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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

(57) Abrégé/Abstract:
The present invention relates to compositions containing novel proteins and methods of using those compositions for the diagnosis and treatment of immune related diseases.

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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

(57) Abstract: The present invention relates to compositions containing novel proteins and methods of using those compositions for the diagnosis and treatment of immune related diseases.

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COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

Field of the Invention

The present invention relates to compositions and methods useful for the diagnosis and treatment of immune related diseases.

Background of the Invention

Immune related and inflammatory diseases are the manifestation or consequence of fairly complex, often multiple interconnected biological pathways which in normal physiology are critical to respond to insult or injury, initiate repair from insult or injury, and mount innate and acquired defense against foreign organisms. Disease or pathology occurs when these normal physiological pathways cause additional insult or injury either as directly related to the intensity of the response, as a consequence of abnormal regulation or excessive stimulation, as a reaction to self, or as a combination of these.

Though the genesis of these diseases often involves multistep pathways and often multiple different biological systems/pathways, intervention at critical points in one or more of these pathways can have an ameliorative or therapeutic effect. Therapeutic intervention can occur by either antagonism of a detrimental process/pathway or stimulation of a beneficial process/pathway.

Many immune related diseases are known and have been extensively studied. Such diseases include immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*

T lymphocytes (T cells) are an important component of a mammalian immune response. T cells recognize antigens which are associated with a self-molecule encoded by genes within the major histocompatibility complex (MHC). The antigen may be displayed together with MHC molecules on the surface of antigen presenting cells, virus infected cells, cancer cells, grafts, *etc.* The T cell system eliminates these altered cells which pose a health threat to the host mammal. T cells include helper T cells and cytotoxic T cells. Helper T cells proliferate extensively following recognition of an antigen -MHC complex on an antigen presenting cell. Helper T cells also secrete a variety of cytokines, *i.e.,* lymphokines, which play a central role in the activation of B cells, cytotoxic T cells and a variety of other cells which participate in the immune response.

Immune related diseases could be treated by suppressing the immune response. Using neutralizing antibodies that inhibit molecules having immune stimulatory activity would be beneficial in the treatment of immune-mediated and inflammatory diseases. Molecules which inhibit the immune response can be utilized (proteins directly or via the use of antibody agonists) to inhibit the immune response and thus ameliorate immune related disease.

T cells play a central role in host defense. T cells are able to modulate the immune response of other cell lineages through the production of a variety of cytokines and immune modulatory molecules. In addition they are responsible for surveying cells throughout the organism for the presence of non-self. This highly sophisticated process utilizes the T cell receptor (TCR), which is able to recognize and discriminate

between self and non-self peptides displayed by the MHC complex on other cells. This process also integrates co-stimulatory signals that provide additional information to the T cell about the nature of the potential non-self threat. These two signals, the TCR signal and the co-stimulatory signal can be experimentally triggered by use of agonist antibodies such as certain antibodies to the T cell receptor component CD3, and the co-stimulatory receptor CD28. While T cells are essential components of normal immune function, it is believed that inappropriate T cell function underlies many very serious medical conditions including autoimmune disease. Diseases that are impacted by pathologic T cell function are thought to include asthma, arthritis, psoriasis, multiple sclerosis, inflammatory bowel disease, diabetes, graft versus host disease and many others. In these diseases the portion of the T cell repertoire that has a "memory" phenotype is thought to contribute to the disease pathology. It is therefore of great importance to understand the molecular events that occur upon activation of memory T cells. In humans, memory T cells can be identified through the use of the antigen CD45RO which is expressed on memory T cells but not on resting naïve T cells. The use of DNA microarrays provides a powerful experimental approach to identify molecular changes that occur upon activation of this critical cell population. Understanding the identity of molecules whose expression is altered upon memory T cell activation can enable therapeutic strategies that target the pathways impacted by these alterations in gene expression. Such therapeutic strategies can include the use of recombinant proteins, soluble receptors, antibodies, peptides, or small molecule drugs.

Despite the above identified advances in T cell research, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of memory T cell mediated disorders in a mammal and for effectively reducing these disorders. Accordingly, it is an objective of the present invention to identify polypeptides that are overexpressed in memory T cells as compared to non-memory T cells, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of memory T cell mediated disorders in mammals.

Summary of the Invention

A. Embodiments

The present invention concerns compositions and methods useful for the diagnosis and treatment of immune related disease in mammals, including humans. The present invention is based on the identification of proteins (including agonist and antagonist antibodies) which are a result of stimulation of the immune response in mammals. Immune related diseases can be treated by suppressing or enhancing the immune response. Molecules that enhance the immune response stimulate or potentiate the immune response to an antigen. Molecules which stimulate the immune response can be used therapeutically where enhancement of the immune response would be beneficial. Alternatively, molecules that suppress the immune response attenuate or reduce the immune response to an antigen (*e.g.*, neutralizing antibodies) can be used therapeutically where attenuation of the immune response would be beneficial (*e.g.*, inflammation). Accordingly, the PRO polypeptides, agonists and antagonists thereof are also useful to prepare medicines and medicaments for the treatment of immune-related and inflammatory diseases. In a specific aspect, such medicines and medicaments comprise a therapeutically effective amount of a PRO polypeptide, agonist or antagonist thereof with a pharmaceutically acceptable carrier. Preferably, the admixture is sterile.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a

PRO polypeptide which comprises contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native sequence PRO polypeptide. In a specific aspect, the PRO agonist or antagonist is an anti-PRO antibody.

In another embodiment, the invention concerns a composition of matter comprising a PRO polypeptide or an agonist or antagonist antibody which binds the polypeptide in admixture with a carrier or excipient. In one aspect, the composition comprises a therapeutically effective amount of the polypeptide or antibody. In another aspect, when the composition comprises an immune stimulating molecule, the composition is useful for: (a) increasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) stimulating or enhancing an immune response in a mammal in need thereof, (c) increasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen, (d) stimulating the activity of T-lymphocytes or (e) increasing the vascular permeability. In a further aspect, when the composition comprises an immune inhibiting molecule, the composition is useful for: (a) decreasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) inhibiting or reducing an immune response in a mammal in need thereof, (c) decreasing the activity of T-lymphocytes or (d) decreasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen. In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or a cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

In another embodiment, the invention concerns a method of treating an immune related disorder in a mammal in need thereof, comprising administering to the mammal an effective amount of a PRO polypeptide, an agonist thereof, or an antagonist thereto. In a preferred aspect, the immune related disorder is selected from the group consisting of: systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody. In one aspect, the present invention concerns an isolated antibody which binds a PRO polypeptide. In another aspect, the antibody mimics the activity of a PRO polypeptide (an agonist antibody) or conversely the antibody inhibits or neutralizes the activity of a PRO polypeptide (an antagonist antibody). In another aspect, the antibody is a monoclonal antibody, which

preferably has nonhuman complementarity determining region (CDR) residues and human framework region (FR) residues. The antibody may be labeled and may be immobilized on a solid support. In a further aspect, the antibody is an antibody fragment, a monoclonal antibody, a single-chain antibody, or an anti-idiotypic antibody.

In yet another embodiment, the present invention provides a composition comprising an anti-PRO antibody in admixture with a pharmaceutically acceptable carrier. In one aspect, the composition comprises a therapeutically effective amount of the antibody. Preferably, the composition is sterile. The composition may be administered in the form of a liquid pharmaceutical formulation, which may be preserved to achieve extended storage stability. Alternatively, the antibody is a monoclonal antibody, an antibody fragment, a humanized antibody, or a single-chain antibody.

In a further embodiment, the invention concerns an article of manufacture, comprising:

(a) a composition of matter comprising a PRO polypeptide or agonist or antagonist thereof;

(b) a container containing said composition; and

(c) a label affixed to said container, or a package insert included in said container referring to the use of said PRO polypeptide or agonist or antagonist thereof in the treatment of an immune related disease. The composition may comprise a therapeutically effective amount of the PRO polypeptide or the agonist or antagonist thereof.

In yet another embodiment, the present invention concerns a method of diagnosing an immune related disease in a mammal, comprising detecting the level of expression of a gene encoding a PRO polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower expression level in the test sample as compared to the control sample indicates the presence of immune related disease in the mammal from which the test tissue cells were obtained.

In another embodiment, the present invention concerns a method of diagnosing an immune disease in a mammal, comprising (a) contacting an anti-PRO antibody with a test sample of tissue cells obtained from the mammal, and (b) detecting the formation of a complex between the antibody and a PRO polypeptide, in the test sample; wherein the formation of said complex is indicative of the presence or absence of said disease. The detection may be qualitative or quantitative, and may be performed in comparison with monitoring the complex formation in a control sample of known normal tissue cells of the same cell type. A larger quantity of complexes formed in the test sample indicates the presence or absence of an immune disease in the mammal from which the test tissue cells were obtained. The antibody preferably carries a detectable label. Complex formation can be monitored, for example, by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. The test sample is usually obtained from an individual suspected of having a deficiency or abnormality of the immune system.

In another embodiment, the invention provides a method for determining the presence of a PRO polypeptide in a sample comprising exposing a test sample of cells suspected of containing the PRO polypeptide to an anti-PRO antibody and determining the binding of said antibody to said cell sample. In a specific aspect, the sample comprises a cell suspected of containing the PRO polypeptide and the antibody binds to the cell. The antibody is preferably detectably labeled and/or bound to a solid support.

In another embodiment, the present invention concerns an immune-related disease diagnostic kit,

comprising an anti-PRO antibody and a carrier in suitable packaging. The kit preferably contains instructions for using the antibody to detect the presence of the PRO polypeptide. Preferably the carrier is pharmaceutically acceptable.

In another embodiment, the present invention concerns a diagnostic kit, containing an anti-PRO antibody in suitable packaging. The kit preferably contains instructions for using the antibody to detect the PRO polypeptide.

In another embodiment, the invention provides a method of diagnosing an immune-related disease in a mammal which comprises detecting the presence or absence or a PRO polypeptide in a test sample of tissue cells obtained from said mammal, wherein the presence or absence of the PRO polypeptide in said test sample is indicative of the presence of an immune-related disease in said mammal.

In another embodiment, the present invention concerns a method for identifying an agonist of a PRO polypeptide comprising:

(a) contacting cells and a test compound to be screened under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and

(b) determining the induction of said cellular response to determine if the test compound is an effective agonist, wherein the induction of said cellular response is indicative of said test compound being an effective agonist.

In another embodiment, the invention concerns a method for identifying a compound capable of inhibiting the activity of a PRO polypeptide comprising contacting a candidate compound with a PRO polypeptide under conditions and for a time sufficient to allow these two components to interact and determining whether the activity of the PRO polypeptide is inhibited. In a specific aspect, either the candidate compound or the PRO polypeptide is immobilized on a solid support. In another aspect, the non-immobilized component carries a detectable label. In a preferred aspect, this method comprises the steps of:

(a) contacting cells and a test compound to be screened in the presence of a PRO polypeptide under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and

(b) determining the induction of said cellular response to determine if the test compound is an effective antagonist.

In another embodiment, the invention provides a method for identifying a compound that inhibits the expression of a PRO polypeptide in cells that normally express the polypeptide, wherein the method comprises contacting the cells with a test compound and determining whether the expression of the PRO polypeptide is inhibited. In a preferred aspect, this method comprises the steps of:

(a) contacting cells and a test compound to be screened under conditions suitable for allowing expression of the PRO polypeptide; and

(b) determining the inhibition of expression of said polypeptide.

In yet another embodiment, the present invention concerns a method for treating an immune-related disorder in a mammal that suffers therefrom comprising administering to the mammal a nucleic acid molecule that codes for either (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide or (c) an antagonist of a PRO polypeptide, wherein said agonist or antagonist may be an anti-PRO antibody. In a preferred embodiment, the mammal is human. In another preferred embodiment, the nucleic acid is administered via *ex vivo* gene therapy. In a further preferred embodiment, the nucleic acid is comprised

within a vector, more preferably an adenoviral, adeno-associated viral, lentiviral or retroviral vector.

