCCTT AGCAGCAGTT 60

TCmGCGATTG TTGAAGGAAA GCCAATCCAC GTTATTTTTT CrGGGAAACC TGGTGTCGGT 120

AAAAGTCaTT TGGCTATCAG TATTTTAGTT GAAGTCTTAG aACGCTCTGC ATATCaAAAG 180

TATTGTTTAT TTGTCAGCTA CTCTGAGTTA TTAGAAAAAC TAAAAATGTC CATGAATGAA 240

TCGGCCAAAA GCCAAGCAAA GGCTCAAGCG TATATTACTA GAATGAAAAA AGCAGACGTT 300

TTGGTTTTAG ATGATTTAGG TGCTGAATTA GGAATTArAA ATAAAGTTAG TACGGATTTT 360

AATAATGACA TCTTAAACCG AATTTTAGAA GCTAGACAGA ATAGAGCAAC TATTTnTACT 420

ACTAATTTTT CCGGAAACAA CTGGTGGAGG CCTATGGAAC ACGCATTAnn CCTCGTCTAA 480

TGAGCACGCC AATGGCTATG TnTCCATATG AAGACACACA GACAACGA 528

(2) INFORMATION FOR SEQ ID NO: 763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

GCTGAAGCTG ATCCAATATA TATCAAAACA CAGCTAGGAC ATAAAGAGAT AATACAGTCA 60

TATGAATACG CATCAGCTAC TGAAGCAAAT AGAAAAAAGA ACAAAGAAAA ATATGAAAAC 120

AAATACAAAG ATATTTTGTA AATACCCAAA AATTACCCAA AGTATATCTA AATTGTTATC 180

TTGATGTATA TATTAAAACA TATAGAATTG TTTTTAATTA AACAGCAATA TTCTTGAATA 240

ATTATCTATG AAGCTGGCAG GTGGCTCTTT ATTAAAAnGC TAAAACCTTT ATTTATTAAA 300

GGTTTTAGCT TTTTTCATTA CCGACATACC CAAAAAGTAC CCAATTTTnT TGTATTATTT 360

TrTATTTCTT GATAGACAAC ACGAACGAAA GTTCGATATA ATTGTATTAG GGAGGACGAT 420

ATCATGAAAA CTAATTATGT AGGAGTAGTT GAAAAGATTA AAATGTnAAG TATGTATCCA 480

AAAATTTTAG GTCGATTCTC 500

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

ATTTATTTTT TTAGTACAAA AAGTCAGCAA TTTTTTGCGT ATGTTTGGGC CATTTTCCCA 60

GTCATCGCCT TTTTTTTGGT TAGTTTTTAT ACATTGGATT TTTTATTTTC CCCAAGCTAT 120

TTAATTATGG TGCCTGTATT TACTATTATG TTTAAAATTA ACTATAAAAA AGATTATTCG 180

TTTGTAGCGC TGCTCAAAAT GAGTATCAGG CAATTTGTGA TCAGTTTTTT AGCATTTATA 240

GCTAGTAGTT CCTTTAGCTG GTCTATTATT TTAAATAGTA GTGTGACATT TTTAATTGTT 300

TATTTATTTT ATTCATCTGC GACACCGATG CGGTATCATA GTTATTTGAT GATGTTTACG 360

TTTTGTCAGT TAATCCAGGT TAAAGGAAAT ACATTTTTGA TGCAATCTCA AGTTGTGGnC 420

TTTTTAATTG GTCTTTTTTT ATTGGC 446

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

TATTTTTTCT GAACTGCTCT TGCTTTCTTC CGCTCCAGAA GTCTGTGTTT TTTTCATTTG 60

TTCTGGTGTG GGATAAATCT GTTCGCCTTC TTTTGAGAGA AGGAAACGGC TACGTGCTAA 120

TTTTGCCACA TAATCATCAT CTTTTAACAA AGCAACGTCT TTTTTTAGAT CCTTGACCTT 180

CTTATCAACT GCTACGGATT CAGCAATTGC ATCTGCTCGT TCTTGTTTGA AAGCACCTAA 240

GCGATGATAA TCTTTCATCA ATTGGATGCC AGAAAAGGCA AAAATAATGA AGGCCACGAG 300

AAAAATCGCT GCCAAGgTCT GCGTCTAAAA ATCAATTGTT TCTGTTGkTT TTGGAATTCG 360

ACATACTGTT CTTTCGTGTA GTCATTTTCC AATGCCGCAA CTTTCyTCGA GTTTTTTtCA 420

TTCTTTCCCA TCGTCTCGCT CCACTCGCTT tGGATTGTCC GTTTTATTAT ACCAACATCT 480

AAGAACCTnG TCTAATGTtA ATTTCAGAGA AGTTAAAGAA AATCAAGCTT TTTTCTAAAA 540

TAATCCTTGC CTTTGGAAAT AAACAGCGGT nGATTAnTAA ATTTTTTCCA AAAG 594

(2) INFORMATION FOR SEQ ID NO: 766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

TGATTATTTT CCCTTGGAAT ACCTTAGCAG GCACAACGGT GAGTCCATTT GTTATGGTTT 60

TTGAAAAAAT GAATATTCCT TTTGCTGCTG ACATCGTAAA TTTTGTGATT ATTTTAGCCT 120

TGTTTTCTTC TATTAATTCT GGAGTATACG CCTCTTCTCG CCTTTTATAT TTTCGCTTAA 180

AAGATAAAAA AGGACCCATG AGTAAACTAG GGGTTTTAAA CAAGCACCAA GTACCTCAAC 240

GTTCAGTTTT CTTCTGCGCC AGTGTTTTAT ATCTGGGCGT TATTCTTTCT TATTTTGTTG 300

GCGATGAATT ATTTGGTTAC TTAGCCGGTT CTCTCTCTTA CACTGTCTTG CTAATTTGGA 360

TTTaATTAGC GCTGCGGCGT TTGTnCTGTC TTTAAAACGA GGGTCTCTCT TTGAAAAAAG 420

TATTAATCTC CTTGCGTTAA TCATTTTAGG TCTCATCTTT ATTGGCATCT TATTtACAAA 480

tTCGTaGGCG TCACTCyTTT AACAGGCCTA CTGTAC 516

(2) INFORMATION FOR SEQ ID NO: 767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767:

TACGGCTTTG AGCGTGTCTT TACTAGTTTA TTGCAAATCA ATGATGATCG GGAAAAGGTA 60

TTAGCAGAGT TTAAAAAAGT CGTAGATTAC GCCAACCAAT TAGGTATGGA AGTGATGGTC 120

GATATTAATC CTGCATTGTT CGAACAaTTA GGCATCTCTT ATGATGATTT ATCATTTTTC 180

CATGATATGG GCGCTTACGG TATTCGTTTA GATCTTGGTT TTACTGGGCA AGAAGAGGCG 240

AATATGACAA GAAACCCTTA TGGtATTAAA ATTGaAATTA ATATGAGTTC mGGGaCAAGT 300

TATGtAGATA ATATTATGGc CTACTCACCa AACACaGaAA ATTTACTAGG CTCACATAAT 360

TTCTATCCAC ATCGCTATAC CGGCTTAGGC TATGAGCATT TTGTTTATTG TTCAGAAAAA 420

TTTAGAAAAT AtAATTTAAA TACGATGGCG TTTGTGAACT CACACGATGC TACATTTGGG 480

CCATGGCCGA CACAAGATGG GTTATGTTCT TTGGAAGACC ACCGCGATTT AGAAATTGCA 540

ACGCAgTTAA GCATTTAGTT TTAACAGGAT TAATCGATGA TATTTCTGTC GGAAATGCTT 600

ATGCCTCAGA AGCAGAATTA GCAGCAATGG CAGAAGCCTT TCATGCACCG TATCCTTCGA 660

TCAAAGTGGA TACAGAACCA GAAATCACAG AAGATGaAAG AATTGcATTG TTCGATAACT 720

TACACAGTTA TCGTGGaGAT CGTTCTGaTT ACGTTTTGCG TTCaACAaTG aCACGtGTTT 780

ACTATAAAGA TCGTCCTTTC CCAGCTCATA CAACCGAGAG ATATGGTTCG GGCGATGTCC 840

TTGnATTGAC AACGnnGGCT ATGG 864

(2) INFORMATION FOR SEQ ID NO: 768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

ATTTGCTTTT AGCAAATAGG AATCTTAAAC TTTAATTACA ACTAATTTAT TCTAATTTAA 60

GGAGAGAAAA ATGATTTCCA GCAAATACAC TATTAGAGAA CAAAATGAAG CTCAAATACT 120

TAATCAAATT ATAAAACATA GAGAAATATC TAGAGCCGAA TTAAGTAAGA TCACCTCTTT 180

AAATAAAGCA TCTGTTTCTT CAATTACAAA CAAACTAATA AACGATGGAT TCATCATTGA 240

AAAAAGGATC GGAGAAGCTA CAAATCGAGG AAGAAAACCT ATCATGCTGA CCTTTAACGG 300

TAGTTCTTCA GCCTTAGTAA TTGCAATTGA TCTAGGCTAT AACTATATAG ATGGCGCATT 360

AGCTTCTTTA GATGGAAAAG AAATCCATAG GGTTCAACTT ATTGATACCT ATGTTAACAA 420

AAAAAATGTC CAAGATTTAA tTCATAAAGT ATTCAATCAG CTTACTTCAG ATTGTCCTCA 480

TACCCATTAT GGCATAGTAG GTATGACAAT AGCTCTTCAA GGTCAAGTTC TAAATAATAA 540

AATTATCAGT ACTTCCTACA ATGATCTTGC TGAAATAAAC CTAGTTGAAA TGTTAAACCA 600

AGAATACAAc TTCCCAGTAT TCTTACAAAA TGAAGCTAAT TTATCAGCGT TGGGTGAATA 660

TACTTTTTCA TCAGATATAG AAmACTTAGC ATCCmTTmGT CTTCATAGTG GCATTGGTGT 720

CGGACTTGTG AAAAATGGTA AACTAGATGk TGGTAATAAm GGTTATGCTG GACAATTaGG 780

ACATACTATT TTGTTTCCCA ATGGAAGAAA ATGTACTTGT GGAAATCATG GTTGCTTAGA 840

AAAATATTGC TCTACACAAG TGATTTATCA CGAAATTTCG AAAGAGAAAA ATCTCAATAA 900

AATAAATTCA GATGTAGTTT CTATTCTATA TAATAACAAA GAATCAAAAG TTGTTAAAAT 960

GATTGAACAA TATGCCTACT ATTTATCTAT TGGTGTTAAT AATGCTATCA TGTTATATGC 1020

ACCTGAATTA GTAATTTTCA ATAGTCCATT AACAAAAAAA ATTCCAGATA TAATAAACAT 1080

AATCCAAAGA AATTTAAACA ATCAATTTAC AAAAGACGTA TTAGTTATTA ACAGCCCTAT 1140

CGAATGGAAT CCTGTAATTA GTGGAGCTAT CTCACTTTCA ATACAGAAAT TTTTAAATAT 1200

TGAACAA 1207

(2) INFORMATION FOR SEQ ID NO: 769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 772 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

nGATAATCAC TGCACCATCA TGTAGTGGTG TATTTGGAAT GAAAATATTA ATCAGTAATT 60

CACCAGTAAT ATCGGCAtCC AAATCAATAC CTGTCTCAAT GTATTCATCT AAACCGGTAT 120

TGCGTTCAAT GGTTATCAAA GCACCAATTT TCCGTTTTGA CATGTACTGA ATGGCTTTGT 180

CAAAGGCCTG AATAATACGC TCATCTTCTT GTTGCGCACC TTTATTCGGG CGGAAAAACG 240

AACTTCTCCC TAGATGTTCC AGCCCTCTTC GCACTTCTGG TTGAAAAATA ACAACCGCGG 300

CGATtACACC ATACATGATG ACTTGATTCA TtAACCAAGA TAATGTATGT AGACCAATTA 360

TCTCACTTAG AATGCGGATA ATGATAAAAA CAGCGACACC TTTTAATAGT TGGACTGCTT 420

TTGTTCCACG AACAAGCATG ATTAATTTGT AAACGAGGTA CCATACGACT AGGaTATCTA 480

TGATATkGAT AACAAAATCC TTAGATAAGA AATCCGTTGA GATGACTTGC TGCCAATAAT 540

TCmAATCTAA TAATTGATTC aATkGAAACG ACaTCATACC CCTCACTTCT CTCtCAAGAT 600

TyCCTAACAA GTATACCACA TTATTTTCTT TCATCACAGA ACGCAAGCGG AAACATCAGG 660

AAAATTTAGG AACTTTTTCA AATAACTTGA AATTTTTCAT CAAAAAATCG CATTTCTAAC 720

TAAAAAACGT GTGCTAAGCn AAAAGCTnCA GACACGTTTT TTTGGACTnC TA 772

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

GACnAGCTTC TAAAACTCGG TCCACGTCTA ATTCGGAGTG CATATACTCA AAAACATTGA 60

ACGTATCACT ATTTGACAAC GTGTTTAAGT CTAAGACCTT AATCTTGTAC TTGCCTTTTT 120

TCAATAAAAG TCCAATCTCT GGCAATATCC CACCGTCTGG GTCTGTTGTG ATAAAGCTAG 180

CATGTCGTTG CATAAGATTG GTTTTGATAA AAGCTAACGT TTTGGCCGCT CCAGAGTCAC 240

CTAGAATGGC GATATTCTTA TTTTTTTGTA GCTTGATTGG TAAACGTTTA TTAAAAAGAG 300

AAATTTTTAC ATGCTTACTA ACAATAATAT TGTTTTCAGG AATTGGATCT TCATATTTTT 360

TCATTTCAGC AGGTGTAGCA AAACGAGCCG AACCGTATTC TTCTCCATGA CGGTAGATTC 420

CACGATCATT ATCTCGCACA TACATTAATA GCCCTAAAAG AAAACCAAGT ATTCCCACAC 480

TAAATCCTAA TAGACTTGGT GTTATAAAAA ACCGATAAAA AGTTTGTTCG ATATACGTTA 540

GAATATCTTT TGTAAAGAGA TAATTCGTTT TTGAAAAATA GTCTGTCCCT GGTAACAGCC 600

AAAAGAAATT TCCTATTCCA AAGCCAATCA CAAATAGAAA AATACCAAGG AGAGATACGG 660

GTTCAGTTCC TTTTTGGTAC GCTGCATCAC AGTTCCCTCC TTTTGG 706

(2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 635 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771:

CCAAAGGGAG GATTTnATGC AAATTAGGCA GGTACATGTT AGGGCATCGA AAATTAAACT 60

GCAAAGAAnC ATTTACGATC GCTTTGGGGA CGATAGAATC AGCGGATAGT GCAATTGTGG 120

AAATTGAAAC AGAAGAGGGA TTAGTTGGAT ATGGAGAAGG AGGGCCAGGC ATTTTTATTA 180

CCGGTGAAAC GTTGGCTGGC ACGCTTGAAA CGATCGAATT ATTTGGCCAA GCAATCATTG 240

GCTTAAACCC CTTTAATATT GAGAAAATTC ATGAAGTGaT GGATAAAATA TCTGCTTTCG 300

CTCCAGCGGC AAAAGcAGCA ATCGATATTG CTTGTTATGA TTtGATGGGT CAGAAAGcTC 360

mACTGCCTCT TTATCAATTG TTAGGCGGCT ATGATAACCA AGTAATAACG GATATTACAC 420

TAGGTATTGA TGAACCAAAT GTGATGGCAC AAAAAGCCGT CGAAAAAGTC AAACTAGGTT 480

TTGATACATT AAAAATTAAA GTCGGAACAG GAATTGAAGC TGATATCGCA AGAGTAAAAG 540

CGATTCGTGA AGcAGTTGGC TTTGATATCA AGCTCCGCTT AGATGCGAAT CAGGCTTGGA 600

CGCCCAAAGA TGCAGTTAAA GCGATTCAAG CATTA 635

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

TnATTAATAT CTATATTTGA AATGTTATCA TCATATAATT CAATTGTCGC TAAAAGTTCA 60

CCTACAGTTC CCTTACACCA ACTATTGTTT TTAGGTTCTT CTTCAAAGTA TGATTCTTTA 120

ATTTTATGAA GTAAAGAATT TGCCTTATCT ATCCTATTGA ATTTTGATAG AAGATGGACA 180

TAGCTATATA TACCGTGTCC GAATCCTCTG AAATTAAAAT AGGGTTCTTC GGATAATTTT 240

TCAAAAATTT CTAATGAAAA TTTTCTATAT TTTTCATCCT CTGTTATCTC GGATAACAAT 300

AATAAAACTT TTATTATACT ATTATGCCCG TGGATCCAAT CATTTTTTAA CTCGCCATTA 360

TTTATCGGTT TCTTTTCAAT CAACATGTCT GGCAATTTCT AnGGACTACA TTTAAAGAGT 420

TTATATCATT ATTTAAGCGG nAATCTACAA GTAAAGGATA TATTAAACTT CCTTTTCCAA 480

AAAAAGCTGA CAATATATCT TCAGATGGTA TTGTATAAAT TGAATTTTTT ATACATTCAA 540

TTACATAGTC AtATTTATGA TycTttGTAA TGTATTTAAG AGCCACATAA AATATGAATA 600

TACCAGGCAA TCCATCGwAC ATATTATTAT TTAGGATTCC CACATTCCAA TCTTGATCCA 660

ACTTTATGTC AATCCAATTT ACAGTATTGG TTTTTTTATT AAAAATAGCT CTCTTGAAAA 720

TTTTTTTCTC TATCTTCTGA CATGCTTGAA TAATTTTACC GTTTAGCTCT AAGCCAGTAT 780

AAATATATTT ATTTGAATTT TGATTTTTCA AATCATTAAT ATATTTATAT GGATTATAAA 840

TATTcAAAGC AATTTCTAGC CAAACGGTTT GAATAGAAAT ATCTTCrTCA CArrGaTCAT 900

TTATTTTATT TAGGCATCTA TTCAGAGCGC TTnCTTGATA AAAATCTTCT ACTAAGCACC 960

CGTCACTAGC TATTAATGAT GTTTTTGAGA TATTGTTATA AAAAATGGGT ATGTCTCCAT 1020

CTATTAAGTC TGAAAATTCG TAATGAACTA CCTTTTTATT CTTATATGGA TAGGCCCACA 1080

TATTATGAAG TACTTTTTCT CT 1102

(2) INFORMATION FOR SEQ ID NO: 773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

TATGATTGTT TAGGTTGTAG TTGTTGCAAT TCGGCTTCTG TTAAGGGCCG ATATTCCCCT 60

AGTTCTAACG TTTCATCCAA CCATAGTTCG CCCATTCGTA ATCGTTTTAA ATACGTCACA 120

GGTTTGCCTA CAGTGGCTAA CATCCGTTTG ACTTGATGAA ATTTCCCCTC TTGAATCACT 180

AAACGGACTA CGGAAGTCCC TTCTTCCTCA TTGATCGTCT CAATGACTAA ACGACTTGGT 240

TTAACCATTT CTCCATCTTT CAAGGCAAAT CCTTGCGCAA ACAGTTGACA ATCTTCCGCT 300

GTCACAAGTC CTTCAACTTC AGCTAAATAw TCyTTATCCA CATGCTTTTT GGGkGaTAAT 360

AATTGATGCG CTAACTGGCC ATCATTtGTT GgTAGAAGCA AGCCyTCGGk AyCTTwATCC 420

AAGCGACCAA CTGGGrACAA GTCGGCACGG kAATCCTGAT CAGTtAACAA GTCAATTACC 480

GTTTCATCTC GCTGATCTTC CGTCGCAGAA ATGACACCTT GTGGTTTATG CAACATGTAA 540

TAAAAGAATT TCTGATACGT AAGAATTTCT CCCATCAAGG CAATTTGATC TGTTTCyTCA 600

TTtACTTGTG kTTTGGCTTC TTTtACGACG TCACCATTCA CCGkAACGaC TTTTTTCTTT 660

AACAATTGTT TGATTTCTTT ACGACTACCG ATACCAACAT CGGCTAAAAA TTTATCTAAA 720

CGCATCGTCA TTCCTCTTTC CTTTAAAAAA ATAGCTTGGG ACATAAATCG AATCGATCGA 780

TGTCTCArGC CTTGTCTCTT AAGAGAATCT GCTGAAAGGA GTTCAATCAG CTATTATTTA 840

ATATTGAATT TTGCACGTAA TTTTGCGGCA TTTTTCCCTA ATAAACGATC AGCTAAGCGA 900

ATCTTCAAGA CCGAATAGCC ATAAAAAGCG CCTCCTGCAG CAGCCACAAT TACAACGATA 960

ATGAAGGCTk GGAAAAnGTC TAGTTGGATC TAAAAATAGA TACAAGAACT GACGGAAAAT 1020

CAAAGnGATA ATCATCATGA TGACTGTnAT ACAGAACATT AACAATGTTC GCCGTAAGGT 1080

T 1081

(2) INFORMATION FOR SEQ ID NO: 774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

TTACTAAAAA ATTGTTTAAG ATTGTCCATA GTACTCCCTC TGTTTACGTT TCTTGGCTAA 60

GTCTACCATA TTCTTGCAGG TACGACCTAG GTCTAAAGCA TGAAAAATTC TTGAAAAACA 120

ATTTCAATGG TCTTTTCGCT GTAGCAAAGG AAATATGGCC TTCACTAGAG GTAAATAATT 180

GCTTACGCTT AGAAACGAGT CTTTATTTAG CCTCTATTCT ATCATGCTTT TCTTCGTTTT 240

TTATGTAAAT TTGTTTAAGA ATCTCTCAAG GAACTGCCTT TCTAACAAAT TTCAGCTTTT 300

TTTCCGTTCT GACTTGACCT TTTGAGTAGC TTTGTTACAC TAAATAGCGA ATCAGTGAAA 360

GGTGGGATTT GGTGGAATAT TCAATGAGAT TACCTGAAAA TTTTTCAACA ATGACTGTAA 420

AAGAACTATT AGAAAATGAn GGCTAGTCCT CGAAAAGTGC GCCATTTTTT n 471

(2) INFORMATION FOR SEQ ID NO: 775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

ATGGAAAGAA AGTAATTAAA GGAGCTTCAA AATAGTTTAA TATATAACTT TTAGGAGGGA 60

ACCCAAATGG AAATTATTTA CCCACCTTTA GTTGAAGAAG GATTAAAGTA TTATCTTGAA 120

ACGACCCAAC AATCGCTAGA TAAAAGTACT TTTTATCGTT CGATGGTAGA GAGAGGAATT 180

ATTACTGAAA CGGGTTTACC GACCCAACAG GCAATTGAAA ATGGATTAGT CAAAGACTAT 240

TACGAGGACC AAGGGTTATC ATTTGATGAT TTTTTAAGAA TCTATCCAAT TTTTGAAGAG 300

TATGACGAGG AGTTATTTCA ATGTATCGAT GGTaTTGGGA GATACCTGTg ATATGAAgAA 360

AATTTAGCTc ACAATgGAAT CTGGCGAGTa cTTTgAgtGC ACAcAGtcAA GCGTtCTgAg 420

AcGtAgaTgA gaGGAAtTtG CGcAAAATAT TAGAGGCGAC GGGACGCGAC CCTGCAAAAA 480

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

GTGAGAACCA ATCTTAATTG GTGATCCAAC AGCATATTGC AAATGCTGCT ATGGCTCGTG 60

GAATCAACAC ATCAAACTTT ATTATTATCA ACCCAAATGA TTATGAAAAA TGGGATGAAA 120

TGGTCGAAGC ATTTGTTGAA CGCCGTAATG GAAAAGCTAC TAAAGAAGAT GCTGAAAAAA 180

TCTTAAAAGA TGTCAACTAT TTCGGTACTA TGTTAACTTA CATGGGTATT GCTGATGGTA 240

TGGTTAGTGG TGCTATCCAC TCAACAGGTG ATACAGTTCG CCCTGCGTTA CAAATCATTA 300

rAACAAAACC AGGCGTGAcC GTGACAAGTG GTGCTTTtCTT AATGATTCGT GGTCGTGACC 360

AAGAAAGATA TkTATTCTCA GACTGCGCGA TTAACGTGAA CCCAACTGCA CAAGAATTAG 420

CTGAAATTGC TGnTGATAGT GCCAAAACAG CTGAATnATT TGACATTGAA CCAAAAGTTT 480

CATTG 485

(2) INFORMATION FOR SEQ ID NO: 777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

GTAAATTACT TCATnATTTG GnAACTACGG ATAATTTACC TAnAnATGAC AATTGGCCAA 60

TAACTATTAA AAAAATTACT TTTTTAAATC AAATATCAAA TGACAGCATA AGTAATTTGT 120

ATAAATTGTG GGTATTACCA CTATACTATA AGGCTATATC GGCTGATAAA CCTAATAATA 180

TGAAATACTT TAGTGTATTT AAAAAGTGTA TTCCATTTAT TTCAGATACT CTTTTTACTT 240

ATAAGTTATT ACTAAGATAT CAAGAAACAC AATACGAAGT TTTAAGAGAT TTAGAAAGTC 300

TATACAGTTC AATTTTTCGT AATTTGTTGA AATTTAAAGC TAATGAAAGT CCTGCTATTA 360

TAGTAGAAGA ATTGAAACGT GAAAGATCGG GCATTCTTAA TAATTCCCAG GAAATAATAC 420

AAAAAGCTAT ACAAGAATTA AGCTATTCAA AAAAAACAAA TTCCCCAATG GATACGGATC 480

TAGTCAGGTA TCTAATTGAA AGACTAAATG AGAATAATTT TAATACTCAA AGTGTTGTAG 540

GTGGAATTGA cACATAATTG AgATGAAAAg GamCGAAtGC AGTAGTAACA TAGGAATTTA 600

GTaTTTTTAG AAGGAAtTAT AATGATATGG CTAATAAGAT TAAACAAGAT TTACTTAAAA 660

AACATAATGA TGATGAAAAC AAGGTTGAAA GACTACTTTT AGAAAAGAAG TTTACTGAAA 720

TATACACTCG TAGTGAGTAT CCTCAAGTGA AGGAGCTATG CCGTACTTAC CCAGATGGGG 780

ACTTTACCGA AGTAGAAGTC AAAGAAAGAG CTAAATATAT GGCAAAGTAT TTTATCGATG 840

AGTATTTAGA AATCAATTAA CAGTTAATGT AAGTAAAATA AAACAATAGT TATTGAATCG 900

ATTACATTTT TTTGAGAATA CCAAATGGAT CTATTGATAT GGGGAGTCAA CCTTAAATTA 960

TTACCAATGT AAGAAAACGA TTCATACAAC TCGAAACAGA GTAAGTCAAA AAGGATATTA 1020

CAAAGAGTTA CACTATTTAT GAAAGAGAAA AAATTTAAAA CGTGCCAACA ATGCTTTTAT 1080

AAATTAAGCA ACGTTGGTTT TTCTGTTACT TAAAATCTAA TATCTTTAGT ATAATACCTT 1140

AATGTATTCT TAGAGTACGC CATAAGTGGT TAAAATACGC ATTCAATCTA GTATTCATGG 1200

TGAACTTTCT AAAAATAATA GTATTAATTA CAATTATTTA CTTGAGCGTT AAAAACAAAC 1260

TTAAAGAAAA ATGACTGTAG ATTTCTGAGC TACTTTAAAT TCAAAATAAT TCGGraAACT 1320

GAAATTTTGT TGkTGCaAAA CAGGACCGTT TGGTCCGGAT AATGGTACTC GGAAAGGCCG 1380

GTTTTTGC 1388

(2) INFORMATION FOR SEQ ID NO: 778:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

ACTACnGAAG AGTACnATnG AGCACCTTGA TCCCGCACAA AATCGGTGCC AGATCCTTAT 60

ATGATTGATA CCACACCCAT GGCTGCCACC ATTAAAGCGG GCGAGACCAT TTCCATGACT 120

TCGAAAAATA TGCGACAAAA AGGTCAAATT CTTTTAGAGA AGACTGGGGT AGAAACAGGT 180

ACTGATCTTT GGAATGACAA TTATTCTCTA GCTGGAAATA CATTTGCCAT TCGTAAAGAC 240

AGCCCAGCTG GTGAAATTGT CCAAGAAATA ACAACGGATG AAAAAGGTCG TGCGGAAACA 300

CCAAAAGAGC TTGCTAATGC TTTGGAACTG GGAACCTATT ACGTGACAGA AACTAAATCT 360

AGTAATGGTT TCGTGAATAC CTTCAAACCA ACAAAAGTCG AGTTAAAATA TGCCAATCAA 420

ACCGTGGcTC TTGTTACCAG TAACGTAAAA GGGCAAAACC AAGAAATTAC TGGGGAAACC 480

ACTTTGACAA AAGAAGACAA AGATACCGGT AATGAGAGTC AAGGGGAAGC TGAGTTTAAA 540

GGAGCTGAAT ATACTCTCTT ACTGCAAAGA TGGTCAGCTG TAAATnGAGT GAGCTTTAAA 600

ACAGATTAGT GAGGGACGAA GCTTCTGTGA ACAGTGCTTG GCTTAGTGAA GACCAGTGCG 660

TAACnCTGCA TTACGGATTC TGCAGACCAG CCTGAGTTCT TGTGACGGAT CTGAnnTAAA 720

GTGTATACGA AAATG 735

(2) INFORMATION FOR SEQ ID NO: 779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

GCTGTACGGC AGCCAGACGT TGCTGTCCGG CACGGTGATA CTGTTCAAGC AGCTCGATAC 60

CGATATACCG GCGTCCGGAC TGAAGGGCGG CCACACAGGT TGAGCCGCTG CCTGCAAACG 120

GGTCCAGCAC AATCGCGTTC GGGTGTGTGA AGCTCTCAAT CAGTGGTTGC AGGCTGGTAA 180

CAGGCTTTTC CGTCGGGTGA TGACGATTGC CTGAATATTT CCAGCCCAGC ACGTCGGGCA 240

ATGGCTTCTG AGGCA 255

(2) INFORMATION FOR SEQ ID NO: 780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

AGATGCTGAT TTCTTTGCAT TTGAAGCGTG TGAGTATCGC CGTCATTTCT TGGCTTATTC 60

ACCAGATTAT GCGATTATGA CGAATATCGA TTTTGATCAT CCAGATTACT ACAAGAGCAT 120

TGAGGACGTT TTTTCAGCGT TCCAAACAAT GGCTCATCAA GTCAAAAAAG GAATTTTTGC 180

TTATGGTGAT GATAAGTATC TTCGCCAGTT AGAATCAGAA GTGCCAGTTT ATTATTATGG 240

CGTCAcGAAG AGGgATGATA TCCAAGCCCG AAATATTCAA CGAACAACGG AAGGCTCATC 300

TTTTGATGTT TATCACAAGG ATGATTTTGT AGGTCATTTT GTCTTACCAG CATTtGGCCA 360

TCACAaTATC mTGAATGCGC TAGgTGTGAT tGCtGTGGcT tATTTTGrAA AACTtGrTAt 420

GCmAAAAGTC GCaGAaGAAa TGCTAAGTTT TAAAGGTGTA AAACGTCGTT TTAGCGAGAA 480

AAAAGTCAGT GACATGATTA TTGTTGATGA TTATGCGCAC CATCCAGCTG AAATTAAAGC 540

AACGATTGAT GGCGCTCGCC AAAAATATCC TGACAAAGAA ATTATTGCTG TCTTCCAGCC 600

ACATACATTT ACACGAACAA TTGCCTTAAT GGATGAATTT GCTGAAGCAC TGGATTTGGC 660

AGATGAAGTA TTCTTAT 677

(2) INFORMATION FOR SEQ ID NO: 781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

TTTAGGGATG AGACAATTAC CGATGGGCGT TTCTTATGCG GTTTGGACAG GAATTGGTAC 60

AGCAGGAGGC GCTATTTTAG GAATGCTCTT AGGTGAATCA AAAGACCTAC GACGGATATT 120 tTTTATTTTT TTAATCATTG TTTCTGTGAT TGGTTTAAAA TTAATTGGTT AGAAGGCGAG 180

AGAACATTGT TTGGATTATT GAAAGACAGG TGAGTAAAAT TTAAAAAGAG ACAGAACCAA 240

GTGCGGTGTT CTGTCTCAAA ATAGCTTTTA TTTTACAAGG TTACTATAAC GtGTCGCAAA 300

TTCATTGTTG TAGGACTTGC CGTTGACATC TkGACCAACG TCCCAATTTG CAGACCAAGT 360

CATTAAGCCA CGG 373

(2) INFORMATION FOR SEQ ID NO: 782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

ATGCATGAAA TTAAGTAAAC GACAAGAGCA AATTATCGCT GTTGTAAAAG AGCATCAGCC 60

AGTTAGTGGT GAACGCATTT CGGACATACT AGCCGTTTCA CGTGCGAmAT TGCGTTCTGA 120

TTTGTCTTTT TTAACACTTT CAGGAATTTT AAAAGCAAGT CCGAAAGTTG GTTATACTTA 180

CGAAAGTGAT AATATGGAGG CTTTTTTCTT TTTTGATGTT TTTCAAACAA AAGTTCAGGA 240

GATCATGAGT CCACCaTTGA TGGTTGCCCA AGACACCTCA ATTCGAGATG CGATTACCAA 300

CTTGTTTATG TATGATGTCG GTTCTCTTTA TGTCAtGGAT GAAGCmAAAG AaTTATTAGG 360

GGTTTTGTCA CGAAAAGATT TATTACGGGC CTCTTTAAAT ACAAATATTG ATGGCACACC 420

TGTTGCTGTT TGTATGACAA GAGTGCCACA TGTGAAAACC TGcACACCAG AATTTACTAt 480

TCTTGAAGCT GCTGACACTT TGCAAAAATA CGAAGTGGAT TCTTTGCCAG TCGTTGAAAA 540

AGAAAATCCT AAAAAAGTTA TTGGAAAAAT TACGAAAACG AAAATTTTAA CCTATATTAC 600

GCAACAAGCG AAAGAAGCCG CACAAAACAG ATAAGGGAGC TTAATTATGA AAAAAGAGAT 660

CATTGTTTAT ACTATTTCCG ATTCACTTGG AGAAACATCA CAAAAA 706

(2) INFORMATION FOR SEQ ID NO: 783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

TGAACAAAAT CGACTTCTTC ATAAGTCACA TCCTTTATCT ATTAATACAG TTAAAAAATC 60

TGTATTACTT ATAGCATAAA TGAAAGCGAT TAAAAAGTAA AGTTCTCTTG AAAATTCCCA 120

TGTTCAACTT TTAGGCTAGG TTCTTTTTAT ATGCTAAAAT AGAATAGAAA CGGAGGTTTT 180

TaATGGAATG GaTTGAAATT AaGCACGCAA CaCaAAATAA TTTGrAGrAT ATCTCTGTCA 240

ATATCCCTAA AAAGCAACTA ACTGTTGTTA CTGGACTTTC GGGTTCAGGA AAGTCCTCCT 300

TAGTATTTGA CACATTAGCC GCTGAATCAC GTCGGGAACT AAATGGATAC CATTTAGTTC 360

GnTTTGGTTC CAAAATTACT TTACCCCAAA TATGGGTCGT CCCAGAAGTT GGAAAAAAAT 420

CGAGAATCCT TCCTGGTTGG CCAATTGGTC CATTGGACCC nGAAAAAAAG TAnGCAGGGn 480

AATTCnCCGT TCCGACAGT 499

(2) INFORMATION FOR SEQ ID NO: 784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