In yet another aspect, the invention provides a recombinant viral particle comprising a viral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide, or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein the viral vector is in association with viral structural proteins. Preferably, the signal sequence is from a mammal, such as from a native PRO polypeptide.

In a still further embodiment, the invention concerns an *ex vivo* producer cell comprising a nucleic acid construct that expresses retroviral structural proteins and also comprises a retroviral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein said producer cell packages the retroviral vector in association with the structural proteins to produce recombinant retroviral particles.

In a still further embodiment, the invention provides a method of increasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is decreased.

In a still further embodiment, the invention provides a method of increasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is decreased.

B. Additional Embodiments

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

In other embodiments, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an

extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700

nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences herein above identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid

sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as herein before described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as herein before described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

BRIEF DESCRIPTION OF THE DRAWINGS

The Figures 1-2442 show the nucleic acids of the invention and their encoded PRO polypeptides.

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO84739 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA329084".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO61679 cDNA, wherein SEQ ID NO3: is a clone designated herein as "DNA273712".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO83580 cDNA, wherein SEQ ID NO5: is a clone designated herein as "DNA327535".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO5: shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO60800 cDNA, wherein SEQ ID NO: is a clone designated herein as "DNA326466".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO: 7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO84740 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA329085".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO84741 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA329086".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO69614 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA329087".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO71125 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA324783".

Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO40279 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA329088".

Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO60747 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA272614".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO71106 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA304680".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO37034 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA226571".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO84742 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA329089".

Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO84743 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA329090".

Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO22637 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA189703".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO81962 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA325438".

Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO11997 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA329091".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO59293 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA270963".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO33667 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA210121".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO84744 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA329092".

Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO49242 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA254127".

Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO4546 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA103216".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO38028 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA328356".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO65 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA324158".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO84745 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA329093".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO84746 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA329094".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO84223 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA328364".

Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO84670 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA328966".

Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO77352 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA329095".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO83815 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA327876".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO12926 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA153752".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO59084 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA270721".

Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO69520 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA287245".

Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO71134 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA327532".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO3632 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA97285".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO84747 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA329096".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO37518 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA227055".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO81277 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA324633".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO81277 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA324633".

Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO70258 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA324058".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO61271 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA327845".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO39268 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA287207".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO84748 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA329097".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO59895 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA271608".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO80773 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA324060".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO69492 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA287211".

Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO38258 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA227795".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO83005 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA326655".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO84749 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA329098".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO83581 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA327537".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO49642 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA254537".

Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO49675 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA254572".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO59358 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA271030".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO81477 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA324871".

Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO80814 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA324107".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO60127 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA329099".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO60127 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA271847".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO69473 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA287187".

Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO62041 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA274103".

Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA328380".

Figure 120 shows a nucleotide sequence (SEQ ID NO:120) of a native sequence PRO61053 cDNA, wherein SEQ ID NO:120 is a clone designated herein as "DNA272974".

Figure 121 shows the amino acid sequence (SEQ ID NO:121) derived from the coding sequence of SEQ ID NO:120 shown in Figure 120.

Figure 122 shows a nucleotide sequence (SEQ ID NO:122) of a native sequence PRO57298 cDNA, wherein SEQ ID NO:122 is a clone designated herein as "DNA327255".

Figure 123 shows the amino acid sequence (SEQ ID NO:123) derived from the coding sequence of SEQ ID NO:122 shown in Figure 122.

Figure 124 shows a nucleotide sequence (SEQ ID NO:124) of a native sequence PRO38005 cDNA, wherein SEQ ID NO:124 is a clone designated herein as "DNA327540".

Figure 125 shows the amino acid sequence (SEQ ID NO:125) derived from the coding sequence of SEQ ID NO:124 shown in Figure 124.

Figure 126 shows a nucleotide sequence (SEQ ID NO:126) of a native sequence PRO36766 cDNA, wherein SEQ ID NO:126 is a clone designated herein as "DNA287217".

Figure 127 shows the amino acid sequence (SEQ ID NO:127) derived from the coding sequence of SEQ ID NO:126 shown in Figure 126.

Figure 128 shows a nucleotide sequence (SEQ ID NO:128) of a native sequence PRO84750 cDNA, wherein SEQ ID NO:128 is a clone designated herein as "DNA329100".

Figure 129 shows the amino acid sequence (SEQ ID NO:129) derived from the coding sequence of SEQ ID NO:128 shown in Figure 128.

Figure 130 shows a nucleotide sequence (SEQ ID NO:130) of a native sequence PRO82352 cDNA, wherein SEQ ID NO:130 is a clone designated herein as "DNA325896".

Figure 131 shows the amino acid sequence (SEQ ID NO:131) derived from the coding sequence of SEQ ID NO:130 shown in Figure 130.

Figure 132 shows a nucleotide sequence (SEQ ID NO:132) of a native sequence PRO71139 cDNA, wherein SEQ ID NO:132 is a clone designated herein as "DNA304713".

Figure 133 shows the amino acid sequence (SEQ ID NO:133) derived from the coding sequence of SEQ ID NO:132 shown in Figure 132.

Figure 134 shows a nucleotide sequence (SEQ ID NO:134) of a native sequence PRO2907 cDNA, wherein SEQ ID NO:134 is a clone designated herein as "DNA89242".

Figure 135 shows the amino acid sequence (SEQ ID NO:135) derived from the coding sequence of SEQ ID NO:134 shown in Figure 134.

Figure 136 shows a nucleotide sequence (SEQ ID NO:136) of a native sequence PRO84240 cDNA, wherein SEQ ID NO:136 is a clone designated herein as "DNA328388".

Figure 137 shows the amino acid sequence (SEQ ID NO:137) derived from the coding sequence of SEQ ID NO:136 shown in Figure 136.

Figure 138 shows a nucleotide sequence (SEQ ID NO:138) of a native sequence PRO11993 cDNA, wherein SEQ ID NO:138 is a clone designated herein as "DNA151697".

Figure 139 shows the amino acid sequence (SEQ ID NO:139) derived from the coding sequence of SEQ ID NO:138 shown in Figure 138.

Figure 140 shows a nucleotide sequence (SEQ ID NO:140) of a native sequence PRO84751 cDNA, wherein SEQ ID NO:140 is a clone designated herein as "DNA329101".

Figure 141 shows the amino acid sequence (SEQ ID NO:141) derived from the coding sequence of SEQ ID NO:140 shown in Figure 140.

Figure 142 shows a nucleotide sequence (SEQ ID NO:142) of a native sequence PRO69632 cDNA, wherein SEQ ID NO:142 is a clone designated herein as "DNA287372".

Figure 143 shows the amino acid sequence (SEQ ID NO:143) derived from the coding sequence of SEQ ID NO:142 shown in Figure 142.

Figure 144 shows a nucleotide sequence (SEQ ID NO:144) of a native sequence PRO81592 cDNA, wherein SEQ ID NO:144 is a clone designated herein as "DNA325001".

Figure 145 shows the amino acid sequence (SEQ ID NO:145) derived from the coding sequence of SEQ ID NO:144 shown in Figure 144.

Figure 146 shows a nucleotide sequence (SEQ ID NO:146) of a native sequence PRO83292 cDNA, wherein SEQ ID NO:146 is a clone designated herein as "DNA326984".

Figure 147 shows the amino acid sequence (SEQ ID NO:147) derived from the coding sequence of SEQ ID NO:146 shown in Figure 146.

Figure 148 shows a nucleotide sequence (SEQ ID NO:148) of a native sequence PRO615 cDNA, wherein SEQ ID NO:148 is a clone designated herein as "DNA329102".

Figure 149 shows the amino acid sequence (SEQ ID NO:149) derived from the coding sequence of SEQ ID NO:148 shown in Figure 148.

Figure 150 shows a nucleotide sequence (SEQ ID NO:150) of a native sequence PRO49824 cDNA, wherein SEQ ID NO:150 is a clone designated herein as "DNA254725".

Figure 151 shows the amino acid sequence (SEQ ID NO:151) derived from the coding sequence of SEQ ID NO:150 shown in Figure 150.

Figure 152 shows a nucleotide sequence (SEQ ID NO:152) of a native sequence PRO69484 cDNA, wherein SEQ ID NO:152 is a clone designated herein as "DNA287198".

Figure 153 shows the amino acid sequence (SEQ ID NO:153) derived from the coding sequence of SEQ ID NO:152 shown in Figure 152.

Figure 154 shows a nucleotide sequence (SEQ ID NO:154) of a native sequence PRO36173 cDNA, wherein SEQ ID NO:154 is a clone designated herein as "DNA225710".

Figure 155 shows the amino acid sequence (SEQ ID NO:155) derived from the coding sequence of SEQ ID NO:154 shown in Figure 154.

Figure 156 shows a nucleotide sequence (SEQ ID NO:156) of a native sequence PRO82678 cDNA, wherein SEQ ID NO:156 is a clone designated herein as "DNA326273".

Figure 157 shows the amino acid sequence (SEQ ID NO:157) derived from the coding sequence of SEQ ID NO:156 shown in Figure 156.

Figure 158 shows a nucleotide sequence (SEQ ID NO:158) of a native sequence PRO84752 cDNA, wherein SEQ ID NO:158 is a clone designated herein as "DNA329103".

Figure 159 shows the amino acid sequence (SEQ ID NO:159) derived from the coding sequence of SEQ ID NO:158 shown in Figure 158.

Figure 160 shows a nucleotide sequence (SEQ ID NO:160) of a native sequence PRO69550 cDNA, wherein SEQ ID NO:160 is a clone designated herein as "DNA329104".

Figure 161 shows the amino acid sequence (SEQ ID NO:161) derived from the coding sequence of SEQ ID NO:160 shown in Figure 160.

Figure 162 shows a nucleotide sequence (SEQ ID NO:162) of a native sequence PRO84753 cDNA, wherein SEQ ID NO:162 is a clone designated herein as "DNA329105".

Figure 163 shows the amino acid sequence (SEQ ID NO:163) derived from the coding sequence of SEQ ID NO:162 shown in Figure 162.

Figure 164 shows a nucleotide sequence (SEQ ID NO:164) of a native sequence PRO12890 cDNA, wherein SEQ ID NO:164 is a clone designated herein as "DNA151802".

Figure 165 shows the amino acid sequence (SEQ ID NO:165) derived from the coding sequence of SEQ ID NO:164 shown in Figure 164.

Figure 166 shows a nucleotide sequence (SEQ ID NO:166) of a native sequence PRO4780 cDNA, wherein SEQ ID NO:166 is a clone designated herein as "DNA103453".

Figure 167 shows the amino acid sequence (SEQ ID NO:167) derived from the coding sequence of SEQ ID NO:166 shown in Figure 166.

Figure 168 shows a nucleotide sequence (SEQ ID NO:168) of a native sequence PRO60513 cDNA, wherein SEQ ID NO:168 is a clone designated herein as "DNA272251".

Figure 169 shows the amino acid sequence (SEQ ID NO:169) derived from the coding sequence of SEQ ID NO:168 shown in Figure 168.

Figure 170 shows a nucleotide sequence (SEQ ID NO:170) of a native sequence PRO61616 cDNA, wherein SEQ ID NO:170 is a clone designated herein as "DNA273645".

Figure 171 shows the amino acid sequence (SEQ ID NO:171) derived from the coding sequence of SEQ ID NO:170 shown in Figure 170.

Figure 172 shows a nucleotide sequence (SEQ ID NO:172) of a native sequence PRO69463 cDNA, wherein SEQ ID NO:172 is a clone designated herein as "DNA287173".

Figure 173 shows the amino acid sequence (SEQ ID NO:173) derived from the coding sequence of SEQ ID NO:172 shown in Figure 172.

Figure 174 shows a nucleotide sequence (SEQ ID NO:174) of a native sequence PRO69595 cDNA, wherein SEQ ID NO:174 is a clone designated herein as "DNA287331".

Figure 175 shows the amino acid sequence (SEQ ID NO:175) derived from the coding sequence of SEQ ID NO:174 shown in Figure 174.

Figure 176 shows a nucleotide sequence (SEQ ID NO:176) of a native sequence PRO62075 cDNA, wherein SEQ ID NO:176 is a clone designated herein as "DNA274139".

Figure 177 shows the amino acid sequence (SEQ ID NO:177) derived from the coding sequence of SEQ ID NO:176 shown in Figure 176.

Figure 178 shows a nucleotide sequence (SEQ ID NO:178) of a native sequence PRO59281 cDNA, wherein SEQ ID NO:178 is a clone designated herein as "DNA270950".

Figure 179 shows the amino acid sequence (SEQ ID NO:179) derived from the coding sequence of SEQ ID NO:178 shown in Figure 178.

Figure 180 shows a nucleotide sequence (SEQ ID NO:180) of a native sequence PRO81979 cDNA, wherein SEQ ID NO:180 is a clone designated herein as "DNA329004".

Figure 181 shows the amino acid sequence (SEQ ID NO:181) derived from the coding sequence of SEQ ID NO:180 shown in Figure 180.

Figure 182 shows a nucleotide sequence (SEQ ID NO:182) of a native sequence PRO84252 cDNA, wherein SEQ ID NO:182 is a clone designated herein as "DNA328405".

Figure 183 shows the amino acid sequence (SEQ ID NO:183) derived from the coding sequence of SEQ ID NO:182 shown in Figure 182.

Figure 184 shows a nucleotide sequence (SEQ ID NO:184) of a native sequence PRO83360 cDNA, wherein SEQ ID NO:184 is a clone designated herein as "DNA329106".

Figure 185 shows the amino acid sequence (SEQ ID NO:185) derived from the coding sequence of SEQ ID NO:184 shown in Figure 184.

Figure 186 shows a nucleotide sequence (SEQ ID NO:186) of a native sequence PRO71133 cDNA, wherein SEQ ID NO:186 is a clone designated herein as "DNA304707".

Figure 187 shows the amino acid sequence (SEQ ID NO:187) derived from the coding sequence of SEQ ID NO:186 shown in Figure 186.

Figure 188 shows a nucleotide sequence (SEQ ID NO:188) of a native sequence PRO62518 cDNA, wherein SEQ ID NO188: is a clone designated herein as "DNA274745".

Figure 189 shows the amino acid sequence (SEQ ID NO:189) derived from the coding sequence of SEQ ID NO:188 shown in Figure 188.

Figure 190 shows a nucleotide sequence (SEQ ID NO:190) of a native sequence PRO4912 cDNA, wherein SEQ ID NO:190 is a clone designated herein as "DNA329002".

Figure 191 shows the amino acid sequence (SEQ ID NO:191) derived from the coding sequence of SEQ ID NO:190 shown in Figure 190.

Figure 192 shows a nucleotide sequence (SEQ ID NO:192) of a native sequence PRO4912 cDNA, wherein SEQ ID NO:192 is a clone designated herein as "DNA329002".

Figure 193 shows the amino acid sequence (SEQ ID NO:193) derived from the coding sequence of SEQ ID NO:192 shown in Figure 192.

Figure 194 shows a nucleotide sequence (SEQ ID NO:194) of a native sequence PRO59943 cDNA, wherein SEQ ID NO:194 is a clone designated herein as "DNA271656".

Figure 195 shows the amino acid sequence (SEQ ID NO:195) derived from the coding sequence of SEQ ID NO:194 shown in Figure 194.

Figure 196 shows a nucleotide sequence (SEQ ID NO:196) of a native sequence PRO84754 cDNA, wherein SEQ ID NO:196 is a clone designated herein as "DNA329107".

Figure 197 shows the amino acid sequence (SEQ ID NO:197) derived from the coding sequence of SEQ ID NO:196 shown in Figure 196.

Figure 198 shows a nucleotide sequence (SEQ ID NO:198) of a native sequence PRO84755 cDNA, wherein SEQ ID NO:198 is a clone designated herein as "DNA329108".

Figure 199 shows the amino acid sequence (SEQ ID NO:199) derived from the coding sequence of SEQ ID NO:198 shown in Figure 198.

Figure 200 shows a nucleotide sequence (SEQ ID NO:200) of a native sequence PRO81854 cDNA, wherein SEQ ID NO:200 is a clone designated herein as "DNA329109".

Figure 201 shows the amino acid sequence (SEQ ID NO:201) derived from the coding sequence of SEQ ID NO:200 shown in Figure 200.

Figure 202 shows a nucleotide sequence (SEQ ID NO:202) of a native sequence PRO11586 cDNA, wherein SEQ ID NO:202 is a clone designated herein as "DNA329110".

Figure 203 shows the amino acid sequence (SEQ ID NO:203) derived from the coding sequence of SEQ ID NO:202 shown in Figure 202.

Figure 204 shows a nucleotide sequence (SEQ ID NO:204) of a native sequence PRO cDNA, wherein SEQ ID NO:204 is a clone designated herein as "DNA".

Figure 205 shows the amino acid sequence (SEQ ID NO:205) derived from the coding sequence of SEQ ID NO:204 shown in Figure 204.

Figure 206 shows a nucleotide sequence (SEQ ID NO:206) of a native sequence PRO59309 cDNA, wherein SEQ ID NO:206 is a clone designated herein as "DNA270979".

Figure 207 shows the amino acid sequence (SEQ ID NO:207) derived from the coding sequence of SEQ ID NO:206 shown in Figure 206.

Figure 208 shows a nucleotide sequence (SEQ ID NO:208) of a native sequence PRO2338 cDNA, wherein SEQ ID NO:208 is a clone designated herein as "DNA88418".

Figure 209 shows the amino acid sequence (SEQ ID NO:209) derived from the coding sequence of SEQ ID NO:208 shown in Figure 208.

Figure 210 shows a nucleotide sequence (SEQ ID NO:210) of a native sequence PRO37063 cDNA, wherein SEQ ID NO:210 is a clone designated herein as "DNA226600".

Figure 211 shows the amino acid sequence (SEQ ID NO:211) derived from the coding sequence of SEQ ID NO:210 shown in Figure 210.

Figure 212 shows a nucleotide sequence (SEQ ID NO:212) of a native sequence PRO84757 cDNA, wherein SEQ ID NO:212 is a clone designated herein as "DNA329112".

Figure 213 shows the amino acid sequence (SEQ ID NO:213) derived from the coding sequence of SEQ ID NO:212 shown in Figure 212.

Figure 214 shows a nucleotide sequence (SEQ ID NO:214) of a native sequence PRO83076 cDNA, wherein SEQ ID NO:214 is a clone designated herein as "DNA326736".

Figure 215 shows the amino acid sequence (SEQ ID NO:215) derived from the coding sequence of SEQ ID NO:214 shown in Figure 214.

Figure 216 shows a nucleotide sequence (SEQ ID NO:216) of a native sequence PRO49881 cDNA, wherein SEQ ID NO:216 is a clone designated herein as "DNA254783".

Figure 217 shows the amino acid sequence (SEQ ID NO:217) derived from the coding sequence of SEQ ID NO:216 shown in Figure 216.

Figure 218 shows a nucleotide sequence (SEQ ID NO:218) of a native sequence PRO37073 cDNA, wherein SEQ ID NO:218 is a clone designated herein as "DNA304459".

Figure 219 shows the amino acid sequence (SEQ ID NO:219) derived from the coding sequence of SEQ ID NO:218 shown in Figure 218.

Figure 220 shows a nucleotide sequence (SEQ ID NO:220) of a native sequence PRO37073 cDNA, wherein SEQ ID NO:220 is a clone designated herein as "DNA304459".

Figure 221 shows the amino acid sequence (SEQ ID NO:221) derived from the coding sequence of SEQ ID NO:220 shown in Figure 220.

Figure 222 shows a nucleotide sequence (SEQ ID NO:222) of a native sequence PRO49210 cDNA, wherein SEQ ID NO:222 is a clone designated herein as "DNA253807".

Figure 223 shows the amino acid sequence (SEQ ID NO:223) derived from the coding sequence of SEQ ID NO:222 shown in Figure 222.

Figure 224 shows a nucleotide sequence (SEQ ID NO:224) of a native sequence PRO80498 cDNA, wherein SEQ ID NO:224 is a clone designated herein as "DNA323741".

Figure 225 shows the amino acid sequence (SEQ ID NO:225) derived from the coding sequence of SEQ ID NO:224 shown in Figure 224.

Figure 226 shows a nucleotide sequence (SEQ ID NO:226) of a native sequence PRO83586 cDNA, wherein SEQ ID NO:226 is a clone designated herein as "DNA327555".

Figure 227 shows the amino acid sequence (SEQ ID NO:227) derived from the coding sequence of SEQ ID NO:226 shown in Figure 226.

Figure 228 shows a nucleotide sequence (SEQ ID NO:228) of a native sequence PRO3647 cDNA, wherein SEQ ID NO:228 is a clone designated herein as "DNA97300".

Figure 229 shows the amino acid sequence (SEQ ID NO:229) derived from the coding sequence of SEQ ID NO:228 shown in Figure 228.

Figure 230 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO84262 cDNA, wherein SEQ ID NO:230 is a clone designated herein as "DNA328419".

Figure 231 shows the amino acid sequence (SEQ ID NO:231) derived from the coding sequence of SEQ ID NO:230 shown in Figure 230.

Figure 232 shows a nucleotide sequence (SEQ ID NO:232) of a native sequence PRO37941 cDNA, wherein SEQ ID NO:232 is a clone designated herein as "DNA227478".

Figure 233 shows the amino acid sequence (SEQ ID NO:233) derived from the coding sequence of SEQ ID NO:232 shown in Figure 232.

Figure 234 shows a nucleotide sequence (SEQ ID NO:234) of a native sequence PRO59324 cDNA, wherein SEQ ID NO:234 is a clone designated herein as "DNA270995".

Figure 235 shows the amino acid sequence (SEQ ID NO:235) derived from the coding sequence of SEQ ID NO:234 shown in Figure 234.

Figure 236 shows a nucleotide sequence (SEQ ID NO:236) of a native sequence PRO37534 cDNA, wherein SEQ ID NO:236 is a clone designated herein as "DNA227071".

Figure 237 shows the amino acid sequence (SEQ ID NO:237) derived from the coding sequence of SEQ ID NO:236 shown in Figure 236.

Figure 238 shows a nucleotide sequence (SEQ ID NO:238) of a native sequence PRO84758 cDNA, wherein SEQ ID NO:238 is a clone designated herein as "DNA329113".

Figure 239 shows the amino acid sequence (SEQ ID NO:239) derived from the coding sequence of SEQ ID NO:238 shown in Figure 238.

Figure 240 shows a nucleotide sequence (SEQ ID NO:240) of a native sequence PRO70425 cDNA, wherein SEQ ID NO:240 is a clone designated herein as "DNA290280".

Figure 241 shows the amino acid sequence (SEQ ID NO:241) derived from the coding sequence of SEQ ID NO:240 shown in Figure 240.

Figure 242 shows a nucleotide sequence (SEQ ID NO:242) of a native sequence PRO60991 cDNA, wherein SEQ ID NO:242 is a clone designated herein as "DNA272904".

Figure 243 shows the amino acid sequence (SEQ ID NO:243) derived from the coding sequence of SEQ ID NO:242 shown in Figure 242.

Figure 244 shows a nucleotide sequence (SEQ ID NO:244) of a native sequence PRO84759 cDNA, wherein SEQ ID NO:244 is a clone designated herein as "DNA329114".

Figure 245 shows the amino acid sequence (SEQ ID NO:245) derived from the coding sequence of SEQ ID NO:244 shown in Figure 244.

Figure 246 shows a nucleotide sequence (SEQ ID NO:246) of a native sequence PRO84760 cDNA, wherein SEQ ID NO:246 is a clone designated herein as "DNA329115".

Figure 247 shows the amino acid sequence (SEQ ID NO:247) derived from the coding sequence of SEQ ID NO:246 shown in Figure 246.

Figure 248 shows a nucleotide sequence (SEQ ID NO:248) of a native sequence PRO34726 cDNA, wherein SEQ ID NO:248 is a clone designated herein as "DNA220748".