TATTCATTTC TCCCCTACTC TCTCTGGTTT TTATGGACGT GTATAgaTTA CTgTTTTTTT 60

ATAGGaAAAG AAATGGGCAT TCTTGTATAT TTTGATGTAC AATATAGTAT AGAAAGCGGA 120

TACAAGTAGG AGTGATTTTT TATGAACTAC ACAAATAGTC GAACGTTTAA TCCTGAAATT 180

TTATATGCCT TTGATCCTTG GAACGAAGAG ACCCACCCTT ATAATTGTCA TCATCATGAA 240

TTTCTGGAAA TATCTATTCT TTTAGAAGGT GAATCTGAAT ATATTGTTCA AGGGCAACAG 300

TACCATGCCA CTGCTGGTAC AGTGTTTCTT TTTAATCCGC GAACGGAACA TGGTGAGCAA 360

CAAAAAGCAG GAACTTACTC ACATCAACTA CACATTGGCA TTTCAAATCT CTATTTAGAA 420

GGCTTAGCGC GAAACGTATT TCCAAATAAA TCAGCTTTAT TAGATTTAAG TCATTTACAT 480

GGTGCTTTTT TAGAAAAAGC TTGGCAAATT GTTCATGAAT TAAACCATCA AGAAGTTGAA 540

TCAGCGTTAC AAATTAAAGC TTTAGTTATT GAACTATTGG TCTATATTTT AAGAAGCTTA 600

GCAGTTGATC AAGAAAATAA AATTGAAACT CGGCTATCGA AAACGGAAAA AAGAAAACGA 660

AATTTAGTCA ATCnCAACCA AAAATnGTTG CGATGGTCCA TGGCGAAACG GCGAT 715

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

ATTAAAATTG GCGCATTTTT CAAAAAAGCC CGTGCTATGG ATAAGCGTTG TCGCTCTCCT 60

CCAGAAAGTG AACTTCCGTT TTCTCCGACC AATGTATGAT AACCGTCAGG TAGTTTTTCA 120

ATAAAGTCTT CGCAGTTAGC TAAACGAGCT GCkTTTTTCA CTTCCTCATC TGACGCTTGA 180

CTATTTCCAA TACGTATATt TTCCAAAATA CTTGTATTAA ACAaAGTTAC CTCTTGCAAA 240

ACAATAGCGA TTTTGCTAAA CAnAGAAGCT GGAGATACAC GTTTAATATC ATACCCATCA 300

ATTAAAATAC AGCCTTCATC ATAATCATAC AGTCTAGACA CTAATTTCAA GATACTAGTT 360

TTCCCGGAAC CACTAGCACC TACTAACGCA tCACTTCTCC TTGTTTAGCC GTAAAAGAGA 420

TATGATCTAA AATTGGGGTA TTGTTATCAT ATGAGAAAGA GACATCTCGC AACTCAACGT 480

CAAAAGATTT CAGAGGACTA TCTGATCCCT CTTGGAnACT GGTTTCCTTC ATAGCTCTAA 540

TTCGCTGTAT TTTAGGnGCT AAATAAAATA TTTCAAGCAC TGCTTCTTTC ATAGAATCGA 600

AGGAATCCTT TAnTTTTATT GCGGCTAGTA AGTAACCAAC GACGTAGAnG TATAGTCACT 660

TCACCCGTTA AAAGTAAGTG AACACCTACT AGAA 694

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

AAGGAACTGT nAACAGAGCA ATTATTTTGG CTAGCTGAAT CTTTTTGGCC ACAAGTGTTT 60

CCAGAAGAGG AAGACTATTT TTTTGGCGTG AGCGGTGGCC TCACATTTTA TCAAAAACAA 120

AGATTGGCCT CGGCACAACT ATCTATAATT ACGCTTGAAA AAGAAAAGAC AGAGGTTCCA 180

ACAATGCCTC GTTATTTTGA TTACTTGGGC AAAGAGCAAT CCTTGCCAGA AGCCTTCAGC 240

GCTTTATATG ACTTGCTAGG GGACGTAAAT CCTGAATACT ATCTTTCGCA AGCGAGAAGA 300

GTCATTAAAC AAGCTCTGCG AGGCCGCAAA GTCAGTACTG TGCCTAATAT TTTTCAAGAA 360

AGTTTGCACT TGACCCAAGT GATTACGATT GACCAGGACC ACTTAAAACT CCTTTTACCA 420

GTAGCAACGG AACAAGCCGA GCCTTTAGAA GCACAGTCGG ATATTCTAGC ATTTTATTAT 480

GAAAAAATTG CTAACCGATC GGCCATCGAA CGCTTAGTTT TTATGCAACA ATTGATTGAG 540

CAACTAGGTA CGAACTCTCT AAGTTATCTT AGAATAAATT AAAGTTACGA TAATTTTATT 600

ATGTAAACTA AAAATCAATA ACAAGAAATG GCGCCGCTTC TTAGTGAGAA ATGGCGTCAT 660

TTCTTTTGCG AACTTTTTTC GTCCAAAAAC CACCGGAAAT GAACTTAGGC TCATAGGAAA 720

TGATAAATGC TCTCGGCTCT AATTGATTGA TTAATTTGTA CAATGTACGT TCGTTTTTTC 780

TTGGGGAAAG GATTTCTAAA ACCATTCGTT CTCCTTCGCG TCCGTAGGCG ACACTTTGCG 840

TAACACCATA GCCGTGTTaC ACGAAGtGTT tCTGGTAAAT GAAATTGTTC AGTAGTAGAA 900

GGGAGGATAA CCGATACCAT AATATAACCC AAGGCCAAAT AGTCTTCGAT TTTAATTCCT 960

ACACTAATGC CAACAGCGTA ACCAAGCGCA TAAACAAGTA AATTTAAAGG ATTGTCTAAC 1020

CGATTCAGAA CCATACTCAG CCCTAAGACA TAAATTGTTA TTTCAGCCAT ACTAACCAGC 1080

GGTGCAATAA CCCGATAACC TTTCATCGTT AACATAAAAC GAATAGTATT TAAGGTAATA 1140

TACGCAAAAT TAATGATAAA AATCATAGCT AACATTTTCA AATCAACGAC CATAAAATAA 1200

GTACCTCTTT TCAAAATCTT TACATCCAGC CCTCATTATA GTACAGaAAA ACTGAGAATC 1260

AAAGGCGAAA CACTTATAGA AATGAATTCT TTTTTGAATA CTCGCTCATA TTATTCGCCT 1320

AATTTAACTG TTATTTGATA TAATCTTAGT ATGAAGTAAG AAGGAGGTAA GCGATGAAAA 1380

TTTTTGTTTG GATTTTGTTA TTTTTATTAG TAATTAACGT TATTGCTGCC TTAATTACTG 1440

TTTTTAGAAA ACCTCGTAGT ATTTCCAGCG TTTTAGCATG GATGATGACG TTGATTTTCT 1500

TGCCTGGTAT CGGCTTTATT ATTTACTTAT TCTGTGGGCG AGGTATCGAT GGACAAGAAG 1560

TTTTTAAATT GTCTGATGAT GAAAAACAAA TGGTTCAACG AATTAAAGAA AAAGTGGACG 1620

TTGATAACAA AAAAGCAGGG CGCGATAAAC GTTATGATTT ACTTTATGAT GCGAAAGTTT 1680

TAAATCGTTA TTTCCGGAAT ATGGACGCAT CACCGTTGGC CAAAAGAAAT AGTTTGCAAT 1740

TATTCACAGA TGGCCAAGAA AAATTCCAAG CATTATTTGA AGATATTCGT GCAGCGAAAG 1800

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 976 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

ATTTGAATGA TTTGTAAAAT TTTTGGTACA AATAGAATTA GTCCTACTAG CACTGCGAAA 60

CCGGCTGTTA ATAAAACAGC TCCTGCGGCC ATGTCTTTAA CTTTTTTTCC GATTGGATGA 120

AAGTGAAAAT CCGTAAACAT ATCTACGACA TTTTCAAAAA TTGTGTTGAT AATTTCTGCC 180

AACCAGACAA GAAAAACGGC CAATAACAAC CACAGCCATT CAGCAAGTGT TAAGGAAAAC 240

AAGAAACCAA ATACAATGGC CGTGACACCA AACGCTACAT GTTTGCGCAT ATTACGTTCT 300

TCTCGAAAAA CTGTTTTGAT TCCTTGCCAG GCAAATTCTA ATGAATTAAT AAAATGTTTA 360

TTTTTTCCTG TTTGCTCATC TTTTAAGGCC ATACGCATCT AAAaTCTCTT cTGTAAcCAA 420

cATTTyTTTy CacTTCAGGT TCCATATGAT CGTACCCaTT CAAATGTAAA AgCCATGTAC 480

TGCCAAAAAG CCCATTTCTC GTTCCAATGT GTGCCCATAT TCAACTGCTT GTTCTGCTGC 540

TCGCTCTGTT GAAATAATTA AATCACCTAG ATtACGTGGT AGCTCTGCCA ACTCTTCATC 600

ATCAAAAATA ATTGGCAATT CGTCTTCCCC TTCATCCTCT AAAGCAAAAC TGATGACATC 660

TGTAGGCATA TCTTTGCCCC GATAGTCACG ATTAATCATT TGGATACCTG CGTTATCTGT 720

AAAAGTCACC GACATCTCCG TATCTTCGGc AATTTCTAGA AAACCCGCTG CAAATTGCAG 780

CAAGTTTTCG ATTTCTTTGA TTTCTTCTGT TGGTACTTTC TCGGTTTCAT CAATGAAAGT 840

AATATCCATT AGTCATCTCT CTTTTCTTGT TCATCTTTCA TTTCTTCTGC TTCAGCTTTC 900

ATTTTTGGAT ACTTAATCCG TGAATGGAAG GTACTGCATA ATCCATTAAT TAATGATTTT 960

TCAATGATGC GAATCT 976

(2) INFORMATION FOR SEQ ID NO: 788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

TTAGGAATGA CCAATTTTGA AAGGGGTTCG ATTGATGAAT TCGATGATAT TTCTAGCATT 60

GATCAATACT ATCGAGCAAT AAAAGAAGGA TTTACGCCCA AAGAAGCCTT GTCACTTGTC 120

AATTTGCGTA GTCGAGACAA TGCCCGCACG CCTTTTCCAT GGAATGATTC TATGTATGGC 180

GGTTTTTCAA GCGTCAAGCC TTGGTTAGGA ATGGTGGATA ATTATAAAGA AATCAATGCC 240

GAAGCAGAAA TAAAAAATAG TCAAAGTATT TTTCATTTCT ATAAGCGGAT GATTGCATTT 300

CGTCaAAAGA GTCCCTATAC AGACATCTTA CTTTaTGGrA CATTTGAGGG tCTGTCaAAT 360

CTTCCmGaTA ATGtTATTGC tTATAAACGC mAATTaAATG aAAAAACGAT TTACGCCtTT 420

TTTAATTTkG GkGAGGcGGk tCCaATCCCy CmTTAtTTAG kTAATGGCAC AGTTATTTTT 480

GATACACAGT CTGAAGAACG AGAGCAATTA GTTCAGCAGG GAACATTATT AAAAAGCTAT 540

CAAGGACTAT TGATTACTAT AA 562

(2) INFORMATION FOR SEQ ID NO: 789:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

CAGTATTAAA AGTACTTnTC AATTACACAC TTAGTGTnCC AGTTTTTTTG GGTCTTTTCA 60

ATAAAAATGA TTCTTTTTTC AtCGTTTTCT TtCAAaTCyA AACAAAGCAT TCGTTTGTTA 120

GAAACAATAG CTACTTATTT CCGAATAATT AGaTTTAATT AAACCAAAAG CAAAGGAATT 180

CACGAACGTC TTTcAATTAA CTTCTTGTTT AAATGGGAAT TTCAGGTCCT CTCACAAAGC 240

ATTTTTTACT TATTTTTCAA AAAAAACAAC GAAAGAATAG ACACAGCCAT TCTCTCGTTG 300

CTTCATATCC TTTTATTTGT AATCTTCTTC GTAAAAACGT CCTAAAATTT TAACATTATC 360

TGAGATGCTG ACAAAGGCAT TCGGATCACT TTCTTTCATG GCTGCTTCTA AACTTGGCAA 420

CTCAAAGCGT GTCACAATAG TTAGCAGAAC AGTTTGGCGG TCGTGGCGAT ACGnCCCTTC 480

CGCTTCATGA ATAATTGTAA TACCGCGGCG CATTTTCTTT TGAAtCTCAT CCACGACTCG 540

ATCTGGGkTT TTAGTGaCAA TCATAACTTG CATTTTCTTT TGCTTAGTAT AAACGGCATC 600

TGTGACCTTC CCACTTACAA AAATTGATAA CGCACTGTAG AACATGTACT GCCAGCCAAA 660

TAAATAACCT GCAACGAAGA CAATTAGTGC GTTAAAATAA ATTGAAATCG AGCCAACGGA 720

ACGCCCCGTT TTTTTCCGAA TGGTAATGCT TAAAATATCT AAGCCCCCAG AAGAAACCCC 780

GTTTTTTAAG ACAAAACCAA TTCCTGATCC AGAAATCGCC CCwCCwAAAA TAGCACAGAT 840

AATTGGATCT TGGGTCATCa CCGTTTGCGG AACAATATGC ATAAATAATG AAGTTAAAGT 900

CACGGTAATG AAAGTAAAAA TTGTAAACTT CTTACCTATT TTTTTCCACG CAATAAAGAA 960

TAACGGCACG TTTAAAAGAT A 981

(2) INFORMATION FOR SEQ ID NO: 790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

TTTTTCGAGA CGATACAGTT TATAGTTTCG TCCTGTGTTA CTAATGAGAA TCGAACTAGC 60

ATTTTTGGGT ACATACTTAA CATTCTAATC TTATCAACTA CTCCTACATA ATTAGTTTTC 120

ATACTATCGC CCTCCTAGTA ATATAATTAT ACCGAATGTA TGTTCGTGTT GTCTATAGAA 180

AAATTTTGTA AATCTATGAA ATGATAAAAA CAAATGGTGA TACATTTGGT GATACATCTG 240

AAATATCTAT GAAAAAAATG TAAATAGTGA AAGACTTCAA TAACTAATAA ATCATTGATA 300

TATAAGTAAT CGGAAAGAAT GAAATCTATG GAAATGTTTa TCTAACAAAC GCAACATGTt 360

CGCtTATTAG GTAAACCAGG TTTgAAGAAT TAGCmAAAGA TTTAAATGCA CGTCTATAAT 420

TgTAAtAAnA GA 432

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

CTGAAAAAAG CAACACTAGA AGTTTTGAAT TTACCTGCGT TGACAGGTAT AACTGATGAT 60

AATTTACGTC GTCTACTCAA CAATCTAATT ATTGAACTGT ACAAGTACCA GGCGGAAGAA 120

GAACGTCGAT ACATTCGTGA AACGCAGCAA CAGGGAATTA CACTGGCTAA AGCAAAAGGA 180

AAATATAAAG GTGGAAAGCC AAAGTACcGA GAAAATGATC CACGTCTTCA GTTAGCATTT 240

AAATTGTTTT TAGACGGATG CACAGATAAA GrAGTAGAAC AACAGACAGG GATTAATAGA 300

AGrACTTTTA GrAGATATAG AATGAAATAT GGAATAACAA ATTCTCTTAG ACATAAGAAT 360

GATTAAAACT ACTAATCCAA TGTAAAACAG ATAATATATT AaAGAGGGCT ATAGAGTAAA 420

ATGCAAAAGA AGTTTGAAGC AAAGCAATGC TCAGTAGACG nGTTACTAAA GGCGAnATAA 480

GCGATTATAT AAGGTTTCGA ATTTTCAAAG AACATATGCA TGGAAATATA AAC 533

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

CGAGTTTTCG CTGGCGCGGG CCACCCTGCT GCTGGATCGC GACGCCAGAT CGGAGGTCGA 60

ACAGGGCGTG CGCGATGCCT GGGACCTGGT CGGCGGtTCG CGtGCGCAAC TGGCAGAACT 120

TCCTGGCCTG GCAGTTCCAC TACGAGCACT ACATCCTGGC GCGCCTGTTC GTGAACCGCC 180

GCACCGCGCG CGTGCTGGAC TTCGGCCATC GCGAATTCGG CGAGAACCGC ATCCTGCCCG 240

ACGAGGAGGC GCATCGCATC CGCATCACGC AGTGnTGGCT GCGCAAC 287

(2) INFORMATION FOR SEQ ID NO: 793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793:

AATAAAATGG CCATAATAAC AAACGCAATG ACTAAATATA AATTACTATC TTTCAAATAA 60

TTTTTCATAT AATCCTCTTT TCTTGGTTTC AAGTTGCCCC GTGCCTGCCA CGGAAAATTC 120

TTTTTTATTA TAGTCGGTTT CGAGGGAAAA AGAAACAACT TCTCTTAGGT CTTATGATAT 180

ACTGAAAAGA AAAAAATGAA AGAAGGATTG GATATGACCT ATTCTATTAC ATGGGATTTA 240

GACAGTATTT TCCCCAAATGG GAGCGAGTCC AAAGAACTTA GCCAACGAAT GACTCAATTA 300

ACCGAACAGA CAAAAGAGTA CCATCAATTA ATCACAGAAT GGACACCAGA AAGTGCCCCA 360

nGCAAnGAAC AATTTGCTG 379

(2) INFORMATION FOR SEQ ID NO: 794:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

CCAAAATTAT CCGACTACGC CATAGATCAT TTAAGAAGGA TAATTTTTGG AAGGGAAAGA 60

GAATCATATA TGAAGTGAAG GAGGTCAGGA CAGAACCGTT TATTTTCGAA GGAATTGGTT 120

CTGTTCTCGC CATTTATCAG GTTTTGAaCC TGGAACAAAA ATCCAAAGTG ATTTTTGTCC 180

CAGGCTCTTT CGCTCTTTTA TTGAGTAAGA AGTCAGTTTA GAATTTATAT TAAGTTTCGC 240

TGTACATTTT AAAATTATCA TCAACAGAAA ATACAACAGG CGAATTTTTA GATAAAAAAA 300

TTAGTAAAAC AAGTATTAAA TAAATAGTAT TTTTGAGGAT AAAGTAAGAG AAATGTTGTT 360

TTTTTAATAG TTGTTAACGG AAAACAAAAT TATTTTATAG CCATAAAATA TATTTTTATT 420

ATAATTATAT TATAAmaymm tGaGCATATG ATTTGCAGAT AAGTTTTTCA GGGCCTATTC 480

TGAATAGGAA CTTAGCTATA AAAATAAAAG AGGAGAGTGG TTTTGATGAG AAAAAATCAG 540

AAGATTGTGC CAATTGTGAC AGCTTCAGAC GAAAATTATG CTCCTTATTT GAATGTAATG 600

ATGACAACTG TTTTAGAAAA TTGTCATGCG GAGAGACCTG TTCATTTTTA TGTGATTGAT 660

GATGGGCTGT CGCTATCTAG CAAAAAAGCA CTCCGAGaAA CGGTTAGTAG TAACTCACAA 720

AATGCAACTG TTGAATTTCT AACAGCAGAC AAAGAAGTCT ATCAAAATTT TTTAGTGAGT 780

GATCATATTA CAACGACCGC ATACTTACGC ATTTCTTTAC CGTCACTTTT ACAAAAATAT 840

AGCTATAAAA AGGTTCTTTA TTTAGATGCA GATACGCTGG TTTTAGATGA TATTGTCCAG 900

TTGTAT 906

(2) INFORMATION FOR SEQ ID NO: 795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

GGGCAAGAAG cATCCAAGTC TTGATTCGCC GAGGAGCAAG TCTTGAAGAT GCACAAGATG 60

CAGTGTCGCA AACGTATACA ACGATTTTTT CAATATTACC TGAAATTACA TCAGAAAATC 120

TACGCCCGTG GTTTTTCCGA GTAACATTTA ATTACTACAT TACGATGTAT CGAAAAAAGA 180

AACGAGAACG CACTTTTGTG GCAAACAGCC ATCCTGTGCA ATCAATAGAA AA 232

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

TTTATTACAT ATCAAGATTC TATCACCTTT ACAAAGAATG TTGCATCTTG GTATACAGCT 60

GTATCTTCGG TATTACCATA AACTTTAGCA GCTGTATGAA CATCAGTGAT TAATGTATTT 120

TCGTATAGTt CTTGkGCTGC ACTTACTCCA CCGCTATTAT GCCCATCGAA tAGaCCTTtA 180

ATTTCTACTT CTACTGTTtC ATCTGCACCT TtCTCATTAT CAGCATCAAA TAAATTAGAT 240

TTaTTTTTAT CTTATCTCCA ACTTTAAGGT TATTTTTTTC AGCTAAATCT TTATGCATTA 300

AGATTTTATT TTTATCTTCA TTTTCTAAAT GCTTTCCTTC TACTAATTTA TATGCTTCTG 360

ATACAAATTT TGTTTCTTTT GTTGAGTCGT TAACCCCAGT TAACATAACT GTTCTTTTAA 420

AATTCTTTGC TCTTTCAGGk GATTGaTTcG CAAGAGTCTC TTGAGTTTCA ATAATATCAT 480

AATCAACTAA ATCTGCAACA CTGTTTATTC TTTTTACATA GGAGTCTATA CTATCTGTTT 540

GAGATATCTT TTTAATATCT TCACCTTTTA CATTTCCCCC ACCTCTAGGT GTTCCTGGAT 600

(2) INFORMATION FOR SEQ ID NO: 797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

TTTTGGAGGA CAAGATGATT CGTATACTCG TACTATTACT CGCCGTTGTC ACAGGCGTAC 60

cAGTTATTAT TTGATGAAGA AAAGTGCAGC TTTTTTACCA CTCTTAAAAA AAGAAACTGC 120

AACAGAAAGT CAACAGTTTA TCGAACGTTT TGGGCGTTAT TACTTGATTA TCGCCATTCT 180

AGGTGTTCTA GCGGCTATTT TTAATCGCCC GTTATTGTCA ATTGGTTTTA TCTTTTTTGT 240

TTTATTACTT TCAACGTTGT TTAGTTTAAC TTTTGCAAAA AAAATGTCAT AAAAGACGAT 300

GAATTTAAAG AGGTCGGGAC AGAAGTGTTT AACTCCGAGA AATAAGAAGG AATTTCCGAA 360

AATTGTTCTT TAATTTTTGG AGAATTTCGG CTTATTTCCG AAGaGTTGCT TCTGTTTCCG 420

CCGTTTATCA ATTTTTAAcG GTGGGACAAA AATCCAAAGT GATTTTTGTC CCAGGtTCTT 480

TTTTTACmAA AAAAATGCCA ATATTCAGaA AAAAAAGAAG CGGnTTCAGT TcCkTTTTtC 540

nTTGnTTGnT TTACnAttAT aTngAAmCAt TAAtGaTTtT GTTaCGCTGA AAGGAGCGGT 600

TATTATGTTA CAACAATATC AnAAAATTAT GATAGC 636

(2) INFORMATION FOR SEQ ID NO: 798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

TGGGTAATTT TTAGGTTTCA CTTCGAAACG ATTATTGACA TACTTTCGTA AATACGCACC 60

TGTTTGTAGG GAAAGTGTTT GTTCCTCTTT AAAAGATAGA AGATTTTTGA CTGTAAAATT 120

AACTAGCATG CTGTTCACTG AGAGATCCCC TCATAATTTC CCCAAAGCGT AACCATGTGT 180

GAATAAATTT TGAGCTAGTA GGGTTGCAGC CACGAGTAAG TCTTCCCTTG TTATTGTGTA 240

GCCAGAATGC CGCAAAACTT CCATGCCTAA GCGAACTGTT GAGAGTACGT TTCGATTTCT 300

GACTGTGTTA GCCTGGAAGT GCTTGTCCCA ACCTTGTTTC TGAGCATGAA CGCCCGCAAG 360

CCAACATGTT AGTTGAAGCA TCAGGGCGAT TAGCAGCATG ATATCAAAAC GCTCTGAGCT 420

GCTCGTTCGG CTATGGCGTA GGCCTAgTCC GTAGGCAGGA CTTTTCAAGT CTCGGAAGGT 480

TTCTTCAATC TGCATTCGCT TCGAATAGAT ATTAACmAGT TGTTTGGGTG TTCGAATTTC 540

AACAGgTAAG TTAGTTGCTA GAAyCCATGG cTCCTTtGCC GACGCTGAGT AGAnTTTAGG 600

TGACGGGTGG TGACmAtGnA kTCCgTGTCG AGCGCTGAtT TTtCGGsCTT TAGAGCGA 658

(2) INFORMATION FOR SEQ ID NO: 799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

TAAAATTAAT ATTTACTAAA TTAAGATTCT TCAATAATTT TTTTGCTTCA TCTACAGTAG 60

AGCATTGGCC CAATACCCAA GGAATAAACT CAAATGGAGA AACATTTTCT TTTCCTTCTT 120

CAATTTTTTT ATAATCTGCA TAGCCTGAAA AGTTTAATCC AGCCATTCCT AATCCTTTTT 180

CATTTATTGC ATCATAATAA AGCGGATAAT CAGCAATCCC AGCAGCAATT CCAAyTATTG 240

CAAAATGATG ATCTAAATTT CCAACTTCTC GAAATGAAAA CTTATAATTT CTCGGCGTAA 300

TAGTAACCAC CTCATTATAA GAmATTTCAT AATCAAAATT CCTTCCAAAG TAATGATCTT 360

TTGATACATA AGTAATTGCT GTACACATAA TCAATTCCTC CTATATACTA ATTCAGTCAC 420

TAAAATAGTA CACCCAATAC TCTTTTTTAT CAAATTTAAC CTATCCACAA AATGGCTAAA 480

CAATATATGA ACATTCAATT TGGTTCTGTT GCAAAGTTTT AAATCTACTA TCAAATAAGG 540

TAGAATAATA GAAAAAGATA GCAGGAGGAA TGACGGTGAA TCATTTTAAA GGAAAGCAAT 600

TTCAGTAGGA TGTGATTATT GTAGCCGTGG GCTACTATCT TCGTTATAAC CTTAGCTATC 660

GTGAAGTTCA AGAAATCTTA TATGATCGTG GGCATTAACG TTcTCATACG ACGATTTATC 720

GTTGGGtGCa AGAATATGGc CAAcTACTCt AtCCAAtTTG GGAAAAAGaA AAATAAACma 780

TCCtTTTAwT CccTGGGAAA tGGGATGaAc gkACcTCCaA ATTAnA 826

(2) INFORMATION FOR SEQ ID NO: 800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

AAACCAGATT GGTCTGCTCT GACTCAATCT GGACACAAAA TCATTATTTA TTTAATTAGT 60

TTTGTTACTT TATTGATTTA TTGGAACAAT CATCATCATT TATTTCAAAG TGTCCGTAAA 120

ATTGATGGAC GTGTCCTTTG GATGAATAAT TTTCTAATTT TGACGTTGAC GTTTTTCCCG 180

TTTGTTACTG GTTGGGTGGG TGAACATCCG TTTTCTTGGC CGCCACAAGC TTTGTATGGC 240

TTAGTAGTAT TmGGmGmTGA TGTTGCTTAT TATCTAGTGG TGCGGGCATT GATTCAGGCA 300

AATGGGCCCA AATCCGAAGT ACAACGkTTG TTkGGCCACT AkCCAAAATT AACGCTTtTCG 360

ATTGTGTTGA ATATTAnTGC GnTGATTGTG GGTAAAATGG TAGCACCAAT CGC 413

(2) INFORMATION FOR SEQ ID NO: 801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801:

TCTTCATTCA CATCAAATGC GCAACTTACA CGAATACTGT TGCTTTGATG GAATTTGTAC 60

TTTAATAAAG CACTTCCTAA ATTACCAACC CCGATTAATG CGACATTGGT TAACTCATCT 120

TCATTCAATG TTTTTGCAAA AAAGTTCATT AAGTTTTCAA CATCATAGCC GTACCCACGT 180

TTACCTAATT CACCAAAATA TGAAAAGTCA CGACGAATAG TCGCACTGTC TACTTGTACC 240

GCTTCACTTA ATTCAGTTGA TGAGACTTTA TTTTTTCCTG TATCATGTAA CATTCTTAAG 300

TAGCGATAAT ATAAAGGAAG GCGTCGCGCC GTTGCTTTTG GAATAACTTG ATCTTTCACA 360

ATTGGACCTC CAATACTTtC ACTTAAATCk TATCCAtTAA CATAATAGCA GTTT 414

(2) INFORMATION FOR SEQ ID NO: 802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

GCCAATTTTT ATAGAAAAAA AACAAAGAAG AATAGAATAC TGGCTAATTG CTTTTnTAGG 60

AATTTTATTT TTAACAACAT TTATTAATCA TACGTATGCT TTTTCAGAGA ACATTAAGTT 120

GATCATTTGG CAATGTATCT TTTTCTTTTC CGTTTACGAA GTAGGGCGTT CGAATGATAA 180

ATCTGTTTTT AAAGCTTTTG AGTATGTACT TTTAATTGTT TGGACCGCAT TAGTCATCGT 240

TGGGTTATAC TTATTTTTTG CGCGAATCAG CTTTTCAAAA CCAGTAGAGT CTTTGTATTA 300

CGGAATGAGA ATCGGTTTTT TTGAAAATCG ATTATATGGT GTTTTgTGGA GCCTAACTAT 360

GCATGTACCA TCTCATTAGk TtGTATTTTG GTTGGCGTGC GGAATTTtAT TAATACCAAT 420

AGCAAATGGT tAAAAGTGGT TtGTGCAATG GTGATTTTtC yACAATTtAG TTATGTAGCA 480

TTGTCTGGAT CAAGATCAGG AGTTATTCAG TTGATTTCAA TGGTAATTTT CGGGATGTTC 540

TTTACAATTT GGTTCTTTCa AAAAAATACA TCCAAAGCAG TTATAAAAAA AGTTGTGCAA 600

GCAGTATTAG TTTCTTTTTT CTGTGGTGCT ATTGTTTTCG GGGGCCTTAC AGTTAATAGA 660

AAAAGGGTAT ATTGCTACTG CAAATTCAGT GAATATGGAA GTACCAAAAG TTTTAGGATA 720

ATAAAGGAAA ATGGAATTCn AGGGAAATA 749

(2) INFORMATION FOR SEQ ID NO: 803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803:

AAGGCTTCGT AGGTTGTATC AATCAGCTTG GCACCAGCAT CCACAATCAT GGTGGTACCG 60

GCTACTTTGA TTTCTTTCAT TTCTGTTAGC ATAATCACGA CATCGCGAAT ACCGCCATCA 120

CGAACAATCA AGTTGCTAGC ATTGCCTAAT ACTAACCATG AAAGTCCTTG TTCTCGGCAA 180

TACGCCACAA TCTCTTCAAC TTCTTTTTTT GTTTTGGGTA AGGCCAACAC ATCAGCTGGG 240

CCGCCTGTTT TGGTAAAGGT TACGTTTTTT AATGGTTCAT CTACTAATAA AGTAATTTCG 300

TTTAATGTTT CTAACATAGC TTTAGTGTTC ACGAAAGTTA GTCCTTTCTT TTCAAAATAT 360

CTGTCTTATT CTAGCATGAT AGAAAGAAAG TTGCTAGTCC TCTTTAAAGA ACATGCCGTT 420

GTTGTTGGCG TACATTTCTT CACATAACGC ATGACTTTCA TAGACTTTTT CTTGCTTTAA 480

CTCTTGCTCT TGCGGTTTTT GAATGGCCTG AATGAAAGCA GTAACCATTT GGTAAAAACC 540

TCTTTTTTCC AATGTTGGCG TCCAATCTCC CATCTCCTTT ACCTGGTATC CTCTTCCGGT 600

TGGAGGGCAA ATGCGTAAAT TTTC 624

(2) INFORMATION FOR SEQ ID NO: 804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804:

TTTTTAGTCA TTTACTCCCT CCTTTTCGAG CAGTACTTAC CTTACTGTAG CATAGTTTTT 60

GATTGGCGCC TATCAGCAAT TTATCTCCAG ATAATAGAAA AGCCCCCCAG CGAAAGTGrA 120

TGGCTTTTCT ATTGTTAATT CTTTCTGATT TgTAGATAAC TTACACCTAA AACGGCAAAT 180

GTACTTGCCA GTATTCCTGC TATTAGCATA AACGGTGTTT TTGTTGTGCC TGTTTTGGGA 240

AGTTCTCGTT GCCCGTTTGC TTCATTTAAT TTTTGAATTG GTTCACTAAG CAGTTGGGGA 300

GCCAACTGTG GGCTTCCTTC ATTTTTCAAT GTATTTAATG GAGCGTTTAG TATTTGTGGT 360

TGATTTTTTG ATGTAACATT TTTATTTTTC TCCACAGTTG TTTCTGTGGA TGGCTGTTTT 420

TTCTCAGTTG TAGTAATTTC TTTTGTTGGT GAGACATGAA CTTCTGGCTG GCTGCTTTCT 480

GCCGTTcCGT TATACCATTC TCTTCAGTgT kACGCTTGGt TnTCAGGtAt GATTGGTGCA 540

ATCGTGCCTA GTGTTCACTT CCATCTGGAT 570

(2) INFORMATION FOR SEQ ID NO: 805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805:

TGCATTTTGC CTGGGACAAT CCAGACGAGG ACTTGACCGG GTATTTCCGG CGCTTTCTGG 60

AACTGACCGC CATTAAGAGn GACCGAAAGC GGCGCGTCTA CGTCCTGACC AATTACGGCA 120

GCACCCATGA GCAGGACTTG TACCGGGTGG AAACCCTGCG CGGCATGrGr TATGACCCCT 180

ATGTGATGGT CTACGACCGC CCGGCCGCAC CGAAAATCAC CCGCCAGCTT CAGCGCTGGG 240

TGAATAATAA GCGGATTTTT TACACGGTCA AAAACTTTGC CGATTACATT CCAAACAGAA 300

CAGGAGGGAT AACGTGAAAA TCGACCGATT AAAAACCGAC CTGGCAAAAG CCAGGGAAAA 360

AGCCGCCGAG TGGCAGGCCC GCGTGCGGGA CTTGGAGAAG CAGATCACCG AGCAGGAAAA 420

CCTTGAAATC TTGCAGGTGG TACGCAGCGT AnGGCTTTCG CCG 463

(2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 611 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806:

AAGnATTnCC GGACGCCGAG AAATTAATTT TAGAAGATGC GGGTGTAATA CCGTTACTTC 60

AAATTGGAAA TGCTAAATTA AGAAATCAAA AAATTTCTGA AATGAAAGTA CACTCTATTG 120

GTGCTAAGTA TGATTATAAA ACCATGGAGA TAAAATAAAA AACCTCTCTT AAAAGAGGTT 180

TTTTTATTTG TCAGATTTTA AATAGCCAAC ACCTTCAAAA GTATCAGCAA TTATATTTAA 240

AGAAGAGGGA ACTTCAAAAT TTTCTTTTCT AGCTATTTCT GTTACTTCTT TAACTAACTC 300

TTTATAAGTA TCATTTTCAC CTAATTGAGA GAATAAATTT ACGATGTTTA CAGCTTTCAA 360

ATATTCCTCC ATATTTCGTT TTTTCAAGAA ATTTCTGAGA TGTTTTAAAT AAATCATttC 420

TAAATTAATA gTaCCATCTA AAATAAAAGA AGGGACTTTT CGAACAATAT CAAATTGTTC 480

AAGGAAGTAA TCAGCTTTTT CAAAATCCTT TTTTTCAAGA AAGACAGTAA CCGCATTCTT 540

GATACATAAC TGAACTGCAT GGTCATGGAT ATCTCCATAA GATTtGGTTA ATtGGGAAAg 600

AGTTTTTCCT G 611

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 552 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807:

AAATGAAGAT AAATTTACTC ATTGGACCCC TAATGTTTAT AGTTATGGTG CATATGCTGA 60

TGATAATAGA ACTATTGTTA AAGGCCACAA CGAAAGAAAC TTGCAACAAA TCAATACTTT 120

TGTAATCGAT TTTGATCGCT CACTAGGTGA AATATTAGAT TCTCAAATGA TTCTCGATGC 180

TGCAATTGAT CTGGAACTGA TGCCAACGCT AATTTTAGAA ACTCCAGGGG GATTTCAAGC 240

GTATTTCATT CTTGAAAATG CCTGGTACAT TTCTTCAAAA AATAATTATC AATCAATCGA 300

AGTGGCCAAG AGAGTATCTG AAAATTTAAG AAAAGCATTT GCTGAAGTAT TGCCTTCGGT 360

CGATTTGGGG TGCAACaTTT TGGTATTGCA CGTATTCCTA GAACAGACAA TGTAGTCTAT 420

TACTACCCAG CACTGACACA TGATATGCAA CAACTAaTCC AGTGGTCCAT GAAATTTGAG 480

GCCAAAAAGA ACACCTnAAA AAACCGGAAT CTTAATGTTG GTTGCnGGTA AAGATGGAAT 540

CnGGATTTAA AG 552

(2) INFORMATION FOR SEQ ID NO: 808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808:

GGCAGTAGAT ATTTTAACAT CTGCAAAAGT CAACGAAACT TCTAATATAG TAGAAGCAAA 60

AATTGCGGAC GAACAAGTAA CTGGCAAATT AACCGCAACA AAAACCGTTA ATAACGCCAA 120

ACCAAAACTA GGGGAAGAAA TCGAATACAC CATCAGCTTC CGCAACACTA TCGAAAACGG 180

CATCCTAAAC AAAGTAGTTA TCACAGACCA ACTGCCAAAA GGACTGACAT ATGTCAAAGA 240

TAGCCTAACA AGTGTTGGTG ATGAACCAAA GCCAACCAGC TTGAAAGAAA CCAACGGCAC 300

AATCACAGCG GAATACCCAA GTATCACCGA TATGAAAGAA CGGAGTATTC GCTTCAAAGT 360

GATCGTTAAC GAAGAAGCCA AAGCGGGCGA AACAATTCTC AACAAAGCCA AAGTAGATGA 420

CACAGTTAAT CCACCAGAAG AACCAGAGGT GCCTGTGGTA CCAGAAACGA ACGCAGGCAA 480

ACTAGCCGCA ACAAAAACCG TTAATAACGC yAAACCAAAA CTAGGCGAAA CTATCGAGTA 540

CACAATTAGC TTCCGCAAyA CCATCGAAAA CGGCGTCCTA AACAAAGTAG TTATCACAGA 600

CCAACTACCA AAAGGACTGA CGTATGTCAA AGATAGCCTA ACAAGTGTCG GTGATGAACC 660

AAAACCAACC AGCTTGAAAG AAGCCAACGG CACAATCACA GCGGAATACC CAAGTATCAC 720

CGATACGAAA GAACGGAGTA TTCGTTTCAA AGTGATCGTT AACGATGAAG CGAAAGCGGg 780

CGAAACAATT CTCAACAAAG CCAAAGTAGG TGATGGCATC AATCCACCAG AAGAACCAGA 840

AGTGCCCATT ACGCCTGAAG AACCAGCGAA AAATaAAAAG GAAACAAACA AAGTTGTTAC 900

AGACCAGAAC AAACCTACAA AAAATAGTAA AAATGAAATT GCCATAAACA AGAAAGAAAC 960

GTCTAAATCA TCCTATTTAC CAAAAACAGG AGAAAAAGTT CAAAAAATAT TTGCGTATCT 1020

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GGGTGTAGGA CTGATCTTAA TTGTATTAAT TCTCTATGTT ATAAAGAGAA ACAAAGAAAA    1080