Figure 249 shows the amino acid sequence (SEQ ID NO:249) derived from the coding sequence of SEQ ID NO:248 shown in Figure 248.

Figure 250 shows a nucleotide sequence (SEQ ID NO:250) of a native sequence PRO84761 cDNA, wherein SEQ ID NO:250 is a clone designated herein as "DNA329116".

Figure 251 shows the amino acid sequence (SEQ ID NO:251) derived from the coding sequence of SEQ ID NO:250 shown in Figure 250.

Figure 252 shows a nucleotide sequence (SEQ ID NO:252) of a native sequence cDNA, wherein SEQ ID NO:252 is a clone designated herein as "DNA329117".

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO37335 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA226872".

Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO37924 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA227461".

Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO38039 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA227576".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO82769 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA326373".

Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO83589 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA327559".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO59136 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA287167".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO69491 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA287625".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO80735 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA324015".

Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO83123 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA329118".

Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO2842 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA88562".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO60337 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA272066".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO11583 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA150805".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO80988 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA324310".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO63048 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA275385".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO37575 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA227112".

Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO62927 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA275240".

Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO4554 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA329119".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO2752 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA329120".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

Figure 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO62097 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA274167".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figure 289.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO62908 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA275214".

Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO83596 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA327567".

Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO36579 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA226116".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO60487 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA272225".

Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO84274 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA328440".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO84695 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA329020".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO84275 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA328442".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO49673 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA254570".

Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO84763 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA329121".

Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO84277 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA328444".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

Figure 311 shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO62362 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA328448".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figure 311.

Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO81689 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA325115".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO58880 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA270502".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1213 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA66487".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO83600 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA327576".

Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO21744 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA188225".

Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO84764 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA329122".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO84765 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA329123".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO84766 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA329124".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO64556 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA277809".

Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO83257 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA326939".

Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO71111 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA304685".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO84767 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA329125".

Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO: shown in Figure .

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO62626 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA274881".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO84768 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA329126".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO49244 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA254129".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO60906 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA272801".

Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO62479 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA274690".

Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO81599 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA329127".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO84769 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA329128".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

Figure 351 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO60248 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA271973".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 351.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO84288 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA329129".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO61349 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA273346".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO12742 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA151878".

Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO60936 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA272840".

Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO34252 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA216500".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO20124 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA329130".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO84770 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA329131".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO81877 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA325334".

Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO60742 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA272608".

Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO80649 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA327584".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO83145 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA329132".

Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO84771 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA329133".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO83605 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA327585".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO71107 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA304681".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO59254 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA329134".

Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO84299 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA328473".

Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO37756 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA227293".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO58102 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA329135".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO37368 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA226905".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO84772 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA329136".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO12879 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA329137".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO38299 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA227836".

Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO84773 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA329138".

Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO84774 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA329139".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO60960 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA272867".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO12770 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA150430".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO71146 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA304720".

Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO60024 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA271740".

Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO60698 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA272449".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO84775 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA329140".

Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO59315 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA270985".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO80660 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA323927".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO51738 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA256807".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO84776 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA329141".

Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO84777 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA329142".

Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO60997 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA272911".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO84700 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA329033".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO84778 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA329143".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO69521 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA287246".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO84779 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA329144".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO80881 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA324183".

Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO37791 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA326322".

Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO37815 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA328513".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1723 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA82376".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO2711 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA88239".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO36378 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA225915".

Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO84780 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA329145".

Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO70001 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA329146".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO37200 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA226737".

Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO84781 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA329147".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO34276 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA216689".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO12313 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA150529".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO61870 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA273919".

Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO37579 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA227116".

Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO60781 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA272655".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO84782 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA329148".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO12481 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA150812".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO4854 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA103527".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO37040 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA226577".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO61763 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA273802".

Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO20111 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA329149".

Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4793 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA325800".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO84783 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA329150".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO84703 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA329036".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO12173 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA151067".

Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO36542 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA226079".

Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO37560 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA227097".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO84784 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA329151".

Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO84785 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA329152".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO81753 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA325192".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO84786 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA329153".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO69568 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA329154".

Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO1207 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA329155".

Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO84787 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA329156".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO49183 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA253585".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO60670 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA272417".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO62861 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA329157".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO2536 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA76503".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO38477 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA228014".

Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO12243 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA150427".

Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO84788 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA329158".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO4660 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA329159".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO81585 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA324991".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO83635 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA327632".

Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure .

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO21960 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA192060".

Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO62760 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA299899".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figure 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO84789 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA329160".

Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 525.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO21708 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA188333".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO37544 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA227081".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure .

Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO37910 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA227447".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO21834 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA188301".

Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO37636 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA227173".

Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO84790 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA329161".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO21885 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA188355".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO51301 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA256257".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO60077 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA329162".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO83644 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA327643".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA329163".

Figure 548 shows a nucleotide sequence (SEQ ID NO:548) of a native sequence PRO84792 cDNA, wherein SEQ ID NO:548 is a clone designated herein as "DNA329164".

Figure 549 shows the amino acid sequence (SEQ ID NO:549) derived from the coding sequence of SEQ ID NO:548 shown in Figure 548.

Figure 550 shows a nucleotide sequence (SEQ ID NO:550) of a native sequence PRO81000 cDNA, wherein SEQ ID NO:550 is a clone designated herein as "DNA324324".

Figure 551 shows the amino acid sequence (SEQ ID NO:551) derived from the coding sequence of SEQ ID NO:550 shown in Figure 550.

Figure 552 shows a nucleotide sequence (SEQ ID NO:552) of a native sequence PRO37843 cDNA, wherein SEQ ID NO:552 is a clone designated herein as "DNA328570".

Figure 553 shows the amino acid sequence (SEQ ID NO:553) derived from the coding sequence of SEQ ID NO:552 shown in Figure 552.

Figure 554 shows a nucleotide sequence (SEQ ID NO:554) of a native sequence PRO63054 cDNA, wherein SEQ ID NO:554 is a clone designated herein as "DNA329165".

Figure 555 shows the amino acid sequence (SEQ ID NO:555) derived from the coding sequence of SEQ ID NO:554 shown in Figure 554.

Figure 556 shows a nucleotide sequence (SEQ ID NO:556) of a native sequence PRO12374 cDNA, wherein SEQ ID NO:556 is a clone designated herein as "DNA150621".

Figure 557 shows the amino acid sequence (SEQ ID NO:557) derived from the coding sequence of SEQ ID NO:556 shown in Figure 556.

Figure 558 shows a nucleotide sequence (SEQ ID NO:558) of a native sequence PRO2541 cDNA, wherein SEQ ID NO:558 is a clone designated herein as "DNA76517".

Figure 559 shows the amino acid sequence (SEQ ID NO:559) derived from the coding sequence of SEQ ID NO:558 shown in Figure 558.

Figure 560 shows a nucleotide sequence (SEQ ID NO:560) of a native sequence PRO4940 cDNA, wherein SEQ ID NO:560 is a clone designated herein as "DNA328576".

Figure 561 shows the amino acid sequence (SEQ ID NO:561) derived from the coding sequence of SEQ ID NO:560 shown in Figure 560.

Figure 562 shows a nucleotide sequence (SEQ ID NO:562) of a native sequence PRO2524 cDNA, wherein SEQ ID NO:562 is a clone designated herein as "DNA75525".

Figure 563 shows the amino acid sequence (SEQ ID NO:563) derived from the coding sequence of SEQ ID NO:562 shown in Figure 562.

Figure 564 shows a nucleotide sequence (SEQ ID NO:564) of a native sequence PRO59203 cDNA, wherein SEQ ID NO:564 is a clone designated herein as "DNA270867".

Figure 565 shows the amino acid sequence (SEQ ID NO:565) derived from the coding sequence of SEQ ID NO:564 shown in Figure 564.

Figure 566 shows a nucleotide sequence (SEQ ID NO:566) of a native sequence PRO2022 cDNA, wherein SEQ ID NO:566 is a clone designated herein as "DNA76516".

Figure 567 shows the amino acid sequence (SEQ ID NO:567) derived from the coding sequence of SEQ ID NO:566 shown in Figure 566.

Figure 568 shows a nucleotide sequence (SEQ ID NO:568) of a native sequence PRO58425 cDNA, wherein SEQ ID NO:568 is a clone designated herein as "DNA329047".

Figure 569 shows the amino acid sequence (SEQ ID NO:569) derived from the coding sequence of SEQ ID NO:568 shown in Figure 568.

Figure 570 shows a nucleotide sequence (SEQ ID NO:570) of a native sequence PRO4611 cDNA, wherein SEQ ID NO:570 is a clone designated herein as "DNA103281".

Figure 571 shows the amino acid sequence (SEQ ID NO:571) derived from the coding sequence of SEQ ID NO:570 shown in Figure 570.

Figure 572 shows a nucleotide sequence (SEQ ID NO:572) of a native sequence PRO84793 cDNA, wherein SEQ ID NO:572 is a clone designated herein as "DNA329166".

Figure 573 shows the amino acid sequence (SEQ ID NO:573) derived from the coding sequence of SEQ ID NO:572 shown in Figure 572.

Figure 574 shows a nucleotide sequence (SEQ ID NO:574) of a native sequence PRO2068 cDNA, wherein SEQ ID NO:574 is a clone designated herein as "DNA83063".

Figure 575 shows the amino acid sequence (SEQ ID NO:575) derived from the coding sequence of SEQ ID NO:574 shown in Figure 574.

Figure 576 shows a nucleotide sequence (SEQ ID NO:576) of a native sequence PRO12876 cDNA, wherein SEQ ID NO:576 is a clone designated herein as "DNA151420".

Figure 577 shows the amino acid sequence (SEQ ID NO:577) derived from the coding sequence of SEQ ID NO:576 shown in Figure 576.

Figure 578 shows a nucleotide sequence (SEQ ID NO:578) of a native sequence PRO38147 cDNA, wherein SEQ ID NO:578 is a clone designated herein as "DNA327657".

Figure 579 shows the amino acid sequence (SEQ ID NO:579) derived from the coding sequence of SEQ ID NO:578 shown in Figure 578.

Figure 580 shows a nucleotide sequence (SEQ ID NO:580) of a native sequence PRO4933 cDNA, wherein SEQ ID NO:580 is a clone designated herein as "DNA329167".

Figure 581 shows the amino acid sequence (SEQ ID NO:581) derived from the coding sequence of SEQ ID NO:580 shown in Figure 580.

Figure 582 shows a nucleotide sequence (SEQ ID NO:582) of a native sequence PRO12612 cDNA, wherein SEQ ID NO:582 is a clone designated herein as "DNA329005".

Figure 583 shows the amino acid sequence (SEQ ID NO:583) derived from the coding sequence of SEQ ID NO:582 shown in Figure 582.

Figure 584 shows a nucleotide sequence (SEQ ID NO:584) of a native sequence PRO84794 cDNA, wherein SEQ ID NO:584 is a clone designated herein as "DNA329168".

Figure 585 shows the amino acid sequence (SEQ ID NO:585) derived from the coding sequence of SEQ ID NO:584 shown in Figure 584.

Figure 586 shows a nucleotide sequence (SEQ ID NO:586) of a native sequence PRO36521 cDNA, wherein SEQ ID NO:586 is a clone designated herein as "DNA226058".

Figure 587 shows the amino acid sequence (SEQ ID NO:587) derived from the coding sequence of SEQ ID NO:586 shown in Figure 586.

Figure 588 shows a nucleotide sequence (SEQ ID NO:588) of a native sequence PRO34330 cDNA, wherein SEQ ID NO:588 is a clone designated herein as "DNA218278".

Figure 589 shows the amino acid sequence (SEQ ID NO:589) derived from the coding sequence of SEQ ID NO:588 shown in Figure 588.

Figure 590 shows a nucleotide sequence (SEQ ID NO:590) of a native sequence PRO37671 cDNA, wherein SEQ ID NO:590 is a clone designated herein as "DNA227208".

Figure 591 shows the amino acid sequence (SEQ ID NO:591) derived from the coding sequence of SEQ ID NO:590 shown in Figure 590.

Figure 592 shows a nucleotide sequence (SEQ ID NO:592) of a native sequence PRO1610 cDNA, wherein SEQ ID NO:592 is a clone designated herein as "DNA329169".

Figure 593 shows the amino acid sequence (SEQ ID NO:593) derived from the coding sequence of SEQ ID NO:592 shown in Figure 592.

Figure 594 shows a nucleotide sequence (SEQ ID NO:594) of a native sequence PRO24922 cDNA, wherein SEQ ID NO:594 is a clone designated herein as "DNA196424".

Figure 595 shows the amino acid sequence (SEQ ID NO:595) derived from the coding sequence of SEQ ID NO:594 shown in Figure 594.

Figure 596 shows a nucleotide sequence (SEQ ID NO:596) of a native sequence PRO83069 cDNA, wherein SEQ ID NO:596 is a clone designated herein as "DNA326727".

Figure 597 shows the amino acid sequence (SEQ ID NO:597) derived from the coding sequence of SEQ ID NO:596 shown in Figure 596.

Figure 598 shows a nucleotide sequence (SEQ ID NO:598) of a native sequence PRO70938 cDNA, wherein SEQ ID NO:598 is a clone designated herein as "DNA329170".

Figure 599 shows the amino acid sequence (SEQ ID NO:599) derived from the coding sequence of SEQ ID NO:598 shown in Figure 598.

Figure 600 shows a nucleotide sequence (SEQ ID NO:600) of a native sequence PRO84795 cDNA, wherein SEQ ID NO:600 is a clone designated herein as "DNA329171".

Figure 601 shows the amino acid sequence (SEQ ID NO:601) derived from the coding sequence of SEQ ID NO:600 shown in Figure 600.

Figure 602 shows a nucleotide sequence (SEQ ID NO:602) of a native sequence PRO84796 cDNA, wherein SEQ ID NO:602 is a clone designated herein as "DNA329172".

Figure 603 shows the amino acid sequence (SEQ ID NO:603) derived from the coding sequence of SEQ ID NO:602 shown in Figure 602.

Figure 604 shows a nucleotide sequence (SEQ ID NO:604) of a native sequence PRO83141 cDNA, wherein SEQ ID NO:604 is a clone designated herein as "DNA329173".

Figure 605 shows the amino acid sequence (SEQ ID NO:605) derived from the coding sequence of SEQ ID NO:604 shown in Figure 604.

Figure 606 shows a nucleotide sequence (SEQ ID NO:606) of a native sequence PRO2768 cDNA, wherein SEQ ID NO:606 is a clone designated herein as "DNA88374".

Figure 607 shows the amino acid sequence (SEQ ID NO:607) derived from the coding sequence of SEQ ID NO:606 shown in Figure 606.

Figure 608 shows a nucleotide sequence (SEQ ID NO:608) of a native sequence PRO84797 cDNA, wherein SEQ ID NO:608 is a clone designated herein as "DNA329174".

Figure 609 shows the amino acid sequence (SEQ ID NO:609) derived from the coding sequence of SEQ ID NO:608 shown in Figure 608.

Figure 610 shows a nucleotide sequence (SEQ ID NO:610) of a native sequence PRO49572 cDNA, wherein SEQ ID NO:610 is a clone designated herein as "DNA254464".

Figure 611 shows the amino acid sequence (SEQ ID NO:611) derived from the coding sequence of SEQ ID NO:610 shown in Figure 610.

Figure 612 shows a nucleotide sequence (SEQ ID NO:612) of a native sequence PRO2693 cDNA, wherein SEQ ID NO:612 is a clone designated herein as "DNA88195".

Figure 613 shows the amino acid sequence (SEQ ID NO:613) derived from the coding sequence of SEQ ID NO:612 shown in Figure 612.

Figure 614 shows a nucleotide sequence (SEQ ID NO:614) of a native sequence PRO60433 cDNA, wherein SEQ ID NO:614 is a clone designated herein as "DNA272165".

Figure 615 shows the amino acid sequence (SEQ ID NO:615) derived from the coding sequence of SEQ ID NO:614 shown in Figure 614.

Figure 616 shows a nucleotide sequence (SEQ ID NO:616) of a native sequence PRO51592 cDNA, wherein SEQ ID NO:616 is a clone designated herein as "DNA256561".

Figure 617 shows the amino acid sequence (SEQ ID NO:617) derived from the coding sequence of SEQ ID NO:616 shown in Figure 616.

Figure 618 shows a nucleotide sequence (SEQ ID NO:618) of a native sequence PRO84798 cDNA, wherein SEQ ID NO:618 is a clone designated herein as "DNA329175".

Figure 619 shows the amino acid sequence (SEQ ID NO:619) derived from the coding sequence of SEQ ID NO:618 shown in Figure 618.

Figure 620 shows a nucleotide sequence (SEQ ID NO:620) of a native sequence PRO7 cDNA, wherein SEQ ID NO: is a clone designated herein as "DNA35629".

Figure 621 shows the amino acid sequence (SEQ ID NO:621) derived from the coding sequence of SEQ ID NO:620 shown in Figure 620.

Figure 622 shows a nucleotide sequence (SEQ ID NO:622) of a native sequence PRO84376 cDNA, wherein SEQ ID NO:622 is a clone designated herein as "DNA328591".

Figure 623 shows the amino acid sequence (SEQ ID NO:623) derived from the coding sequence of SEQ ID NO:622 shown in Figure 622.

Figure 624 shows a nucleotide sequence (SEQ ID NO:624) of a native sequence PRO38213 cDNA, wherein SEQ ID NO:624 is a clone designated herein as "DNA227750".

Figure 625 shows the amino acid sequence (SEQ ID NO:625) derived from the coding sequence of SEQ ID NO:624 shown in Figure 624.

Figure 626 shows a nucleotide sequence (SEQ ID NO:626) of a native sequence PRO61201 cDNA, wherein SEQ ID NO:626 is a clone designated herein as "DNA273159".

Figure 627 shows the amino acid sequence (SEQ ID NO:627) derived from the coding sequence of SEQ ID NO:626 shown in Figure 626.

Figure 628 shows a nucleotide sequence (SEQ ID NO:628) of a native sequence PRO84799 cDNA, wherein SEQ ID NO:628 is a clone designated herein as "DNA329176".

Figure 629 shows the amino acid sequence (SEQ ID NO:629) derived from the coding sequence of SEQ ID NO:628 shown in Figure 628.

Figure 630 shows a nucleotide sequence (SEQ ID NO:630) of a native sequence PRO34451 cDNA, wherein SEQ ID NO:630 is a clone designated herein as "DNA218655".

Figure 631 shows the amino acid sequence (SEQ ID NO:631) derived from the coding sequence of SEQ ID NO:630 shown in Figure 630.

Figure 632 shows a nucleotide sequence (SEQ ID NO:632) of a native sequence PRO83661 cDNA, wherein SEQ ID NO:632 is a clone designated herein as "DNA327674".

Figure 633 shows the amino acid sequence (SEQ ID NO:633) derived from the coding sequence of SEQ ID NO:632 shown in Figure 632.

Figure 634 shows a nucleotide sequence (SEQ ID NO:634) of a native sequence PRO84800 cDNA, wherein SEQ ID NO:634 is a clone designated herein as "DNA329177".

Figure 635 shows the amino acid sequence (SEQ ID NO:635) derived from the coding sequence of SEQ ID NO:634 shown in Figure 634.

Figure 636 shows a nucleotide sequence (SEQ ID NO:636) of a native sequence PRO38214 cDNA, wherein SEQ ID NO:636 is a clone designated herein as "DNA227751".

Figure 637 shows the amino acid sequence (SEQ ID NO:637) derived from the coding sequence of SEQ ID NO:636 shown in Figure 636.

Figure 638 shows a nucleotide sequence (SEQ ID NO:638) of a native sequence PRO36999 cDNA, wherein SEQ ID NO:638 is a clone designated herein as "DNA226536".

Figure 639 shows the amino acid sequence (SEQ ID NO:639) derived from the coding sequence of SEQ ID NO:638 shown in Figure 638.

Figure 640 shows a nucleotide sequence (SEQ ID NO:640) of a native sequence PRO36859 cDNA, wherein SEQ ID NO:640 is a clone designated herein as "DNA226396".

Figure 641 shows the amino acid sequence (SEQ ID NO:641) derived from the coding sequence of SEQ ID NO:640 shown in Figure 640.

Figure 642 shows a nucleotide sequence (SEQ ID NO:642) of a native sequence PRO73 cDNA, wherein SEQ ID NO:642 is a clone designated herein as "DNA36718".

Figure 643 shows the amino acid sequence (SEQ ID NO:643) derived from the coding sequence of SEQ ID NO:642 shown in Figure 642.

Figure 644 shows a nucleotide sequence (SEQ ID NO:644) of a native sequence PRO848001 cDNA, wherein SEQ ID NO:644 is a clone designated herein as "DNA329178".

Figure 645 shows the amino acid sequence (SEQ ID NO:645) derived from the coding sequence of SEQ ID NO:644 shown in Figure 644.

Figure 646 shows a nucleotide sequence (SEQ ID NO:646) of a native sequence PRO84381 cDNA, wherein SEQ ID NO:646 is a clone designated herein as "DNA328597".

Figure 647 shows the amino acid sequence (SEQ ID NO:647) derived from the coding sequence of SEQ ID NO:646 shown in Figure 646.

Figure 648 shows a nucleotide sequence (SEQ ID NO:648) of a native sequence PRO2023 cDNA, wherein SEQ ID NO:648 is a clone designated herein as "DNA304473".

Figure 649 shows the amino acid sequence (SEQ ID NO:649) derived from the coding sequence of SEQ ID NO:648 shown in Figure .

Figure 650 shows a nucleotide sequence (SEQ ID NO:650) of a native sequence PRO84383 cDNA, wherein SEQ ID NO:650 is a clone designated herein as "DNA328600".

Figure 651 shows the amino acid sequence (SEQ ID NO:651) derived from the coding sequence of SEQ ID NO:650 shown in Figure 650.

Figure 652 shows a nucleotide sequence (SEQ ID NO:652) of a native sequence PRO84384 cDNA, wherein SEQ ID NO:652 is a clone designated herein as "DNA328601".

Figure 653 shows the amino acid sequence (SEQ ID NO:653) derived from the coding sequence of SEQ ID NO:652 shown in Figure 652.

Figure 654 shows a nucleotide sequence (SEQ ID NO:654) of a native sequence PRO36800 cDNA, wherein SEQ ID NO:654 is a clone designated herein as "DNA226337".

Figure 655 shows the amino acid sequence (SEQ ID NO:655) derived from the coding sequence of SEQ ID NO:654 shown in Figure 654.

Figure 656 shows a nucleotide sequence (SEQ ID NO:656) of a native sequence PRO37797 cDNA, wherein SEQ ID NO:656 is a clone designated herein as "DNA227334".

Figure 657 shows the amino acid sequence (SEQ ID NO:657) derived from the coding sequence of SEQ ID NO:656 shown in Figure 656.

Figure 658 shows a nucleotide sequence (SEQ ID NO:658) of a native sequence PRO24924 cDNA, wherein SEQ ID NO:658 is a clone designated herein as "DNA196426".

Figure 659 shows the amino acid sequence (SEQ ID NO:659) derived from the coding sequence of SEQ ID NO:658 shown in Figure 658.

Figure 660 shows a nucleotide sequence (SEQ ID NO:660) of a native sequence PRO84802 cDNA, wherein SEQ ID NO:660 is a clone designated herein as "DNA329179".

Figure 661 shows the amino acid sequence (SEQ ID NO:661) derived from the coding sequence of SEQ ID NO:660 shown in Figure 660.

Figure 662 shows a nucleotide sequence (SEQ ID NO:662) of a native sequence PRO37393 cDNA, wherein SEQ ID NO:662 is a clone designated herein as "DNA226930".

Figure 663 shows the amino acid sequence (SEQ ID NO:663) derived from the coding sequence of SEQ ID NO:662 shown in Figure 662.