AGAGGAGTAA ACAAAATCGA TTGTTTTAGA ACGACTAATT AGCTGAAAAT TTAnGnGTTG    1140

ACGACATAAG TCAAAATGAC CTATGTCGTC AACTCTTTTT GGATTTATAA CAAGGAAATC    1200

CAACATATTG TGTGTGC                                                   1217
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(2) INFORMATION FOR SEQ ID NO: 809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:

```
GCGGCGAGCG AAcGGaAGAG CCCAAnCCAA CAAGCTTGCT TGTTGGGGTT GTAGGACTCC      60

AATATGGTAG TCTGTTAGTA TAGTTGAAGG ATTTGGAAAA TTCCGCTAAA GAGGGTGAAA     120

GCCCCGTAGA CGAAATGCTG ACAACACCTA GGAGGATCCT GAGTACGGCG GAACACGAGA     180

AATTCCGTCG GAATCCGCGG GGACCATCCC GCAAGGCTAA AtACTcCCTA GTGACCGATA     240

gTGaACCAGT ACCGTGAGGG AAAgGTGAAA AgCACCCCGG AAGGGGAGtG AAATAGATCC     300

TGAAACCGTG TGCCTACAAC AAGTCAAAGC TCGTTAATGA GTGATGGCGT GCCTTTTGTA     360

GAATGAACCG GCGAGTTACG ATTGCATGCG AGGTTAAGTC GAAGAGACGG AGCCGCAGCG     420

AAAGCGAGTC TGAATAGGGC GAATGAGTAT GTAGTCGTAG ACCCGAAACC ATGTGATCTA     480

CCCATGTCCA GGTTGAAGGT GCGGTAAAAC GCACTGGAGG ACCGAACCCA CGTACGTTGA     540

AAAGTGCGGG GATGAGGTGT GGGTAGCGGA GAAATTCCAA ACGAACTTGG AGATAGCTGG     600

TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CGGAATTGAG AATGATGGAG GTAGAGCACT     660

GTTTGGACTA GGGGCCCATC TCGGGTTACC GAATTCAGAT AAACTCCGAA TGCCATTCAT     720

TTATATCCGG GAGTCAGACT GCGAGTGATA AGATCCGTAG TCGAAAGGGA AACAGCCCAG     780

ACCACCAGCT AAGGTCCCAA AATATATGTT AAGTGGAAAA GGATGTGGGG TTGCACAGAC     840

AACTAGGATG TTGGCTTAGA AGCAGCCACC ATTTAAAGAG TGCGTAATAG CTCACTAGTC     900

GAGTGACCCT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGACTACA     960

CCATTAGGTG TAGTGGTAGG AGAGCGTTCT AAGGGCGTTG AAGGTCGATC GTGAGGACGG    1020

CTGGAGCGCT TAGAAGTGAG AATGCCGGTA TGAGTAGCGA AAGACAGGTG AGAATCCTGT    1080

CCACCGTATG ACTAAGGTTT CCTGGGGAAG GCTCGTCCGC CCAGGGTTAG TCGGGACCTA    1140

AGCCGAGGCC GATAGGCGTA GGCGATGGAC AACAGGTTGA TATTCCTGTA CCAGTTGTTT    1200

TTGTTTGAGC AATGGAGGGA CGCAGTAGGC TAAGGAATGC ATGCGATTGG AAGTGCATGT    1260

CCAAGCAATG AGTCTTGAGT AGAGTTAAAT GCTTTACTCT TTAAGGACAA GTTGTGACGG    1320

GGAGCGAAAT AATAGTAGCG AAGTTCCTGA TGTCACACTG CCAAGAAAAG CTTCTAGTGA    1380

GAAAACAACT GCCCGTACCG TAAACCGACA CAGGTAGTCG AGGAGAGTAT CCTAAGGTGA    1440
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GCGAGCGAAC TCTCGTTAAG GAACTCGGCA AAATGACCCC GTAACTTCGG GAGAAGGGGT 1500

GCTGACTTCG GTCAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC 1560

TCTGCAAAAT CGTAAGATGA AGTATAGGGG CTGACGCCTG CCCGGTGCTG GAAGGTTAAG 1620

AGGATGGGTT AGCTTCGGCG AAgcTCAGAA TTGAAGCCCC AGTAAACGGC GGCCGTAACT 1680

ATAACGGTCC TAAGsTAGCG AAATTCCTTG TCGGGTAAGT TCCGACCCGC ACGAAAGGCG 1740

TAACGATTTG GGCACTGTCT CAACGAGAGA CTCGGTGAAA TTTTAGTACC TGTGAAGATG 1800

CAGGTTACCC GCGACAGGAC GGAAAGACCC CATGGAGCTT TACTGTAGTT TGATATTGAG 1860

TGTTTGTACC ACATGTACAG GATAGGTAGG AGCCGATGAG ACCGGAACGC TAGTTTCGGA 1920

GGAGGCGCTG GTGGGATACT ACCCTTGTGT TATGAACCCT CTAACCCGCA CCACTAATCG 1980

TGGTGGGAGA CAGTGTCAGA TGGGCAGTTT GACTGGGGCG GTCGCCTCCT AAAAGGTAAC 2040

GGAGGCGCCC AAAGGTTCCC TCAGAATGGT TGGAAATCAT TCGAAGAGTG TAAAGGCAGA 2100

AGGGAGCTTG ACTGCGAGAC CTACAAGTCG AGCAGGGACG AAAgTCGGGG CTTAGTGATC 2160

CGGTGGTTCC GCATGGAAGG GCCATCGCTC AACGGATAAA AGCTACCCTG GGGATAACAG 2220

GCTTATCTCC CCCAAGAGTC CACATCGACG GGGAGGTTTG GCACCTCGAT GTCGGCTCGT 2280

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCCATTA AAGCGGCACG 2340

mgAGCTGGGT TCAGAACGTC GTGAGACAGT TCGGTCCCTA TCCGTCGCGG GCGTTGGAAA 2400

TTTGA 2405

(2) INFORMATION FOR SEQ ID NO: 810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

AGAATATGCT AAAGTATTAA GAAAGAATAG TCTGGAGTTG ATAAGAATGA ACTTTAAAGA 60

AAAAATTACA GAAATGGTTG AAAATGTTTA CGATTTAGCA CGCGATGGTA AGTATGATGT 120

CAAAGTTGAC TTAATTCCTC GTAAAAAAGG CAACATCAAA AGTGGTGTTA AAGTCACTTC 180

TTCAAGAAAT ACAGCCCACA ATATCAAATG GCGTTCAAAA AACTAAkTCG TCTTTAACAG 240

AAACACCGGA GCAGACAAAA TTATTGTCTA CTCCGGTGTT TTTATTTTTC TAATTCGATA 300

CCTAAGACAG TTAAATGCCC ATTACCAACT AATTTGATAA CTAATTGGGC TAAGTGGTTG 360

GGTGTCATAT CTGTTTCGCT nGTGGTCCAC CAATGAAGGG TACCGATGAA GATAGAGGGC 420

ATGTATTCAA TnACAAAATC nTATCGGnAC ATCAATAATC ATTTTCGGTA ATACGCAACT 480

GCGGAAAAAA ATCGTCGCCA TATTTTCCTT CGAnAATTTC AGCTAAGCGT TTTCGAA 537

(2) INFORMATION FOR SEQ ID NO: 811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811:

GCTTTTACTT TTAAACTGAG CGGTACTATA ATTTCTGCTG AATTTGTTAA ACTTTCTGCA 60

CTAGTAATTT GTGGGGATTG TAGTGAAACT AAAGCTGCTG TAGATAGTAG CAAACCGCCA 120

AGAATTATCT TTGATTTCAT AATATCATTC TCCTTAAATT CTATTTATTA AGCTCAAAAA 180

AATAGTTTTT ATCTTAACAT TCTAGCTACT TTAATTCTTA ATACTACAAA AGGAAAACAT 240

TGTTATATTG AATAAAAACA TGTCCCTATC TCCTTTCTAA TTAGttTCCA CAAAACGTAA 300

TGATTACGTT TTGTGGAAAC TAATTTTACA AATTTTTTTA AGAATGTCAA TAAAAATGAA 360

GGTTCATTTT ATTTAAGTGt CAAAAATAGA TTAATATAAA ATTTAACTCG ATTATTTTTC 420

AGATAGCTAA AAAGCAATTT CATCTTTATT AGCTAAAAAG TAGTCAAGTC CAGACTCCTG 480

TGTAAAATGC TATACAATGT TTTTACCATT TCTACTTATC AAAATTGATG TATTTTCTTG 540

AAGAATAAAT CCATTCATCA TGTAGGTCCA TAAGAACGGC TCCAATTAAG CGATTGGCTG 600

ATGTTTGATT GGGGAAGATG CGAATAATCT TTTCTCTTCT GCGTACTTCT TGATTCAGTC 660

GTTCAATTAG ATTGGTACTC TTTAGTCGAT TGTGGGAATT TCCTTGTACG GTATATTGAA 720

AGGCGTCTTC GAATCCATCA TCCAATGATG CGCAGCTTTT GAATATTTGG GTGATCGATA 780

TAATCATGAA TCAATCGAT 799

(2) INFORMATION FOR SEQ ID NO: 812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812:

TTTGCAAGTT AGTTTACTTT TAGGCTTCCT TTTAATCTGG ATTCATTCAT TTATGGAAGA 60

TATTTTATTA GCGCCTCATT GGATGCCGAT AGTTTATAGT TTCCTTGGGC TAGCCTTCTA 120

CTTCCGGCCA GAGAAAAAAC GAGGAAGACA TGAAAGACCA ACGACACCTA AAAGAAGAAA 180

ACGAGTGAAA CAAACAAGTC CTGTTAGCAA TGAAGAGCGC CCGATAGCAC CTGTTGACGA 240

AGAGGGCTGG GaCCAACCTG AAGAATTAAG TCGTGtCCAA AGACATCGCm GATAATTTTc 300

ATCCTATAGA ACTTTCTTGT CCGCTGACAT TATGGkrATA TAgGGGTTGC ATGTTATTAC 360

AAATAATGTA ATTACTGGAA GTGAAGAGAG GAAGTTTTTA ATGACATCAA AAAGTGAATG 420

GAGTAATGCA AGACGGATTG TAATTATTTT AGCAGACGTT TTGCTCTATA ATTTATCAAT 480

(2) INFORMATION FOR SEQ ID NO: 813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

TTAAGCGATA AATCAGCTGA AGTCCTTTTA GATTTAGATG CTAAGAGCTT CCCAATGAAC 60

GGCAAAACAG TTCGCGTTGC CCAAGTAAAT ACCGTCGATT TAGCAGAAGT TTTAGATCGT 120

CAAGCTGAAT TAGAAGCAGC TATGGCCGCA GAAAATGCAG CCAATAATTA TGACTTGTTT 180

GTCTTAATTA TTACGAATAT CCTAGACAGT GATTCTGAAT TATTAGCGAT TGGTGCGGAA 240

CAAGCCAAAA TTGAAGCAGC GTTCAATGTA ACATTAGTTA ACAATCGTGC GTTCTTACCC 300

GGCGTTGTTT CTCGTAAAAA ACAAGTAGTA CCACAATTAA CAGAAGTCTT TAACTAAAAC 360

CGTArGgscC TAAGcAACGC GATTAAATTC CTTGTTGCTT AGGCGCTTCA ATAGTAAAGG 420

GGCGTTAACA TGAATGATTT AGCAATTTAC TATCATTCTC CGCAACAAAC GAAACAATAC 480

AATCATTTGC TCAACCAATC ACTTTTTTTC CCTCTTGTTA CTTTTATGTA TGAACATCGG 540

GAAGAAAGAA TCATTTTAAG ACAATTAAAA GCGGCCTTTG CAACAGAAGC CAAGTTAGAA 600

CAATTTTTAT CAGAAAGGAT TGATTGTCAG TTAATCATnG GGAAAATCGT CAATATCGTT 660

TGAATTTTCC TATTATACGG CAGCTGAAGT GCGAGTTG 698

(2) INFORMATION FOR SEQ ID NO: 814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814:

CTTAATCGTT TTTCTTTTAT AGGATATCGC AnTAATCGTA AnACATAATT CATnnGAAAG 60

GATTAACCCA TGACCTTAAG AAAATCAAGT TTAATTATTT TAGTCCCATA CATTACGCTT 120

TCTTCGGGCC GTTACTTTTT TCGGGTATTT CCCCCAATGC AGCGATTAAT GTGACAACTG 180

CTCTCTACAT TATTGGCGCC CTTGTAATGA TTGGCATCTT TTTAAAAACA ACAGAACCTT 240

CTCCTTTAGA GGAAACAGCA ACCTTGAAAT CACCTATTTT TATTTTTTTA CTAGGTGTTA 300

GTGGGATTTT CATTGCCATG CTGATTCAAG GGGTTACTTT TGCCATTGAA GTAGCCATCA 360

CAGGAgAACA AGCTACTTCT CAAAATACAC AAGCTATTGT AGCGGTGATT TTGGCAAATC 420

CTTTATTTAT TTTGGCAACT ACTATCGGTG GTCCGATTAT GGAArAAwTC GTCTTTCgTT 480

ATGCATTTAT CCATTTaATC CAsCCTTTtA CAAATTTCyG GawTGcGGsT ACTGtTAnTT 540

CGGCGATTTT TTCACTCGCA CATGCCGATG GTCACTTTTT TGTTTATTTC TTTATGGGAT 600

TTTTCTTTGC TCTTTTGTAC AAGCAAACTG GAAAAATTTG GACtCAATTA TTGCCCATTG 660

CGGCATGAAT ACGATTGTGA TTATTGTTCA ACTACTTTTG CATAATGGTA CAATTCAATA 720

AGAAAAGGGC CTnTCGTCTA AACGACTAGG CCCTTG 756

(2) INFORMATION FOR SEQ ID NO: 815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

GATACGCTGC AAGCGAcrGT TTCaAGTGCC yGcGTTTTCT GGTTGTTCCA AGTCGTTAAA 60

CCTTGGACTT CTGCTAACGT TAACGAAGGC TTTGCTTGAG GTCGACTAAA AATTAAGTCC 120

ATGACATATA AAAGTTCTTT TCGTCGGGCA ACGATTTGTA TCTCATCCGT TGGCAGTTTT 180

AGCATTTGCC ATTGCTCAAA AATATCATTT GCGGCTTGGG CAACTTCTGA CGCATTCGGT 240

CCCTCTAGGC GAAATGTCTC AACTGGCCAA TTCACCATTC CTGCGTTGAT TAAAGGATAG 300

TTAGCTAACT CAACATATTC TGAAATGCTC GCTTCGGCTA ATGGAAATTG TTGCAAACCC 360

GTTTGATAAT AGACATGCTC ATTTTGTTCA AAGTCAGCAT CAATCCCAGC AAAATAATGA 420

GGAAAGACCT CAACAATTTT CAACAATTGC TGAAAAGTCT TAATTGAACG TTTCGCTGAC 480

TGATGTTTTT CAAACGCAAT CACACCTTGT TGCTGATATT GTGCCTGTTT TACAAAGGAA 540

AACCCCCAGC TTTCGCCATC TAAGTTCATT CGAATCACTC GATGGTTCGT AGTCGCAGGA 600

AATTGCTGAC TTCCCTGGTA GCCTTCTGTT GCCATGCACC ATTCACAGCG GGGATAGCTT 660

TGTGCAGAGA GCGTTGCTTT TGACGCCTCA CTGTGGACCT TATTTGCTAA AAAATCTCCA 720

TAGACTGTTG AAAAAACAAC AGGTTCTTCC TGTTCAATGA CCGTACCGTT TTTTTGACAA 780

AGTTGGTAAA AATACTCGGT AGCCTCTTGT GGCTCTTTGG CATAATGTTG TGCAAAAAAA 840

GCATTAACCA CAGAAGGTGG CGGTGTTAAC AAATCCATCA ATTGCACCAT GAACTGTTCT 900

TTTTGTTGCT CTGTTTTTAC AAGTTGGTTG GCACTCGCAA CTTGACACAA TTGTTCCGCC 960

AAATCAGCGG CGGGTGTTGC CACAGGCCGT ATGTCTACTT CGCCTAATTC TTGTTCACCA 1020

ATCATTGATA ATAAACGGTT CTGAAGATAT AAGCGATCCA ATTCCATCCA ACCACCTGCT 1080

TGAATAGCAA GTGTGGTAAA ATCGGCAATC ATTTGACTCG TGGTCATCGA TTCATTCCTC 1140

CTATTACTTT TCTTGATATC CATGTGGATG AGCTTGATGC CATTGCCAAG CGGTGGCGAT 1200

AATATCCTTG ACCTCAGTTA CTTCTGGTTG CCAGCCTAAA ACTCGTTTGG CTTTTTCACT 1260

AGAAGCAATT AACGTACTAG GATCCCCTGC TCGGCGTGGG GCGATTGTTG CAGGAATTTC 1320

TTGGCCTGTC ACTTCGCGAG CAGCATCTAA CATTTCTTTA ACAGAATAGC CGTTGTTGCT 1380

ACCCAGGTTA AAGACGTCAC TTTCGCCACC ATTTTTCAAG TATTCTAAAG CCAAAATATG 1440

TGCTGCAATC AAGTCTTCAA TGTAAACATA ATCTCGAATG CACGTGCCAT CTGGTGTATC 1500

ATAATCATCC CCAAAAATAC TTAGCTCTGC TCGTTGGCCT AATGCCACTT GTAAAATAAT 1560

TGGCACAATA TGCGTnTCTG GCGTGTGATC CTCACCAATT GA 1602

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1008 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816:

ATTTCCTTTG GCGTGGCTTC TCTCGTCATT TCAAAAATAG ATGCATTCTT TTTTATCTGC 60

ACAGACATTA CAACACGCAT TGAAACAGTT GAGTGCTTCG GATGTGGATA TTCATGTGTT 120

AACGATACCT ACCAATAGCT TTTCATGTTC TCTCTCCTAA TTGTTTTTAT GTATATTTGT 180

TTATTGTAAG ACAAACACTT TAATCCCTGT TATACTCATT GAAAGACAGC AACTCCTTTT 240

TGCTTCATGT AACACTTCCA GTTATTTCAA AACATAATCT GCTGTCTGGC CACTAGATAT 300

TTTATCTGGT GGTTTTTCAT GCGAAAACAA TCCAAATATC CGACAAAACT TGACAGCTAt 360

GTkACACTTG ttTTAGGkAG CACTCTkTCA TAATAGCkAA AGTTCATAAA CTACAAGTGA 420

CACGAGATTT TCACTAACGC TACCTAGCCA CTAGATCCCA TTTCTAGTGG CTTTTTTTGC 480

ACAAAAAATA AGTTTTGATG TGAATAAACG CTCTTTTATT CTTTATTCTT ATTTGATATA 540

ATTTTTTAGG TAGCAACTCC TTTTTGTAAA TAGCAACCAA CAAAAATTTT GCACGAATGC 600

TACCTAGCCA CTAGATCCCA TAGTCTAGTG GTTTtTTATG TACGArAAAA rGmCCACTTA 660

CTGAGTGAnC TTwATAyCGm CGTGsCAGGA GTkGAtCtGC AgCCATkGAT TAAAAAwTAm 720

CkGTyCTTAT TTATTAAkGA mCCTTTyCTT TTTTGGTTCA GwTTCAAAAA CTATTTCTAA 780

mCTCAAAwTA wTAGTCTGTA AAGACmACgC CATAAmCAGC CCTGAGAAAA ATGTCCATAT 840

ATAAAATATT AGGATTGAAG CAAAGGTCTC TTTATACTGA AATATTTGGA GCATCATTGA 900

TAGTATCAAA GTAGTAAATG CACTTAATAA AGATATAAAG AGTTGATATT TTAATTTTTT 960

TCTATAGCAG ATCCTCGTAT ATTCTTCATA AAACTAGTAT CTTTTATA 1008

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

GTCATAGCTG TTTCCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGAGC 60

CGGAAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG AGCTAACTCA CATTAATTGC 120

GTTGCGCTCA CTGCCCGCTT TCCAGTCGGG AAACCTGTCG TGCCAGCTGC ATTAATGAAT 180

CGGCCAACGC GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC 240

TGACTCGCnG CGCTCGGTCG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT CAAAGGCGGT 300

AATACGGTTA TCCACAGAAT CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA 360

GCAAAAGGCC AGGAACCGTA AAAAgGCCGC GTTGCTGGCG TTTTTCCATA GGCTCCGCCC 420

CCCTGACGAG CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT 480

ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG cGCTCTCCTG TTCCGACCCT 540

GCCGCTTACC GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCATAG 600

CTCACGCTGT AGGnnTCTCA GTTCGGTGTA GGTCGTTnGC TCCAA 645

(2) INFORMATION FOR SEQ ID NO: 818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

ATGCAAGCCA GTGGATTAAA ATATACTAAA AAACGAGAAT TACTGATGAG CTATTTGATT 60

AAGCGAAATC nGTATGTTTC TGCACGTGAA GTGTATGAAT TTATGAATGA AACCTTTAAA 120

GGAGTCAGTT ATGATACGGT TTATCGTAAC TTGCATGACT TTGAGCGCTT AGAATTACTG 180

GAAAAAACAG AATTAAATGG CGAGCAAAAG TTTCGCTTCC GTTGTTGCCA AGAGGTGGAA 240

CATCATCATC ACTTTATTTG TACGGTTTGT GGCAAAACGG AAGAAATTCA CATGTGTCCG 300

ATGAATTTTT TTGAAGAACA GTTAAAAGGT TGTTCAATTG AAGGACATCG CTTTGAAATC 360

CTTGGTCGTT GTGCCGATTG TTGCGAAAAA TAGCGAATAA GACGAAAAAT CAAACAAAAA 420

TTTCGTATTT TATCAGTAGA GTGGTTGACG GTTATTTATG CTTTACTATA ATATAACAAG 480

GACAGTATTT TAATTTGTGG GTTTTTCCCA CAAATAAGAA AAACGGTTAC TTTTTAAGCT 540

CGGAGGGGAG GGAATAACAT GTCCAAAAAC AGTCGTTCGT AAAAACGAAT CnCCTGGATG 600

AnGGCTCTTC GTCGCTTCAA ACGTTCCGTT TCCAAAGCnG GGTACTTTTA CCAAGAATCC 660

ACGTAAACGG GAATTTCCAC GAAAAAC 687

(2) INFORMATION FOR SEQ ID NO: 819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

TnGTAnGCGT TCTTTTTTTA AGAATACCAA AACATTATTT AAAATAAAGC AATTTTTATT 60

TTTAGTAGTA AGATAGTAAA GTAGTAAGAT AGTAAAGTAG TAAGATAGTA AAGTAGTAAA 120

ATAGTAGAAT AGTAAAGTAG TAGAATAGTA AAATAGTAAG ATAGTAAAAA ATGTTTATTT 180

TTTAATAAAT ACGTCTAAAA ATCCTTTTGT AGAAAGGTTA ATATCATTCT TTTAAAACAA 240

TAAGATAGTA AAATAGTAAG ATAGTAAAGT AGTAAGATAG TAAAATAGTA AAGTAGTAGA 300

ATAGTAAAGT AGTAGGATAG TAAGATAGTA AAATAGTAAA TTTTATAAAT ATnATTTGTA 360

GTAAGAnAAT 370

(2) INFORMATION FOR SEQ ID NO: 820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:

AAAGTAAAAA TTGGCTTAAA TATGTTGTTA ATGATTATCG TTTTAGGCGT AATCTTTTAT 60

GTCATGGATA ATTCATTAAG TGATATTTTT GCTCAACTGA TGGAAACGAG TTGGCTGGTG 120

CTGATTGCTG TTATTTTTTT TGGAGTAGTT TATCAATTTG CAGAAGGGCG CTCAATCAAG 180

GAAATAGCTC GTTATTTTAA CAAAGACTTT ACGACAGTGG ATGGTtTTTT TACTTCTTGT 240

TATGTAGCAT TTaTCGGATT AATTCATTGG CACGGGGAAC CTTGCCTTTC AGAAATTTAA 300

TTTTTAATAG GAAAAAGGGG AATTCCCGGT TTCC 334

(2) INFORMATION FOR SEQ ID NO: 821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821:

CTTCAGACTC ACACCCATTC TACACTGGTC GTCAAAAATT nTTGACAAGC CGACGGACGT 60

GTGGACCGTT TCAACAAAAA ATACGGTCTC AAAGACGAAA ACGCAAATCC AGACGCATAG 120

TCTTTCAAAA CATTGTTATG ACAAGGTTTA TAGAGGTTTT CCACTGTGGT GGGAAACCTC 180

TTTTTTTGTT GGATAGGCAG TTTTAAATTC AGAGAAATTA TTTAAATATT ATTTTATTTA 240

ACTGAAATAT AGCTAGTCCG TATACCGTAt AATTTAAATT ATTTGGATAG TATACATATk 300

GTAAAGTGCA ATTGTCTTTT TAGAATCTTT AAGGTATAAT TTGTTTTAAT GAGTTTATAT 360

GTAAGCTTTt tCtcTTTAAA GmCTTtGAyC AtAyCTTTTT tATAagaGAA aCTATgTTtG 420

TGAAaaGGaT ATAAAAGTGn TAAAACAATT GTACTTAACA GTATTAAGAT GGGAGACCGT 480

ACAAGGCATA AAA 493

(2) INFORMATION FOR SEQ ID NO: 822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822:

TTTCAATTCC CTCTTCATAT ATCGAAATAA GATAACTATA ACCTTCCAAT AAATAATTAA 60

TTTGTTCATC AATAGTTTTA TTCCAAGAAC CTTTCTCTTC TTTTAATTTA GAATTTATAA 120

AAAACTCTTC TAGAGTTGAA TACGGAGATC CGTCAAGCGT AATCAGTCGT TCTGAAATTA 180

CATCCAACTG ATCATTAATT TGCTCCATAA GATCATCCAT TTTTGGATGT AGCGTTAGAA 240

ATCTTCCTCC ACGCATATAC CAATGAACTT GATGAATTCT TACTGAAAAT ACGCTTAAAT 300

CGGCTACCAA TTGATTTAAT ATTTTTkTTG TTTCACAAAA TTTCATAGTA TCACTCCTAA 360

TTTAGTGTTA TTTAAAAAGA AATCATTCCG ATTTACGTAC AATTTAATAT AATAAATATA 420

TCTTGTCAAA AATAAAATGA ACGTTTATAT TAAAAAAGTG TTTATAAAAA TCTTTACAAC 480

TTATTCATCC TTT 493

(2) INFORMATION FOR SEQ ID NO: 823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823:

TAGAACGGAa CTAACAGAAT CATGCAGATT gCAACnTTTG GTCTGATTAA TGAGATGGAA 60

TCAGTGAAAA AATAATGAAt TTTGTTATCT CAAAGCtTCG aTTcTTCAAG TATTATTGAG 120

ATATaTTTAA AAGCTCGTAG ATTTATCTAT AAAcGTTTCT TCaCAGTACc AtCAAAATCG 180

GGAAACCGGG TGGCGACGGT GAATAATGTG CCAATCGGAG ATAGGCATCG GATAGTATCA 240

AATTCACTAC GCATGATGCG TAGCAATTAC AT 272

(2) INFORMATION FOR SEQ ID NO: 824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824:

CGCGGCCTAC GAGAACACGA GGTTTTCnTG AACTATCnTC ATGTTGACTC AATACATAAC 60

CACCGTAACG CCCTAATTTA AAAGCTAATT CAGGTGTTAA CTCCTTATTT GCAATTCCTC 120

TTACACCATC TGTTCCAAAA TATTTACCCA TTTTGATTCT CCTTAGTCAC TTGATTCTCT 180

GTATTTTCAG TTGAACCAGC AGTTGTACTT TCTACTGTTG ATCCCTCACT TGTTGTTTCA 240

GAAGTATTTG AT 252

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825:

GACATCTAAG GTGCCTTCAG CTTTTGAATA AAAGGCATTA TTCGGnGATC GTAACCCCAT 60

TTTGTTACTA TCAGTTTTAT AAATGGTATA AGGTCCTTTG CCTTTTAAGG ATAAGTGAAG 120

TTCTTCGCCT GCTTGTTTAT TTTTTAGTGT ATAACTTTCT TTTAGCGGTG TGACTGATTT 180

TTCCGCTTGC TTGTAATAAT AGACGGCGCC AGATCCACCA ATTGCCCAGC AAAAAATTCT 240

TGTTTGGCTT TTGGTAAAAA CAATGTGATA GATAAGAGGA TTTGTTCTTT AAAGATTGAC 300

CAATCTGCGA ATATTTCTTC ATTGGTTAAA ATCATTTCTA TTTTTTCTGC TATTTTTTTC 360

CAGAGGATCA TTCGCCAGTT ATTTTCACCC ACTTCcATAt TCTTTAAACc ATGCTTAATA 420

aCtGrAGrAT AaTGGGGAAC ATTTGGckGA CAtCgCsGCA AATnAAAAAT CCATTA 476

(2) INFORMATION FOR SEQ ID NO: 826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826:

TTAATGACAT GTGACAATTG AATAATTTGT GGGTCGGTTA ATTCTTTGGA ATCACGAACA 60

CCTAATGATT TTAGTTTGCT AATCATGCTT TTGTCAACAT AGGnCAGCAC AGACAGTTAC 120

TGGACCAAAA TAGCTACCAk TACCGrCTTC ATCGGaACCT ATCACAGACC AGTTGCCAAA 180

ATCAGCAGGC AGTGTAGTAG TCTGGGGAGA AACTTTTTTC TTTGGTGTGG TACTCGTTCC 240

TTCCCAACGA GCGGCCTCTT TTTCAGCTTG ArGTCCCTGA AACATGACTT TACCTGATTG 300

ATAAGCGGTG ATAGTAGTGG TGCCAACCTT GGCCACAAAG ACAGTATAAG GGACCGTTTt 360

ATTTAAACGa TgGGTTGtAA ACAGTGGTCA TCcTGCTAAT GnTTnTACTA ACT 413

(2) INFORMATION FOR SEQ ID NO: 827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827:

TTAAAAGATA CAATGTAATG sAGACAGGCA CATTAAAaCC GACAATTTTT GTTGAGAGGG 60

TTGTTAAAAT TTGTGCCAAG CCTGTTAAGC CACTGGAATA AATATTTCCT GGTTGATAGA 120

AAAAGTTCAT GGCAtTGATG CAAGAATAGC ATAGACAATC GACACAGAAA ATTTTGTTGT 180

ATAGTCATGA ACTGGCAGTC CGTCATA 207

(2) INFORMATION FOR SEQ ID NO: 828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828:

AACGTTTGGC TAAATCACCT AGAATTGAAT CAGGCACATC CATCCATTGT GTAAAGTACG 60

TAGAGAGGAC GCCATCATCC AATTTnAnGG GGGCTTATAA nGTGAAGTCC CCTTTAAAGA 120

ATGGTACAAG CAGAGAGGCT TGTAAATCAT AGTCAAATTC AGGGTTTTCA AATAATTCTT 180

TCGCCCGATG CAATAAATGA TCAAGAATCA CTTCCATCCC ACGAGAAACA GGGTGAAAAT 240

AGACTTGGAC ATACATTTGG TAACGACTAA CGATATAGTC TTCCACCGCA TGCATCCCAT 300

TCATAGCAAA GGCAATGCCT CCTTT 325

(2) INFORMATION FOR SEQ ID NO: 829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829:

TTGACGGTTn TTTAAGTCTT TACTTCGTAn TTACAACTTC TTCCATTAAC TTATnATTTC 60

CTCGCTATTC CTATCGTTGT CTAACAATAA GTTGATTCGA TCATATTCTT TGTCTTTATA 120

CTTCACTGTT TTCTTACGGA TTTTATTAAC ATCACTTGTT CCTAGTTCTG AGCAAGTAAG 180

GTTCCnTACA CATTGGTGTA AAAAACACGT GAAGCCAATT AAATTTCCTG CACTTTTTGC 240

TCGTTGATCT GCAGATAATT TTTGCTCTAC TTCATTTCCG TTCTTATCTT TCCCTTTCTC 300

TGTCATTGGT ACACTAACAT CACCTAAGAC CGGATTAATA TTTACAAATG CGGTCTCAAC 360

TTCTTTATCT ACACTAAaCA TCATATCAAA CAAAGAATTG GACGTGTTGG CATCTTTTAG 420

GACGGAAAGA CCCGTAAAAA TAAGAATCGT CATTAAAAAA ATACCAAAAA ACCGTTTGTA 480

TCGTTGTTGT CCAATAAATT TACACCTAAA ATAACAAAGA CAAAGGCAAT nCCAATCGTT 540

CCCGCAATGC CCAACATGTT AGTTGCTATG CTAGACGTTA GGTTCATAAT CGGTTGCTTA 600

ATAGCAGTTA TAATATCCAT ACTAAATAGT GTTTTTACCA TAACTGCATT AAACTCTCCG 660

AGTCCTTTTA CCATTGACCA GACAAAAGTC TTTATTGTCG CAGAAGCATT TGTGATGGCT 720

TCTTCAACnC CTGTCCATGA ATCTTGTTTT TTTTCTTTGG TCATtAACTC GAAAGCGTTG 780

TCTTTGTAaG TATCGTAAAT CAAATCTACA TTAGTGGTTG GCTCTGTAAC AATAACTTTA 840

TTTTCATCAG GTTTAGGTTC GGCATTAACC GCTGTAaGTT TGgCGTAAAC ACcAAAAAAA 900

ACCnGGCCTA CTAAAAAATn GTAAGGACTG GCTTTTACCC CGTGGATTTC TTAATTC 957

(2) INFORMATION FOR SEQ ID NO: 830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830:

GGATTTTnAC TCCAAAAAAA GTTTAGCATC CGCTTACATT GTTGCCAAGA AAAATGGAGA 60

ATTTTGGAGT TTTTTAATTy TTATAGTGTA TAATAAACAA AAATTACATT CTAGAGGAGA 120

TTTTATGAAT TACATTTATT TAATTAATGA ACATTATCCC TTATTAACAA AATCGGAACG 180

AAAAGTTGCT GATTTTATTC TTAACTCTGG AGAATCTATT ATTTACAGTA CTATGAATGA 240

nATTAAAAnA AAAGCGAATG T 261

(2) INFORMATION FOR SEQ ID NO: 831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831:

ATTGCTATTA AACCAAATGG GAACACTATA TATTCTCCAG TAGATGGTAT TGTCCAAGTC 60

GTATTTGAAA CTGGGCACGC TTATGACCTC AAATCAAATA CTGGTGCTGA AATATTAATT 120

CATGTTGGTA TTGACACAGT ATCATTGAAT GGTAAAGGAT TCACTAAAAA AGTTGGTGCT 180

AAACAAAAAG TAAAAAAGGG AGAGGTTCTT GGAACATTTG ACAGCACAGT AATTACAAAT 240

TCAGGACTTG ATGATACAAC AATGGTTATT GTAACAAACT CTAAAGATTA TTCAGAAGTT 300

ATTCCTATAA CTAAAAATAT AGTTACTGAA gGTGCAGCCT TATTGAsrAT TAAATAGCTT 360

ATTAAAAGTT AATAGACTCT CtATACmAAG AGAGTCTATA TTTTTATTAT AGTTAATTAT 420

AACTATTCTA AGCTAATTAA TTTGACATAA A 451

(2) INFORMATION FOR SEQ ID NO: 832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832:

CCCTTTATGC CCTnTCCGnC TGTAATGTTG TCCGGTTGTG GAACCnGTAT GGAAAAgrTA 60

TTGACTGCCG tGGTGGTAAA TGGGAACTAG AAAATAAAAG TCCAACTACT ACTTACACTT 120

TTTTTGATGA TGAAACTTTT TCGAGGTATA ATTCAAAAAT TAGTGATAGT GGAACGTACT 180

CTTACGATGA AAATAATAAA AAACTCACTT TGGATATAAA AAATAAAGAA CAATTAATAA 240

TGGAAAATGT TGAATATAAA GACGGTAAAT TAAAAGGTGA AATTGGAGGC GTAGAAGGAA 300

CTCTGATAAA AAAATAAAAT AAAGAGGTGA TCTTTTGAAT AAGAAATCAC TGGTAAAAGC 360

AGTCTTACTA TTTTTAGTAG GCTGTTTTTT TGTGTTTACG CAAACTACAG CGGTTAATGC 420

CGAACCTAAA CCTGATGAAA ATAAAGTTAT TGTTACAGAG CCAACCACTA ATGTAGATTT 480

GATTTACGAT ACTTACAAAG ACAaCgCTTT CGAGTTAATG ACCAAAGArA AAAAACAAGA 540

TTCATGGACA GGGTTGAAGA AGCCATCACA AATGCTTCTG CGACAATAAA GACTTTTGTC 600

TGGTCAATGG TA 612

(2) INFORMATION FOR SEQ ID NO: 833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:

CACTTACGGC AAAACTTTGA ATCGACCGTG TCAATTTTTT CACGAATATC TTCCAATGAA 60

TCTTTGAGGC CTAACCACCG GATAATACCT CTTTCCTGCC AAATCTCCGC TTCACGTTTA 120

TTACACATCG ATTGTGaACG TcGATAAATC GGcTTcTcTA ACGATGaAAG ACTTCCTAAT 180

AATCtCAAGC AATCGTTCTG AGATAGTGTT TCGCTTAATA CAATTGCATC AAAATAATTA 240

AAAAAAGTTA ACTCATGTTC TATAGTTTCT TCACAGCAGT TCGTACAAAA GACTTCATAA 300

TTTAAATGTT GTAATTGCTG CTGAAATGTT TGCTCAACTA AAATGTTCTT TGTTAATACC 360

AAAATCCTkC kCATTTcTTC TTTCCTCCTA GAACTCTTTC TGCTACCAAT AACTAAACGC 420

ACCAATCAAA ATACGTTACC AAATCGCGTG TTTTCTCCAT CGATTGGTTA ATAAACACCT 480

TTTTATCTTc ATCTCTCTTC GCTCCTTTAT TCTTTATTTT GGTGGTTATT TATATnATAT 540

nAGAaATGgA TTTTgTTTGk GTGTAAAATT TTTTTAtCCc CGTAAAAAAA AATGaATTyC 600

CTTTAATATC AACTAATAAA GCkGATTTTT aACAAAAAAg TGCCGAAACT TCCTACTTTT 660

TGCTAAAACA CGCCAAAAnT CTGTAATTTT ATTATTTTTT TCTCGAGAAA ACATCAAAAT 720

GTTGATGTTT AACACTAACA TTTTGATGTT TTCGACAAAA ATCTTTACAA TTAATCGGTA 780

ATTTCTCTA CTTTTAACGA TAACTACTTT TAAAAAAGAG TTATTTTAAA AGTGACTTAA 840

ATATTTATCA TATAAAAAGT AAGGGACTAA AATCTTTACG ATTCTAGTCC CTTACTTTTT 900

ATAATCCACA ACGTTTTTAG TTAGAAGAAT TCTTTTTTGC TTTCCTAGCA GAACGATCTT 960

TTTGACGACG TTCAATTTTA CGTTTTTTCT TATTG 995

(2) INFORMATION FOR SEQ ID NO: 834:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:

```
CGTTGGGGTA GCGAAATTGG TTCTTGGTTA GTTCAAGGGA GTAGACACCT TACGGATATG      60

GGGTTATGGA CGCATATTCT TTCTGGATTC ATTGTATCAG TAACAGGGAT TATCATTGTT     120

TACTCTTTTC ATAAGAAGCT ATCTCTTTTA GCTTTAACAG CAGCCATGTT GGTTGGCTTT     180

AATCCTTGGT TTTTACAAAA TTTAAGTTTC AGGTTCGACA GTCCTTACAT GTCTTTGAGC     240

CTTTTATTTT CTGTTCTTCC ATTTCTATTT TGGAATAAAA ATAAAGTCTT ATTTTTAGTT     300

GTTTCTATTT TaAGCaTTTT TTTGATGTGt AATACTTATC AGGCGTCTTC GGGGATCTAT     360

GTCGTGATGG TGTTAGCATT ATCACTGAAG CAGCTGTTAG ACAATCAATC GTTTATTGCT     420

GTGCTTAAAA AAGCGATTGT AGCTATGATT AGCTATATAA GCGCCATGTT TCTTnATCTT     480

ATTGAAACAA AATTTAATCC TGAAATAGCA ACGCGAGGCG GTATGnCAAC AATCGCGAGT     540

GTTAAGGATA TACCCAAAAC AATCCTGGTA AATAGTCAAA TGTATCTGTC AAAAaTAaCT     600

GAACAGAGTA CAAAACTATG GaTACTTTTG TTTTTTATTC TAGTAATTTT CTTTGTTTTA     660

AGTACGGTTC TTAATGCGAA AGTATCGCCT GTTAAAAGCT TTTTATACGC AGTATTATTT     720

CTATTTTTAG GCTCTATTTT GAGTTAnGGC GTC                                  753
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(2) INFORMATION FOR SEQ ID NO: 835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

```
TGAGCGTGGA GCAAAAATCC AAAGTGATTT TTGTCCCACG CTCTTGTTTA TTACGGAAAA      60

ACCATCAATT TTTTATTAAA TTCTGATATT TATTATTGCT TTTTCATTAT AGTTGGCGTA     120

ACTTTAGAGT ATAAATTTGT GAAGCGAGGG AGTCCGTGTG AGAAATTTTA AAAAATCCGA     180

TAAATTAAAT AACGTAAGTT ACGATGTCCG TGGTCCTGTT TTAGAAGAAG CAGAACGCAT     240

GCAAGAAGAG GGCATACGTA TTTTGAAATT AAATACAGGG AATCCAGCGC CATTTGGTTT     300

TGATGCCCCm AATgAAAwTG TGCGCgACAT GATTGTAAaT GTtCGCGATy CAGAaGGTTA     360

TtCCGATyCA AAAGgTATTT TttCTGCAaG AAAaGCGATT GAmCAaTATT GCCAATTAAA     420

AAAaTTtCCy AATGkAACGA TtAATGAwAT TtACACkGGT AATGGCGTGA GTGAACTAAT     480

TACCATGTGT ATGCAAGGCT TGTTAAATAA CGGCGATGAA GTACTTGTGC CAATGCCAGA     540

CTATCCTTTA TGGACTGCAT CTGTTTCTTT GGCGGGCGGT ACACCCGTTC ATTATATTTG     600
```