Figure 664 shows a nucleotide sequence (SEQ ID NO:664) of a native sequence PRO84803 cDNA, wherein SEQ ID NO:664 is a clone designated herein as "DNA329180".

Figure 665 shows the amino acid sequence (SEQ ID NO:665) derived from the coding sequence of SEQ ID NO:664 shown in Figure 664.

Figure 666 shows a nucleotide sequence (SEQ ID NO:666) of a native sequence PRO84804 cDNA, wherein SEQ ID NO:666 is a clone designated herein as "DNA329181".

Figure 667 shows the amino acid sequence (SEQ ID NO:667) derived from the coding sequence of SEQ ID NO:666 shown in Figure 666.

Figure 668 shows a nucleotide sequence (SEQ ID NO:668) of a native sequence PRO84805 cDNA, wherein SEQ ID NO:668 is a clone designated herein as "DNA329182".

Figure 669 shows the amino acid sequence (SEQ ID NO:669) derived from the coding sequence of SEQ ID NO:668 shown in Figure 668.

Figure 670 shows a nucleotide sequence (SEQ ID NO:670) of a native sequence PRO21795 cDNA, wherein SEQ ID NO:670 is a clone designated herein as "DNA188271".

Figure 671 shows the amino acid sequence (SEQ ID NO:671) derived from the coding sequence of SEQ ID NO:670 shown in Figure 670.

Figure 672 shows a nucleotide sequence (SEQ ID NO:672) of a native sequence PRO34286 cDNA, wherein SEQ ID NO:672 is a clone designated herein as "DNA217244".

Figure 673 shows the amino acid sequence (SEQ ID NO:673) derived from the coding sequence of SEQ ID NO:672 shown in Figure 672.

Figure 674 shows a nucleotide sequence (SEQ ID NO:674) of a native sequence PRO34287 cDNA, wherein SEQ ID NO:674 is a clone designated herein as "DNA217245".

Figure 675 shows the amino acid sequence (SEQ ID NO:675) derived from the coding sequence of SEQ ID NO:674 shown in Figure 674.

Figure 676 shows a nucleotide sequence (SEQ ID NO:676) of a native sequence PRO34447 cDNA, wherein SEQ ID NO:676 is a clone designated herein as "DNA218651".

Figure 677 shows the amino acid sequence (SEQ ID NO:377) derived from the coding sequence of SEQ ID NO:676 shown in Figure 676.

Figure 678 shows a nucleotide sequence (SEQ ID NO:678) of a native sequence PRO36753 cDNA, wherein SEQ ID NO:678 is a clone designated herein as "DNA226290".

Figure 679 shows the amino acid sequence (SEQ ID NO:679) derived from the coding sequence of SEQ ID NO:678 shown in Figure 678.

Figure 680 shows a nucleotide sequence (SEQ ID NO:680) of a native sequence PRO84806 cDNA, wherein SEQ ID NO:680 is a clone designated herein as "DNA329183".

Figure 681 shows the amino acid sequence (SEQ ID NO:681) derived from the coding sequence of SEQ ID NO:680 shown in Figure 680.

Figure 682 shows a nucleotide sequence (SEQ ID NO:682) of a native sequence PRO84807 cDNA, wherein SEQ ID NO:682 is a clone designated herein as "DNA329184".

Figure 683 shows the amino acid sequence (SEQ ID NO:683) derived from the coding sequence of SEQ ID NO:682 shown in Figure 682.

Figure 684 shows a nucleotide sequence (SEQ ID NO:684) of a native sequence PRO37687 cDNA, wherein SEQ ID NO:684 is a clone designated herein as "DNA227224".

Figure 685 shows the amino acid sequence (SEQ ID NO:685) derived from the coding sequence of SEQ ID NO:684 shown in Figure 684.

Figure 686 shows a nucleotide sequence (SEQ ID NO:686) of a native sequence PRO61770 cDNA, wherein SEQ ID NO:686 is a clone designated herein as "DNA329185".

Figure 687 shows the amino acid sequence (SEQ ID NO:687) derived from the coding sequence of SEQ ID NO:686 shown in Figure 686.

Figure 688 shows a nucleotide sequence (SEQ ID NO:688) of a native sequence PRO80638 cDNA, wherein SEQ ID NO:688 is a clone designated herein as "DNA323896".

Figure 689 shows the amino acid sequence (SEQ ID NO:689) derived from the coding sequence of SEQ ID NO:688 shown in Figure 688.

Figure 690 shows a nucleotide sequence (SEQ ID NO:690) of a native sequence PRO84391 cDNA, wherein SEQ ID NO:690 is a clone designated herein as "DNA328609".

Figure 691 shows the amino acid sequence (SEQ ID NO:691) derived from the coding sequence of SEQ ID NO:690 shown in Figure 690.

Figure 692 shows a nucleotide sequence (SEQ ID NO:692) of a native sequence PRO81872 cDNA, wherein SEQ ID NO:692 is a clone designated herein as "DNA325329".

Figure 693 shows the amino acid sequence (SEQ ID NO:693) derived from the coding sequence of SEQ ID NO:692 shown in Figure 692.

Figure 694 shows a nucleotide sequence (SEQ ID NO:694) of a native sequence PRO72 cDNA, wherein SEQ ID NO:694 is a clone designated herein as "DNA36717".

Figure 695 shows the amino acid sequence (SEQ ID NO:695) derived from the coding sequence of SEQ ID NO:694 shown in Figure 694.

Figure 696 shows a nucleotide sequence (SEQ ID NO:696) of a native sequence PRO84393 cDNA, wherein SEQ ID NO:696 is a clone designated herein as "DNA328611".

Figure 697 shows the amino acid sequence (SEQ ID NO:697) derived from the coding sequence of SEQ ID NO:696 shown in Figure 696.

Figure 698 shows a nucleotide sequence (SEQ ID NO:698) of a native sequence PRO82391 cDNA, wherein SEQ ID NO:698 is a clone designated herein as "DNA325944".

Figure 699 shows the amino acid sequence (SEQ ID NO:699) derived from the coding sequence of SEQ ID NO:698 shown in Figure 698.

Figure 700 shows a nucleotide sequence (SEQ ID NO:700) of a native sequence PRO9824 cDNA, wherein SEQ ID NO:700 is a clone designated herein as "DNA327689".

Figure 701 shows the amino acid sequence (SEQ ID NO:701) derived from the coding sequence of SEQ ID NO:700 shown in Figure 700.

Figure 702 shows a nucleotide sequence (SEQ ID NO:702) of a native sequence PRO84808 cDNA, wherein SEQ ID NO:702 is a clone designated herein as "DNA329186".

Figure 703 shows the amino acid sequence (SEQ ID NO:703) derived from the coding sequence of SEQ ID NO:702 shown in Figure 702.

Figure 704 shows a nucleotide sequence (SEQ ID NO:704) of a native sequence PRO84809 cDNA, wherein SEQ ID NO:704 is a clone designated herein as "DNA329187".

Figure 705 shows the amino acid sequence (SEQ ID NO:705) derived from the coding sequence of SEQ ID NO:704 shown in Figure 704.

Figure 706 shows a nucleotide sequence (SEQ ID NO:706) of a native sequence PRO61545 cDNA, wherein SEQ ID NO:706 is a clone designated herein as "DNA273567".

Figure 707 shows the amino acid sequence (SEQ ID NO:707) derived from the coding sequence of SEQ ID NO:706 shown in Figure 706.

Figure 708 shows a nucleotide sequence (SEQ ID NO:708) of a native sequence PRO66271 cDNA, wherein SEQ ID NO:708 is a clone designated herein as "DNA281431".

Figure 709 shows the amino acid sequence (SEQ ID NO:709) derived from the coding sequence of SEQ ID NO:708 shown in Figure 708.

Figure 710 shows a nucleotide sequence (SEQ ID NO:710) of a native sequence PRO84810 cDNA, wherein SEQ ID NO:710 is a clone designated herein as "DNA329188".

Figure 711 shows the amino acid sequence (SEQ ID NO:711) derived from the coding sequence of SEQ ID NO:710 shown in Figure 710.

Figure 712 shows a nucleotide sequence (SEQ ID NO:712) of a native sequence PRO59579 cDNA, wherein SEQ ID NO:712 is a clone designated herein as "DNA271268".

Figure 713 shows the amino acid sequence (SEQ ID NO:713) derived from the coding sequence of SEQ ID NO:712 shown in Figure 712.

Figure 714 shows a nucleotide sequence (SEQ ID NO:714) of a native sequence PRO69487 cDNA, wherein SEQ ID NO:714 is a clone designated herein as "DNA287203".

Figure 715 shows the amino acid sequence (SEQ ID NO:715) derived from the coding sequence of SEQ ID NO:714 shown in Figure 714.

Figure 716 shows a nucleotide sequence (SEQ ID NO:716) of a native sequence PRO71112 cDNA, wherein SEQ ID NO:716 is a clone designated herein as "DNA304686".

Figure 717 shows the amino acid sequence (SEQ ID NO:717) derived from the coding sequence of SEQ ID NO:716 shown in Figure 716.

Figure 718 shows a nucleotide sequence (SEQ ID NO:718) of a native sequence PRO84401 cDNA, wherein SEQ ID NO:718 is a clone designated herein as "DNA328619".

Figure 719 shows the amino acid sequence (SEQ ID NO:719) derived from the coding sequence of SEQ ID NO:718 shown in Figure 718.

Figure 720 shows a nucleotide sequence (SEQ ID NO:720) of a native sequence PRO69475 cDNA, wherein SEQ ID NO:720 is a clone designated herein as "DNA287189".

Figure 721 shows the amino acid sequence (SEQ ID NO:721) derived from the coding sequence of SEQ ID NO:720 shown in Figure 720.

Figure 722 shows a nucleotide sequence (SEQ ID NO:722) of a native sequence PRO84710 cDNA, wherein SEQ ID NO:722 is a clone designated herein as "DNA329048".

Figure 723 shows the amino acid sequence (SEQ ID NO:723) derived from the coding sequence of SEQ ID NO:722 shown in Figure 722.

Figure 724 shows a nucleotide sequence (SEQ ID NO:724) of a native sequence PRO3645 cDNA, wherein SEQ ID NO:724 is a clone designated herein as "DNA97298".

Figure 725 shows the amino acid sequence (SEQ ID NO:725) derived from the coding sequence of SEQ ID NO:724 shown in Figure 724.

Figure 726 shows a nucleotide sequence (SEQ ID NO:726) of a native sequence PRO83679 cDNA, wherein SEQ ID NO:726 is a clone designated herein as "DNA327696".

Figure 727 shows the amino acid sequence (SEQ ID NO:727) derived from the coding sequence of SEQ ID NO:726 shown in Figure 726.

Figure 728 shows a nucleotide sequence (SEQ ID NO:728) of a native sequence PRO69684 cDNA, wherein SEQ ID NO:728 is a clone designated herein as "DNA287427".

Figure 729 shows the amino acid sequence (SEQ ID NO:729) derived from the coding sequence of SEQ ID NO:728 shown in Figure 728.

Figure 730 shows a nucleotide sequence (SEQ ID NO:730) of a native sequence PRO69498 cDNA, wherein SEQ ID NO:730 is a clone designated herein as "DNA287219".

Figure 731 shows the amino acid sequence (SEQ ID NO:731) derived from the coding sequence of SEQ ID NO:730 shown in Figure 730.

Figure 732 shows a nucleotide sequence (SEQ ID NO:732) of a native sequence PRO4911 cDNA, wherein SEQ ID NO:732 is a clone designated herein as "DNA329189".

Figure 733 shows the amino acid sequence (SEQ ID NO:733) derived from the coding sequence of SEQ ID NO:732 shown in Figure 732.

Figure 734 shows a nucleotide sequence (SEQ ID NO:734) of a native sequence PRO82935 cDNA, wherein SEQ ID NO:734 is a clone designated herein as "DNA326573".

Figure 735 shows the amino acid sequence (SEQ ID NO:735) derived from the coding sequence of SEQ ID NO:734 shown in Figure 734.

Figure 736 shows a nucleotide sequence (SEQ ID NO:736) of a native sequence PRO84403 cDNA, wherein SEQ ID NO:736 is a clone designated herein as "DNA328621".

Figure 737 shows the amino acid sequence (SEQ ID NO:737) derived from the coding sequence of SEQ ID NO:736 shown in Figure 736.

Figure 738 shows a nucleotide sequence (SEQ ID NO:738) of a native sequence PRO84811 cDNA, wherein SEQ ID NO:738 is a clone designated herein as "DNA329190".

Figure 739 shows the amino acid sequence (SEQ ID NO:739) derived from the coding sequence of SEQ ID NO:738 shown in Figure 738.

Figure 740 shows a nucleotide sequence (SEQ ID NO:740) of a native sequence PRO10404 cDNA, wherein SEQ ID NO:740 is a clone designated herein as "DNA287169".

Figure 741 shows the amino acid sequence (SEQ ID NO:741) derived from the coding sequence of SEQ ID NO:740 shown in Figure 740.

Figure 742 shows a nucleotide sequence (SEQ ID NO:742) of a native sequence PRO61502 cDNA, wherein SEQ ID NO:742 is a clone designated herein as "DNA273521".

Figure 743 shows the amino acid sequence (SEQ ID NO:743) derived from the coding sequence of SEQ ID NO:742 shown in Figure 742.

Figure 744 shows a nucleotide sequence (SEQ ID NO:744) of a native sequence PRO83682 cDNA, wherein SEQ ID NO:744 is a clone designated herein as "DNA327699".

Figure 745 shows the amino acid sequence (SEQ ID NO:745) derived from the coding sequence of SEQ ID NO:744 shown in Figure .

Figure 746 shows a nucleotide sequence (SEQ ID NO:746) of a native sequence PRO80665 cDNA, wherein SEQ ID NO:746 is a clone designated herein as "DNA329191".

Figure 747 shows the amino acid sequence (SEQ ID NO:747) derived from the coding sequence of SEQ ID NO:746 shown in Figure 746.

Figure 748 shows a nucleotide sequence (SEQ ID NO:748) of a native sequence PRO38019 cDNA, wherein SEQ ID NO:748 is a clone designated herein as "DNA227556".

Figure 749 shows the amino acid sequence (SEQ ID NO:749) derived from the coding sequence of SEQ ID NO:748 shown in Figure 748.

Figure 750 shows a nucleotide sequence (SEQ ID NO:750) of a native sequence PRO38337 cDNA, wherein SEQ ID NO:750 is a clone designated herein as "DNA227874".

Figure 751 shows the amino acid sequence (SEQ ID NO:751) derived from the coding sequence of SEQ ID NO:750 shown in Figure 750.

Figure 752 shows a nucleotide sequence (SEQ ID NO:752) of a native sequence PRO83683 cDNA, wherein SEQ ID NO:752 is a clone designated herein as "DNA327700".

Figure 753 shows the amino acid sequence (SEQ ID NO:753) derived from the coding sequence of SEQ ID NO:752 shown in Figure 752.

Figure 754 shows a nucleotide sequence (SEQ ID NO:754) of a native sequence PRO82667 cDNA, wherein SEQ ID NO:754 is a clone designated herein as "DNA327701".

Figure 755 shows the amino acid sequence (SEQ ID NO:755) derived from the coding sequence of SEQ ID NO:754 shown in Figure 754.

Figure 756 shows a nucleotide sequence (SEQ ID NO:756) of a native sequence PRO83684 cDNA, wherein SEQ ID NO:756 is a clone designated herein as "DNA327702".

Figure 757 shows the amino acid sequence (SEQ ID NO:757) derived from the coding sequence of SEQ ID NO:756 shown in Figure 576.

Figure 758 shows a nucleotide sequence (SEQ ID NO:758) of a native sequence PRO70339 cDNA, wherein SEQ ID NO:758 is a clone designated herein as "DNA290237".

Figure 759 shows the amino acid sequence (SEQ ID NO:759) derived from the coding sequence of SEQ ID NO:758 shown in Figure 758.

Figure 760 shows a nucleotide sequence (SEQ ID NO:760) of a native sequence PRO82739 cDNA, wherein SEQ ID NO:760 is a clone designated herein as "DNA326343".

Figure 761 shows the amino acid sequence (SEQ ID NO:761) derived from the coding sequence of SEQ ID NO:760 shown in Figure 760.

Figure 762 shows a nucleotide sequence (SEQ ID NO:762) of a native sequence PRO84407 cDNA, wherein SEQ ID NO:762 is a clone designated herein as "DNA328629".

Figure 763 shows the amino acid sequence (SEQ ID NO:763) derived from the coding sequence of SEQ ID NO:762 shown in Figure 762.

Figure 764 shows a nucleotide sequence (SEQ ID NO:764) of a native sequence PRO84812 cDNA, wherein SEQ ID NO:764 is a clone designated herein as "DNA329192".

Figure 765 shows the amino acid sequence (SEQ ID NO:765) derived from the coding sequence of SEQ ID NO:764 shown in Figure 764.

Figure 766 shows a nucleotide sequence (SEQ ID NO:766) of a native sequence PRO84411 cDNA, wherein SEQ ID NO:766 is a clone designated herein as "DNA328633".

Figure 767 shows the amino acid sequence (SEQ ID NO:767) derived from the coding sequence of SEQ ID NO:766 shown in Figure 766.

Figure 768 shows a nucleotide sequence (SEQ ID NO:768) of a native sequence PRO83795 cDNA, wherein SEQ ID NO:768 is a clone designated herein as "DNA327851".

Figure 769 shows the amino acid sequence (SEQ ID NO:769) derived from the coding sequence of SEQ ID NO:768 shown in Figure 768.

Figure 770 shows a nucleotide sequence (SEQ ID NO:770) of a native sequence PRO83688 cDNA, wherein SEQ ID NO:770 is a clone designated herein as "DNA327706".

Figure 771 shows the amino acid sequence (SEQ ID NO:771) derived from the coding sequence of SEQ ID NO:770 shown in Figure 770.

Figure 772 shows a nucleotide sequence (SEQ ID NO:772) of a native sequence PRO84413 cDNA, wherein SEQ ID NO:772 is a clone designated herein as "DNA328635".

Figure 773 shows the amino acid sequence (SEQ ID NO:773) derived from the coding sequence of SEQ ID NO:772 shown in Figure 772.

Figure 774 shows a nucleotide sequence (SEQ ID NO:774) of a native sequence PRO62131 cDNA, wherein SEQ ID NO:774 is a clone designated herein as "DNA274202".

Figure 775 shows the amino acid sequence (SEQ ID NO:775) derived from the coding sequence of SEQ ID NO:774 shown in Figure 774.

Figure 776 shows a nucleotide sequence (SEQ ID NO:776) of a native sequence PRO84813 cDNA, wherein SEQ ID NO:776 is a clone designated herein as "DNA329193".

Figure 777 shows the amino acid sequence (SEQ ID NO:777) derived from the coding sequence of SEQ ID NO:776 shown in Figure 776.

Figure 778 shows a nucleotide sequence (SEQ ID NO:778) of a native sequence PRO84814 cDNA, wherein SEQ ID NO:778 is a clone designated herein as "DNA329194".

Figure 779 shows the amino acid sequence (SEQ ID NO:779) derived from the coding sequence of SEQ ID NO:778 shown in Figure 778.

Figure 780 shows a nucleotide sequence (SEQ ID NO:780) of a native sequence PRO82573 cDNA, wherein SEQ ID NO:780 is a clone designated herein as "DNA329195".

Figure 781 shows the amino acid sequence (SEQ ID NO:781) derived from the coding sequence of SEQ ID NO:780 shown in Figure 780.

Figure 782 shows a nucleotide sequence (SEQ ID NO:782) of a native sequence PRO81832 cDNA, wherein SEQ ID NO:782 is a clone designated herein as "DNA325285".

Figure 783 shows the amino acid sequence (SEQ ID NO:783) derived from the coding sequence of SEQ ID NO:782 shown in Figure 782.

Figure 784 shows a nucleotide sequence (SEQ ID NO:784) of a native sequence PRO84815 cDNA, wherein SEQ ID NO:784 is a clone designated herein as "DNA329196".

Figure 785 shows the amino acid sequence (SEQ ID NO:785) derived from the coding sequence of SEQ ID NO:784 shown in Figure 784.

Figure 786 shows a nucleotide sequence (SEQ ID NO:786) of a native sequence PRO84418 cDNA, wherein SEQ ID NO:786 is a clone designated herein as "DNA328642".

Figure 787 shows the amino acid sequence (SEQ ID NO:787) derived from the coding sequence of SEQ ID NO:786 shown in Figure 786.

Figure 788 shows a nucleotide sequence (SEQ ID NO:788) of a native sequence PRO84419 cDNA, wherein SEQ ID NO:788 is a clone designated herein as "DNA328643".

Figure 789 shows the amino acid sequence (SEQ ID NO:789) derived from the coding sequence of SEQ ID NO:788 shown in Figure 788.

Figure 790 shows a nucleotide sequence (SEQ ID NO:790) of a native sequence PRO81387 cDNA, wherein SEQ ID NO:790 is a clone designated herein as "DNA324766".

Figure 791 shows the amino acid sequence (SEQ ID NO:791) derived from the coding sequence of SEQ ID NO:790 shown in Figure 790.

Figure 792 shows a nucleotide sequence (SEQ ID NO:792) of a native sequence PRO82674 cDNA, wherein SEQ ID NO:792 is a clone designated herein as "DNA326267".

Figure 793 shows the amino acid sequence (SEQ ID NO:793) derived from the coding sequence of SEQ ID NO:792 shown in Figure 792.

Figure 794 shows a nucleotide sequence (SEQ ID NO:794) of a native sequence PRO59443 cDNA, wherein SEQ ID NO:794 is a clone designated herein as "DNA329197".

Figure 795 shows the amino acid sequence (SEQ ID NO:795) derived from the coding sequence of SEQ ID NO:794 shown in Figure 794.

Figure 796 shows a nucleotide sequence (SEQ ID NO:796) of a native sequence PRO59258 cDNA, wherein SEQ ID NO:796 is a clone designated herein as "DNA329198".

Figure 797 shows the amino acid sequence (SEQ ID NO:797) derived from the coding sequence of SEQ ID NO:796 shown in Figure 796.

Figure 798 shows a nucleotide sequence (SEQ ID NO:798) of a native sequence PRO84816 cDNA, wherein SEQ ID NO:798 is a clone designated herein as "DNA329199".

Figure 799 shows the amino acid sequence (SEQ ID NO:799) derived from the coding sequence of SEQ ID NO:798 shown in Figure 798.

Figure 800 shows a nucleotide sequence (SEQ ID NO:800) of a native sequence PRO84424 cDNA, wherein SEQ ID NO:800 is a clone designated herein as "DNA328649".

Figure 801 shows the amino acid sequence (SEQ ID NO:801) derived from the coding sequence of SEQ ID NO:800 shown in Figure 800.

Figure 802 shows a nucleotide sequence (SEQ ID NO:802) of a native sequence PRO58159 cDNA, wherein SEQ ID NO:802 is a clone designated herein as "DNA269750".

Figure 803 shows the amino acid sequence (SEQ ID NO:803) derived from the coding sequence of SEQ ID NO:802 shown in Figure 802.

Figure 804 shows a nucleotide sequence (SEQ ID NO:804) of a native sequence PRO84817 cDNA, wherein SEQ ID NO:804 is a clone designated herein as "DNA329200".

Figure 805 shows the amino acid sequence (SEQ ID NO:805) derived from the coding sequence of SEQ ID NO:804 shown in Figure 804.

Figure 806 shows a nucleotide sequence (SEQ ID NO:806) of a native sequence PRO62821 cDNA, wherein SEQ ID NO:806 is a clone designated herein as "DNA275106".

Figure 807 shows the amino acid sequence (SEQ ID NO:807) derived from the coding sequence of SEQ ID NO:806 shown in Figure 806.