TGATGAGCmA GCAGAATGGT ATCCAGACAT TGrTGaTATA AAaTCmAAAA TAACTyCGAa 660

TACAAAAGCA ATCGTTATTA TCAATCCCAA TAATCCGACT GGTGCTTTAT ATCCGAAAGA 720

GTTATTACTA GAAATTGTCG AAGTGGCACG TCAAAATGAT TTAATTATTT ACTCCGATGA 780

AAtTTATGAT CGCTTGGTCA TGGACGGTTT GGTksaTGTA CCGATTGCTA CATTAGCTCC 840

TGaTTTAwTT GTCGtAACAT TGAATGGTTT GTCAAAATCA CATCGAGTGG CAGGCTTCCG 900

ATGCGGTTGG ATGGTGkTAA GTGGAGATAA ATCACGAGTA AAAGGGTATA TCGAAGGGCT 960

AAATATGCyT GCTTCCATGC GGTTATGCTC AAATGTGTTG TCACAmCAAA TCATyCAAmC 1020

kGCATTAGGT GGCTATCAAA GTGTCGATGG TTTACTTTTG CCAGGTGGCA GAATTT 1076

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:

AGACAGCTTA AAGGTGAGCA AATGGnGGTT GTTACGCATG TTAnTGATGG CcAGCATCAA 60

TTTAAAATCA ATGATTTTAT CGATTTTACA GGCAACAATC ATACATCAAA AGATAGCATG 120

ATTGGGATGC TAGTAGGCAT ATTAGGTGGT CCTCTGGGCA TTCTTTTTGG CTGGTTTGCT 180

GGAAGTATGT ATGGTGCAAG CAAAGACGCC AAAGAAATTC AAGAAGCACA AACGGTTTTT 240

GAACATGTGA TTCAAAAGAT TGATGAAGGA CAAACGGGAT TGTTATTAAT TGCAGAAGAA 300

GAAGACAACC GTCCGCTCAA CCAATTGGTT ATGTTTGACT TAGGTGGCGA AATCACGCGG 360

CTTGATTTAG AGGAAGTCCA CCAAGAATTT ACGATGCGAA CGAATTGCCC AATGGAAGCG 420

GAACCATCCG TGGGCAGCCC AAAAAAAGGn CCACCCCCnA GGAAGCCACC TTCCGGAAAG 480

nAGGATTAAG GGnGCCAAGA C 501

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 856 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:

AGGTTCATTG GTTGTTTCAG GGCTTACTAC TGGTTGTTCT TGTGCTnGAT TTTTCACTCC 60

TACTGTTGGT TGTTGGACGT TTGTGGTATC ATTTGGGGTA GCTGAACTCT GTTacTCmAT 120

TTTTTTcrGA CGCTACTTCT TCTGCTTTGG TCGGTTGAGA AGTAGTGTCT TTTTGTACTG 180

CAGATTCTTC AGATACTGCC GTATTAGGCG TTGCACTACC TAACTGCGGA TCGGGGTTAT 240

CGGGGTGCAC TGTCGTTGAT CCTGGTTGCG TATCTAATTC CGCTGcTTGt ACATTATCAG 300

TAGCTAATCC TACAACTCCT AACACGCCTA GAAAAAGAAT AGGAGCTACG ATCCAATGCT 360

TCTTTGcCTT ATACATTTTA AAACGTTTTT TTACTTCAGT CTGTTGATTC ATGTATCATT 420

CTCCTCGATT TTTTATTTTT TTGTTTGTAA AATAACTCAC GCAACACAAG GCGCTCGTTG 480

CTTTTTCATT GTCATTTCCC TCCTTACTAA AAAAAGAGAA CCGAAAGTAT CTTCGATTCT 540

CTTAGTTATT TTATATTCTT ATAAAACACG ATATATATCT TTGTTTTGCT ATATCAAACA 600

ATTATTAACT ATTTTTTTTA CGTTTTTTGT TCTTGAAATT GATCGTACCT GCTGCCATCA 660

ATAATCCAAT AATAGTCAAC CAAATACTTT GTTGTTCTCC CGTTTGTGGT AAGGATTCTG 720

GTGCTTTTGC TACTTGTTTC GTCTTACGAG GTTCTGAATG TGTTAATGCT TGTGCTTTTG 780

GTTGTTCTTT TTGTTTAGAA AAAGATAACT GTTGGAGACC AGGTGTTTTG TCTGCTGAAG 840

TAGCACTTGC TACTAA 856

(2) INFORMATION FOR SEQ ID NO: 838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838:

TGTGCCTCTT GGGATTTCGC TGTGCCATTT TTTACTTTCA AACCCAGGTG TGCCACCGTG 60

AAGTGTTGTT TGAGTAGGAG TATTAATCAT CGTTTGATAC TTTTTACCCG CTAGTTcAAA 120

GGAGCCATCG GCAATTCGGC CAGCTGgTTC GACCAATtGT TGcACCAAAA TATaAGTCTT 180

TAGACAAATA TTCATCTTGC TGAGGGGAAA GCCTAGCACG AGTGATCGGG ATCATTTnTG 240

TAAGGGAACG TCGGCGCAAC A 261

(2) INFORMATION FOR SEQ ID NO: 839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839:

ATATAGCTAA AAATGATATA CCTGATGCAG ATATTATTAT GTACAATGAG ATGGATATGG 60

CATATCTTGA TGAAAAAATC AAGAATACTG GATTGCCTGT ATCATATATA GATTTACAAA 120

CAAAAAATGC TGATAGTATA AAGAAAAAAT TAGAAAAATT TGCTGAAAAT AAAATACAAT 180

AATAACTACT ATAAAGTTAC TGATGAAAAG AGCCAACAGG GTATACCCTG TTGGTCTTTT 240

TGTATGTTCA TGATATACTT GAATTTCTAA GAGGkCaACA GAGTTGAGCA mCAGAATTTT 300

AAAATAAAGT AATTTTTTrG AGGrGAtTTT CTATGGCAAA AATTGGATAT GCnCGAGTAA 360

GAGTGGGATC AAAATTTAGA TCGACAGTTA GAATTATTAT CnCAGTGTGA TAAAATTTTT 420

ACTGTAAGCA AGTGGGAGGA ACTAAnCGnA TGGTTCCAGA AATGTGAATT TATCGGG 477

(2) INFORMATION FOR SEQ ID NO: 840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840:

GCAACAAGTT CGCTATATTC AACAATTATT GGAATATACG GCAGAAACAT TTGCAGAGAA 60

TAATGATGGA CAAGAAATTA TGAATCGAAT TAAGACCGTT TATGAAACCT ATCGCACAAA 120

ACCATTGCCG CAAACAAGAr GTGAATTTGA AAATCGGGCG CGACTCTTTC AGTTTTTACA 180

ATTGTTTCAG TCATTCATTC AAGTCAAAGC GGACTTTGCC AAATTACAAC TAGATAAATA 240

AACAGAAAAA GAAACCTTTT TAAACAGAGG TTTCTTTTTT GTnCTCTTAA AAATTCAGGC 300

AAGTTCTTTA GTATTCATTG AGAATGTGTT AAACTAATGA GAAAGAAAnn TAAC 354

(2) INFORMATION FOR SEQ ID NO: 841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841:

AAGCCAGAAA TATGTTGTAA AAGTTGAGCA CTCGCTGTAT TCACATCAAC ACCAACTTGG 60

TTTACCGCAG TTTCTACAAC AAAATCCAAT TGCTCGGCAA GACGTTTTTG CGATACGTCA 120

TGCTGATATT GACCGACCCC GACTGCTTTG GGATCAATTT TTACTAATTC TGCCAACGGA 180

TCTTGCAAAC GACGTGCAAT GCTGACCGCA CTTCGTTCTT CGACTTGTAA ATCAGGAAAC 240

TCTTTACGAG CCACTTCACT CGCAGAGTAA ACGGAAGCCC CTGCTTCATT AaCAATCACG 300

TAAAAGACGT CACGCTTCAC CGCTTTTAAT TGCTCTGCCA CAAACAATTC AGATTCACGA 360

CTTGCCgTTC CGTTTCCAAT AGCTACCATG TCCACtTGAT AGTCTTCArT GATCTTTTTA 420

AAGGCTGGAC CAGnGGCTTC ACGTTTCGCA GCAGTCGC 458

(2) INFORMATION FOR SEQ ID NO: 842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:

ATTTGkCGTA CTTTTTCTTC ATAATTTGTC GTACTTTTAG TCGCAACTGC TTGAAGACTA 60

GCCAATGTCG CTTTATGAAC AGATAGTtCT TTTTCTGCTG TTGCTTGTGT TGTTTTGGCT 120

GTATTTAAGA CTTGCTGACT TGCACTTTTT GCTTGTTGAG CGTCTGATTC TGCTTGTTGT 180

GCAGTAGCTA ATTTTTCTTG ATTGGTTGCT ACTTCTTTTT GAAGGGTTTC TTTACTCTTA 240

AAGACTGGAG CAGTGCCTTC TTCATAGGTA TTTGCTTCAA CTAATTTTGA TTGATTATAG 300

CTAATGATAT GGATTTTTGC CGAAATATCA TTTAAATCTC CTGAAATAGA AACTGCCATG 360

TTTGTTGTGT CCCCTTTTAG CAATGAATCT ATATGAGAAT ACGCTGAACT TTCATCGTCA 420

AAGAGCATAT CAGCAATTGT TTTTCGAGCA GCTTTTTCAA ACTCTAGTTG AGAAATAGTG 480

CCATTAATCG TTTCAAAATA GCCCATACTT AGATTTTCAT AAAAGTTTTG CCCTGGATAC 540

TCTTTAAAAC CATTTTCTTT TGCTGCACGA TTAATTGCAT TTACGTCATG ATCAAACTCT 600

TTGGGATTAT CATATTTTGC TACATCCCAA GCAAATCTCA TAGCTTGGTT AGAAATCTTC 660

AACTTTTGTA ACCCAAGCTT TTCGCGAACA TCATTGATAA GTCCTACAAC GTAATCGCTC 720

ATTTGTTGCT TTTGTTTTyC GGTAGGATTT TTGACATTGA TCATTTCCGT TrCTTTTGCC 780

rCATCTGCTT GATTTTCAGG AAAAACTTTA TTTAATGCTA ATGCTTCTTT TTCCATTGCT 840

TGCTTTTCTT GTTCAGwTAA TTTTTTGTAA TAATCAGGTG TGAAGTTAGC AGGyAAGTTA 900

AkTCCTTTAT GyCCyTTTAr CTCTTCTTTT GAkyTATCTA AAGTATTCTG CGCTTGCTTT 960

GTTGCTGCTT GCTTGTCTTT yAAAGCATTt TCTTTyGmAG TTAAATCTGC CTGTTTCGCA 1020

GCTGTATCTG CTTTTGCGTC TGCTACTTTC TCTTGACTAG TTGTCACAAC rGTTTGTTGG 1080

TCTGCrACTG CTTGATCGTC CTTCGTyTTT TGATCTTTAG CTTTkGCTTC TTCTTTCTGT 1140

TTGTTAGCCA GTTCAGCTTC TTTTGCTGCT TGTTCTTTTT CTGCCTTTAC TTTTTCCGCT 1200

TCCGCATTTy TCGCTAATTC TTCAAGCTTG GCTTGTTCTT GTTTTGCAGC TGTTACTGCT 1260

TGTTGATCTT TTTCATTTTG CACTTTAGCA GCATTCGTTT CTTTTGCTTT TTCATCGACA 1320

ACAGCTTGTT GTTGGTTAAC GTCTGTTTGA GCTTGATCCA CTACTTTTTG TTGTTCATCA 1380

ACAGCCTGTG TATCCGTAGC CACTTGCTCT TTAGCTTTTT CAATGGCTGA AGGTGTTGCT 1440

TCATCCACGA CTTTTTTAGC TTCGTCTACA ACTGCTTGTT GG 1482

(2) INFORMATION FOR SEQ ID NO: 843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843:

GGAATCATGG CTAAAAATGA CCCTAAATAA GGGATTAAAT TTAAAAAGCC TGCTGCAATA 60

CCTAAAGTGA CTGCATAATC TAAGCCAATG ACAGAAAAAC CAATCATAAA CATAATTGCC 120

ACTGCGAAAG CGACAGTTAa TTGTCCTCTA ATATAAGAAG AGACTTGATC ATTGACTTCT 180

GCAgAACTTT TAgGTTGGTT TACGCATCTT CACTGGTAAA AACTTCATTA AATtGGCGCT 240

AgTTTTTGCC ATCTTTCAGT AAATAAAATA GAATAAcGGC AtCGTAATGA TGGCGACAAA 300

GATCGTAGCC ACCGC 315

(2) INFORMATION FOR SEQ ID NO: 844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844:

TTTTATTCTA TTAACCAATC CGGCGCATTG GAATATCATT GTTATCTGGA TGAACCAATA 60

AATATTGAAT AACATCAATA TTGCkTGCTT GGAATGAGGc TGCACATGCT TGCAAATATA 120

AgTCCCACAT TCGATAGAAg CGCTCGCCTT TTTCGTCAAC AATTTCTGCn TCTATATTAT 180

GGAAGTTTTT TGTCCAATGT TCCAACGTCA ATTGAnAATC TCTGCGCAAA CT 232

(2) INFORMATION FOR SEQ ID NO: 845:

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845:

TCGCTGCATT TACATCTGGA TATGGGCCCA AnATATAACG CTTTGTCTTT TAAAACCTTT 60

CGAGTAATCA TTAAACGAGG ATATTTTTCG TTTGTGATTT TGATAAAAGG ATAGGTTTTA 120

TCGTCTTTTA ACATGATGTn ATATTTGGGA TTATTTTTAT GGATTAAATT AATTTCTAAT 180

AAAAGTGCTT CAATATTCGA TTCTGTCACA ATATATTCAA AATCATCGAT TTCACTGACT 240

AATCGTTCTG TCTTAGTATC ATGGCTACCA CGAAAATAAG ATCGGACACG GTTTTTCAAA 300

ATTTTGGCTT TCCCAACATA GATAATCGTG CCGTTTTTAT CTTTcATTAA ATaACAACCA 360

GGTTGATCAG GAAGCAGTGC TAATTTATTT TkTATTCGTT CGTTCATACG ATACTTCCTT 420

TCTAACAAAA TGCTTCGtCT ATTATACACC TCTTTTTGTA ATTAAACAAA AAAAGCCGCT 480

ACTTTATGTA CGAAAGAAAC AGCCTGAAAA GACAAtCGCT AATGATTTCc TCTTCAGACT 540

GAATCAAACT ATTCGTAATG ACTAATCACG TTTATAAGTG TTTGGCAATC ATTGCTTGCA 600

ATTGGTCTTT TGTATGAACA CCGACTGCTT TTTCAACAAC TTCGCCATCT TTTTTCAATA 660

GCAATGTTGG GATGCTCATG ATTCCAAAAC TTGCTGGTGT TGCAGGATTT TCATCCACAT 720

CCATTTTGAC GATTTTCACT TCGTCTTCAT CATATTCTTC AGATAATTGT TCTAAGATGG 780

GTGCTTGCAT ACGGCAAGGG CCACACCAAG TTGCCCAAAA GTCGATTAAG ACTAATCCTT 840

CATCTGTTTC TGTTGCAAAA TCTTTATCGG TAATTGCTTG TGTCATTTCA CGGGATC 897

(2) INFORMATION FOR SEQ ID NO: 846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846:

```
TCGAACTGCC GACACACGGA GCTTCAATCC GTTGCTCTAC CAACTGAGCT ACCACGCCTA      60

AAACAAAAGC TTGTTCAAAT AATTTTCAAG TAACAACATT AAATGGCGGT TCCGACGGGA     120

TTTGAACCCG CGATCTCCTG CGTGACAGGC AGGCATGTTA ACCCCTACAC CACGGAACCA     180

ACCGAGTAAT GGAGGTTAAC GGGATCGAAC CGCTGACCCC CTGCTTGTAA GGCAGGTGCT     240

CTCCCAGCTG AGCTAAACCT CCAAAAAGGA ATGTTACTAT TAAAATAAAT GACCCGTACG     300

GGACTCGAAC CCGTGTTACC GCCGTGAAAG GGCGGTGTCT TAACCGCTTG ACCAACGGGC     360

CAGTTTGTAA ATATGAAACG GAGAGTAAGG GATTCGAACC CTTGAGACAG TGTTTACCGC     420

CTACATGATT TCCAATCATG CTCCTTCGGC CTCTCGGACA ACTCTCCATA GCTGAAAGAA     480

GCACATACTC ATGATATTTC ATATGTTAAA CTCCGGCAGT AGGACTCGAA CCTACGACAT     540

CATGATTAAC AGTCATGCGC TACTACCAAC TGAGCTATGC CGGAATAAwy GCGTGGCGAC     600

GTCCTACTCT CACAAAGGGA AACCCTTCAC TACAATCGGC GCTAAGAAGC TTAACTTCtG     660

TGTTCGnCAT GGGAACAGGT GTATCCTTCT CGTATCGCCA CCACACTGGG TGTTGTnTCT     720

TATTGAGTTG AATCTTCATT                                                 740
```

(2) INFORMATION FOR SEQ ID NO: 847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847:

```
CATTAATACA GGTATTAATC TCTATAATGA TGGTCAACTA GACGATGCGC CTGTAGCTGG      60

GGAATATAGT AAGCAATTAG AAAATnACAA AGATTTCATA CGAGAATTAT CTGCTACAAC     120

TATGTTTTTA GAGGTAAATC AACGAAATAA AAAAAGTATA ACTTCAAATA AACATGCTCG     180

ACAAGCGATT AATTTTGCGA TTGATCGTGA GGCTATATCA AACAAGATAT TAACAAATGG     240

AAGTATACCA GCTAAAGGTG TAGTACCGAG TAAACTAGTA TATAATCCAA AAACAGGAAA     300

AGATTTTACT AATTCAAGTT TAGTGTTTTT GGATAAGAGT AAAGCTAAAG ACAGCTGGGA     360

AAAAGCTAAA AAAGAATTAA AAGGTACTGA TTTATCTATC GATATTATGG TCAATGAAGA     420

AGATTTATCA AAAAAACTAG GTGAATATCT TCAAAATGAA TTGCAAGATA CTTTGGATGG     480

ACTTAAAGTT TCAGTTACTG CAGTACCTGC CACGTTACAA ACTGAACGAT TAAATTCTGG     540

GAACTTTATG ATTGCATTGA GTGGTTGGCA AGCAGCTTTG CCGATCCAGT TAGTTTTTTA     600
```

GCAAATTTTG AGAGT 615

(2) INFORMATION FOR SEQ ID NO: 848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 926 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848:

CGTTGTAACG CCTTTTGCAA CCATGCTTGC TTTACGCAAT TGACGGCGTT GTTTTTTAGT 60

TTTACCGTGG AAACGGTGAG ATGTAAAGGC ACGGCCACGT TTTAAGCCGC CTCCACCAGT 120

ACGTTTTACA CGTTTTGCTA ATCCGCGGTG TGTTTTTTGT TTTGGCATGA CTAATTTTCC 180

TCCTCAAAAT CTTTGCTTCA AGTGAAAGAC TCTAACAGTC ACAACTGTCG AATATCCTTC 240

TTGTAGAAAT TACCAAAAGT CCGAATGCTC GGTCTCTTCG TTTACTTGTC GTTTTTCGGT 300

GCCAGCGTTA GAAACATGCT GCGTCCGTCC ATTTTCGCTT TTTGTTCCAC TGTGGCGATG 360

TCCGCAGTTT CTTCAGCTAA GCGATCAAGA ACTTTCTGAC CAATCTCTTT ATGGGTAATG 420

GCACGGCCTT TGAAACGGAT AGAAGCTTTC ACTTTGTCTC CTTTTTCTAA GAACTTACGC 480

GCATTACGAA GTTTTGTATT GAAGTCATTT ACGTCAATTG TTGGACTTAA ACGAACTTCT 540

TTGACGTTGA TCACTTTTTG TTTCTTGCGA GCTTCACGCT CTTTCTTTTG TTGTTCGAAA 600

CGGAATTTTC CATAATCCAT AATTCGCGCA ACTGGTGGTT TCGCTCCTGG CGCTACAAGT 660

ACTAAATCCA AGTTTGCAGA TTCAGCGATT TGTAATGCTT CTGCTTTGGT TTTTACACCT 720

AATTGTTCAC CATCTTGTCC GATCAAACGT rACTCGCGTG cACGAATGCC GTCGTTAACC 780

ATCATATCCT TtGCTATGGT CATTCACCTC CAAAATTTTn AAGAGAAAAT CCTAACGGAA 840

GTCTGCTTTG TTTGCTAAAT GCAATAAAAA AACAGGTTCC TATCCAGAAC CCGCCAACAG 900

TCTGCCTTAC TTAAAAAAAT AAGGAA 926

(2) INFORMATION FOR SEQ ID NO: 849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849:

ACTCAAACTA TTTCGAACGA TAATCGTATA CCAGCTGAAT TTGTCCGTCA TGTTGATGGA 60

GATACCACCG TGTTAAGAAT AGACGGAAAA GAACAAAAGG TTCGCTTTTT ATTAGTAGAT 120

ACACCCGAGA CTGTAAAGCC GAAAACAAAA GTACAGCCAT TTGGTTTGGA AGCCAGCAAC 180

CGTACAAAAG AGCTTTTGTC TACTGC 206

(2) INFORMATION FOR SEQ ID NO: 850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850:

ATCAAATTCT TTTTCTTACA ATAATTAAAA ACCATATTTA GAACCTGAAC AAGAGATTGT 60

AAACTATTTT TAGCATAACC AACATTAACG CCATCAATTC CCTTTTCTTT TAAAATGAAA 120

AGGAATTTTT GTAGTTCTTC TGATGATAAA CTACTTAATT TTTTACCACC AATCCATCGA 180

TTAAGTATTT TCACCTGTnC TTCTCGTTTA TCATACGTTG CCACCTTTTG TTCGTTTAGT 240

GATCGATAAT ATTCAAACCA CTTTTGACTA ACAACACTAA ATTTATCATT ACTAGCAAGC 300

CTnTnTTGCT 310

(2) INFORMATION FOR SEQ ID NO: 851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851:

CCTTTGAACA TTACTGAAGC CAACACGTAA TCGACTTCTT CCCACGGAAT TTGGATAAAC 60

TTACGTGGAT CTTTGGCATG GTAAAATTCA AACCCGCGGT CACCTATCAT AATTTGTCCA 120

TAATCTGTTA ATCCTGTAAA TGCCGTCGCA TCTATAACTA AATCAACTTT TGTGTTTAAT 180

GATTGTACCA TGTTATCTkC TCCATTTCAT TCAACTAATT CCTCTTTATT ATACTTTTCT 240

TTCCTCATCT AAACAAA 257

(2) INFORMATION FOR SEQ ID NO: 852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852:

CACACCTTAC TCAGCAAATC TCGTCACAAA TAGTACTACA AAAACCTTCG TGTTATTATT 60

AAATAGCCAT GAAACTTTTG AGGCTTGGGT TACGAGCTTT ATTGATAAAG CTCAAGAAAA 120

TGGCTATAAC TGCTTGATTT TAAATAGTCA CGGTAGTTTA GAACAAGAAC TGAAAAATAT 180

TACCTCGCCA ACTTTAAAAC AAGCCAGTGG CATTATTTGG GACCCAATCA ATGAAAACAG 240

TAAACAATAC GCGAAATTTA TAGAAGAATT AACGATTCCT TACTATTTCG TCAATCACTC 300

AACTAACGAA TTACCTTCTC TAGCGGGGCT TTATGAAGAA GCTAGTTATG TTTTAACCCA 360

AGAATTATTA CAGAATAACC ATAAAAAAAT TAGTTATTTC GTCACTAACC CmAAATwTAA 420

AGrrGCmATT ATTGCmGGcT ATAAAAAAGC CTTGTTTGAT GTCAATTTAC CCTTTAGTAA 480

AGAAAATATT TTAACTACTA TCCCTGCTGG ATTTCAGTAA TCAGCTTATC ACAGATGGGA 540

TTACGGGTAT CCTTACTGGA TGACTATACC CAGGCTGTTT TTTTGGAACA GCTTTTAAAG 600

CAGAGCGGTT TGCGAACCCC CGATAATTAC TCTTTACTCG CAATTAAGCG GAAAAATGGA 660

TCGGTGCCAT TTTACCGGAT CCnAnTTCCT nCGnCCTAAT TAGATACCGA GACGGTTGGG 720

TAGCCAGTTA G 731

(2) INFORMATION FOR SEQ ID NO: 853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853:

TCACTCGTTT ACATACGAAA GACAGCTGCG ATTTTGTAGA mGCATCTGGT TCTTTCTGCC 60

AAAGCAAGCG ACAAATTTGA TCACGATCCA ACCCTTCGTG GGCATGCTGA TACAAGATTT 120

TTAAAAAGCG TTGCTCGTTT TT 142

(2) INFORMATION FOR SEQ ID NO: 854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854:

AACATACACA TTTCCTTCTT TAACCAATGG ATTTAATTGA TCTAACACAC CAGCTAATTC 60

GCCAGAGTTC TTCTCTGCGT AAAACTTGGC CCCAAATAAA CCACCACCAA TAACAATTGC 120

TGTCACCACT AAAAATTTAA TAAATTTCAT CACATAAATC CTCCCGAGTA ATTATTCTCT 180

GTTACTTCTT CCAAAGTATA GCAAGTTTTA AACAATCCTT CCTCGGGCGC AACGACCAGT 240

TTTTCCTCAG ACTTATGTCG TATnTnTGTT ATTTTGAATA AATAACAAAA CACTACTCnT 300

C 301

(2) INFORMATION FOR SEQ ID NO: 855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855:

TGCAGCAGCT GCAGTTGCCG ACTGAAAATC CCCGTTGTGA TCCCAAAATA AAGCTTCTAA 60

CATTTTTGCA CCTCGATAGT TTTATTTTAA TTATCTACTA ACTATCGATA TCTTTCAACT 120

TAAGATTATC CTCAATCAAT ATTTTTAAAT CAGAAAATTA ATTCAATTTG CATTCTAATC 180

CATCAAATTC TkGTTAATAT TATTTTGAAT GTCTGCTTCA TCAAAGAAAC CATGCCCACA 240

ATAAACCAAG CTTACAATCA TCAATTTCCC TTGGCGTGGC TCCCTCGGnC ATTTCCAAAA 300

ATAGGAnGCA TCCTTTTTAA TCTGGCACAG 330

(2) INFORMATION FOR SEQ ID NO: 856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856:

AAGGTGTTAG AAAAAATGCT ACCTAACTCT TCTGATGTTA CTTTTTACAA ATTTTTAAAT 60

AAACAGCATA GTTTGTATGA ACAACAATTT GAATTTTTAA AAGAAGTAAT TCAATTTAGA 120

AAAAATAATG AATATGACCA ATATAGCCAA ATAGGGTGTA ATTTATTACA CTATGATTTA 180

TTAATTTCAG GATTACTTTT TGATGTTAAG TCTTATGATT ATTCATATCA ATACTTTTTA 240

AAATTAGATT TAGCTAACTA TTTTTCTGAA TTAGAGATTC CTGATGAATA CAAAATGTTA 300

ATAAATAAGT ATCGGGAGAA TGAATCATGA TTAAGAGACC TCATGkAATG CAAGAkAGTA 360

TACmAGATgT GGTGkTgCAT GCATAGrAAT GrTATGkAAA TTCyaTAATA TTAATATAGr 420

TAGaaGATAT ATCCAAGAAG AAACTGGCTA TGGAATGATA GGAATATCAT TAAAAGCTAT 480

GGAAAAATTT TTTTCAAAAG TAGATGCAAA CCCAGAAATA GTAAATATAT CTAAAATTAA 540

TAGGTTAAAC AAAGAAAATA GGGAAATGAT TAATAACTCA CT 582

(2) INFORMATION FOR SEQ ID NO: 857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857:

TGCAnAAATT AAAAGAATTG CAATAGCTAA ATAGTTAGTT tGATTAAAAT CTATTACAAA 60

TTTTTTTAAT AGTTCTAAAA CTGTAGATAG TGCAAGTAGA GCTATAAATA TTAATATTAT 120

ATTTAAGGAA GTTTGTATAT TTTTTTTTAA AGTTTGACTA TTGTTATTTA CACTAAAAAA 180

TGTTATTAAT GACTCTTTTT TACACATTTC AATAACTTTG ATTCTAAACA GTAATATTTT 240

TTTTATATTT GTTTTTAAAT CGACTTTTCG TTTTTTTTCA TCTAGAATGA CTTTTCCATC 300

TCTGGTTAGT TCAACAACAC CCAGAAACAG TTCTTCTTTA TTACTATTCC ATAATAATAT 360

CGGCCCCTGA CCATGATTTT TATCAATATC AAAATCAGAw ATAATAACTT TATCTGCAAC 420

TTTTCTTAAA TCATTTTCTA GTGTTTCTGA AGTTAAGTTC TTATTTAATT TATGGATCAA 480

TGTG 484

(2) INFORMATION FOR SEQ ID NO: 858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858:

GCGTAACTCA TGTGTTCACC CCCTGTCCGT TGCTCTCTGA AACAAATGGT ATAAGGTAAA 60

GGGCAGGTGA ACCTTGGTCT TTACGAAAAA AGTTTTGAnA ATTTTTTTGT GCCTGATTGC 120

GCATTTTGCT ACCTCCGAAA ATTTGAAAAT TAGTGAAATT CCAAACCTTT TTGGAGGTTT 180

AATGTCTGAT TAGCATATCT GTATACGTTT GATAATGCGC TTAAATGATT TTGAAGCGGC 240

GCGnTCTGTG CCACACTTTT TTTGACGGGA TACCCGCCGT GTATATAAAA ATAAAACCAT 300

CCATGTACTG TCCCTTTCTA CGGACAGACA CAAATGGCAA AGGAAGTAAG CCCTGATGGC 360

GGTATTCTTC TTTGCGCTGG CGTTCCATTT CACGCTCATA GTCGGCAAAG ACCTGATAGA 420

TTcTCTGGAT ACCTCGACCG TGATGGGCTT ACCGCTACCA TCAAAAATCG TAACGTAACA 480

CATGGcTCCC TCCTGTGCAG CGTCATCCAg GCAGAGAAGA ATGCCAkGGG GGAAATGTCG 540

TCATCAGGAT CAAGGGGAGC GnCCCATGCT GCACAACCGA GGGGCAA 587

(2) INFORMATION FOR SEQ ID NO: 859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

GCCnCCnTTC AAAGGAGTnG CACCATCAGG AAAATTAGCT ACTGCACAAC AAGCAGAATC 60

AGCGCTCAAC AGCAAAAAGT GCAAGTCAGC AAGTCTTAAA TACAGCCAAA ACAACACAAG 120

CAACAGCAGA AAAAGAACTA TCTGTTCATA AAGCGACATT GGCTAGTCTT CAAGCAGTTG 180

CGACTAAAAG TACGACAAAT TATGAAGAAA AAGTACGACA AACTGCAACG GCAGAAAAAA 240

GCCTTCAACA AACAAAAGAT CAATTGGCAA CAATCAATGA GTTAATTCAG AATCGAGCTG 300

CTGTTTTAGA AAAAGCGAaA ACAAACGTTT CGGAAGCACA AGCAATTGAA CAAACGTCTG 360

CTAAAGTGCT GAAAGAAAAA CAAGCAGCCC AAAAAGCAGA AGAAAACACA TTGAATAGCT 420

TGAAGGAAGT ATTGAATTTA GCAAAAGAAA ATTTAAATCA AAAACAAGTT GCATTTAAAA 480

CAAGTACACG TTCATTGTCT CGTTTAGAAA ATGCTCAACC AACATACGAA AAAGCATTAA 540

ACGAGTTAAA CAAAGCAGAA GCAGCAGCGG TCCAAGCACA AGAAGCCTAT GAAAATTCTC 600

TGAAATCATT GGAGGAACTT AAAGAACAAC AAGCCGTTGC TACACTTGCT TATACACAAG 660

CACAAGAAGA CCTTTCTAAC GCGAAGTTAG AGCTACAGCA GTACCAGGGC GTATTAAGAG 720

AATTAGAAGC aCAACAAGCC GaACAGCAGC GACAAGAAGC GTTGCAAGAA CAAGTAGCAA 780

AAGAACAACA ACGCCTTGAA CGAGAAGCAA AACAAAGCCA AACGTTAGTA GCAAGTGCTA 840

CTTCAGCAGA CAAAACACCT GGTCTCCAAC AGTTATCTTT TTCTAAACAA AAAGAACAGC 900

CAAAAGCACA AGCATTAACA CATTCAGAAT CTCGTAAGAC GAAACAAGTA GCAAAAGCCC 960

CAGATTCTTT ACCACATACA GGAGAAAAAA ATAATAAATG GTTAGCTATA GCTGGTCTGA 1020

TATTTGCTTT GTTAGGAGCT GCGGGTATTA TAAGTTTTAT TAGTAGAAAC GAGAAGAAAG 1080

TAAAAAATAT CTTTAAAATT AAATAATAAA GTCAAAGGAG CGACATATTT CGCTCCTTTT 1140

TATTGTAATC ATTGGAATAA ATTGAAAAAT AAAAAAATAG CCAACCAAAA TGGTTGGCTG 1200

ATTGTATTAA AGGCAGAAGA ATCTACCAAA TTTAGGAGCC AACCAGTTTC CGCTGGTCAA 1260

CAAAAAATAA ATGGATTGTC TCGGATGGAG ACACTTAAAT AGTACCTGAC AATAAAATTT 1320

TAGGCAACAA AAAAGTCAGC CGTTTTCCGC CGACTGACTA AACGAATAAG ATTTGTAAAG 1380

AAGTGATTTG TACTTTTTAC ACAATTATGA TAGCACGTTA AATGTTTTTA ACGCAAAAAA 1440

AAGCTAAGGG AATCGAAAAa CTTTCGGTTC TCTTTTTGTG AGGAGGAATG GAAATAATGA 1500

TGAAAAAGCA ACGAGCTCCT TGTGTTGCGT GAACTATTTT TACAAACAAA AAATAAAAAA 1560

TCGAGGAGAA TGATACATGA ATCAACAGAC TGAAGTAAAA AAACGTTTTA AAATGTATAA 1620

GGCAAAGAAA CACTGGATTG TAGCCCCTAT TCTTTTTTTA GGTGTATTAG GAGCTGTAGG 1680

ATTAGCTACA GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGGAA CAACGACGGT 1740

GCAACCCGAT AATCCCAACC CGCAGTCACG AAATGAAACA CTTAAAACGG CAGTATCTGA 1800

AGAAGCAGCA TTACAAAAAG ACACTACTTC TCAACCAACC ACAGCAGAAG AAGTAGTGCC 1860

GAAAGGAATT GCTGCTGAAC AAAGTTCAGC TACCTCAAAT GATACCACAA ACGTCCAACA 1920

ACCAACAGCA GAAGCAGAAA AATCAGCACA AGAACAACCA GTAGTCAGCC CTGAAACAAC 1980

CATTGAACCT CTAGGGCAGC CAACAGAAGT TGCACCAGCA GAAAATGACG CTAATAAATC 2040

AACGTCAATT CCTAAAGAAT TTGAAACACC AGACGTTGAC AAAGCAGTTG ATGAAGCGAA 2100

AAAAGATCCA AACATTACCG TCGTGGAAAA ACCAACTGAA GACTTAGGAA ATGTTTCTTC 2160

TAAAGATTTA GCTGCAAAAG AAAAAGAAGT AGACCAACTA CAAAAAGAAC AAGCCCAAAA 2220

GATTGCCCAA CAAGCAGCTG AATTAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAATGC 2280

AGAAATTGCG GCAAAAAATA AAGCGGAAAA AGAGCGCTAC GAAAAAGAAG TGGCGGAATA 2340

CAACAAACAC AAAAATGACA AAGGCTATGT GAATGAAGCA ATCAGCAAAG ACTTAGTTTT 2400

TGATTCAAGC ATTGTGACTA AGGATACTAA AATAGACAAG ATTACAGGTG GCAAGTTTAT 2460

TAAAGCTTCC GATTTTAACA AAGTAAACCA AGGACAATCC AAAGATATTT TTACAAAATT 2520

AAGTAAGGAT ATGAATGGAA AAGCAACAGG CAACTTCCAA AGCTCAAAAG TGGCTGCTGT 2580

TGAATTTGGC CCTAAAGGAG GATACGCGGT TCTTTTAGAA AAAAACAAAC CGGTCAATGT 2640

CACGTATACA GGATTAAATG CTAGTTATTT AGACCGAAAA ATCACAAAAG CAGAGTTCAT 2700

TTATGAACTT CAATCTGCAC CAAGTCAAAG CGGCACCTTA AATGCAGTAT TTTCGAATGA 2760

TCCTATTATT ACAGCATTTG TTGGTACTAA AAATGCCAAT GGGAAGGACG TAAAAGTTCG 2820

CTTAACCATT AAATTATATG ATGCTAATGG CAAAGAAGTT TTACCAGATA AAGACCATGC 2880

CTTTGCCTAT GCGTTATCGT CATTAAACTC TAGTCTAGGA ACAAATTATA GTGTAGAACA 2940

TGCGGAATTT GTTTCAGACT TTGGCTCAAA AAATGAGTTC AAGTATATTA ATGGTTCCTA 3000

CGTAAAGAAA CAAGCGGATG GGAAATTCTA CTCAACCGAA GACCTTGATT ATGGGACAGG 3060

TCCTTCAGGA CTAAAAAATA GTGATTGGGA CGCTGTAGGT CATAAAAATG CGTACTATGG 3120

TTCTGGTGTA GGTCTAGCTA GAGAGGGTGG ACGTATTTCT TTCTCTTTTG GTATGACAAC 3180

CAAAGGAAAA GTCAACCTAT CTGGTGCGCA ATGGTTTGCC TTTAGTACCA ATTTAAATGC 3240

GAAATCAATT AGACCATACC AAAAGAAAGG GAATCCaAAA GAACCAGAAA AAGCAACAAT 3300

TGAATTCAAT CGATACAAAG CCAATGTCGT TCCTGTTCTT GTGCCgAATA AAGAAGTCAC 3360

TGATGGTCAG AAAAATATCA ATGATTTAAA TGTGAAACGA GGCGATtCTT TACAATACAT 3420

TGTGACAGGG gATACGACAG AACTTGCCAA AGTAGATCCG AAAACAGTGA CAAAACAAGG 3480

GATTCGGGAT ACCTTTGATG CAGAAAAAGT GACGATTGAT TTATCCAAAG TGAAGGTTTA 3540

TCAAGCAGA 3549

(2) INFORMATION FOR SEQ ID NO: 860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:

AATTCTAAAA TTTATTTTAA AATAAGAATT TGCATTGGCA TTTACTTTGT CAGCGGGTAT 60

ACTTATACTT GATGTATTTT GCATTTATTT CAGAAAGGAA TGGTGACATG CTTTTTGCTA 120

ACCTATGGAA AGCAATTATT CTTGGTATTA TCGAAGGAAT TACCGAGTGG CTTCCAATTA 180

GTAGTACCGG ACATTTAATT TTAGTGGATG AGTTTATTAA ACTCGATCTA AGTAAAGATT 240

TTATGGAAAT GTTCAACGTC GTTATCCAAT TGGGAGCGAT TATGGCGGTT GTnATtTTAT 300

ACTTCCAC 308

(2) INFORMATION FOR SEQ ID NO: 861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

CACTATCACA ACAAATCAAC AGTTTGGAAT GCTCAGGAAA AGATTTAGCA GATATAAACC 60

CAACTAACAC TACAGGTTGA AGAGTCCAAC GCTTGCAAAA CAAGAGATGA AATTACTGCA 120

TGCAGCATAA AGCTGCAGCT TTCAGGACCA ATAGCAGGGG ATCTCCCCAT CCACC 175

(2) INFORMATION FOR SEQ ID NO: 862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:

TTCCTTTAGT GAAGAGAGTC TTTGGTTGGT GGAAAAAGAC GTAAAGAAAC AGCGAACCAC 60

ATCTGGGAGT TGACTTTTTG AACCCTTAGT AGGAAAGTCC GGGACCACTC GTTAACAGGC 120

GAaGTTATGA ACTTCATAAG GtCGTGTTGC GAAACACGAA TAAACTAAGG TGGAACCACG 180

ATAATTGATT ATTCGTCC 198

(2) INFORMATION FOR SEQ ID NO: 863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

TGATTATTTT AATAGATTGG TGTAGTTTAA TATCAAAATC AATATTATAG GTGATAATAC 60

ACATAGAGAA ATAAArATAA TCAAAAAATA GAACCATTTT TTAGAAACTA GCATACCTAA 120

TCCTATCGTT CCTAGTGTGT ACAGTACTAT CAAAATAAGA TAGATTTkkG TTCCATTTCC 180

TGAAAAATCC GTCTTGCTCA CACTAGTTAT CATTCGAAGA ATAGCATATA TAATCCCCAA 240

AGAGCACAAC ATCCAAATAA AGCTACTAAT ATATTTAAGG AGATTCATAA CCAGACCTAC 300

TTTCTATTAn ATTACTnAGA GTAGCCTTTC CAAGTTTGTG TGTGCGTCGC TCTAACATCA 360

AAGTAATCAG GA 372

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

CATTGGTTTA AAAATGACAA ACGGTCTTGA AATTTTATTA CACATGGGTA TTGATAnGGT 60

AGAGTTAAAC GGGGCACCGT TCACTATTAA AGTGAAAGAA GGnGACCAAG TGACTGCAGA 120

TACGGTGGTC GCAATTGCTG ATTTAGAAGC AATTAAAGCA GCTGGTAAAG GAACTGAAAT 180

GGTTGTCATT ATTACCAACA TGGATAAAGT AACACAATTT TCGTTAGAGA AAACTGGCGT 240

GGTTACAGC 249

(2) INFORMATION FOR SEQ ID NO: 865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

ATTTTCCGAG GAAATATTTA TAAAATGCAT ATTTACCGCC tAAAGCAAAC GGTGGCGATA 60

TGAGTTTACC TGTTACCTAT TTGTTAAAAA ATGCCACAAA ATTTATTTAT GTCAACACTT 120

CATTTTTCAA GGTATTTTTT ACTATTAAAG AACTGCCTTA CATTGCTGTT TTAGATGAAA 180

ATAATTATTT TTACGGCATk TTAACACACA GCACCTTATT AAATATTTTA GCGCAATCTT 240

GGAATGTAAA ACAAGGGAGC TACGTTTTAA CAATTGCTTC AGTTGGTCAA CAAGGCGACT 300

TAGCAGCCAT TTCAAAAATC ATTGCCAAAT ATAGCAGCAT CGCCAGCTGT ATTACATTGG 360

ATGTCGATAG TGAAGAATTT GTTCGTCGCA CACTTATTAC TTTACCAGCC GGCACAACTG 420

CCGAAACGTG TACAGCCATT GTAGAACATT TAGAGCGGAA AAACTTTAAA GTTGTAGAAT 480

TGGAAAATTT AGAAgACGAG TAAAATTTAC GACCTTTAGC TTAGGATTTA mAGCTAGGGA 540

GGTAAGCCAA TTTGACTTAC CTCCcTAGCT TATTTTTTTA GACTTCTTCA CCAATAATTC 600

GAACTTCCGT TTGCAATTCA ACATCAAATT TTTCTTTAAT CACTTCTTGG ATATGTGCAA 660

TTAATTCCAC ATAATCTGTT GCG 683

(2) INFORMATION FOR SEQ ID NO: 866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866:

AATGTAATAA TGCCCATTTG AACTTGTGCA TTTGGTTGGT TTTCTTTATC AAAAAAAATC 60

GTCATTTCTT CTGATTCTGC TGATTTAATA AGCAATAGCT TCCCCTCCTT TTTTAAATCT 120

TGTATCTTCC ATTATTCCTT TAAATAGAAT CAAAGTCAAT CTTTTTATAG AAAATTCTGA 180

ATATTCTACA CAAAAAAAGA GAGCATGAAT TCTCTCTCTT TTGnCTCTTT AAACTTTTAC 240

AATCCAGCcT TCTGGCGCTT CTTTGTCACC AAACTGTATG CCAACCAGTT CATCATATAG 300

TTGcTTAGtC ACTGGtCCAA CTTCCGTTTC ACTATAAAAT ACATGGaAAT CTGTGCCGTT 360

TTGaATCCCA CCAATAGGAG AAATAATCGC CGCTGTGCCA CAAGCACCCG CTTCGGAGAA 420

GTCCGCTAAT CGATCAATGT AAACGTCTCC TTCAAGCGCC GTCATCCCTA AACGTTCTTT 480

TGCTAGCGTC AATAATGAAT ATTTAGTAAT ACTTGGCAAA ATAGACGnTG ATTTCGGCGT 540

AATAAAAGTA CCATCTTTGG TTATGCCAAA GAAATTGGCT GCACCAACTT CTTCAATTTT 600

CGTATGCGTA TACGGATCTA AATAAATGCA ATCACTAAAT TCTTTCTCAT GTGCTTCTGC 660

ACCTGGTAAA AGACTAGCTG CATAATTGCC CCCCACTTTA GCTGCCCCAG TTCCTC 716

(2) INFORMATION FOR SEQ ID NO: 867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867:

TACGTTTCAT CCATTTTCCA TGAATAAAAG GATTTTTTAT TTTTCTTTTT CCAAATTTGA 60

TAGAGTAGTT TGCCATATTC TTGCACCCAA CGATAAATCG TCGTATGAGA AACGTTAATG 120

CCaCGATCAT ATAAGATTTC yTGaACyTCa CGATAGCTAA GGTTATAACG rAGaTaGtAG 180

CCCACGGCTA CaATAATCAC ATCCTGCTGA AATTGCTTTC CTTtAAAATG ATTCATCGTC 240

ATTCCTCCkG CTATCTTTTT CTATTATTCT ACCTTATTTG ATAGTAGATT TAAAACTTTG 300

CAACAGAACC AATGGTATTA TAACAAGAAT TACTAATGTT AACTTTGCAC TAAGGTTAAT 360

TAGGACTATC CCATATAAAA GAACTTCAAA TATTGATAAC ACAACTTTGG GTATTGTAGA 420

ACTAACTAAA GTATACATAC TACTTGCATC ATTTGATAAT ATACTAGCGA TATTACCAGr 480

AAGAGAATGC TCAAAGAAAG AAGTTCGCAT ATTTAGTATT TGTTTTATAA CTTTAGCTCT 540

TACTTTATTT ACAATAATTA TTCCTATTTT TTGTAGATAA AA 582

(2) INFORMATION FOR SEQ ID NO: 868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868:

TGATGTCACT TTCTGTAACG GTACATCGTA AAAAGGATCT TCACGACGTC CTAAAAAGTC 60

TTTTCCTTGT TGCGGGAACA TCGCATATAA TAGGACATCC TCTTCAGATT TTGCATATTG 120

TTGGATTTCC TTTTCTAAAC TATGCAACTC TGGTTTCAAT AAATCCGcgG TCGACAAtGA 180

TTACCTCTTC ATCCCCAtGA TTTTTGCTTA ATCTCTcgCG ATAGTGcGGT GATTGCCATA 240

TcTCCGCGCA CATAAyCTTG ATTCATtCGk gATtAAgGAT ATCTTCCCCA GAAATCACAT 300

CCTTAAGGCT GTGGTCCAAC CATTGTGAAA GCGGCGGACT AGGGGGAACC CAAACTGCCT 360

ACTTAGGCTC AGCAAAACTC TCAATTGCTG GAACTGCCCG GAATGCTAAA AGGTGAnACA 420

AC 422

(2) INFORMATION FOR SEQ ID NO: 869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1069 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869:

TACTCAGGGA AATCGAATTT tCTTTCTCTT CCTGCAGGTA CTAAGATGTT TCAGTTCTCT 60

GCGTCTACCT CTAATCAGCT ATGTATTCAC TGAAAAGTAA TATCCTATAA AAGATATTGG 120

GTTCCCCCAT TCGGAAATCT CTGGATCATA GCTTACTTAC AGCTCCCCAA AGCATATCGG 180

TGTTAGTCCC GTCCTTCATC GGCTCCTAGT GCCAAGGCAT CCACCGTGCG CCCTTATTCA 240

CTTAACCTTA TCAACCTTAC GGTTGGGTCT TrATCACTTC TTCTAGCGAT AGAAGGTTAA 300

TCAATAAATA AGCAATTGAA CTTATtAAAA AACTCATTCA ACGCGGTGTT CTCGGTTTGT 360

TTTGATTCTT TTTACTTCAA TATCCAGTTT TCAATGAACG AATCTGATAG CAAAAGCTAT 420

CAATGGAGCc TAGCGGGATC GAACCGCTGA CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA 480

GCTGAGCTAA GGCCCCGAAT TTATTTGATT GAGAGTAGAC CTCTCAAAAC TGAACAAAGT 540

AAAGACGAAA TGTGTATTTC CGTAATATTC CTTAGAAAGG AGGTGATCCA GCCGCACCTT 600

CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATCT ATCCCACCTT AGGCGGCTGG 660

CTCCAAAAAG GTTACCTCAC CGACTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG 720

TGTGTACAAG GCCCGGGAAC GTATTCACCG CGGCGTGCTG ATCCGCGATT ACTAGCGATT 780

CCGGCTTCAT GCAGGCGAGT TGCAGCCTGC AATCCGAACT GAGAGAAGCT TTAAGAGATT 840

TGCATGnCCT CGCGGTCTAG CGACTCGTTG TACTTCCCAT TGTAGCACGT GTGTAGCCCA 900

GGTCATAAGG GGCATGATGA TTTGACGTCA TCCCCACCTT CCTCCGGTTT GTCACCGGCA 960

GTCTCGCTAG AGTGCCCAAC TAAATGATGG CAACTAACAA TAAGGGTTGC GCTCGTTGCG 1020

GGACTTAACC CAACATCTCA CGACACGAGC TGACGACAAC CATGCACCA 1069

(2) INFORMATION FOR SEQ ID NO: 870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870:

CCTGATGAAA TTGTCGACTT TTATGAAGAC TTACAAGAGA TTGATTTATC AGGAAAAATC 60

TTCGGCGTTT GTGGTTCAGG AGACACGTTT TATGATGATT TTTGTAAATC GGTGGACGAC 120

TTCGAAGCAG TCTTTACTCA AATT 144

(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871:

TCnGAAAGTT ATCCACAGAT GTGGATAATG TGGACAATCA GTGGCGAATA TGTGTTTGTA 60

TTGAAAAAGC TGTTAAATAA AGTAATTTTT TAGTTTGTTC TGTGGATAAC TCTGTGTATA 120

TGTGTATAAT TATGTGGAAA CGTTGTGGAA AGTAGCCAAA CTTCGTGCTA AAATAAGAAA 180

GAAGAGAAAA CGAGAAAGTA GTGGAATAGG TGAAAATTAA ACTAGTAACA GTCGGAAAAC 240

TGAAAGAAAA ATACCTGATT CAAGGCATTA ATGAATATCT GAAACGTTTA AATAGCTATG 300

CCAAGATGGA AATCATTGAA GTACCAGATG AAAAAGCCCC AGAAAAACTC AGTGACGCTG 360

AAATGCTTCA AGTCAAAGAA AAAGAAGGCC AACGTATTTT GGGGAAAATT AATGACAACG 420

AATACGTCTT TGTTTTAGCC ATTAATGGCA AACAATTATC TAGTGAAGAA TTTTCAAAAG 480

AnATTGAACA ATTAGGGATT AGTGGCAAAA GTAATCTAAC CTTTGTCATT GGTGGCTCCT 540

TAGGTCTCAG TGATTCAGTC CTTCAGCGAA GTAACCAACA AATTTCTTTT GGCcGCTTGA 600

CTTATCCACA TCAGTTAATG CGTTTGGTAT TAGTGGAACA AATTTATCGC GGTTTTCGGA 660

TTATGAAAGG GGAACCGTAT CATAAATAGG AAATAGGCTG GTTGCTCAGT AAGTTCTATG 720

AATCAAGnCA TTGCTTGAAA AATATATGAA GTAAAATATC TTTAGTCTGT TTGTCTGATA 780

GAAAATAAAA AAATTCAATC AAACTGGATT GAGAGAAACG TtACCGTTCA AACAATAAAT 840

AAAAaTGAgA GGAATGGCAA AAAmCAtGGC A 871

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872:

AATATTTTTA TTAGCGTGTT CAAATCCTGA TTTCTTGTAT CAATTATTTT CTGTTCACTT 60

TCAATAAGAA AAAaGTCTTT ACTTCCATGG CTAATAATAa GTCTCTATTT TtCAtAATAT 120

gCAAAATtAT ATCTTAATag AAAaTATTTT TATTTTAAAG ATAAAAAATT CTTCATCCTG 180

CAATACTTTA TATTCTATAT TGTAATTATT CAGAATATTA CTTACAATAT ATAAACCTAA 240

TCCATTACTA TTTCCCTTAT TTAAATCAAA TTTAACATCA AATATTTTAT CCATATTCGA 300

AATTTTATTG TTACCGTATG AATTCTCTAT ATATAACCAA TCATT 345

(2) INFORMATION FOR SEQ ID NO: 873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873:

nCCCCCATTA TATGGAATAA CACCTGGAnC TATATTTCCA AAGGATCCCT AAAATTAnGG 60

TTTATGTCCA TGGTTTCAAA TGTATCTAAA TACTTTTCCG ACAAnCCTTC aCkGAGTAAA 120

TCaAATTGTA AAAGTAACTT TTGGCACTGC ACCTCCaGTG CCTTTTCGTC CAAATGATAA 180

TCTATTAATT GAGAATATAA TTTTTTAGTT TCTTTrGTTC TGTTGCAAAG TTTTAAATCT 240

ACTATCAAAT AAGGTAGAAT AATAGAAAAA GATAGCAGGA GGAATGACGA TGAATCATTT 300

TAAAGGAAAG CAATTTCAGC AGGATGTGAT TATTGTAGCC GTGGGCTACT ATCTTCGTTA 360

TAACCTTAGC TATCGTGAAG TTCAAGAAAT CTTATATGAT CGTGGCATTA ACGTTTCTCA 420

TACGACGATT TATCGTTGGG TGC 443

(2) INFORMATION FOR SEQ ID NO: 874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874:

ATTTGTTTAT GAGCATCAAG ACATTCTCTT CTAGAAATGA AAAGTAGGTT ATTTATCCTT 60

TCGTAACATG TTAGGCTTAT TCAACTATGC TTCCAATCGA AATTTAATTA ACTTAACAAC 120

TTAAAATGTT CTCTTTATTG ATTTTCATAA TTTaAATTGT TCAAATTGAA TTAGATAAAT 180

AGTAATACTT CCCATATTAA AATTTATTTT TTTTCAGCCC TATAATACTT ACAATTACCG 240

TGAATAATCC TAAATACATG GGAAGACCAT TATACTTTTC TCCAGTTTTC GGTAACTCCA 300

TAGTATTTTT ATTTCGATTA CTnCn 325

(2) INFORMATION FOR SEQ ID NO: 875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 428 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875:

GATCAATCCA ATTATTTGTA TTGnATATTC ACATCGGTCT TGCAACATTG CGTAAGCTAT 60

TTnACTATCA TTAGACATAG TTTTATAAAA TTCTGATGTA AAAAGTACTT TAGGTAATTG 120

GTAATACAAA TTTCTATAGG TTTCATTAGC TGAAATAAAT TGAAAATCGT TCATAGCTTT 180

ACCTCTCTGT TTTTGTTAGT TTATAGTTTA ACCTACTTTT ATTTCCCTTG CAAATACTGA 240

TATAACAGTA TTTGCCTGCT nTCTTAGTAT ATCACGATAT TGCGATATAA CGCAATTGTA 300

ATATTGGAAT ATCGTGATAT TACAATATTT AAAAGATTAT TATTGATACA ACAGCGTTTG 360

TAGAAAAAAA ACAACAACAA TATTATGATA TTGTTGTTGT CTAATATTGT AATATTGTGA 420

TTCCACAA 428

(2) INFORMATION FOR SEQ ID NO: 876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876:

GGAAAGnAGT AGTCTATGAT AAAATAGTAA AAAGAGCAGA AATGAGGACA AcgAATGAAA 60

ATTGGAGTCA TTGGTTTAGG AAATATTGCA CAAAAAGCGT ATTTGCCAAC TTATAGTGAA 120

TGCCGCCACT TGGCAGAGTT TGTATTAGCA ACTAG 155

(2) INFORMATION FOR SEQ ID NO: 877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877:

GCCGAATAAA AGAAGTTTCT GATGATATTG AAGTTGTGGC TATCAATGAT TTGACTAGCC 60

CAACAATGTT GGCTCACTTA TTACAATTTG ACTCTACGCA TGGCACCTAT CCTGGCACCG 120

TGACAGCCAC TGAAAATGGC ATTGTGGTTG AnGGCGAAGA nACCCGTGTC TACGCAGAAC 180

CAGATGCAAG TAAAATCCCT TGGGTTAAAG AAAACGGAGT AGACATTGTC CTTGArTGTA 240

CAGGTTTTTA TACCTCTgAA GnAGAAGCAC AAGCTCA 277

(2) INFORMATION FOR SEQ ID NO: 878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

AAAAGTATAC TAGTATACTG GTATACTTTC CTTTAGCAAA CCTTTTAACA AGCAAGATTT 60

CTAAGGTATA CTGGTATACC TTTGAATAAA AGTTTAAGTA TACCAGTATA CTGnCACGAT 120

AAAAGCAACA GTATACCAGT ATACTTACGA TCATATTTTG GAGTATACTG GTATACTATT 180

GCTAAaGAAA ATAAAAAATA ATGATTTACA AATwTAATTA TGTACGGTAT TTTTTAAGAG 240

TATTGAATTT ATAAATATTA AGATAAAAAA ATAGAGACGG TAACTTACTT GATCGCCAAA 300

TCAAATAAGT TACAGAATCA AAAATGTACA CCCATTTTCA ATTCTTTTGC GTCCCTGGAT 360

GATA 364

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879:

CATGAGTGTT GCCTGGCAAT ATTTGTGGGG ATTTTTTGAT TATTGTTAGC ATTTTTCTAG 60

ACAAGAACAA CTGAAAAAAG AGTTTCTTTT TTCCATTATG TTTTGTTTCT GAGTTTAACC 120

AAATCACTCA TTATTTCAAG GAGGAATTAG GTTATGTCAG TaCAATTAGA AGTCAAAGAC 180

AGAGCCTATC CGTCCAAGGT TCAACTAAGG A 211

(2) INFORMATION FOR SEQ ID NO: 880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880:

ATCTTTTATT TAGAATGAAT AGGgATCTGA AaTaTAAGaT TTTTTGATGG AGAAAaCCAG 60

GATGATTTAA TAGTTATyCA TATACATATG ACTCAACACG nAATAGATGG TGATTAACAG 120

AGAGTTATCC AAATTATTAT ATATAGAAAT AATTCAAAAT TATTTTAAAG AAATTCTAAC 180

TTTTCACTCG ATAAAATATA GTGTAAAAAC GCAACTTGAT TCAGAGGATG AAAATGAAGT 240

GTTCAGATAT GAGTTGAAAA ATACTTATTT CAATTGATTG AGTAAAGCTG TTTTATCATT 300

ATTAGTAATA TGAAGATTTT TATATCAGAC TTAGAGAAAA GCTTTACTAC ACTCTTGTTA 360

ACTATAATGC TTTTAGCGAG AAATAATACC TAAAGTGTAA GCTAAAAATT TATCATAT 418

(2) INFORMATION FOR SEQ ID NO: 881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881:

ACATCTTTTT TnCTGGnACA TTAATTGnGC TACTTTTTTT AATTGTGTCG AGTTAAATCT 60

CCAAGGAACG AACAGTAATT TTAGCGCATG AATTAACCCC TAGTnAGCTA CGTCGATTTT 120

GGCAAAACTG ATTTATGAGT ATCTAAAAAA CGAACAAATC ATCGGCCTGG AAAAATTCTA 180

TACCTTTAAC TGTGCCGATT ATGCCAATAA TCCCGAATTG CTATCATCTA TTCTCTTCGG 240

CCATACCAAA GGCGCATTCA CTGGGGCTGA ATCAGAAwAA CrAGGACTCT TGGCCCAAGC 300

TaATAATTCC GTACTCTTTT TAGATGAAGT ACATCGATTA TCCAACGAAA ACCAAGAAAA 360

ACTCTTTCAG TTTATGGATA CAGGGACCTT CCGCCCTATT GGTGAAGA 408

(2) INFORMATION FOR SEQ ID NO: 882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882:

CTTCAAAAAT CTCGCGATTG TGATCGCGAA TAATATACGT CATTGTAGCT TCTTCTGGCG 60

TTCCAGCAAA CGCTGCTAAA TGATAAAAGC CTTCTTCACC TGCTGTTTTT TCTGGAACTT 120

CGTCAGCAGG TAAGGCATTA TGGAAATCAA TTCCTAATTG TAACGCATTA ATCATTGTAT 180

TTTTGGCTGT TCCTGGATGA ACGTTTTTCC CTTGAATTGT AATTTCTGCT TGCGCCGCAT 240

TAAACGTTTC AAATTGTAAT TCGCCTACTG GCCCACCATC CATTGTATAA GCAAAATCCA 300

CGTTAAATTG AGCGACATCA AATTTGTCGG GCACCTACAC CAATTTCTTC GTCAGGACCG 360

AAAAGCCACA CGAATGGGGG CCATGTTTAA TTTCnGGGGn GATTAAATTA AATATTCCCn 420

GGGCGGTCAA TAATTCCGCA ATAnCCGGAT TTATCAACCA GCTCC 465

(2) INFORMATION FOR SEQ ID NO: 883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

AAAGTTTTGA TGATAAAAAT TACTATTGCT AACTTATTAG AAGGGGTCCC ATTATTACTC 60

TTATTAACAT TATACAAATA ATCTTTCCAA TCACTCCTGC AAACGGGCTT CGTCTCTAAC 120

TGAAGGTCTA TTACATTAGC ATTGTGCGCA CATGCATTCC TAACAAAATT TATACATTTT 180

AGCCATGATA ATAATTCAAT ATCCGTACAT CTAAACATTT TTGAAAGTTT TCGTTTATTT 240

CTAGTAGACA TAATTTCTAC TAATCTAACA AGTTCACCAA AAGTAAGAAC TTCCACAGCT 300

AACCAAATAC TTGGaAAATT ATCTTTTTCT TTAnTCCTnn T 341

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

AAAGATGGAT TCTTCTTTAC TCACACCTAA AAGAnGTTTT TCTGAATCCT TTAGTAAGAA 60

AAACCGGTGA CTCTATCGTT AACAGAGAGT AGTTGTCAAC GCAACTACAT AAGGCTTATC 120

TTGTGAAAGA TAAGTAAATT GAGGTGGCAC CACGAATGCG ATTCGTnCTC TTGGCTCACA 180

GCCAAGAGGC TTTTTTG 197

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1548 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

CGGAATTGGA CTAnCCnATT GAAAACCATT TCTTTTTnTC CTAAAAAAAT CGAAGATGGG 60

TAATAAAAAG AATGGGTAAT CTGATAAAAA AACGAACTTT ATCTAATCGG ATAAGAAAGA 120

ATAATCGGTA TTGAAAAAAA GTTTAAAAAA AGTGAAAATA ATGATTGACC AATGCTTGAA 180

ATCTTGGTAT ATTATTTACA TGGTCGCAAG GCGAGTCACA CAGCTGAGCG ATTCAGAAGT 240

CAATAATTAA ATAACAATTC TTGATTTCAA ATCTCTCGAA AAAAGTTTGA AAAAACAACA 300

AAAAAGTTGT tGACaAATAm CAAACGAGAT GATAAGATwT AGAAGTTGTC ACAACAGACg 360

ACaACAACCG AGCAAAACAA CTTAAAAAAA CTTTTTTAAA AAAGTTCTTG ACATTCrAAy 420

GAAAGTTTGT TAwGaTATAA AAGTTGCTGC GAGGTAACGT AGACCTTTGA AAACTGAACA 480

AAGAATAGAC GAACCAAATG TGTAGGGCGT CTTGATTCAA TTCAAGACAA CAAACATTTT 540

TAACAAGCAA GCAATATGCT AGCAAACAAA TTGAGCTTAA CAATCGwAAG ATTGTTCTAA 600

CTTTTATTAT GAGAGTTTGA TCCTGGCTCA GGACGAACGC TGGCGGCGTG CCTAATACAT 660

GCAAGTCGAA CGCTTCTTTC CTCCCGAGTG CTTGCACTCA ATTGGAAAGA GGAGTGGCGG 720

ACGGGTGAGT AACACGTGGG TAACCTACCC ATCAGAGGGG GATAACACTT GGAAACAGGT 780

GCTAATACCG CATAACAGTT TATGCCGCAT GGCATAAGAG TGAAAGGCGC TTTCGGGTGT 840

CGyTGATGGA TGGACCCGCG GTGCATTAGC TAGTTGGTGA GGTAACGGCT CACCAAGGCC 900

ACGATGCATA GCCGACCTGA GAGGGTGATC GGCCACACTG GGACTGAGAC ACGGCCCAGA 960

CTCCTACGGG AGGCAGCAGT AGGGAATCTT CGGCAATGGA CGAAAGTCTG ACCGAGCAAC 1020

GCCGCGTGAG TGAAGAAGGT TTTCGGATCG TAAAACTCTG TTGTTAGAGA AGAACAAGGA 1080

CGTTAGTAAC TGAACGTCCC CTGACGGTAT CTAACCAGAA AGCCACGGCT AACTACGTGC 1140

CAGCAGCCGC GGTAATACGT AGGTGGCAAG CGTTGTCCGG ATTTATTGGG CGTAAAGCGA 1200

GCGCAGGCGG TTTCTTAAGT CTGATGTGAA AGCCCCCGGC TCAACCGGGG AGGGTCATTG 1260

GAAACTGGGA GACTTGAGTG CAGAAGAGGA GAGTGGAATT CCATGTGTAG CGGTGAAATG 1320

CGTAGATATA TGGAGGAACA CCAGTGGCGA AaGCGGCTCT CTGGTCTGTA ACTGACGCTG 1380

AAGCTCGAAA gcsTgGGGAG CnAACaGGAT TAGATACCCT GGTAGTCCAC GCCGTAAACG 1440

ATGAnTGCtA ArTGTTGGAA GGTTTCCGCC CTTCAGTGCT GCCAGCnAAA CGCCnTTAAG 1500

CACTCCGCCT GGGGGAGTAC GACCGCCAAG GTTGAAACCC CAAnGAAT 1548

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

AAAAAACAAC CATTGCCTAT GTAGAACAAC GTAGCGCCTT GGATCTTAGT TTCCCAATTA 60

GCGTTTTTGA AACGGTCTTG CTAGGAACCT ATCCAAACTT GGGGACTATT AAAACGCCCA 120

GGAAAGAAAG AaAAGCAAGC AGCCATGGCT GCATTAAAAA TGGTGCAATT AGAAGACTAT 180

GCGCAACGCC AGATTGGCGA ACTTTCTGGT GGCCAATTAC AACGTGTGTT TATCGCCCGT 240

GTTTTGGCCC AAGGTGCTGA GGTGATTTTT TTAGATGAAC CTTTCGTCGG CATTGATATG 300

TCTAGTGAAA AAGTGATTAT GGATATTCTT AAATCATTAA AAAATCAAGG TAAAATGATT 360

ATCATGTTCA CCATGATTGC ACAAAGTGTC CCACTATTTT GATGAATTAA TCGTTTGAAA 420

AAnCGGCTAA TTGCTGCnGG GCCTGGTGnA CCAAACATTA CTGCAGAACG CTCCCAAGAA 480

CATACC 486

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

CAGACGCGCA CAACCATTAA AACAGGTGAC GATTCTCTTT TATGTGACTG TGCCAGAAGC 60

CTTTCGnGAA CGGGCGACAC GGTGTTTGAA GCTTGTCTCC CCAAACTGTC CAGTGATTCA 120

ATCATTGGCT GAAAGAATTA CTGTCGAAGA AACAGTTGTA TTTAAAAAGT AAACCATTAG 180

AGACATTATC GTTACGAGCG CTTTTCCCTT TTTGGATGCC TCGTTTCTGG GAATGTCTTT 240

TnTTAGAGGA GCGTAGGGAA ATAGCTGTAG A 271

(2) INFORMATION FOR SEQ ID NO: 888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888:

GCAGGCAGAG GAGGCACCTG TAGGGGGTGG TGGGCTGGTG GCCCAGGAGA AGTCAGGAAG 60

GGAGCCCAGC TGGtGaCAAG AGAGCCCAGA GGTGCCTGGG GCTGAGTGTG AgAGCCCGGA 120

AGATTTCArC CATGCCTCAC AGCTCCGACA GCAGTGACTC CAGCTTCAGC CGCTCTCCTC 180

CCCCTGGCAA ACAGGACTCA TCTGATnGAT GTGAGAAAAT TCAnAGGAAG GAGAAAAATT 240

CGTATTGCCG CCCAGAAGAG CCGACAGAGG CAGACCACnG AAGGCCGAAA CCCTGCAACT 300

TGGAGAGCGA AGACCT 316

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889:

AGTCAAGACC ATAGCCTTCT AAATTGATTT CAGCAATATC AGCTAaGGGC GTGCGCTGCA 60

TCGATGTCTT CwTGTGTGCA AGTTGGTGAT nTAAATAATA ATGTATCAGA AATAATCGCT 120

GAGACCATCA TACCAGCAAT TTGAGCTGGA ATTGTCACGT TATTTTCTTT AAA 173

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890:

AAGAAGGCGG CAAAAAAGCG TTTGAATTAA TTAAAGAAGG TATGAACAAT GGTGCGAAAG 60

TTTTAGGCTT AGCAACAGGT AGTACACCAG nAACATTATA TAAAGArATG ACTGCAAtGA 120

tGTCGACTTT ACAGAAATGA CTTCTGTAAA CTTAGATGAA 160

(2) INFORMATION FOR SEQ ID NO: 891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891:

AGGTGTTATT TTAACATTAG TAATAATTGC AGCATTACTT ATTTTATCTA GTAGCTTAAA 60

GTTGCAAGTT TTATTGGTTA AGTTTGCCAA TCGTTGGTTT AAACGACCAA AACTAAGAGA 120

TTGGGTGGAT AATTGTAATT TACAAATCTA TTCCTTGCGG GCAGCTGTCC AAACAATTAC 180

ACAAGAyCGC TCAGCGTTGC TTCGAATCTT TTCATGGAAT GTATTTAAAT TATTATTTTG 240

GTACATTATT CCTTACATTG TTTTAGTAGA AAATCACCCG AATATTGATT TATTATTAGT 300

GATGTCCTTT ACCAGTTTTG CTGGTTATTC TTTCCAGGAn TTATTCCCGA CACCTGCTGG 360

CATTGGTCCA TTTGAAATTG TTTACTTATT GGTTGTTTAA ACC 403

(2) INFORMATION FOR SEQ ID NO: 892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892:

nAAATACGAA TTCGAGCCCG GTACCCAAnA AACAATTCAA ATTAATTGAT TGTCGCAGTG 60

AAGGAACTAC CAATTATTAC TCACTTTCTC ACGATACCAC CAAAATTGAG CAACTCCAAC 120

AACTATTGAC CCACATTACG TCGATTATGC CAGGGAGGAA GCAAGCATGA AAAAAATTCT 180

CGTGGTCCTC ACAAACGTCT CCCGTTATCA CGGCACCGrA raACCAACGG GsCTCTGGcT 240

AGGTGAAGCC ACGGAGTcGT GGAAGAAGTA ACCAAAGCAn GATTTTCAGT TGACTATGTT 300

AGTCCCCAAG GAGGCTATGT CCCTTTGGAT CCCCGGAGTA TGAAATATGT AGATTCATCC 360

ATTATGGCAG TTTATGAAAG TGCTGATTTT CAAGAACGAG CGCTAGCACA TTCCCTCTCT 420

CTTGAAGAAA TTGAGCCAGA TGAATACGCA GCAATTTACT TTACAGGAAG CCATGGCGTT 480

ATGTGGGGAC TTTCCTGAT 499

(2) INFORMATION FOR SEQ ID NO: 893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893:

CTGATGCGtA TTTTCTCCTT ACGCATCTGT GCGgTATTTC ACACCGCATA TGGTGCACTC 60

TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC CCGACACCCG CCAACACCCG 120

CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG 180

TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGACGAA 240

AGGGCCTCGT GATACGCCTA TTTTTATAkG TTAATgTCAT GATAATAATG GTTTCTTAGA 300

CGT 303

(2) INFORMATION FOR SEQ ID NO: 894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894:

ATCAATTACG CCTTATCAAG AAAAAGGACG TCCAAAGCAA CCAGAAAAAG CAACGrTTGA 60

ATTCAATCGA 70

(2) INFORMATION FOR SEQ ID NO: 895:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895:

GGACCATTTT AAGGAAATTA CCCGGGGGGG AAAATTTTAA AAAGCCCTTT TGGGGGCCGG 60

CCAAAACCCA AATTTTTAAG GAAAGGTTTT TGGGGGTTAA ATnTTTTAAA TTTGGGGGGG 120

GTTGGcaATT TTTTTtCCCC CAAAACCCAA TTTTTTTGGG GGTTCCCTTG GCCCCCGGAA 180

CCAAAAATTG GGGGCCTTAA CCGGGAAAAA ACCCCCAAGG AATTTTTTAA ATGGGTTT 238

(2) INFORMATION FOR SEQ ID NO: 896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 456 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896:

TTTCAAATAG TATAGTTTGA ATGCTCAAGT ATTTCAGCAA CTTTTATAAC ACAGGAGGTA 60

ATAAATATGG CTGTACCAGC GAGAAGAACA TCGAAAACAA AAAAAAGATT GCGTCGAACA 120

CATGAAAAAT TAAAATCACC TGAAATTTCG TTTGATGAGA ATCTTGGTGA TTATCGTAAA 180

AGTCATCATG TATCTTTAAA AGGCTATTAT GGTGGAAAAA AAGTGATGGA TAAAAAATAG 240

GAGGTAATAG TATTGAAGAA AATGAATATT ATTTATCCAC CACTTGTGGA ACAGAGCTTT 300

CAATTTTATC AAGATTATGA ACAAGAAAGA TATGATAAGT CTGAATTATA CAGAATAATG 360

GTTATGAAGA ATATTATTAA TGAAAATGGC ACTCCAACAG AAGAGGCTCT TAAAAAAGGA 420

TTAGTTAAAG CTTTTATGAA GATATGATTT ATCTTT 456

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897:

TCAAAAAGCG GGTTGGCTTT GAGCGGTCCA GTTGTGAGAC GATTAAACAA ACCTGAATGG 60

ATTCAATTGT ATTTAGATGA ATCAAGATTA GCATTGTTTG TAATTCCCTG TAAAGCGACG 120

GACGAAGGCG CTAGAAGTTG TGTAAATCCG AAGTCAAAAA AGAAAGCAGG GTATCGTAAA 180

AGCTGGTCAG GTAGCATTTT AGAGAAGGTA GCAAAAGCCA GCAAGATGGA TATTGAAAAT 240

CATCGTTATC ATGTTGAACC AGnAAGCGTT GAAGGCTATC CAACTGACTC TTGGTTTTGA 300

TTTAACGA 308

(2) INFORMATION FOR SEQ ID NO: 898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898:

CAAGTGCTTG GTACTTTAGC CACTGGTTCT GTTACCGGCA CGTTGCTTGG TCCTCTTTTG 60

GG 62

(2) INFORMATION FOR SEQ ID NO: 899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899:

TTCATTAATC ATATTCGTnG CTGCATTATT TTTATTCGTT ACATAGCTGT CAATTTGGGA 60

AAnGGnGTTA TTTTTTTGTG AATCAATTGA TAAGTTAATT GTATAAGTAA CATAAACGCA 120

CAAAGCAGCC ACCGTTAACA AAATAATACT TGTTAACAGT AGACTGTATT TTTGTACTAA 180

TCGATTTAAT AAATATTTTT TTTTAAACAG TTTTTTGAAG ATTCGCTTCA TTTTGTTCCA 240

ACTTTCCATC AATAAACTGG CGATTTTTGC GCGTGACATA GGCACACCAC ATCATAATTA 300

AGGGCAAACG AAGCAAATAG TAGCAGTnCT TTCATTTTCC AGTTAAAGCA ACGATACTAA 360

TTACACCGAA TAAGACTTTA AAAAATACAC CGAGGTTTAA AAAGATACTG ATAAATGGAA 420

GGCTCATTAA ATCAATAGGT TGAGATAAAA TAGCTCCCTC CTATAGTAGC CTATAAATGT 480

AAAA 484

(2) INFORMATION FOR SEQ ID NO: 900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900:

AAAGTCTCTT TTCAATCATT TAGTATACAC CTGAAAAGAA GAATAAACTA TCATTAATTA 60

AAAGAAAAAG TGAAAsAACT AGCGGATTTT TTGTTCAGCT GATTATCTTA AGAATTAGAA 120

AATGAGGTCG GGACAGAAGT GTTTAACTCC TAGAACCAAG TAGGTACTGT TTAACATCTA 180

n 181

(2) INFORMATION FOR SEQ ID NO: 901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901:

TTCCGTGAAA TACGGCGTTT GGACAGGCAA AGAATTAACA AATCAAGGGA GCTTTCCAAC 60

ACCTGGCTCT TGGGAAGAAA TGAAAGCGCA TTTATATTCG GTTTATGCAG ACAAAAGAAA 120

TGAGTCGATT AGTGGTGTTG CTTTTAGTTC ACCTGGAGTA GTTGACGAAA AAAGTCAACA 180

GATTTTAGGG ATTTCCGCCA TTCCATATAT TCATCATTTT AACATTTATG AAGAATTAGA 240

AGCGTTGTTT GGCTTACCAG TGACTATCGA AAATGATGCG AATTGTGCTG GTTTAGCTGA 300

GATATATGAA GGCGCGGCGA AAGGGAAAAA AGAAGTGCTT TTTGTCGTTA TTGGGACAGG 360

AATTGGCGGA CGATTTTTCG CAATGGTGAA TTGTACAAAG GCGCTCATTT ATATGGAGGC 420

GAGTTTGGAC TGAACTTTTT AAGTAATGGC CAAACaTTCA GTGAAATTGG CACAGCTGTC 480

AAAATGGCTC AgCGCTATTG TGAACGAATT GGAGTCGAAA AACAGGCGGT GACAGGAGAA 540

GAAGTTTTTG AACTGGCACA ACGAGGGGAT GAGATTGCTC GCGAAGAAGT CAATAATTTT 600

TATGATTATT TAACACAAGG ATTATTCGGC TTACAGTTTT CTTATGATCC TGAAATGATT 660

GTACTCGGAG GCGGTGTTTC TGCTAAAGAA GGCTTATTAG CAGAGATTAA TCGCCGGATG 720

CTAACGCATT TACAAACCTT TGAATTAAAA GATTTTGTTC CAGAAATCGT GACCTGCCAT 780

TATCAAAATG ATGCCAACTT GAnTGGCGCA CGCCCAACTT TCAAGCCAAA ACGATTGGGA 840

CTATA 845

(2) INFORMATION FOR SEQ ID NO: 902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902:

ATATCAAATG AGAAAAAGTT AAATTGATCA TCCTCTTCCG TCAACAATTC TTTCATCAAT 60

GTTGTTTTAA ATAATTCnGT TAAATAAAGT TCTGTTCCTA TTAATAAATA CACTGGAGCG 120

ATTTTTTGCT CTCGCACTTC TTTCAAAGCT TTTTGTAACT CCATTGGCTC GCTCCTTTTC 180

TCGTTTCTCT TGTTTATCCT ATCATGTTAC TTCTGGAAAT ACTAGTCTTG TTCkTTAACA 240

AATTTGGCTT TAGAAAGCCC TTGCCaAGGt AACCATTGAT AAGAAATCAT TCCTGGAAGA 300

TCGGTCCGAn AATAATnTAT GGTGTGCTCC 330

(2) INFORMATION FOR SEQ ID NO: 903:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903:

ATAAGGGGCG TTTTTCTAGT GCTTAGTCGA AAAAAATAGT TGATTCATAA GTTCATTGTC 60

TTATGAATCA ACTATTTGAT AACTTTCTCT CTTGCTTATT GCGCATTCAG GATCCACATG 120

AATCCGACAA AAACAAAGAA CAAGCCATAC ATAATTGGCG AAACTTCnTT CCCACGTTTT 180

GCCGCAATCA TTGTAATTGG ATAGAAGATA AAGCCTAAGG CAATCCCATC TGAAATGCTG 240

TATGTCAATG GCATTCCTAA CAAGATTAAG AAGGAA 276

(2) INFORMATION FOR SEQ ID NO: 904:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904:

CGCTTAAAAC TTCTCCTTCA ATAGGTGCAT AAATTTCACC ATTTTCTGGA ACTACTGCAT 60

AGCCATCkCC CATCATTTTT TGTGAGAAGG CAGGATCATT CACTTCACTG GTTGGGATAA 120

TGGG 124

(2) INFORMATION FOR SEQ ID NO: 905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905:

GGTTCCtCTA TGCCAACAAA TAACCCGGTT TGTGTCACAT AGCTAACCaT TCGATAGTTG 60

CCAGAAGCAA GCnCAATTCG GCTCATTGTA TCTTCAACAC GGTACATTTC TGCATCGCTT 120

TCTATCATAA TTTTACCAGC TAA 143

(2) INFORMATION FOR SEQ ID NO: 906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

TATCAAGAAA AGTCTAACAA AACTAGATAC AGAGAGATAG AACTAGGGGA AAAAAGTCCT 60

ACCATTGAAG AATTAATTTC TTTTACAGAT ACTTTAGGTA TAAGAtTATC TGAATTTCTG 120

TATCGGGGTG ACATTACACC TCTAGCAGCA TCTTACTATG GTAAAAGAAA AATTGAGGTT 180

GCTTCTTTAA TTAATAACTT CCCTGAATTA GAGAAACAAT TTCCTGAAAT ATACAAAGAT 240

CGCTTTAAGA ACCTACAGTG TTACACTTTA TTTACCTTAT GCTTAATAAT CTCTAAATCT 300

TTAAATAATT CCTTGTATAC TTTTAAAAAC AAAGATATTA GAGAACTTAA AAATTTTTAC 360

AAAAATAGAG AAGTAATATT AGGTGCTGGA CTATGCTATA CTAAGTCATC TTTACAGGGC 420

AGTTCCCAGA ATATTCGAnG GAACTGGATT TTCTAACGGG AAAACnCTTC CCATTAACCA 480

nC 482

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907:

TGGAGAACGT CTGTATCTCA CTGAGCAAAA ATAAACGGAA TAACCCTGAA CGGATAGAAT 60

TAAAAAAGTA TTCTCCAAAA TTGCGCAGAC GGGCAATTTT CAAAGAAGTG AAATAGGCAA 120

GTGGtAAAAA GGrGACaAAA TGGGGCC 147

(2) INFORMATION FOR SEQ ID NO: 908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908:

AAGGATGCCC TACGAGCTTT TGCnAAAGCT GGCGGACAAA ATGTAACTGA ACAACAAGAA 60

GAAGGCTTCT TTGATAAAAT GAAAGATGCG TTTGGCGGTA AGAAGAAAAA ATAAACCAAA 120

CGAGTCAGAG ACAAAAGCAG TTAGCTCCAA GTGTTCATCA CTCTCGAAGG CTAAATTGCA 180

ACGAGTAATT GTAGGTGCTG CTTTTGTTCA ACTGATTATT TTAAGATTTA GnGAGTGGG 239

(2) INFORMATION FOR SEQ ID NO: 909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909:

AAATAGAAGG ATGATTAGAG TTAGCTTGTT TATCACTAGC TTTACTATCC GAACTTTGTT 60

TAGAATTTGT 70

(2) INFORMATION FOR SEQ ID NO: 910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910:

CGCATTGCCA GCAGTAGAAA CGCTAGGAAA CTGCGaATGT TATCTGTTCT GATAAGACAG 60

GAACACTGAC ACAAAATA 78

(2) INFORMATION FOR SEQ ID NO: 911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 887 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911:

TCATGAAAGG GATTCGTTCC ACGGAACnTT CCGAaGaGGA atGCcTmCTT AGTCGATTTA 60

TCATTAmAAA TTAAAGAAGC GATTAAAAAT GGGTATTATC CGCAACTGTT AAAAAACAAA 120

TCTTTAGGAA TGATTTTCCA ACAATCTTCA ACTCGAACAC GAGTATCTTT TGAAACTGCA 180

ATGGAACAAT TAGGCGGACA TGGCGAATAT TTAGCACCTG GTCAAATTCA ATTAGGGGGA 240

CATGAAACGA TTGAAGATAC CAGCCGTGTA TTGTCACGTT TAGTAGATAT TTTGATGGCT 300

CGTGTGGAAC GTCACCATAG TATTGTTGAT TTAGCTAATT GTGCTACCAT CCCAGTCATT 360

AACGGTATGT CTGATTACAA TCATCCAACC CAAGAATTAG GTGATTTGTG TACCATGGTT 420

GAGCATTTAC CAGAAGGCAA AAAATTAGAA GATTGTAAAG TTGTCTTTGT CGGAGATGCG 480

ACACAAGTTT GTTTTTCTTT AGGATTAATC ACAACAAAAA TGGGCATGAA TTTTGTTCAC 540

TTCGGTCCAG AAGGCTTCCA ATTAAATGAA GAGCATCAAG CGAAATTAGC AAAAAATTGT 600

GAAGTTTCAG GCGGTAGCTT TTTGGTCACA GATGATGCAA GTTCTGTTGA AGGCGCTGAT 660

TTCTTGTACA CGGATGTTTG GTATGGCTTG TACGAAGCGG AATTATCTGA AGAAGAACGT 720

ATGAAGGTTT TCTATCCAAA ATATCAAGTG AATCAAGAAA TGATGGATCG GGCcAGGksC 780

CAATTGtAAA TyCATsCaCT GTTTaCCAGC AACmCGTGGG GAAGAAGTAm CTGATGaAGk 840

AATTGACGGT AAAAATTCTA TTTGTTTCGA TGAAGCAGAA AACCGTT 887

(2) INFORMATION FOR SEQ ID NO: 912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912:

GAACAGCATC CGTTACGATT TAAGACCCTG GnCGGTAACT ACTCGTCACT TTTTCTAACA 60

TTGACGAAAC GATAGACCAG GAnACACTAC CATGGCTAGT GATTAGCGAC AAAAATTCTT 120

ACGAACGATT TTTCTTTACa GCTCAaGAAA GCACGCmAGA ACAaGCTTTT GAGAAAATGT 180

TAAAaGAACT AGAAACCGAC CaTGACAGTA CACTAGAAGT TGTTCATAAC TGGTTATGCC 240

GACAAACAGA CGAAGCGCTT TTTCTAGGTA TTCTCAAAGA AGATAGAACG TTAAAAGGTG 300

CTATGACTTA CTGCATAGGA AAAGCCCAAG AACAATCCAA AGACCAATCA AGCGCCATGG 360

TGGCGGACGA AGTGGTTTTC AGTTGGATAA AAGAGTATTT CTTATTAGAG AAATTACCAG 420

AAACCAAAGC AGTTGGTAAA GTAACGACCA AAAAATCAGA AACAAAACCT GAAAGAAAAG 480

AGGTGGACGA ACAAATTGAT TTGTTCGAGT GCGTATGAAT AAAAAACACC AAAACCATTA 540

ACCCCACCCA AAGCCTTTTT TAACTGGTGT ACTGCACAAA TACCAACGTA TGAATGGCAA 600

AACAAAAAGG AGAcAATTCT TGCGAGTTCT CGCAAGAATT GCCCcaCCAT AAAAAAACGA 660

TTAACGAAAT ACTCACGATT ATCGTTTCCA ACGAAATTTT ACTCCTTTGT GATAAAGTnC 720

GACTTTTGCA AGCnCAGTTn TC 742

(2) INFORMATION FOR SEQ ID NO: 913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913:

TGAACTTTGT TTCGCTATCA AGTGAAGAAA GATATCGAGG AATGTTAGAT CCATTGCTAT 60

TTCTGCCAAG AGAAGAAGCT ATTCAAACCG CACGAAACGT GTTAGAAAAT TTTGGTGAAG 120

TTACGACAGA CAGTCACACT GCAGTGAkaA GAAGACGCTr ATTTTAGATT CTGTCAATGC 180

GGTGATGAAA GGTAAAGGaA AAAAaCACCT AACGAAArTA ATCGAGGTTA TTCGCGAAAA 240

AGACCCTAAA TTAGCCAATT TAATCTCTGG CCACAATGTT GGGTTAGGTA AAATTCTTTT 300

AGGGGAACGA TTACAGCGAA CCTATTCGCT TTGGAAAATC CAAATCCATG TCTTAnGTAC 360

CCAGGGGCTT TAAATCCCTA CACAGCGGAA ATTAGACAGC GGACGATTAA ACATGGAACC 420

AATCGCCGGC TGTCCATTAT GGnAGTTATT ATGGAAATGT C 461

(2) INFORMATION FOR SEQ ID NO: 914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914:

CTTACAAATC TATCGTTTAT CATCGCGGAA AACGGCTGAC TTTTTTGTTG CCTAAAATTT 60

TATTGTCAGG TACTATTTAA GTGTCTCCAT CCGAGACAAT CCATTTATTT TTTGTTGACC 120

AGCGGAAACT GGTTGGCTCC TAAATTTGGT AGATTCTTCT GCCTTTAATA CAATCAGCCA 180

ACCATTTTGG TTGGCTATTT TTTTATTTTT CAATTTATTC CAATGATTAC AATAAAAAGG 240

AGCGAAATAT GTCGCTCCTT TGACTTaTTA TTaATTTTAA AGATATTTTa CTTTCTTCTC 300

GTTcTACaAT AAAcTaTAAT ACCgCAGCTC CTAACAAAGC AAtATCAGAC CAGCaTAGCa 360

ACCATTATaT TTTcTCCGTA GTGGTAAgAA CyGGGcTTgC aCTGTTCGcT ACGAGATCgA 420

AGGTAAGCTG gCTTGGcGTC TTGTTAGAAA gAAcGTGGgA CAGGTTGcGC GAGAGCCTGC 480

ACACGTGCTG TTGCCCGTCA GGTGTGCTTG CACGnCTnAC C 521

(2) INFORMATION FOR SEQ ID NO: 915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915:

TCCTTGTCAC ACAGCGTTTA TGGnTTATGG TTAAGGnGGT TAAAAAGGAC TACTGTCTTA 60

ymAATTTGCG TTCCGGCCAA mCCAAAaaGA aGCmCmGrAA AAAGTTTTAG AATTTTTTGG 120

TATGGATACG AmCCCAGCAA ATATTCaGTT AATTAATGAA CTAAAATCAG GAACTTGTTT 180

ATTCCAAGAC CATCGAGGGC GTAgcCAnCC TATTGCAATT GATGTTTTAT TCGATAGTTG 240

GTTAATGGCC ATTTCGTCTA CTAATAAAGA GGATGAAGCT ACTCAAaTGG CGTTGGCAaT 300

GGAACAAGGA TCATAAAAAA GGAGAAGTGA GCATGAAAAA AGTACTACCT TTTATTGCCT 360

TAGTCGGCTT GTTATTGTTG TCaGGTTGTG GAmCAGATAT GAAAAAGATA TTGACTGCCG 420

ATGGTGGTAA ATGGGAmCTA GAAAATAAAA GTCCAACTAC TACtTACACy TTTTTTGaTG 480

ATGAAmCTTT TcCGAGGTAT AATTCCAAAA ATTAGTGATA GTnGGACCGT ACCCCTTACG 540

TGGAAAATAA TAAAAAACTC nCTTTGGnTA TAAAnA 576

(2) INFORMATION FOR SEQ ID NO: 916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916:

CGTCTGCAAC TTTGGTTTCG CTTTTCTAAA ACAACAGCTC GATTCTGAAT AACTCATTGA 60

TTGTTGCCAA TTGATCTTTT GTTTGTTGAA GGTTTGTTTC TGCCGCCGCA GTTTGTCGTA 120

CTTTTTCTTC ATAGTTTGTC GTACTCTTAG TCGCAACTGC TTGAAGATTA GCCAATGTCG 180

CTTTATGAAC AGATAGTTCT TTTTCTGCTG TTGCTTGTGT TGTTTTGGCT GTATTTAAGG 240

CTTGCTGACT TGCACTTCTT GCTTGTTGTG CGTCTGATTC TGCTTGTTGT GCGGTAGCTA 300

ATTTTTCTTG ATTGGTCGCT ACTTCTTTTT GAAGGGTTTC TTTACTCTTA AAGACTGGTG 360

CAGTGCCTTC TTCATAGGTA TTTGCTTCAA CTAATTTTGT TTGATTATAG CTAATGATAT 420

GGATTTTTGC TGAAATATCA TTTAAATCTC CTGAAATAGA AACTGCCATG TTTGTTTCAT 480

TTGCATCTAA TAAAGAATCT AAATGGGAAT AGCCAGAATG TCCATCGTTC ATCAACATGC 540

TTACAAGTGC ATTtCGAGCA GCTTTTTCAA AGTCATACAT AGAAACTTTA CCtTCtgTGT 600

CGTAAATCTT CCCaTACTTA GGGtTTCCAT AAAAgTTTnG TCCaGGGaAT TCCTTtAAAA 660

ACaATTTcCT TTgcCGGCCA CCGAATTGGA TCCGCCAATT TACGGGCCCA nGGATTCCCA 720

AAATTCCCTT TGGGGGGATT AAnCCCAAAA 750

(2) INFORMATION FOR SEQ ID NO: 917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917:

ATTCTGGnTT GGnATGTTAC CATTGCTTGG TTGCGCTGAT TGTGAAATGC TTAAAAATGA 60

CAAGnAAAAT ACCGTCTACT TGACCAAGCA CGGTTATTTT TAAATnATAA ATTGGTCACC 120

GTCTTAAACG GCTCTACATC AGAGAGATAT GTTGGAAGCA TATCTCTCTT ATCTTnATCA 180

TTATAGCACA ACAACCCTAA AAAGACCATC AATAAAAAAT GCCTGAGCCT CCTATTTCAA 240

GGCTCGGGCA TTTTTATTTT AGGGACCAGT CACCAAATTC CAAGTGACCG CAGCATTGTA 300

CTGTTGTCCT TTGGTTCCTT GGTTGGCTGG TACTTCTAAT TTAATGTTCT CAAACGTAAA 360

ATCCAGTTGG TAGACGTCAC TACCTGTGAA CTGTTGGTTT GCGACAACAC TGGTTGCCAC 420

ATTATTCGCC GTTAAGCTCA AAGAACTAGT CTTACCAACT GCTTTGATTT GTTCGGTTGC 480

TTCGTTATAA TTTGTAAAAC TTGAAACATT CGCTGGACCT AACAATAAAC GAGTCGCTGT 540

TGGCAGACTA TCTGTGGTTG CTTTCGGTTG AGATAGTTGC GCTGTCATCT GCCAATTCGG 600

TTGATTTTTC TTAATTCGCA AGTAAGGGAT TGCGTGTACC ATTTTCGTAG TAATCGGCCG 660

CTTTTTTCAA GCCTGATTGT TGCGTTTTAC TAGCAATATT CATTTTCCAA AATCAAAGGT 720

TGGGCACGCT GATnAAGCCT TCnGTTGGGT GTAATGGTCC nTGGGGTTGT AACCGTCAGA 780

CGTAACGCAT CGGGGCGGCT CATGGTCGGC AAATTCCCGT AACACAAG 828

(2) INFORMATION FOR SEQ ID NO: 918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918:

AGTTATCTTA ACGACTAATT TTGCAGATAA AATTGGTTAT TATACCATTG AAAATACAGC 60

GCAAGAAGGT AGTCTAGCAA TAATCAAAGT AGACAAAGAT TCAAGAAAAC GTCTAGCAGG 120

TGCAGAGTTC AAATGGCGTG ATACGGTGAC AGGAAAAGAA GGAACAGTTG TAGCTGACAA 180

AAACGGACAA GCCCTGATAA CGAATTTGCC AGTCAATCGT GTATACGAAA TTACAGAAAT 240

TAAAGCACCA AACGGCTATA TCTTAAATAA CAAGACTTAC CGAGTTATCT TAACGACTAA 300

TTTTGCTGaT AAAATTGGTT ATTATACCAT TGaAAATACA GCGCAAAArG GTAGTCTAGC 360

AATAATCcAA GTAGACCAAG tTCagAAAaC GTCTAGCaGG TGCAGAGTTC CAaTGGCGTG 420

ATACGGTGAC aGGaAAGagG AACAGTTGTA GCTGACAAAA CGGACAGnCC TGTTACGATT 480

GCCAGTCATC GGTATCG 497

(2) INFORMATION FOR SEQ ID NO: 919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919:

TGATCTGCCA CAGTTTGCGC TTGCTTCAAT GCTTCACTGT AGACTTTCCA ACTGCTTGCG 60

GTGTAGTCTT TTTCTTGGTG TTTCTCGTTT TCTTTGATGA TTTTCAACAA GTTGGTTTTA 120

TCTACTTCTT TAGTTGGCAC TTTTACCAAT TGCTTCACTG CCGAACGTAA CTCTGTTTCT 180

GCTTGGTCTA CTTCTGCTTG CGTTGCTGTT GTTTGATCTG CCACAGTTTG TGCTTGTTTC 240

AATGCTTCGC TGTAGACTTT CCAGCTGCTT GCGGTGTAGT CTTTTTCTTG GTGTTTCTCG 300

TTTTCTTTGA TGATTTTCAA CAAGTTGGTT TTATCTACTT CTTTAGTTGG CACTTTTACC 360

AATTGCTTCA CCGCCGAACG TAGTTTTGCT TCTGCTTGGT CTACTTCTGC TTGTGTCGCT 420

GTTGTTTGAT CTGCCACAGT TTGTGCTTGT TTCAATGcTT CGCTGTAGAC TTTCCAGCTG 480

CTTGCGGTGT AGTCTTTTTC TTGGTGTTTC TCGTTTTCTT TGATGATTTT CAACAAGTTG 540

GTTTTATCTA CTTCTTTAGT TGGCACTTTT ACCAATTGCT TCACTGCCGA ACGTAACTCT 600

GTTTCTGCTT GGTCTACTTC TGCTTGCGTT GCTGTTGTTT GATCTGCCAC AGTTTGTGCy 660

TGTTTCAATG cTTCGCTGTA GACTTTCCAG CkGCTTGCGG TGTAGTCcTT TtCcTGGTGT 720

CyTTtTGTTC CTGAAATTAA TTTTCTAACG CTCTTCGGTA ACTTCAGGAG TGGTTTAACn 780

ATGAATGAAC GCGAGC 796

(2) INFORMATION FOR SEQ ID NO: 920:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920:

AACTTCAGAA AATATTAACA GGnAATAGCC GAATnAAGTA ACGTCTACCA AGAAGAAGGA 60

CTCTACCGTT CACAnGCGTG TTCAAATCCT ATTGTTCCGA GGTCATTACT TTACATTCGG 120

CTTTTCTTTA TAATTCTGGT TCACGATTGG CATCTTTGGA ATAAACGTAC ATTAGCGGTT 180

CTTCACGACC AACCGCATAG GCTGCTTGTG GCACATAGGC ACTCATGAAA ATATAGTCCC 240

CTTTTTCCAC TGGATACCAT TCGTTGTCCA AATTGTACAT CCCTTGGCCA CTAATTAAAT 300

ACGCGCCATG CTCTTGGACA TGCGTTTCAA TGTAGGCATG ACTAGCACCT GGTTCAAAAG 360

ATAAGATATG CATATTCATA TCAAAGTCAA ACTCTTTCGG CAATAAACTC CAAAGTAACA 420

CGTCTGTCAT cCTTCATATT CTTCGGGTTG TTGGkCaTGA ATTGACCCAA CCACTTTaTA 480

AGGtTGATGG cCTGCCAACG GGCTGAnAAG CGGnTTTTAA TAT 523

(2) INFORMATION FOR SEQ ID NO: 921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921:

TTTCATCAAA CGACGTTCTT CATGTTTAGT CATTTTTTGT TTTCGTTCTT TTTTATCGGG 60

AATTTTTTCA GTAATCGAAC AGAATTTACA TTTGAAAGAA CGACCATTTT TTCCTTCTAT 120

GATGACCATT TTTTTGGCTT CTGGCCGCCC GACTAACGGT ATGCGGCCCT TAGCAGATGA 180

ATTGGAGATG GCTCATTATA ATGGACACTT ACTTTCCTAT AACGGCGCTT GTGTCACCCA 240

TCACGGcAGT CAGCAACAAC TATTTAATCA GACAATTTCA AAGTCATTGa GTCAACAAAT 300

TTTAGAGCAT TTGAAACAAT TTGaCGTAAT yCCAAkGATT AATGATGrAA CATTaTGTAT 360

GTCAATGATG TTTTTCATAA CACCTTACAT TTAGAGACTG GTGATTTTAA TATTATTGAA 420

TATGAAn 427

(2) INFORMATION FOR SEQ ID NO: 922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922:

TTGATTTTTA nGGATnGGTT CCGGTGGCAT AAGGACAACT AGGTCTTTCA CTGGCAATCG 60

TCAATGGCCT ATTGGnAAAG ATGCCCCTAT CTGTATTATC TGAAAAATCA nACAATCATA 120

ACCAATTAGA AAGGTGGTTA TTATGTATAA CTTATTAACC AAACAGGAAA TTCAGTTACT 180

TTCCCTAATT GAATACTTGT ATGACAGTAA AGAAAAAGTC CCCATGCAAG TACTCCGACG 240

AAAATATGAA TTTTCCCATT aCAATATCAA CAATTTATTG AATCAATTAA CTTTGTTAAT 300

TTCTCGAGTC AATACACATG AAAATGTACA TATTCGTATT ATTAATAATC AACAGTCCAT 360

AGAATTAGTC GCCGATGAAA ATATCCCGAT TGAGTTAATG AAAGAAGCTG TTGTCCGCGG 420

GTCACTAACC TATATGTTAG CCCTGGATTT ACTTTTAAAA CGCTACACTT CAGCCAAAGA 480

TTTTTGTGAA GAGCACTTTA TTAACTTTTC nATTTTTAAA CAAGTCAGTG GCCGGTTAAA 540

TAATCCATCC AGCTAGGATT AATTGGGTAA TTAAACCTAA AAAGGnGGGG AAAAATTTGn 600

GGGAACGAGG AAGGATTTCG CAGGTTnCTT TAATCCCTAT CCTCCATTCC 650

(2) INFORMATION FOR SEQ ID NO: 923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923:

GGGCCCCCAG TTCCCCGTAC TTTAACGGAA TCATCAGTAG GTCGCCTCTG TCGTGTTGGA 60

CTnCTnGCTT TTCGCCACTr rTTTTAAATT GACTCCCAGA GAAATACACG aaCACCAGGA 120

AaTTTCATTT AATTGTCCTC TGaTAATTTT AGGTAAATAA TAGACAAcTT GTAAAAAACT 180

AACTTAGGTA AAATGATAAT GTGGACTTCG CCGTCATCTG GCGTAcATTG GCATCGAAAT 240

TGGTAAAGCC ACCAGCAGAA TTCGTCATGG TCATCGTTAA TAATTGGGCT TTGCCATGCC 300

AACGTCTTTC ATCGCCATCA ATTTTTAGTT TGTATTTTTT CTTTTTCATT AATAAGCGGA 360

AAAATTGCTT TGTAAAGGCT AAAGGACCAT ATkTTTGTTT CTCCTGTTGG GTCACATTTG 420

CTGCTGTATC TGCTAATAGT CCAATCGTTA AGGTCGAAAT CATCACATCT TGATTTACCA 480

TCCCAAAGTC AACT 494

(2) INFORMATION FOR SEQ ID NO: 924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924:

TTTGGCTGTA TnTAAAGGCT TGGCTGACTT GCACTTCTTG CTTGTTGTGC GTCTGATTCT 60

GCTTGTTGTG CGGTAcTAAT TTTTCTkGAT TGGTCGCTAC TTCTTTTTGA AGGGTTTCTT 120

TACTCTTAAA GACTGGTGCA GTGCCTTCTT CATAGGTATT TGCTTCAACT AATTTTGTTT 180

GATTATAGCT AATGATATGG ATTTTTGCTG AAATATCATT TAAATCTCCT GAAATAGAAA 240

CTGCCATGTT TGTTTCATTT GCATCTAATA AAGAATCTAA ATGGGAATAG CCAGAATGTC 300

CATCGTTCAT CAACATGcTT ACAAGTGcAT TTCGAGCAGC TTTTTCAAAG TCATACATAG 360

AAACTTTACC TTCTTGTGTC GTAAATCTTC CCATACTTAG GTTTTCATAA AAGTTTTGTC 420

CAGGGAATTC TTTAAAACCA TTTTCTTTTG CTGCACGATT GATCGCATTT ACGTCATGAT 480

CAAA 484

(2) INFORMATION FOR SEQ ID NO: 925:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925:

GCAACnTATT TnACACCTTG GATTAnCAGG TTGGCCCATG TGTTCTCTAC CGTCAGATAA 60

TCAAATATGG AACCCCnCGG CAATCGCTCT TCTTGGCTAC ATCCGAATCA TTTTAAAAAT 120

ACCTGCACAA CTAAGTTATA TATTTTGTCC GCTTTAAATG GTTTTGAAAA CAAACCGATA 180

TCAAAAACAG TTACTCGCAA ACTGTCTGAT TTATCTTACA AAGATTTATA TTATCAAGAG 240

ATGAAACTTT TAAAAATTAT TCGTTAATAT ACTTATAGTG GTCTATCAAA AAAAGAATAT 300

TTATTCCGTT ACATAAACTT TGAAAAAATG AAAAATAAGA CCTTCAACAT ACTCTATCCT 360

GTTGAAGGCC tTCTCTCTTA TTTAACCCTT TAATTTTTAC GACCtCTAAA TAATCATACC 420

CAAAATGTGC ATACGCAATG GCGTGCAATT CGTCCTCGTG GGTGTCGTTT AATGAAnCCT 480

TTTTGAATAA GAAnGGGTCA TACATACCTC CACCGTTCGG TTCTCACGAT ATTACAGCAA 540

GGACTAACCA CGGACGCGCG ATAATCATAT GTTCACATTT GTCGCATATC AGCTGAGACA 600

CTGCGAnGTA CnTTGCGCAC GCGCGTTGCA CGA 633

(2) INFORMATION FOR SEQ ID NO: 926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926:

TAGTTTTAGC AGCAACGTCG GTCAGCATTT CAGTAGAAGT ATTAAGAGAG TTGAATGTTT 60

TAAGTAGTAA AGAAGGTGCA CGnnTTCTTG GGGCTTCCGT CGTTGACGAT ATCGTGGTCG 120

TGATTATTTT AAGTGTCGCT GTCGGCATGA TTGGTGCAAG TACAGGCGGC AATACAGAAG 180

TCAGCTTTAT TGTTAAGTTA ATTGAACAAG GCTTATTCTT TATTGGGATw TTCTTTTTGG 240

TCCGCTTTAT TGCTCCCTAT kTACTACGTT TAAGTCAAAA AATGAACATT GGGTCGTCTG 300

TTATTATCAT GTCATTGATT ATCTGTTTGG GCATGGCTTA TTTGGCTGAT TTAGTTGGTT 360

TAAGTTCTGT CGTAGGTGCT TTTTTTGCAG GGATTGCTGT GGGACAAACG GATGCAAAAA 420

CAGAAATTGa TTTCAATATT GAAGCTATTG GCTATGCCGT GtTTAATCCC gyCTyCTTgc 480

CAGCATgGCy TAtCAGTGAC ATTwACACGT AnGAAAGGAT TAnCTTTTAT TTGGGAATGA 540

CGATATGGCG AATTTAACCG AAAnTA 566

(2) INFORMATION FOR SEQ ID NO: 927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927:

TTTTTGTTGG CGTGATTGGG TATGCCAGTT ATCTTTTTAC CCAAAAGTTA TTCCAAGTTC 60

CTTACCTCGA TTCATTCGCA GCCGCTTTTG TCATTGGTTT GTTGGCCTAT TTGGCTGTGC 120

ATTTTCACTT AGCGGTCAAC ATCGATAATA TCATTATTGG TGCGGTAATG CCGTTAGTTC 180

CAGGTGTGGC GATTACGAAC TCTTTTCGCG ACATTTTAGC GGGCCACCTC ATCAGCGGGA 240

CGGCGCGAGG GACAGAAGCT ATTTTTATTG CTGGGTCTGT TGGCCTGGGa ATTGCCTTGA 300

tTTTTAAATT ATTTaTGTAA GGAGTGTTCA AATGGAcTAA TTTTyCATCT cyCTTTAGTT 360

TTTTAGCGAC TGTGACGTTg GaTTATTACG AcATcCTCGT AAAcAcTGGg GCTGgGCATA 420

CTGGCATGAC AGGCTGaTGA tTATAwGcTA ACGcaACtTg wgCaGCaACt TGCAACTTTA 480

GGACGCCGGA 490

(2) INFORMATION FOR SEQ ID NO: 928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928:

ACGCTTTTTC TGGTGTGACG GCcAGTTGCG GAAACCGTGA CGATTGAAAG TAGTCCGACC 60

GCCGAAAGTA GTGCCAAGGA AGAGACGCAA GCAAGTAGCG TGAAGGAAGA AACAACGAAA 120

GCCAGTACGG AAAATAGTCA AGTAACAACT GACACGAGTC AGGAAGAAGC AACGAAAGAA 180

GCGGAGAAAG AAGAACCGCA AGCAGAAGTG GAACAAGCAG AAACACCAAT CATTCCTAAA 240

CCAAAAAAAA TCAATATGAG GCACTTATTC ATTTTCTGCA GAACTTATCA GTTTGGATTG 300

TGATGATCAG GTCATTATAA TCCAGTATTT ACCATTACGT TACTATGCCA AGGTCATGGA 360

GGCAGATGGT ATAATCGAAG GGnCTAGTTG GTCAAGGATG CTTCACCGTG GAACTTAAGG 420

ATGTATATGC CACACTCTGn GTATGCnCCA GnCGCATTGA 460

(2) INFORMATION FOR SEQ ID NO: 929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929:

CCTATGTAGG CTGCGATATT CAAAGCTCCG CAGCTTGCAT GGACAAATCA CTGGCCTACA 60

TTCTTACnAA AAAATGCGGG CATCGCCGTC CCCGAATTTC GGTTTTCACA ACGCGGCCTT 120

CCATCATGAT ATGAACAACA TCTGGCGTGA TATAGTTCAA TAAGCGTTGA TAAtGGGkAA 180

TAAtTAACGC ACCAAAGTTC TCGCCGCGCA TTTCATTAAC CCCTTTAGAA ACTACTTTTA 240

ACGCATCGAT ATCTAAGCCT GAATCAATTT CATCTAAAAT GGCAAACGTT GGCTCTAACA 300

TCAATAATTG TAAAATTTCA TTTCGTTTTT TCTCGCCGCC AGAAAAACCT TCGTTTAAGT 360

AACGCTCAGC CATTTCTTCA GGCATATTTA ACGG 394

(2) INFORMATION FOR SEQ ID NO: 930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930:

CTCCAGCATT GTTGGTCATT TTTTCTAATT CTnCATAGGA GTGTTCTGCA TCACTAAATT 60

TAACCATTTC TACTTTATGA AACTGGTGTA AACGAATTAA TCCTCGGGTA TCACGACCTG 120

CACTACCCGC TTCCGAGCGA AAAGAAGGAC TTAAAGCAGT AAAATAAATC GGTAACTCTT 180

GCGCATCTAA AATTTCATTA TTATAGTAGT TAGTTAACGG GACTTCCGCT GTGGGGATCA 240

GCGTCAAATC ACTTTCTGCA ACTTGGAAAA CATCTTCTTT GAACTTAGGA AACTGACCGG 300

TGCCAAACAT TGCTTTGCTA TTGACCAAAT AAGGAGGAAT CACTTCGGTA TAACCATGTT 360

CATTAACATG TTGATCTAAC ATAAAATTAT AGACCGCTCG TTCTAAACGA GCCCCTAAGC 420

CTTTGTAATA AAGAAAACGG CTACCAGATA CTTTCGCGCC TCTTTCAAAA TCTAAAATTC 480

CTAAGGCTTC ACCGATTTCC CAATGTGGTT TTGGTTCAAA TGAAAAAGTT TTCGGCGTAC 540

TCCACCGCCG AACTTCTACG TTGGCGGCTT CGTCTGCGCC AACAGGTACG CTCTCATGAG 600

GTAAGTTAGG CAAACGTTCT GCAATGGCTG TGCATTGTTC TTGCAAATGA ACAACTTCTT 660

GATCTAAAAC TTTAATTTGC TCGCTAACTT CTTGCATATT TAGCAATTGT TGTGAAGCAT 720

CTTTTTGTGC ACGCTTTAAT TGTGCAATTT CTCCTGACAC CTGATTACGG TGTTTTTTCA 780

GTTCTTCAAC TTTAACAAGT AACGCTCTCC GTCCTTCATC TAAAGCCAAA AAGCGTAATA 840

AAACTTCCTC GTCCACACCA CGTGTTTTTA ACTTTTTCTG TACCACTTCT ACATTTTGGC 900

GAATTTTTTT CATATCCAGC ATCTTATTTC CCTCTTCATG ATTAAATTTT AAACAATGGT 960

GAATTTTACT TTTTCAAAAA TTTCATTCTT CATTCGTTGG CCAGTCGCTG TGCCAGCTAA 1020

GCCACCTAAA CCCGTTTCTC TCAATTCTCG TGGTAATTGA CGGCCGACTT TATTCATGGC 1080

TTCCACCACT TCATCTGCTG GTATTTTATT TACAATTCCA GCTAAAGCCA TATCTGCAGC 1140

GATTAACGCA TTGCCTGCAC CTACTGTATT TCGTTTGACA CAAGGAATTT CGACTAACCC 1200

AGCCACTGGG TCACAAACTA AACCTAATAA ATTCCCTAAA GCCATAGCAA AAGCTTCAGA 1260

AGATTGGCGT GGTGTTCCGC CAGCCGCTTC AACAGCTGCA GCGGCGGCCA TCGCTGA 1317

(2) INFORMATION FOR SEQ ID NO: 931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931:

CCCTTGTCAC ACAAGCGTTT ATGGTTTATG ATAAAGTAGT AAAAAAGAAC TACTGTCTTA 60

CAAATTTGCG TTCCGGCCAA ACCAAAAAGA AGCACAGAAA AAAGTTTTAG AATTTTTTGG 120

TATGGATACG AACCCAGCAA ATATTCAGTT AATTAATGAA CTAAAATCAG GAACTTGTTT 180

ATTCCAAGAC CATCGAGGGC GTAGCCAACC TATTGCAATT GATGTTTTAT TCGATAGTTG 240

GTTAATGGCC ATTTCGTCTA CTAATAAAGA GGATGAAGCT ACTCAAATGG CGTTGGCAAT 300

GGAACAAGGA TCATAAAAAA GGAGAAGTGA GCATGAAAAA AGTACTACCT TTTATTGCCT 360

TAGTCGGCTT GTTATTGTTG TCAGGTTGTG GAACAGATAT GAAAAAGATA TTGACTGCCG 420

ATGGTGGTAA ATGGGAACTA GAAAATAAAA GTCCAACTAC TACTTACACT TTTTTTGATG 480

ATGAAACTTT TTCGAGGTAT AATTCAAAAA TTAGTGATAG TGGAACGTAC TCTTACGATG 540

AAAATAATAA AAAACTCACT TTGGATATAA AAAATAAAGA ACAATTAATA ATGGAAAATG 600

TTGAATATAA AGACGGTAAA TTAAAAGGTG AAATTGGAGG CGAGAAGGAC TCTGATAAAA 660

AATnGAATAA GAGGTGTCTT TGAATAGAAA TCCTGGTAAG CGTCTnCTAT TTTTGnGGCG 720

TTTT 724

(2) INFORMATION FOR SEQ ID NO: 932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932:

AAGGTACCTC CAGTAGTTGT ATTGCCACTT GCCAATAATT GTTCACTGCT ATTGTAAAAT 60

TGAACCGTGA CATTTGGATC AGCAGTTCCA GTGACTGTAT AGCCATTGGC TTTGTTTCCT 120

TCAACCTTCG TAATAGTTGG CGCCGCTAAA ACAACATCCG CTGGAATAAC GGCTGTAGCT 180

GGTTGACTTT CATTACCTGC GCCATCTTTG CTAATAATCG TAaTCGTwTC TCCTGGTGTC 240

ACTACGcCAG CtGGTAGAGT CACCGTATAT TGGCCGGTTT CGTTAGCAGT TGTAGCAGCA 300

ATGATGGTTC CGTCTGCGTC ACGGACATCA ATAGTGGTTT Tn 342

(2) INFORMATION FOR SEQ ID NO: 933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933:

AAATTGCCAG ACCTACTTTT TATGGAGACG ACTTTGGAAA TTATTAAAAC GACGAAATAA 60

CTTCATTCAG GATTTCATGC CAAAAGGGAT TACGAAAGCC TATGGTATTT CCTGTTAGCC 120

AAAGATTTAG GAATCCGTGG CAGAAGAAAT CATGACCCTA GGGACGAAGA AAACGATTTA 180

CCGATGATCG AATACGCGGC TAGTGTCGCC AGGCAAATGC GATTCCATaG TTAAAGAAGC 240

CGCAGATGTC GTCACAGACA CGAATGACCA GnGGCGTTGC CAAAnCGGTC GAAAAATATA 300

TTTTAACGCC GTTGGAAAGG AGGCCATTAA GAnGGGGATT T 341

(2) INFORMATION FOR SEQ ID NO: 934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934:

GACTTAATGC TATTGAAGCC CGATGGATGG TGnGTAAGGT CnCGAAGCTn GnGGAATCAT 60

AAAAGTTAAT AAGCCTGGTT TTCCTAATGG GGGCGTCACT TAGGATAGTT TTCTTCCATT 120

CTCCAATCCT GCCGGATAAG AAGGTATTCG CTTCCTCCTT TGGAGTTAGC TTGATAAACA 180

GCCCTTAAAG TCATCCACAG ATTTCTTTTC GGTCTTTGAC ACGTACTTTA TGAGCGATAT 240

TACGAGATAC ATGGATACAA CAATGCTGAT ATTTTGCTTT AGGATAAATT TGATGGATAG 300

TATCTTTCAT GCCTTTTAAG CCGTCCGTAA TAAAAAGCAA GACTTCTTGa ACTCCTCTGG 360

AGTTAATATC CTGTAGCAGC TCATTCCAAA CGTATGTgAT TCAGTTGGAG CAATCGCATA 420

ACTCAGTACT yCTTaGTGCC GTCCTCCCCG AAAACCATnG GCCAAAATAA ACCGCTCCTT 480

GGGATAACGG TTTGACGTTT nAGTGGAATG nAAGAAGCG 519

(2) INFORMATION FOR SEQ ID NO: 935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935:

CATATGGGGC TATACGTCAC GATTGGCATT GGAGATAACC CATTGTTAGC CAAGCTGGCC 60

CTAGATAACG AAGCAAAAAA TACACCAGGT TTTGTTGCAG AaTGGCGATA CGAAAACGTA 120

GAAGAAAAAG TTTGGACGAT CTCCCCTATC ACTGAATTTT GCGGGATTGG cmAGCGTATG 180

GCArCTCGTT TAAAGATGTC aGGAATTGAr TCgaTTnATG ATTTAGCACA TGCAGATCCG 240

TACATTTnAA AACAACGTTT TGGTGTCATG GGTTTACAGC TGTACGCTCA TtCTTGGGGG 300

ATTGATCGAa GTTTTTaGGA GGAAAAAAGA CAAGTTGCTA AAGAAAAGTC nTTTGGAAAT 360

AGTCCAAGTA TTACCnTAGA GATTACCGCA 390

(2) INFORMATION FOR SEQ ID NO: 936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936:

CTATTAAAAA ACGTCAAGAA GAAGCAAGGA AACATGGTAA AGCAGAAACT GGCTTAAAAC 60

AACGGCCATT AAATAAAGAA CAAGAAAAAC GTATGCnACT ACGCCGTGAA TTGAAGCCAA 120

GACCTCAACA TAAAGCGCCA AATGCTATCG AAAAAGCACA AGAAGGATTA AGACAAGCGC 180

ACGAAAAAGG ACGTATGCAA GAACAGAAAT CTGAAGAACA ACTCAAACGG CAGCAACATG 240

AATCAGCTCG CCAAAAAGAA TATGAAAAAG ATCGATTGAA AAAACAGGAA TCACTTAAAA 300

AAATTAATGA TCAAAGCGAC GAATCAACCA tTTAACAGCT TraGAAtCaA ATCGGCGTAC 360

TGGACAGCGA GTTAAAAACG CGAACAGGnC TTCAACACTT TTGAACGCCA GGGGGAAAGn 420

TCTTCACCAC AATTAnCCAA AGT 443

(2) INFORMATION FOR SEQ ID NO: 937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937:

AGGAATCACT TAAAAAAATT AATGATCAAA GCGACGAATC AACCAATTTA ACAGCTTTAA 60

GAAATCAAAA TCGGTCTGGA CAGCGATAAA GGGGGCGAAA CAGGTCATCA AACACTTATG 120

AAACGACAAG GAGAAAAAGT ACTTCAACCA ACAAATAAAC CAAAAGATAT GAAAAArCAA 180

GTGGTTGnTC GTAGTCCAAG ACGAACAGGA CAACCAACGA CTCGTCAA 228

(2) INFORMATION FOR SEQ ID NO: 938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938:

AAGATGTTTA GTTGTAGAAA ATAAACAGGT TTGGGAAGAA AGTGGGACAG GAGTATTTAG 60

CTTCAAGAAT GAAGAAGCTA CTCCTGTCCC GCCGTTTATT TTAGGATTGG GaCGGATGTT 120

CTAAGTTCTT CCTAAAtCGT TTCTGAAAAA AtGAAgGAGT GAGGGAGAAG ATGACAGrAC 180

CAAtGTGgAa TtGAGAaGTt AGGATtaGAA aGCGCATCCt GAaGGgCcGG TtATTTtAAa 240

CcAAACCAAT AAAAGTGAAC AATTGATTCC GACCAAACGA GGCGAACGGG CCGTnGCATA 300

CAGCGATTTA ATTnCTATTA AATnCAGAAA 330

(2) INFORMATION FOR SEQ ID NO: 939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939:

TACGGTCAAG ACCGAGTATG GGGAACTTCA TCTCCAGATT CCGCGCGACC GCAATGGCGA 60

GTTCAAGCAA CAGACTGTTC cTGCTTaTAG ACGGACGAAT GACACGTTAG AGGAGAnCCG 120

TCATTCACCT CTTTCCGAAA AAGTATTAnC CATGTCGGAA TCGCAGACTT GATTGAGAAA 180

TGTTGGGGCA TCATACACGC CCAAACCATG TCCATATACC AAATCATTAC AGAGGGTACG 240

CGTTAAnGGG GGACTCATGC CGTATGCGTA TTATATGCGC ACGATATCGT AACGGAACGC 300

GCAAGAGCAT CTAC 314

(2) INFORMATION FOR SEQ ID NO: 940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940:

CATCATATCA AACAAAGAAT TGGACGTGTT GGCATCTTTT AGGACGGAAA GACCCGTAAA 60

AATAAGAATC GTCATTAAAA AAATACCAAA AAACCGTTTG TATCGTTGTT GTCCAATAAA 120

TTTTACACCT AAAATAACAA AGACAAAGGC AATACCAATC GTTCCCGCAA TGCCCAACAT 180

GTTAGTTGCT ATGCTAGACG TTAGGTTCAT AATCGGTTGC TTAATAGCAG TTATAATATC 240

CATACTAAAT AGTGTTTTTA CCATAACTGC ATTAAACTCT CCGAGTCCTT TTACCATTGG 300

ACCAGACAAA AGTCTTTATT GTCGCAGAAG CATTTGTGGA TGGCTTCTTC AACACCTGTC 360

CATGAATCnT GGTTTTTTTT CTTTGGtCAT TAACTCGAAA GCGTTGTCyT TGTAAGTAtC 420

GTAAATCmAA TCTACATTAG kGGTTGGCTC yGTAACAAtA ACTTwATTTC ayCAGGGTTA 480

GGGTCGGGCA TTAACCGCTG GAGTTTGCGG TAAACACCAA AAAACAGCCT ACTAAAAATA 540

GGTAAGACTG GCTTTACCAG TGGT 564

(2) INFORMATION FOR SEQ ID NO: 941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941:

AATAATTGAA GACGAAAAGA GGACGAACTG ATTGTCCTTC TTTTTTTAGT TATGGAGGGG 60

AnCCATTGGA AGCAGTAGTA GTAGAAAGAG AGGCAAAGGG GATGAAAGAA ATTGCCATCC 120

AAGAAAAAGA TTTGACCTTA CAGTGGAGAG GAAACACAGG TAAGTTAGTT AAAGTTCGAT 180

TAAAGAATAC ACGTGCAATG GAAATGTGGT ACAACAAACA AATTACCGAA GAAAACATTC 240

AAGAGATCAC CACGTTGAAT ATCATTAAAA ATGGAAAATC TTTGGCATTA GAAGTATATC 300

CAGAAAAAAG TATCTATGTG AAACCAAATT TAGGCAGAAT CAATGTGCCT GTCTTTTTTA 360

TCAAAACACC TATTAACAGA GGAGTATTTG AAGAGATTTT CGGCGAAACG TTAAAAGCAT 420

AAGTAAAGGA GAAAGAAAAG CCAATGTATG TATCTTTTGT TCTAAGTTGT TTGCTTssaT 480

TTTCTGCCTA CAGTCTATTA AATAGGCTAA ATTCGTTGGA ATTTGTGGAT GTTTGGTTAG 540

ACAAAGrAAC ACAAAAAATC ACACTAAAAC GCTGTTTTTA TGATACGTCT TTCAAGAAmC 600

AAaCACTAAA aGAGTtAGca CGAGTaTATT TCCAATTAAa wGAAATaATC aaCGTGCAAA 660

TAAACAAGCG GTCTTTAAAT ACGAATGACA TACGTAATGT ACGAGAACTA GAGGAAAAAC 720

AACAAGAAAT AAAACGATTC ATGTTAGACG TTTTAGAAGA TGCTTATTGG AAAGAATTAG 780

CAAATATGCC AGAAGACCAA CGACACTTAG ACGATTGGGA TTTCTTTTAA AATGGGTTAT 840

TGAAAGGAAG CAATAATAAA AAAAATGATG CCTAACACAA AAATATAGGA GGGAAAAAAT 900

GATTATTTTA TCAGGACTTT TTATTTTAGg GATAGGAATA GTTGGAGGTT ATCAGCTAGC 960

CACGTTACCT AAATTGATTG AAATGAAACA GCACAAAGCA ATACAGAACC ATTTCAATGT 1020

TAAAGGAAAT GAGTACACCT ATTATCAAGA AGACAGTGAA AATTACATTT TATCCTTGGA 1080

AGATACAGAA TATCGAATTA AATTTTCCAg AACACCCCGT TAAAAGTGGT ATTCCTGAAT 1140

TTTAGAnCCn 1150

(2) INFORMATION FOR SEQ ID NO: 942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942:

TTTAATTCCA CGGAGACnTT GATTATGGAC GGTTCTTTCA GGATTAAAAA ATAGTGATTG 60

GGACgCTGTA GkTCATAAAA ATGCGTACTA TGkTTCTGGT GTAGGTCTAG CTAGAGAGGt 120

GGACGTATTT CTTTyTCTTT TGGTATGACA ACCAAAGGAA AAGTCAACCT ATCTGGTGCG 180

CAATGGTTTG CCTTTAGTAC CAATTTAAAT GCGAAATCAa TTAGACCATA CCAAAaGAAa 240

GGGAATCCAA AaGAACCAGA AAAAGCAACA ATTGAATTCA ATCGATACAA AGCCAATGTC 300

GTTCCTGTTC TTGTGCCGAA TAAAGAAGTC ACTGATGGTC AGAAAAATAT CAATGATTTA 360

AATGTGAAAC GAGGCGATTC TTTACAATAC ATTGTGACAG GGGATACGAC AGAACTTGCC 420

AAAGTAGATC CGAAAACAGT GACAAAACAA GGGATTCGGG ATACCTTTGA TGCAGAAAAA 480

GTGACGATTG ATTTAn 496

(2) INFORMATION FOR SEQ ID NO: 943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943:

AAAATGTAAA TCCCATTCTC CAGGCACCAC GTGATGTATG GGGTnCGGGA TGACTTGCCG 60

GAATGTTAAA ACTAACGGAT CCCCCAATTT CGTCGCACGA TCAATGGCTC TGCACAAAAT 120

TTTAGCAAAG CCGTACACCG CATCATGACG GTAACTCATT GGCGTAGTAC CTGCATGATT 180

GGCTTGCCCT TTTAAGTTAA CCGTGTAGCG ACGTTGCCCT ACAATACTAT GAACAACACC 240

GACTTGGAGC TTTTCGTTCT CTAAAATATT GCCTTGTTCA ATATGAATTT CGACAAATGC 300

TTCAATGTCC TCACGTCTAG TTTGCTCTTG CCgAAAATCA AAGCCTTGGC GATGCATCTc 360

ATCAACAAAC TTTTTACCTT CGTTGTCAGA GATATCGACT ACTTCTTCAC GTTTGGCTTC 420

ACCAACGACA TTTTTGCTTC CCCAGAAAAC CGTTGGAAAA CGACTC 466

(2) INFORMATION FOR SEQ ID NO: 944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944:

TTAAAAACTT GGGCCTCCCG ATGGCACGCn GCCCCAAATG CTCAAAAATC CCCnGATTTT 60

TAGAGGCCCn TCCnCCGTAG CCACGGTGTA TTATCCCGGA CTAGCGAGTC CATCCTGGTC 120

CACGAATTGC GCAAAAACAG ATGTCGGGAT TTTAGTGGCA TGATTTCTTT TGAATTAGCC 180

AAGGATGAGC AAGTCGTTCC TTTCGTAGAA GCGTTGGAAA TTTTTACTTT AGCGGAAAGT 240

TTAGGTGGCG TAGAAAGTTT AATTGAAGTA CCTGCCATTA TGACTCACGC ATsTAkCCCC 300

AAAGAAAATC GTGAAGCCGT GGGAATTAAA GATGGACTCA TTCGTTTATC TGTAGGAATT 360

GAAGCAGTCG AAGATTTATT GGCTGATTTA GAAAAGGGAT TACAAGCATA ArCAAAAGGs 420

CCTCGTCTTT AGACGAAGGC GTTG 444

(2) INFORMATION FOR SEQ ID NO: 945:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945:

GATTTCnGCA CAGTCCAAAG TTATTGGTnA TTATTCCACC GGCnGATTGG AGGGAAAGAT 60

TTTTTAGTTG AAAAAGTATT GGTnCCTAaT GAAGTCAGkT TGaCgTwTmC CCACAATGAT 120

CGcATGATCt TTGGCGGTGT AACcACCGAC GACTGAGTcG TTAGAGATTA TTTTGAAmnA 180

AGAATTAGGT GTCGATTATT TcTTGGAACG GcGTGAATTA GGAGTCATTA ATATTGGCGG 240

TCCGGGTTTT ATTGAAATCG ACGGTCGAAA AGAAGCGATG AAGAAGCAAG ATGGCTATTA 300

TGTCGGGAAA GAAACTCGAC AAGTGATTTT CTCTTCAGAA GATGCAGCTG ATCCTGCGAA 360

ATTTTACATT AGTTCTGCTC CGGCGCATCA CAAGTACCCA AATGTAAAAA TCAGTATTGA 420

TGAGATTAAG CCAATGGAAA CTGGGGAAGC ATTGACATTA AATGAACGTA AAATTTATCA 480

ATATATTCAT CCCAATATTT GTGAAAGCTG TCAGCTGCAA ATGGGCTATA CGATTTTAGA 540

GCCGGGCAGT TCTTGGAATA CCATGCCG 568

(2) INFORMATION FOR SEQ ID NO: 946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946:

CTTTCCACTC CGCTTTTCGC AATCCTCAAG CTGGCTGtCT gTTCGCAcTG TAcgCTGtGA 60

tCTTATCATT gcACTTAgCA GCATctTTCt TTGcTTTTTC tCGACAACgC yTGTTGTTGG 120

TTAACGTCTG CTgAGCTTGA TCCACTACTT TTTGTTGGTC ATCAACAGCT TGTGTATCCG 180

TAGCCACTTG GTTTTTGGCT TTTTCAAkGG CTGAAGGTGT TGCTTCATCC ACAACTTTTT 240

TTGCTTCGTC TACGACCGCT TGTTGGTCAG TCACTGcTTG TTGACTTTGA TCCAATGCAC 300

CTTTGTTTTG ATCGACCACT GCTTGTTGGT CTTTAACAGA TTGATCAATG GTGTCTTTTT 360

CTTTTTTCGC AGTGTCAGCA ACTTGTTGTT TTTGATCGAC AATTGCTTGT TTCTCTGTTA 420

CTTGTTGCTG TTTTTCAGTA ATGGCTTGCT CCGTTGTTTC TGTAGCTTTC ACTGCTGGTT 480

GTTCTG 486

(2) INFORMATION FOR SEQ ID NO: 947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947:

ACATAACGTT CCACGATCCC ACAAAAATGG CCCAATGCAC ACCCCTCAAT GATTCCTTTC 60

AAGACGCTAC TAAAAAAGCT TATCACGATA TCGCtTCATA GAAAtCGCTt GTTgCATGAA 120

CTGCTGAACG ATATCCCGTT AATAAATA 148

(2) INFORMATION FOR SEQ ID NO: 948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948:

CTTGGTAAnn CTTCTTTGTG AAGCCAAGCC TTTCAATCGG GAAATATTTA AATGGAACTG 60

CCCCCCATGT CTTTCAACAA TTTGATGGCG GTTTCGATAG GCACTTnCCG CCGTGGCGCA 120

CCAGAGCTTA ACGGACCTGT CGCAATGTTG ACATAGCCAA CTTTGCCTGT GGGTGAAACC 180

AAGCCATTAA TCACkGTTTC GTCTTGACGA AGTAAGGcCC CGCGAAGCGC CGACACCTGT 240

GAAGACTTGG TTCACGTGTT GCGGTTGTAG AACTTCTGAT AAGCGAGCCA CCATTTGACT 300

TTGATTAGGA TCGCCAGCCC CTAAGCCGAC AGATAAAGCG TTGTTGGTTG CTGCTTGGTA 360

TTTTTTCATG TCGTCAATAG CTGCTTCATC GGTTTCATAG TTTTTTGAAA GGACGCCTAA 420

CACAACATGC CCTTCTGCTG CTTCATAACA GGCTTGGGCA TTTTCTACTG AATTGGCTAA 480

GACGTTTAAA CAAATGCGTT CTTCTAAATA ATTAGGTTTT AATGACATGA CTTATTTCTC 540

CTTTTTGTCC ATAATTTCTT GTCAATnTTG CACGATTTTG TTCATTn 587

(2) INFORMATION FOR SEQ ID NO: 949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949:

ATTnCGTTGG GGTTGCCACC AATTATCCCC CCCnCAATTT AAGTGAAGTG ATTGATsCAm 60

CAAGTTTATT GATGGACaAT CCtGATGTAA CGACGAATGA ATTGATGGAA GTGTTACCTG 120

GACCAGATTT TCCAACAGGC GnTTTAGTGA TGGGGAAATC AGGGATTCGC CGAGCATATG 180

AAACAGGGAA AGGTTCGATT ACTGTTCGTG CAAAAGTTGA ATTGACTGAA ATGCCGAATG 240

GAAAAGAACG TATTTTAGTA ACTGAATTGC CTTATATGGT GAATAAAGCC AAATTAATCG 300

AACGAATTTC TGAATTACAC AGAGATAAAC GAATTGAAGG AATTACTGAT TTGCGGGATG 360

AATCTTCTCG TGAAGGCATG CGGATTGTCA TCGATGTTCG TCGAGATGTG AGTGCCTCTG 420

TTGTGTTAAA CAACTTGTAC AAAATGACTG CCTTACAAAC ATCTTTTG 468

(2) INFORMATION FOR SEQ ID NO: 950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950:

CGGGGAAATG AAGTACAGGC AGCAGAACAA GCGCAACCAA AAACACCTGA AAACAGTTCT 60

ACAGA 65

(2) INFORMATION FOR SEQ ID NO: 951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 730 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951:

ATCAAGCAGA TGCAAGTCTA AACGAGAAAG ACTTAAAAGC TGTTGCTGCA GCGATTAATT 60

CAGGAAAAGC TATAGACGTG ACTGCTTCTT ATGTTCTTAA TTTAGATCAA AACACCGTCA 120

CAGCaATGAT GAAAACCAAC GCAGACGGTT CCGTTGTTTT AGCAATGGGG TATAAATATT 180

TACTTGTCTT GCCGTTTGTA GTGAAAAATG TAGAAGGCGA TTTTGAAAAT ACAGCTGTTC 240

AGCTGACAAA TGATGGCGAA ACGGTAACAA ATACAGTGAT TAACCATGTG CCGGTTAGTA 300

ATCCTTCCAA AGATGTAAAA GCAGATAAAA ACGGTACAGT TGGCAGTGTT TCTCTACATG 360

ATAAAGATAT TCCGTTACAA ACAAAAATTT ATTATGAAGT GAAATCTTCC GAACGTCCAG 420

CTAACTATGG CGGAATTACC GAAGAATGGG GCATGAATGA TGTCTTGGAC ACGACCCATG 480

ATCGTTTCAC AGGTAAATGG CACGCTATTA CAAACTATGA CCTTAAAGTA GGGgACAAAa 540

CGTaAAAGCA GGAaCAGATA TTTCTGCCTA CATTCTTTTA GAAAACAAAG ACAATAAAGA 600

CTTGACGTTT ACAATGAATC AAGCATTATT AGCAGCGTTA AATGAAGGAA GCAATAAAGT 660

AGGCAAACAA GCTTGGTCTG TATATCTGGG AAGTCGAACG GGATCAAAAC AGGTGACGTA 720

GAAAATACGC 730

(2) INFORMATION FOR SEQ ID NO: 952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952:

TTTCAATAGG GACTGTTGGC TGTTGTGTAC CATTTCCAGC GTGATTTAAT TCCCCTGTTG 60

GCGTTACAAC AACGTCGATT GGCTTGCTTG GTTCTGCTGG TTGTACTGGT TTTTCAGGTT 120

CTGTTGGTTT AGTTGGTGTC ACAGGTTTTT CGGGTTCTGC TGGTTTGCTT GGTGTAACTG 180

GTTTTTCAGG TTCTACTGGT TTACTTGGCT CCGTTGGTTG TTCTGGTTCA CTTGGCTCTG 240

TAGGAGTTGT CGGTTCTGTT GGTGTTGTCG GTTCCGTTGG AACTACTGGT TTTTCAGGTT 300

CTGTTGGTGT TGTCGGCTCT GTCGGTTCTG TTGGCTCCGT TGGTGTAATA GGTGGCTCTA 360

CAGGGTCTAC AGGTGGCTCA ATTGGCGGTG TTGGATCTGT TGGCTTTTCT GGTGTACTTG 420

GTTCTGTTGG TACTTCAATG GGCGGTGTCG TAGTATCATC AGGGATAATT TCTTGTGCAA 480

AAGCAGAAAT TTCACTTCCC CCAAATAGTA GTGTGGCACT AAATAAACTA GCAAAAAGAT 540

TTTTTTTCAT CATTATTTCC TCCATTTTAA TTTTAATTTG TAAGTTCAAA ATCTTCTTCT 600

GTCGGTCGTT CCATTACGAC CAGTTGTTCT TTTGTTcTTC AGCTGTAAAC GTAATTTTCT 660

TTGTCGATgC TCGTCTTTtT CATTGATTAA TACAACAATG AACGcTaTCG TCCATkGTTg 720

kCTTCCTCTT TACTCCCAGG GAAACATACT TCTCGCTC 758

(2) INFORMATION FOR SEQ ID NO: 953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953:

AATGCCACGG TTGAnATCCG AAATGCAGGA GGnGCCGTGA TaGGTACAGG TACTGCTGAT 60

GGGACAGGGG CATTTACAGT TACCATTCCC GCAGGTGAAG CAGGTGCGAA TGAAACGTTA 120

ACCGCCGTAG CGAAAAACGC CAGCGGTACA GAAAGTACGC CAACAACGTT CCAAACGCCA 180

GCGGATCCTA ATACGCCCGT GGCGACGCCA ATTGTTGAGA CTGTAACAGG TAGTACAACA 240

AAAGGCTATG AGGTCAAAGG GACTGCTGAA GTTGGCACCA CCATTGAGGT TCGCGATGCA 300

GCTGGCACGG TCCTTGGTAC TGCAACAACT GGAACTGACG GAAAATATAC AGTGACTTTA 360

GATTCAGGAA CAGCAACAGC AAATCAAACG CTGAGCGTTG TAGCGAAAAA CGCTAGTGGC 420

ACGGAAAGTC AACCAGCAAC GGCGACAAAC ACCAGCTGAT GTCACTGCAC CAACAGTTGA 480

TTACATCACA GGnAACTTT 499

(2) INFORMATION FOR SEQ ID NO: 954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954:

CTGTTAGGCA TTCATTTACT ATTTTGAGGT GTCTGGCTGA ACAnTTGTTG TTCCTTTTAT 60

TTCGTGGTCC TCAGCGTAAT GGCACTTCTG GTCTTCTGGT GGATGnGCCA TCACCTACTT 120

TGGCTTTGTG AGAATGTTCG CnCCTTCGCT TCAnCGTTAA CGATCACTTT GAAACGAATA 180

CTCCGTTCTT TCGTATCGGT GATACTTGGG TATTCCGCTG TGATTGTCCG TTGGCTTCTT 240

TCAAGCTGGT TGGTTTTGGT TCATCACCGA CACTTGTTAG GCTATCTTTG ACATACGTCA 300

GTCCTTTTGG TAGTTGGTCT GTGATAACTA CTTTGTTTAG GACACCATTT TCGATGGTGT 360

TGCGGAAGCT AATTGTGTAC TCGATAGTTT CGCCTAGTTT TGGTTTGGCG TTATTAACGG 420

TTTTTGTTGC GGCTAGTTTG CCTTCTTTCG CTTCTGGTAC CACCGGCACC TCTGGTTCTT 480

CGGGCGGATT AACTGTGTCA TCTACTTTGG CTTTGTTGAG AATTGTTTCG CCCGCTTTCG 540

CTTCTTCGTT AACGATCACT TTGAAACGAA TACTCCGTTC TTTCATATCG GTGATACTTG 600

GGTATTCTGC TGTGATTGTG CCATTGGCTT CTGTCAAGCT GGTTGGTTTT GGTTCATCAC 660

CGACACTTGT TAGGCTATCT TTGACATACG TCAGTCCTTT TGGTAGTTGG TCTGTGATAA 720

CTACTTTGTT TAGGACGCCG TTTTCGATGG TATTGCGGAA ACTGATTGTG TACTCGATCG 780

CTTCCCCTAG TTTTGGTTTA GCGTTATTAA CGGTTTTTGT TGCTGTTAAT TTGCCTTCTT 840

TCGCTTCTGG TACCACCGGC ACCTCTGGTT CTTCGGGCGG ATTAACTGTG TCATCTACTT 900

TGGCTTTGTT GAGAATTGTT TCGCCTGCCT TGGCTTCTTC GTTAACGATC ACTTTGAAAC 960

GAATACTCCG CTCTTTTGTA TCGGTGATAC TTGGGTATTC CGCTGTGATT GTGCCGTTGA 1020

TTTCTTTCAA GCTGGTTGGT TTTGGTTCAT CACCGACACT TGTTAGGCTA TCTTTGACAT 1080

ACGTCAGCCC TTTTGGTAGT TGGTCTGTGA TAACTACTTT GTTTAGGACG CCGTTTTCGA 1140

TGGTGTTGCG GAAcTGATTG TGTACTCGAT TTCTTCCCCT AATTTTGGTT TGGCGTTATT 1200

AACGGTTTTt GTTGCGGTTA ATTTGCCTAC GTTCGTTTCT GGTACCACAG GCACCTCTGG 1260

TTCTTCGGGC GGATTAACTG TGTCATCTAC TTTGGCTTTG TTGAGAATTG TTTCGCCTGC 1320

CTTAGCTTCT TCGTTAACGA TCACTTTGAA ACGAATACTC CGCTCTTTTG TATCAGTGAT 1380

ACTTGGGTAT TCCGCTGTGA TTGTGCCGTT GATTTCTTTC AAGCTGGTTG GTTTTGGTTC 1440

ATCACCGACA CTTGTTAGGC TATCTTTGAC ATACGTCAGy CCTTTTGGTA GTTGGTCTGT 1500

GATAACTACT TTGTTTAGGA CGCCGTTTTC GATGGTGTTG CGGAACTGGA TTGTGTACTC 1560

GATTTCTTCC CCTAATTTTG GTTTGGCGTT ATTAACGGTT TTTGTTGCGG TTAATTTGCC 1620

TACGTTCGTT TCTGGTACCA CAGGCAnCTC TGGGTTCCTC GGGCGGAATA ACTGGGGCCA 1680

CCAACTTTGG GCTTGGTTGA nAAATGGTTC GCCTGCCCTA nCCTCCTCCG GTAAAGATCA 1740

ACTTGnAACG AAA 1753

(2) INFORMATION FOR SEQ ID NO: 955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955:

GAGGATCCCC GTGACTATGC TACTGCAATT CTTGTTGTAC CAACCGGGAG CGTCAATAAT 60

TTTGTGTAAA TAACTCGTCC TTCTGCAAAA TAATGGGTTA CTCAGTAAAC ATTGAAGCTA 120

ATGTATCCGT CACTTGTTGG AAGCCTTTAT GGCTTCTATT TAAGAATTTT TGATTGTATG 180

TATCAAAGAT GGATACTAGG AAACGCTCTA GTGATTCTTC ATTTTGAAAC TGCTCTTTTC 240

TGCGGCTGTA TTTCTTGATT TGTTTATTGA AAGATTCGAT TAAATTAGTT GAGTAAATGC 300

TTCGGCGGAT ACCAGGCGGA AACTCATAAA AAGTCAATAA ATCTTGATTT TTTATCAGTG 360

ACTGCGTCAC TTTAGGATAA GTTTTCTGCC ACTTCTCAAT CATACTCCCT AAAAAGGTAT 420

TTGCCTCTTC CTTTGAGCTA GCTTGATAAA CAGCCTTAAA ATCATCACAG ATTTCTTTTC 480

GATCTTTGAC ACGTACTTTA 500

(2) INFORMATION FOR SEQ ID NO: 956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956:

ACGACACGTG TAGGCACGCT AGAATTAAAA GTACCCAGAA CACGTGATGG CCATTTTTCA 60

CCCACAGTGT TTGAACGTTA TCAACGAAAC GAAAAAGCCC TCATGGCTTC AATGTTGGAA 120

ATGTATGTAT CAGGCGTTTC AACTCGTAAA GTATCAAAAA TTGTGGAAGA ACTTTGTGGT 180

aAATCCGTCT CTAAGTCCTT CGTTTCTAGC TTAACAGAAC AGCTAGAACC TATGGTTAAC 240

GAGTGGCAGA ATCGTTTATT ATCAGAAAAA AATTATCCTT ACTTAATGAC CGATGTACTC 300

TATATAAAAG TACGAGAAGA AAATCGAGTA CTCtCAAAAA GCTGTCATAT AGCGATTGGA 360

ATAACCAAAG ATGGCGACCG TGAAATTATC GGCTTCATGA TTCAAAGTGG CGAAAGgAAG 420

AGACCTGGAC AACATtTTTT GnATACCTAA AAGAcGCGGT TTACAAGGTA CGGgAACTCG 480

TTATTyCTGA TGCGCACAAA GGGATTAGTC TCTGGCCATT AGGAAAATCC TTCACCACGT 540

AGGnGCCAAA AGATGCCAAG TTCACTTCCT AAGAnATATC TTTACCACCA TTCCTAAAAn 600

ATTCAAATCT TTCAGAGAGC GGTTAAGGAA TTTTAGTTCC AGTATTACTA GCGCGG 656

(2) INFORMATION FOR SEQ ID NO: 957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957:

CCCTTATTGG GGAAaGgCGG CAAtAAAAAA GTAATTGTAA AATACTGTTA GGGAATCATT 60

AGATAAAGTC CGTATAATTG TGTAAAAGTA AAAAGGCCAT ATAACAGTCC TTTTACGGTA 120

CAATGTTTTT AACGACAAAA ACATACCCAG GAGGACTTTT ACATGACCCA AGTACATTTT 180

ACACTGAAAA GCGAAGAGAT TCAAAGCATT ATTGAATATT CTGTAAAGGA TGACGTTTCT 240

AAAAATATTT TAACAACGGT ATTTAATCAA CTAATGGAAA ATCAACGAAC AGAATATATT 300

CAAGCAAAAG AATATGAACG AACAGAAAAC CGACAAAGTC AACGAAATGG CTATTATGAG 360

CGCAGyTTTA CGACACGTGT AGGCACGCTA GAATTAAAAG TACCCAGAAC ACGTGATGGC 420

CATTTTTCAC CCACAGTGTT tGAACGTTAT CAACGAAaCG AAAAaGCCCT CATGGCTTCA 480

ATGTTGGrAA TGTATGTATC AGGCGTTcAA CTCGTAAAGT ATCCAAAATT GTGGGAGACT 540

TGTGGTAATC CGTCTCTAGn CCTCGTTCTA GCTAACAGAC AGCTAGACTT GGGnACGGGG 600

CGATCGTTAT TCAGAAAAAT TCCTCTTATG nCGTGACCTT TAAGTCGGAG AAACGG 656

(2) INFORMATION FOR SEQ ID NO: 958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958:

CTGTCGTTTC TTTTTGGTAG TACTCACCTT CTTTATTTTT GTGTGTATTT TTAAGCTTAT 60

CGAACAACGC TTCATACTCG TTATTTATTT GCGCCATTTC TTTATCAGTA CCGCCCATGT 120

CTGGGTGGTA CTTTAAAGCT AGCTTTTTAT ATACGCGTTT CAATTCTTCT AATGTCGTTA 180

CATCTTTGAT AAATTTCATG CTAATCGCCC TTTCTGATTG CTGCTGAACA GCTAAGCTGC 240

CCAGCGTTCC AATTTTTCAA TTGATTTTTT ATCATTTTCA AGGTCTGCTT TTGTGTACCA 300

TGCTGGTATC TCTTTATCAG AAAATAGACT GTAGATAAAT TCTAAGATTT CCATGCkTtC 360

TCTAGCTTTA ACAGCTGATT CACATTGATA ACGTAATATC tTACAyCTgg CTAAGTCTAT 420

CGACATAgAA TAATGAAACG TTgGtTCCTc yACCATTtGt TAACcGtTTT TCCnTnG 477

(2) INFORMATION FOR SEQ ID NO: 959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959:

GTAAAGCCCC nGCCCACCTT AGAACCACTT AGTGGTTTAA TTCCATAAAC TATTTTTAGG 60

AGGCTTACAG AAATGAAAAA AGCAAAATTA TTCGGTTTTA GTTTGATTGC ATTAGGTTTA 120

TCCAnTTCAC tTGCAGCATG TGGTGGTGGC AAAGGCAAAA CCcTGAAgCG GCGGTgGcAA 180

AGGGGATGCA GCGCATAGTG CTGTAATCAT TACAGATACA GGCGGCGTGG ATGACAAGTC 240

GTTCAACCAA TCTTCTTGGG AAGGATTGCA AGCTTGGGGT AAAGAACATG ATTTACCAGA 300

AGGTTCAAAA GGGTATGCAT ATATTCAATC GAATGATGCA GCTGACTATA CAACCAATAT 360

TGACCAAGCG GTATCAAGTA AATTCAACAC AATCTTTGGT ATTGGcTACT TGCTAAAAGA 420

TGCAATTTCT TCTGCAGCAG ATGCCAACCC TGATACAAAC TTTGTTTTAA TCGATGATCA 480

AATCGATGGG CAAAAAGAAT GTCGTTTCTG CAACCATTTA GGAGATAATG AAGCCAGCTT 540

ACTTAGCCGG TGTTGGCTGC TGCAAATGGA AACCAAAACG AACCAAAGTC CGGTTTTGGT 600

TnGGTGGTTG AAGAAGGGGT CCGTAATT 628

(2) INFORMATION FOR SEQ ID NO: 960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960:

CTTTACCTCn TGnGAAATAG TACCTGCACT GCCACAATnC CAGGCGTTTC CATTCGTAAT 60

CGATGATGGA GCCAGGAATT GCTATCCCAT AGCCATTGGC GCCCTTGGTC ACATCGTTAT 120

CGCCAATAAA TGTTTTTCCA GTCGCTTTTT CAATCCCATG AAACGTTGTT GGCGTAAGTT 180

TTGTAGCATT ATTGACCGTT GGATTAATCG TCAAGACCTG ATAGGCTTTG ACATTTCCAA 240

ACCAAGTCCC TGTGCTATCC ACCAAAGCAG TTGTATCTGT CGTTGGTTTA ATCCATAAAA 300

GTTCATCTTT TGTTGGATCG ACAGCTTCAA AATCCGCAAT GTTTACTTTA CtGTACCAGG 360

AATTGTTTCT AATGTTGCAT GATCCTGaAC CGTTAGTTTG CTAGCTGAGA TTAAATTGGc 420

TGTGTTGGTG aTCCCAATTC CAGCGTTTTT AGATAGATGA ATkGATCCGA ATTCATGGnA 480

AGTCGTACnG GGGTCGCGGC AGTAGCAGAA CGCCATTTTG GATGTnCCAC CATAGCCATA 540

AATTAAnGCC ATGGGGGCAT TAATCC 566

(2) INFORMATION FOR SEQ ID NO: 961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961:

GTGTTCGATT TTTATGATGA TACCAATGTG AAACTAGTCC GGCCCTTTGG CGATACGATG 60

GGGCTACATG AAGAATTCCT ACCAGCTAGT AAACGGTATA TGAATGACTA TATCCAGTAT 120

GTAACATCTG ACTTTTTAGC AGGACTTGGC TTTGGCGCCA CTCAAATGTT AGGAGAGTTG 180

GAAgGGATTT ACTTTGGCTA CAATGCGGAT ACGGGGCGTA ATGTTTACCT GAAACCCGCA 240

TTAGCCTCAC AAGGAGTAAA GGGCTCAGTA ACCAATGCAT TAGCTGCGGC TTTTCTTGGT 300

TCTCTTGGTG GCGGAAAATC CTTTAGTAAC AATCTCTTGG TCTACTATGC TGTTCTTTTT 360

GGTGGCCAAG CTGTGATTGT CGATCCAAAA GGAGAACGAg TGGTTGGAAA gAAAACTTGC 420

CAGAAATTGC nGATGAAATC AATAtCCyCA cTTGACyAGt AAaCCrGAAA TCAAGGCnTA 480

CyTGATCCCT AATGGGATTA TGAAGAAAAG AAGATCAGAA GTTAGCATTA TTCC 534

(2) INFORMATION FOR SEQ ID NO: 962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962:

TAAAAATTCT AATTTGATTT TATCCAGCCC AATTTCTTTT TTCCCTTTTT CCCAGAATTC 60

TTTTGCTTTC GCTGTATCGT AGGTTAAGTA GTTATTTTTC TTAGCAGCTA GTTTTGTGAA 120

ATCTGTTCCA TCTGGCGCAA TCGTTTGTCC CGGCGGAATT ACTTGATCTG TAGCCGTTGA 180

TTGATCTTGC AAGACTTCkT TTACAAAACT TTCTTTATCA AAAGCTTGTG CCAACGCTTT 240

ACGAATATTG TTGTTCGCTA AAGCCGGATT TTCTTTTCCA TCACGAACGC TGTTCATTTT 300

TAAAAAgTAT GTGACGAATT GAGGAATTGA AAGAAAGGCT GGATTAwCmA CaTAACCAGG 360

AATAAATTCA CCAcTaGCTT AwTCACTAcA TCCAtTCATc GAGyCAAmCA AtTCACCGcT 420

GTCGTGGGGC CCTAATACTG AACTTTCGCT CnGTAATTAC TT 462

(2) INFORMATION FOR SEQ ID NO: 963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963:

GCATTATTAG CAGCGTTAAA TGAAGGAAGC AATAAAGTAG GCAAACAAGC TTGGTCTGTA 60

TATCTGGAAG TCGAACGGAT CAAAACAGGT GACGTAGAAA ATACGCAAAC AGAAAACTAC 120

AACAAAGAAC TTGTTCGTTC TAATACGGTG GTGACGCATA CACCTGATGA TCCAAAACCA 180

ACCAAAGCCG TTCACAACAA GAAAGGGGAA GATATTAACC ATGGAAAAGT TGCTCGTGGT 240

GATGTTCTTT CTTATGAAAT GACGTGGGAs TTAAAAGGGT ACGATAAAGA CTTTGCTTTT 300

GACACAGTCG ATCTTGCGAC AGGAGTTTCT TTCTTCGATG ATTACGACGA AACGAAAGTG 360

ACcCAATCAA AGACTTACTT CGTGTCAAAG ATTCTAAAGG GGCAGACATT ACGAACCAGT 420

TCACGATCTC TTGGGACGAT GCCmAAGGCA CGGTGACmAT CTCTGCCaAA GACCCmCAAg 480

CCTTTATTCT AGCGTwTGGT GGGCAAGAAT TGCGTGTAAC GTCCCTACAA AAGTCAAAGC 540

CAATGTTTCT GGTGATGTTT ATAATTCAGC GGAACCAAAT ACATTTGGTC AACGAATTAA 600

AACAAATACC GTTGTCAACC ATATTCCAAA GTGGACCCTA AAAAAGACGT GGTTnTAAGT 660

G 661

(2) INFORMATION FOR SEQ ID NO: 964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964:

AAGAACCGGA TATTTTTCTT TGATTTTATT CCAAAAGACA TTGTACATTT TCACATTTTG 60

GACATAGTAA AGTTCGGCAA ATAAATGTGT AGCAAACAAA TAATAAAAAA TTTGCGGACG 120

AATTTTCTCC AATTGCGGCG TCATGTGTAT TTCTTCTAAT AAGAAATGTT GGACTAAATG 180

AGTCAACATG TAAACAGGTG CTTCAGTCTC ATCAAAATGC GCTAAAATTG CTTGTGCAGT 240

GGCTTCATCT TGATAAAATT GGTCATTGGC TAACAAGAAA AAGTACACAA AAGTTAAATC 300

GTTTTTGTTA AGGAAAAGGG TTGTAGCTGT CATCTCkkCT ATAAAGGCTg GTAATGTTTA 360

TTACCTTCTA AATAAGTtTC TTGCTCGGCT GAAGGTCGAT ATTCGGCGCC TTGCGCACTA 420

CGGACTTTTG AGATAGCGAC CATATAwTTA ACTCGGCGTG kCACCGTTTC CGCAACTTCT 480

ACGTGAAAAA AGCCATCATT TTGGCGGTTG TGCGACTTCC GTTCTGTAAT AGnCAAAAGC 540

CAGTACACGG ATTAnTCATA AAATAGTGTA CCAAAGGGCA ATCGC 585

(2) INFORMATION FOR SEQ ID NO: 965:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965:

nCGGGAAGGn AACTGTAAAG CCCCTTCCCA TCAGCAGTAC CTGACCTATC ACGGCACCTC 60

CGCATTCGnA TCTCAACCGT GGCATGGCAT CGGCAGTTCC TTAAACTCGT AACCTGCTGT 120

GGAATTACCT GTCACTCCTG TGATTGTTGG TGCGGTTACG GTTGCTTCAT CCGCTGGTGT 180

nTGGAACGTT GTTGGCGTAC TTTCTGTGCC GCTGGCGTTT TTCGCTACGG CGGTTAACGT 240

TTCATTGGCA CCTGCTTCAC tGCGGGAACG GTAACTGTAA ACGCTCCTGT CCCATCAGCG 300

GTACCTGTGC CTATTACGGT GCCTCCTGCA TTTCGGATTT CAACCGTGGC ATTGGCATCG 360

GCAGTTCCTT TAAtTCGTAA CCTGCCGTTG AATTACCTGT CACTCCTGTG ATTGTTGGTG 420

CGGTTACGGT TGCTTCATCC GCTGGTGTTT GGAACGTTGT TGGCGTACTT TCTGTACCGC 480

TGGCGTTTTT CGCTACGGCG GTTAACGTTT CATTGGCGCC TGCTTCACCT GCGGGAACGG 540

TAACTGTAAA CGCTCCTGTC CCATCAGCGG TACCTGTGCC TATTACGGTG CCTCCTGCAT 600

TTCGGATTTC AACTGTGGGC ATTGGCATCA GCAGTTCCTT TAACCTCGTA ACCTGCCGTT 660

GAATTACCTG TCACTCCTGT GATTGTTGGT GCGGTTACGG TTGCTTCATC CGCGGGCGTT 720

T 721

(2) INFORMATION FOR SEQ ID NO: 966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966:

AGAAAAAGTG TGAGCCTTGT GCTCACGCTT TTTTGTGCAA TTGAAGTTGG TGAATCTCAG 60

CGAAAAGAGA AAGGTACCTT AAATAGTGTG TTTCTGGTCA ATAGCACAAT GAAATATCTA 120

AATACATTAT GAACTGCTTT TCGTTTTATG AAGAGCAGTT TGTGCTATTT GAGAAATTGC 180

TCAATTTAAT CATTAAGTAG TTTCATCAAT GGTGACTATG CTACTGCAAT TCTTGTTGTA 240

CCAACCGGGA GCGTCAATAA TTTTGTGTAA ATAACTCGTC CTTCTGCAAA ATAATGGGTT 300

ACTCAGTArA CATTGAAGCT AATGTATCCG TCACTTGTTG GAAGCCTTTA TGGCTTCTAT 360

TTAAGAATTT TgATgTATGT ATCAAAGAtG GATACTAGGA AACGCTCTAg TGATtCTTCA 420

TTTGAAACTG CTCTTTcTGC GGCgTATTct GATTGTTaTg AAgATCGATA AATAGTgAGT 480

AAAgCTCsGC GaTACCAGcs GAAACTCATA Ann 513

(2) INFORMATION FOR SEQ ID NO: 967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967:

CAGTTATCCC CCnGAGACCC AGAGGTGCnT GTGGTnCCAG AACGAACGCA GGCAAACTAG 60

CCGCAACAAA AACCGTTAAT AACGCTAAAC CAAAACTAGG CGAAACTATC GAGTACACAA 120

TTAGCTTCCG CAATACCATC GAAAACGGCG TCCTAAACAA AGTAGTTATC ACAGACCAAC 180

TACCAAAAGG ACTGACGTAT GTCAAAGATA GCCTAACAAG TGTCGGTGAT GAACCAAAAC 240

CAACCAGCTT GAAAGAAATC AACGGCACAA TCACAGCGGA ATACCCAAGT ATCACTGATA 300

CAAAAGAGCG GAGTATTCGT TTCAAAGTGA TCGTTAACGA AGAAGCTAAG GCAGGCGAAA 360

CAATTCTCAA CAAAGCCAAA GTAGATGACA CAGTTAATCC GCCCGAAGAA CCAGAGGTGC 420

CTGTGGTACC AGAAACGAAC GTGGcAAATT wACCGCAACA AAAcCGTTAA TAACGCCAAc 480

CAAATTgGGG AgAATCGgTA CACmATCAGt TCGCACACCA TCGAAACGGG TCTT 534

(2) INFORMATION FOR SEQ ID NO: 968:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968:

TAATAAAATC CGTAAGAAAA CAGTAAAGTA TAAAGATAAA GAATATGATC GAATCAACTT 60

ATTGTTAGAC AACGATATGA ATAGCGAAGA AAATAATAAG TTAATGGAAG AAGTTGTAAA 120

TTACGAAAGT AAAGACTTAA AAAACCGTTC AATTATGTAT TATAACAACT GGACCAATAC 180

TTTTTATGGC TTGTTTTATC TGGTAGTTAA CTTCATTCAA ACAGTGGTGT ATTTCCTGTT 240

AAGTTTCTnA CGATTAATTA TTGCGGTCAT TCAATTGTTC CTATTGCCGT TGTTACCGTT 300

ATTGTTGTTC GCAGGACTCT TTTTAACTGA AACGAACGTC TTTGCGAATT ACTTTAAAAC 360

CTTTGGCATG ACTATTTTTA TGAAGGGAAT GGTTGGTTTT GCGACTATTT TCTTTGCAAG 420

TTTCTTATCA CTAGGGTTTC AATTAAGCAA TCAGACAGAA AACGTGTGGC AGAAGATATT 480

AACGATACTT ATTTATCTTC TTACACCGCT TGGCTTGTAT GTCTTCCGGA AATTCTTTGC 540

TAATCTTGTC ACGGGACGTG TTTCACTTTC TGATGGTGTC GGGTTTATCG GAAaTCCTTT 600

TGGCACAGAA GCTAATATGC GTAGAGCGGC AAAAGAACAA AAGCaAGAGa ATAAGGAGCG 660

CAnGnAACAG GCACAAGAAG AACGTAAAAG CAGCTATTAA AAAACGTCCA GAAGnAGCCA 720

AGGGAACCAT GGTAAAGCAG GAAACTGGCn TAAAACCAAn GGCCATTAAA TAAAGGACCA 780

AGGAAAACGT G 791

(2) INFORMATION FOR SEQ ID NO: 969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969:

TGCTCGCGAA CAAAGAGCTG CCACACAGAA GGAGTTGTTA GAAACAGCAC CAGAAGCTAG 60

TCTCTTATCT GCCACAATGA ATATTCCTGG AGAAGTAAAA AATTCGCCCA CCTTAACGGC 120

TGTTTTTTTA GAAGTAATTG ACGAAtCGAG CAACAATTGC TGGATCAAGT ACCGATTGTT 180

AATTTTTACC GGAATGAAAA AACAGGTCCT GAATATTATT TGGCGGTTTC GTTAGCCCCA 240

CAAGAATTAA AACAAAGAAT GGTCAAAATT GAAGAAACAC ATCCTTATGG TCGTTTAGTG 300

GACCTAGATG TTTTATGGGG AAtGAGGAGC TAAAAAGCCT TCATCGAGGA GATTTAGGCT 360

kGCCACCACG GCGCTGTTTT AtTkGCCAAG aAGTGGCcGA AAaGTCTGTn GaCGAAATCG 420

asGTCACAGT CTtGaAGCAt GCCAgaAgAA ATaCCggAAT AATTTgaCcC GaAAGGGcac 480

CAAGTGGGTA AAAAAATCCG TTTAACGGAA A 511

(2) INFORMATION FOR SEQ ID NO: 970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970:

CGTTTGATGT CTTATCCGAT GAGGTCGTGA TGCAGTTGCC TTCTGCACCT AATTATCCTT 60

CAATTTATAG TTCTCTAAAC AAATTATTAA CCTTTGAGTC CTACAAATTA GAAGAGTTAA 120

CCCCGAATCG AATTTATAAT AAAGTTGTTG TTGCGATTGA TGAAGCGTAT TTAAATGAAC 180

GCATCAAGGA AATTCCAGCC TCTTTTTATG AGCGCTTTGA AATTATTAAA ACGCGAAATA 240

ACTTATTAGA ATTTATGCCA AAAGGGATTA CGAAAGCCTA TGGTATTTCC TTGTTAGCCA 300

AAGATTTAGG AATCCGTGCA GAAGAAATCA TGACCCTAGG GGACGArGAA AACgATTTaC 360

CGATGATCGA ATACGCTGGG CTTAGGGTGt CGCCATGGGC AAATGCGatT CCaTTAGGtT 420

AAAgAAGCCG CaGATGTCgT CACaGACmCg GATGrCCCAg AttGGCGkTG cCAAAGCGGG 480

TnGAAAATnT AnTTTAACCC CGTTGGGAAG GGGGCCATAA GA 522

(2) INFORMATION FOR SEQ ID NO: 971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971:

GGCGGACGAG CCTTCCCCAG GAAACCTTAG TCATACGGTG GACAGGATTC TCACCTGTCT 60

TTCGCTACTC ATACCGGCAT TCTCACTTCT AAGCGCTCCA GCCGTCCTCA CGATCGACCT 120

TCAACGCCCT TAGAACGCTC TCCTACCACT ACACCTAATG GTGTAGTTCC ACAGCTTCGG 180

TAATATGTTT AGCCCCGGTA CATTTTCGGC GCAGGtCACT CGACTAGTGA GCTATTACGC 240

ACTCTTTAAA TGGTGGCTGC TTCTAAGCCA ACATCCTAGT TGTCTGTGcA ACCCACATCC 300

TTTTCCACTT AACATATATT TTGGGGACCT TAGCTGGTGG GTCTGGGGCT GGTTTTCCCT 360

TTCGGACTAC GGGATCTTAA TCACTCGGCn GTCTGACTCC GGGATATAAA TGAATGGGCA 420

TCGGAGTTTA nCTGAATCGG TnACCGAGAT GGGGCCCAAG GTCAAAAGnG 470

(2) INFORMATION FOR SEQ ID NO: 972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972:

CGCGTAGAGG ATCCCGCCTG ATGATCCAAA ACCAACCAAA GCCGTTCATA ACAAAAAAGG 60

GGAAGACATT AATCATGGAA AAGTGGCTCG TGGTGATGTT CTTTCTTATG AAATGACTTG 120

GGACTTAAAA GGGTACGATA AGGACTTTGC CTTTGATACA GTCGATCTTG CGACAGGCGT 180

TTCTTTCTTC GATGATTACG ATGAAACGAA GGTGACACCA ATCAAAGACT TACTTCGTGT 240

CAAAGATTCT AAAGGGGAAG ACATTACGAA CCAGTTCACG ATCTCTTGGG ATGATGCCAA 300

AGGcACGGtG ACGATTTCTG CCAAAGAcCC ACAAGCCTTT ATTTTGGCGC ATGGTGGGCA 360

AGAATTACGT GTAACTTTAC CAACAAAAGT TAAAGCCAAT GTTTCTGGTG ATGTGTATAA 420

TTTAGCGGAA CAAAATACAT TTGGTCmACG AATTAAAACC AwTACCGTTG TCAACCATAT 480

TCCAAAAGTG rACCCTAAAA AAGACGTGGT TATTAAAGTC GGTGATAAAC AAAGTCAAAA 540

TGGTGCCACA ATCAAATTAG GGGAGAAATT CTTCTATGAA TTTACAAGTA GTGACATTCC 600

TGCAGAATAC GCTGGTATTG TGGAAGAATG GTCGATTAGC GATAAACTAG ACGTCAAACA 660

TGACaAATTT AGTGGCCAAT GGTCTGTGTT TGCCAATTCT ACGTTTGTCT TaGCAGACGG 720

AACCAAAGTG AATAAAGGGG ACGACATTTC GAAACTATTC ACGATGACCT TTGAACaAGG 780

GGTAGTGAAA ATCACAGCCA GTCAAGCCTT TTTaGATGCG ATGaATCTAA AaGAAAaCCA 840

AAACGTTGcA CACTCATGGa AGCGTcATTG GTGTAGACGA tTGCGGcAGa GcGTtcACaC 900

aTCGAGAtCT TTCaCaTGGG aGTTaACyaT ccGGTTTGnC nCT 943

(2) INFORMATION FOR SEQ ID NO: 973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973:

nCCAGGTACT AAGAkGTTTC AGTyCTCkGC GTCTACCTCT AATCAGCTAT GTATTCACTG 60

AAAAGTAATA TCCTATAAAA GATATTGGGT TCCCCCATTC GGAAATCTCT GGATCATAGC 120

TTACTTACAG CTCCCCAAAG CATATCGGTG TTAGTCCCGT CCTTCATCGG CTCCTAGTGC 180

CAAGGCATCC ACCGTGCGCC CTTATTCACT TAACCTTATC AACcTTACGG TTGGGTCTTG 240

ATCACTTCTT CTAGCGATAG AAGGTTAATC AATAAATAAG CAATTGAACT TATTAAAAAA 300

CTCATTCAAC GCGGTGTTCT CGGTTTGTTT TGATTCTTTT TACTTCAATA TCCAGTTTTC 360

AATGAACGAA TGTTTTGAGA GTAGACCTCT CAAAACTGAA CAAAGTAAAG ACGAAATGTG 420

TATTTCCGTA ATATCCCTTA GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGG 475

(2) INFORMATION FOR SEQ ID NO: 974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974:

TTGAAGACAG CCGATTCAGG TTACTTwACA CGTCGTTTAG TTGACGTTGC CCAAGACGTA 60

ATCATtCGTG AAGACGACTG TGGCACTGAC CGTGGTCTTG AAATCGAAGC AATTCGTGAA 120

GGTAACGAAA TTATCGAACC ATTAGACGAA CGTCTATTAG GTCGTTATAC ACGTAAATCA 180

GTTGTTCATC CAGAAACTGG TGCAATCATC ATTGGTGCGG ATCAATTAAT CACTGAAGAT 240

CTTGCCAGAG AAATCGTGGA CGCTGGTATT GAAAAAGTAA CCATCCGTTC TGTCTTTACA 300

TGTAACACAA AACATGGTGT ATGTAAGCAC TGTTACGGAC GTAACCTTGC AACTGGTTCT 360

GACGTTGAAG TCGGAGAAGC AG 382

(2) INFORMATION FOR SEQ ID NO: 975:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975:

AACATAATAA TCTTTCGGAT ACAAATAATA AGAAATGTTA TTTTTAAAAA TAAAACAATA 60

TTTTTTAAGT AATATTAAGA ATGTGAGAGT GTAAAATATT TTGTGTAAAT GAAAAAATCC 120

ATACAAAAAA GGAAGTCGCT TCTGTAGAAT AAAGTTAACG ACAACCAATT CACAGArAAG 180

AGGACTTCCC TATGAATGAT TTTACTACAG AAATTGTGCA AACTCTAGTC ACTAAAGGCG 240

ATTTAAATGA ATTATTCCGT TCGCACTTAG AAAAAGCGAT AAACACACTC CTACGGACTG 300

AATTAACGGC TTTTTTAGAT TACGAAAAAT ATGATCGCAC TGGTTTTAAT TCAGGTAATT 360

CGAGAAACGG TTCTTACTTT CGATCAATCA AAACCGAATA TGGTGAATTA ACATTGGAAA 420

TACCTAGAGA TCGTAATGGT GAGTTTAAAC ACCAAACTTT ACCAGCCTCC AAAGACAACG 480

AnCATTGGAA CCCTAT 496

(2) INFORMATION FOR SEQ ID NO: 976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976:

CTTGCATAGT AAACTTCATA ATATCCCCAG TAATCGAAAC TTTCGCTGGA TCAATAAAAC 60

GACCACTTTC ATCTAAAAAC GACATTTTGT ACGTCTTCTC TGGAATATCG AATGTCTGCA 120

CTGCTCGCTG CGCACGCAtG ATTTCTGGTG TATTAACTAT TATTGGACTC GTCACTGACG 180

CTTCAACTTG CCCGACTACT TGTTCAGTCT GTTCTGGTAG tCTTCATCAG CTGGCGGTAC 240

cTtACTTCCG TATCTGCCTC TGGAAAAGAA ACGGGCGCCC GTCCTTGgAA CCCCCTCTGg 300

AcGGGgACTA CTGtTTGGGC GGGTCCTCCC CTTGGAACAT CTGGGGGnCG CCATGGGTTT 360

TCAGCAATTG GCTGGGGGAT GGCCATTTTA ATGGAACTGG ATTAGGTnAA GGAACCACAC 420

AAAGCGGATT GGCnAATAAA CGGGTTTCCT TTTTT 455

(2) INFORMATION FOR SEQ ID NO: 977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977:

CTTGTTGTGC CTCTAAGTCT CTTAATACAC CTTGGTACTG CTGTAGCTCT AACTTCGCAT 60

TAGAAAGGTC TTCTTGTGCT TGTGCATAAG CAAGTGTAGC AACGGCTTGT TGTTCTTTAA 120

GTTCCTCCAA TGATTTCATA GAATTTTCAT AGGCTTCTTG TGCTTGAACC ACTGCCGCTT 180

CTGCTTTGTT TAACTCGTTT AATGCTTTTT CGTATGTTGG TTGAGCATTT TCTAAACGAG 240

ACAATGAACG TGTACTTGTT TTAAGCGCTA CTTGTTTTTG ATTTAAGTTT TCTTTTGCTA 300

AATCCAATAC TTCCTTCaAG CTATTCaATG TGtTTTCyTC TGCTTTTTGT GCnTCyTGtT 360

TTCTTTCAGC ACTTtAGCAG ACGtTGkTCm ATCGCTGgtG CnTCCGmACG tTGgTTTcGg 420

CTTTyCaAAA CAGCAGCCgA TCcGaATAAC cCATGATGnG CATGACCTTG TTGTGAAGCT 480

TTCCGCGTG 489

(2) INFORMATION FOR SEQ ID NO: 978:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978:

AATTAATTAC ACAGTTATTT AGTCAATTTT GTTTAGGAAA ATAAGACAAG AGAGGAATTT 60

TTTATGAATC mATATCAAGC AGAATCATAT GATGTTATTG TCGTCGGTGC TGGACATGCT 120

GGCTCTGAAG CAGCCTTAGC AGCCGCACGA ATGGGCGTTA AAACGTTACT TTTAACGATT 180

AATTTAGaTA TGGTTGCTTT aTGCCATGTA ACCCTTCTGT TGGTGGACCT GCCAAAGGAG 240

TCGTTGTCCG AGAAATCGtG CATTAGGCGG CGAAATGGGT AAAAACATgA TAAAACCTAC 300

ATCCAAATGC GGATGCTAAA TACTGGTAAA GGTCCAGCAG gCGTGCGTgC GCGCGCAAcT 360

GgACAACATG CCAAGCGCCA nAATGAACAT ACCATGAAAA AGAGAATTTA CCCTCGCAAG 420

GATGTnGAGA TTAACGGGAA ATGCGTTTGC GGGGTGACTC ACAGGCCCAA CGn 473

(2) INFORMATION FOR SEQ ID NO: 979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979:

ACAACGTTCC AAACACCAGC GGATGAAGCA ACCGTAACCG CACCAACAAT CACAGGAGTG 60

ACAGGTAATT CAACAGCAGG TTACGAATTA AAGGAACTGC CGATGCCAAT GCCACGGTTG 120

AGATCCGAAA TGCAGGAGGT GCCGTGATAG GTACAGGTAC TGCTGATGGG ACAGGGGCAT 180

TTACAGTTAC CATTCCCGCA GTGAAGCAGG TGCGAATGAA ACGTTAACCG CCGTAGCGAA 240

AAACGCCAGC GGTACAGAAA GTACGCCAAC AACGTTCCaA ACGCCArCGG rTCCTaATTA 300

CGCCCGTGGG GACGCCAATT TGTTTGAGAC TTGTTAACCG GkTAGTTACC AcCAAAGGsT 360

TATgAGGkTC CAAGGGGACT TGCTTGAAGT TTTgGGCACC aCCATTTnGA GGGTTTCCGC 420

GATTTCAnCT TTGGCACGGT nCCTTTGGTT ACTTTGCAAC AACTTTGGAA CTTTACGGGA 480

AnT 483

(2) INFORMATION FOR SEQ ID NO: 980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980:

CCTnTGGGCC GCCCACGGAA TTGCCCCGGC GGAAATTGCC GCTATTAATT CACGTCCATT 60

CCTAAGGATT TGAACCCCCn GnCTTGACAA GCCGTTGGTG GAGCGAAAAA GGnTCCAAAC 120

TTTACCGTCG TGGAAAACCC AACTGGAGGA CTTAGGAATG TTTCTTCTAA AGATTTAGCT 180

GCAAArGAAA AAGAAGTAGA CCAACTACAA AAAGAACAAG CCCAAAAGAT TGCCCAACAA 240

GCAGCTGAAT TAAAAGCCAA AAATGAAAAA ATTGCCAAAG AAAATGCAGA AATTGCGGCA 300

AAAAATAAAG CGGAAAAAGA GCGCTACGAA AAAGAAGTGG CGGAATACAA CAAACACAAA 360

AATGACAAAG GCTATGTGAA TGAAGCAATC AGCAAAGACT TAGTTTTTGA TTCAAGCATT 420

GTGACTAAGG ATaCTAAAAT AGACaAGATT TACAGGTGGC CAGTTTATTA AAGCTTCCGA 480

TTTTAACAAG TAAACCCAAG GGACAATCCA nAGATATTTT TTACAAAATT TAAGTAA 537

(2) INFORMATION FOR SEQ ID NO: 981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981:

TGTGGGTAGC GGCGAAATTC CAAACGAACT TGGAGATAGC TGGTTCTCTC CGAAATAGCT 60

TTAGGGnTAG CCTCGGAATT GAGaATGATG GAGGTAGAGC ACTGTTTGGA CTAGGGGCCC 120

ATCTCGGGTT ACCGAATTCA GATAAACTCC GrATGCCATT CATTTATaTC CGGGAGTCAG 180

ACTGCGAGTG ATAAGATCCG TAGTCGAAAG GGAAACAGCC CAGACCACCA GCTAAGGTCC 240

CnAAATATAT GTTAAGTGGA AAAGGATGTG GGGTTGCACA GACAACTAGG ATGTTGGCTT 300

AGAAGCAGCC ACCATTTAAA GAGTG 325

(2) INFORMATION FOR SEQ ID NO: 982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982:

GTAATATCCT ATAAAAGATA TTGGGTTCCC CCATTCGGAA ATCTCTGGAT CATAGCTTAC 60

TTACAGsTCC CCAAAGCATA TCGGTGTTAG TCCCGTCCTT CATCGGCTCC TAgTGCCAAG 120

GCATCCACCG TGCGcCCTTA TTCACTTAAc CTTATCAACC TTAcGGTTGG GTCTTGATCA 180

CTTCTTCTAG CGATAGAAGG TTAATCAATA AATAAGCAAT TGaACTaTTA AAAAACTCAT 240

TCAACGCGGk GTTCCgGTTt GGTTTgAAyC TtTtACTCmA AAATCCAGTT TTCAATGAAC 300

GAATGTTTgA GAGTAGACCC CCCCAAA 327

# INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

**A.** The indications made below relate to the microorganism referred to in the description
on page 8 , line 27

**B. IDENTIFICATION OF DEPOSIT** Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution (*including postal code and country*)

10801 University Boulevard
Manasas, Virginia 20110-2209
United States of America

Date of depositMay 2, 1997

Accession Number 55969

**C. ADDITIONAL INDICATIONS** *(leave blank if not applicable)* This information is continued on an additional sheet ☐

**D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE** *(if the indications are not for all designated States)*

**E. SEPARATE FURNISHING OF INDICATIONS** *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later (*specify the general nature of the indications, e.g., "Accession Number of Deposit"*)

For receiving Office use only

☑ This sheet was received with the international application

Authorized officer

For International Bureau use only

☐ This sheet was received by the International Bureau on:

Authorized officer

**What Is Claimed Is:**

1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-982, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-982.

2. The computer readable medium of claim 1 having recorded thereon any one of the fragments of SEQ ID NOS:1-982 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Enterococcus faecalis* genome of commercial importance comprising the following elements:

a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-982;

b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and

c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Enterococcus faecalis* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-982 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Enterococcus faecalis* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-982, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-

982 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *Enterococcus faecalis* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-982 depicted in Tables 2 and 3, or a degenerate variant thereof.

9. A vector comprising any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

10. An isolated fragment of the *Enterococcus faecalis* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading of claim 8.

11. A vector comprising any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *Enterococcus faecalis* genome of claim 8.

13. An organism which has been altered to contain any one of the fragments of the *Enterococcus faecalis* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule to a a nucleic acid molecule of claim 10.

15. An isolated polypeptide encoded by any of the fragments of the *Enterococcus faecalis* genome of claim 8.

16. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 15.

17. An antibody which selectively binds to any one of the polypeptides of claim 15.

18. A method for producing a polypeptide in a host cell comprising the steps of:

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Enterococcus faecalis* genome of claim 8, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

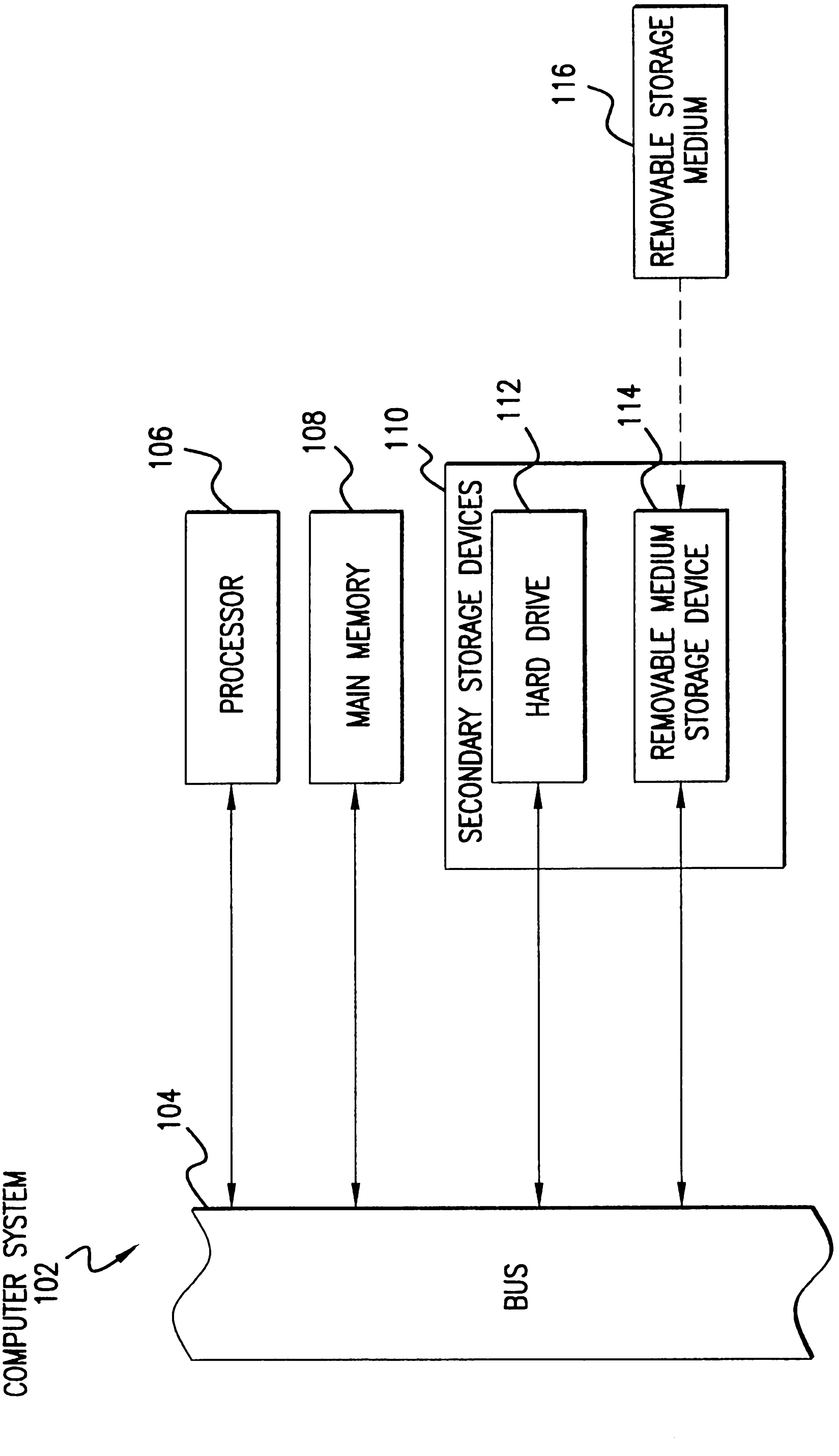
COMPUTER SYSTEM
102
104
BUS
106
PROCESSOR
108
MAIN MEMORY
110
SECONDARY STORAGE DEVICES
112
HARD DRIVE
114
REMOVABLE MEDIUM STORAGE DEVICE
116
REMOVABLE STORAGE MEDIUM

FIG. 1

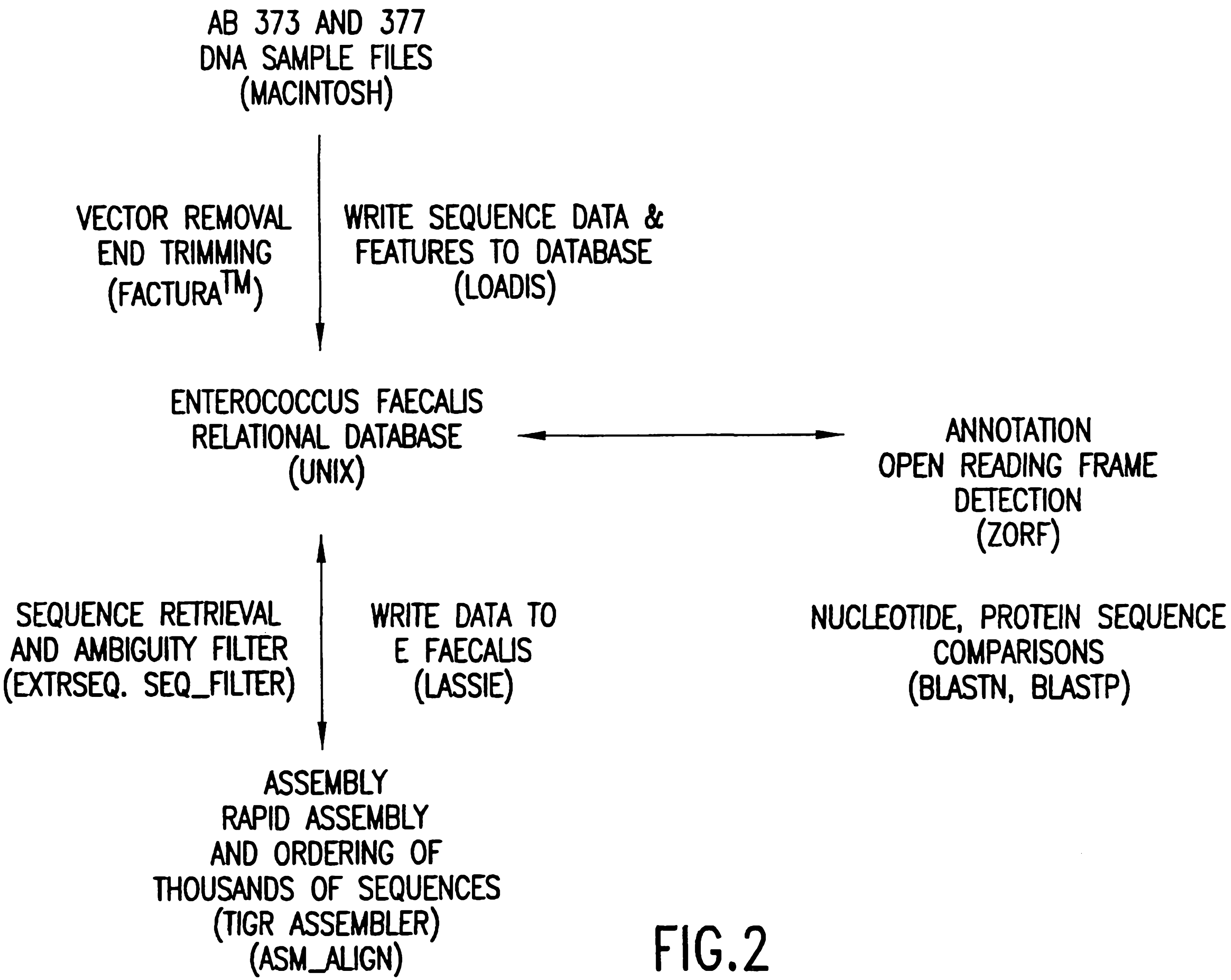
AB 373 AND 377
DNA SAMPLE FILES
(MACINTOSH)
VECTOR REMOVAL
END TRIMMING
(FACTURA™)
WRITE SEQUENCE DATA &
FEATURES TO DATABASE
(LOADIS)
ENTEROCOCCUS FAECALIS
RELATIONAL DATABASE
(UNIX)
ANNOTATION
OPEN READING FRAME
DETECTION
(ZORF)
NUCLEOTIDE, PROTEIN SEQUENCE
COMPARISONS
(BLASTN, BLASTP)
SEQUENCE RETRIEVAL
AND AMBIGUITY FILTER
(EXTRSEQ. SEQ_FILTER)
WRITE DATA TO
E FAECALIS
(LASSIE)
ASSEMBLY
RAPID ASSEMBLY
AND ORDERING OF
THOUSANDS OF SEQUENCES
(TIGR ASSEMBLER)
(ASM_ALIGN)

FIG.2