Figure 808 shows a nucleotide sequence (SEQ ID NO:808) of a native sequence PRO58042 cDNA, wherein SEQ ID NO:808 is a clone designated herein as "DNA269630".

Figure 809 shows the amino acid sequence (SEQ ID NO:809) derived from the coding sequence of SEQ ID NO:808 shown in Figure 808.

Figure 810A-B shows a nucleotide sequence (SEQ ID NO:810) of a native sequence PRO84432 cDNA, wherein SEQ ID NO:810 is a clone designated herein as "DNA328658".

Figure 811 shows the amino acid sequence (SEQ ID NO:811) derived from the coding sequence of SEQ ID NO:810 shown in Figure 810A-B.

Figure 812 shows a nucleotide sequence (SEQ ID NO:812) of a native sequence PRO49214 cDNA, wherein SEQ ID NO:812 is a clone designated herein as "DNA253811".

Figure 813 shows the amino acid sequence (SEQ ID NO:813) derived from the coding sequence of SEQ ID NO:812 shown in Figure 812.

Figure 814 shows a nucleotide sequence (SEQ ID NO:814) of a native sequence PRO36183 cDNA, wherein SEQ ID NO:814 is a clone designated herein as "DNA328663".

Figure 815 shows the amino acid sequence (SEQ ID NO:815) derived from the coding sequence of SEQ ID NO:814 shown in Figure 814.

Figure 816 shows a nucleotide sequence (SEQ ID NO:816) of a native sequence PRO84818 cDNA, wherein SEQ ID NO:816 is a clone designated herein as "DNA329201".

Figure 817 shows the amino acid sequence (SEQ ID NO:817) derived from the coding sequence of SEQ ID NO:816 shown in Figure 816.

Figure 818 shows a nucleotide sequence (SEQ ID NO:818) of a native sequence PRO70367 cDNA, wherein SEQ ID NO:818 is a clone designated herein as "DNA329202".

Figure 819 shows the amino acid sequence (SEQ ID NO:819) derived from the coding sequence of SEQ ID NO:818 shown in Figure 818.

Figure 820 shows a nucleotide sequence (SEQ ID NO:820) of a native sequence PRO84819 cDNA, wherein SEQ ID NO:820 is a clone designated herein as "DNA329203".

Figure 821 shows the amino acid sequence (SEQ ID NO:821) derived from the coding sequence of SEQ ID NO:820 shown in Figure 820.

Figure 822 shows a nucleotide sequence (SEQ ID NO:822) of a native sequence PRO60104 cDNA, wherein SEQ ID NO:822 is a clone designated herein as "DNA271823".

Figure 823 shows the amino acid sequence (SEQ ID NO:823) derived from the coding sequence of SEQ ID NO:822 shown in Figure 822.

Figure 824 shows a nucleotide sequence (SEQ ID NO:824) of a native sequence PRO84382 cDNA, wherein SEQ ID NO:824 is a clone designated herein as "DNA328599".

Figure 825 shows the amino acid sequence (SEQ ID NO:825) derived from the coding sequence of SEQ ID NO:824 shown in Figure 824.

Figure 826 shows a nucleotide sequence (SEQ ID NO:826) of a native sequence PRO cDNA, wherein SEQ ID NO:826 is a clone designated herein as "DNA".

Figure 827 shows the amino acid sequence (SEQ ID NO:827) derived from the coding sequence of SEQ ID NO:826 shown in Figure 826.

Figure 828 shows a nucleotide sequence (SEQ ID NO:828) of a native sequence PRO cDNA, wherein SEQ ID NO:828 is a clone designated herein as "DNA".

Figure 829 shows the amino acid sequence (SEQ ID NO:829) derived from the coding sequence of SEQ ID NO:828 shown in Figure 828.

Figure 830 shows a nucleotide sequence (SEQ ID NO:830) of a native sequence PRO84820 cDNA, wherein SEQ ID NO:830 is a clone designated herein as "DNA329204".

Figure 831 shows the amino acid sequence (SEQ ID NO:831) derived from the coding sequence of SEQ ID NO:830 shown in Figure 830.

Figure 832 shows a nucleotide sequence (SEQ ID NO:832) of a native sequence PRO34255 cDNA, wherein SEQ ID NO:832 is a clone designated herein as "DNA216503".

Figure 833 shows the amino acid sequence (SEQ ID NO:833) derived from the coding sequence of SEQ ID NO:832 shown in Figure 832.

Figure 834 shows a nucleotide sequence (SEQ ID NO:834) of a native sequence PRO84821 cDNA, wherein SEQ ID NO:834 is a clone designated herein as "DNA329205".

Figure 835 shows the amino acid sequence (SEQ ID NO:835) derived from the coding sequence of SEQ ID NO:834 shown in Figure 834.

Figure 836 shows a nucleotide sequence (SEQ ID NO:836) of a native sequence PRO36899 cDNA, wherein SEQ ID NO:836 is a clone designated herein as "DNA226436".

Figure 837 shows the amino acid sequence (SEQ ID NO:837) derived from the coding sequence of SEQ ID NO:836 shown in Figure 836.

Figure 838 shows a nucleotide sequence (SEQ ID NO:838) of a native sequence PRO84822 cDNA, wherein SEQ ID NO:838 is a clone designated herein as "DNA329206".

Figure 839 shows the amino acid sequence (SEQ ID NO:839) derived from the coding sequence of SEQ ID NO:838 shown in Figure 838.

Figure 840 shows a nucleotide sequence (SEQ ID NO:840) of a native sequence PRO61801 cDNA, wherein SEQ ID NO:840 is a clone designated herein as "DNA327732".

Figure 841 shows the amino acid sequence (SEQ ID NO:841) derived from the coding sequence of SEQ ID NO:840 shown in Figure 840.

Figure 842 shows a nucleotide sequence (SEQ ID NO:842) of a native sequence PRO84448 cDNA, wherein SEQ ID NO:842 is a clone designated herein as "DNA328676".

Figure 843 shows the amino acid sequence (SEQ ID NO:843) derived from the coding sequence of SEQ ID NO:842 shown in Figure 842.

Figure 844 shows a nucleotide sequence (SEQ ID NO:844) of a native sequence PRO84448 cDNA, wherein SEQ ID NO:844 is a clone designated herein as "DNA328676".

Figure 845 shows the amino acid sequence (SEQ ID NO:845) derived from the coding sequence of SEQ ID NO:844 shown in Figure 844.

Figure 846 shows a nucleotide sequence (SEQ ID NO:846) of a native sequence PRO84449 cDNA, wherein SEQ ID NO:846 is a clone designated herein as "DNA328677".

Figure 847 shows the amino acid sequence (SEQ ID NO:847) derived from the coding sequence of SEQ ID NO:846 shown in Figure 846.

Figure 848 shows a nucleotide sequence (SEQ ID NO:848) of a native sequence PRO220 cDNA, wherein SEQ ID NO:848 is a clone designated herein as "DNA329207".

Figure 849 shows the amino acid sequence (SEQ ID NO:849) derived from the coding sequence of SEQ ID NO:848 shown in Figure 848.

Figure 850 shows a nucleotide sequence (SEQ ID NO:850) of a native sequence PRO36583 cDNA, wherein SEQ ID NO:850 is a clone designated herein as "DNA226120".

Figure 851 shows the amino acid sequence (SEQ ID NO:851) derived from the coding sequence of SEQ ID NO:850 shown in Figure 850.

Figure 852 shows a nucleotide sequence (SEQ ID NO:852) of a native sequence PRO84823 cDNA, wherein SEQ ID NO:852 is a clone designated herein as "DNA329208".

Figure 853 shows the amino acid sequence (SEQ ID NO:853) derived from the coding sequence of SEQ ID NO:852 shown in Figure 852.

Figure 854 shows a nucleotide sequence (SEQ ID NO:854) of a native sequence PRO63226 cDNA, wherein SEQ ID NO:854 is a clone designated herein as "DNA326562".

Figure 855 shows the amino acid sequence (SEQ ID NO:855) derived from the coding sequence of SEQ ID NO:854 shown in Figure 854.

Figure 856 shows a nucleotide sequence (SEQ ID NO:856) of a native sequence cDNA, wherein SEQ ID NO:856 is a clone designated herein as "DNA154921".

Figure 857A-B shows a nucleotide sequence (SEQ ID NO:857) of a native sequence PRO37597 cDNA, wherein SEQ ID NO:857 is a clone designated herein as "DNA227134".

Figure 858 shows the amino acid sequence (SEQ ID NO:858) derived from the coding sequence of SEQ ID NO:857 shown in Figure 857A-B.

Figure 859A-B shows a nucleotide sequence (SEQ ID NO:859) of a native sequence PRO84824 cDNA, wherein SEQ ID NO:859 is a clone designated herein as "DNA329209".

Figure 860 shows the amino acid sequence (SEQ ID NO:860) derived from the coding sequence of SEQ ID NO:859 shown in Figure 859A-B.

Figure 861 shows a nucleotide sequence (SEQ ID NO:861) of a native sequence PRO37121 cDNA, wherein SEQ ID NO:861 is a clone designated herein as "DNA226658".

Figure 862 shows the amino acid sequence (SEQ ID NO:862) derived from the coding sequence of SEQ ID NO:861 shown in Figure 861.

Figure 863 shows a nucleotide sequence (SEQ ID NO:863) of a native sequence PRO82342 cDNA, wherein SEQ ID NO:863 is a clone designated herein as "DNA325886".

Figure 864 shows the amino acid sequence (SEQ ID NO:864) derived from the coding sequence of SEQ ID NO:863 shown in Figure 863.

Figure 865 shows a nucleotide sequence (SEQ ID NO:865) of a native sequence PRO22818 cDNA, wherein SEQ ID NO:865 is a clone designated herein as "DNA329210".

Figure 866 shows the amino acid sequence (SEQ ID NO:866) derived from the coding sequence of SEQ ID NO:865 shown in Figure 865.

Figure 867 shows a nucleotide sequence (SEQ ID NO:867) of a native sequence PRO64 cDNA, wherein SEQ ID NO:867 is a clone designated herein as "DNA328686".

Figure 868 shows the amino acid sequence (SEQ ID NO:868) derived from the coding sequence of SEQ ID NO:867 shown in Figure 867.

Figure 869 shows a nucleotide sequence (SEQ ID NO:869) of a native sequence PRO2081 cDNA, wherein SEQ ID NO:869 is a clone designated herein as "DNA287620".

Figure 870 shows the amino acid sequence (SEQ ID NO:870) derived from the coding sequence of SEQ ID NO:869 shown in Figure 869.

Figure 871 shows a nucleotide sequence (SEQ ID NO:871) of a native sequence PRO7078 cDNA, wherein SEQ ID NO:871 is a clone designated herein as "DNA329211".

Figure 872 shows the amino acid sequence (SEQ ID NO:872) derived from the coding sequence of SEQ ID NO:871 shown in Figure 871.

Figure 873 shows a nucleotide sequence (SEQ ID NO:873) of a native sequence PRO80521 cDNA, wherein SEQ ID NO:873 is a clone designated herein as "DNA323769".

Figure 874 shows the amino acid sequence (SEQ ID NO:874) derived from the coding sequence of SEQ ID NO:873 shown in Figure 873.

Figure 875 shows a nucleotide sequence (SEQ ID NO:875) of a native sequence PRO84825 cDNA, wherein SEQ ID NO:875 is a clone designated herein as "DNA329212".

Figure 876 shows the amino acid sequence (SEQ ID NO:876) derived from the coding sequence of SEQ ID NO:875 shown in Figure 875.

Figure 877 shows a nucleotide sequence (SEQ ID NO:877) of a native sequence PRO34295 cDNA, wherein SEQ ID NO:877 is a clone designated herein as "DNA217253".

Figure 878 shows the amino acid sequence (SEQ ID NO:878) derived from the coding sequence of SEQ ID NO:877 shown in Figure 877.

Figure 879 shows a nucleotide sequence (SEQ ID NO:879) of a native sequence PRO2313 cDNA, wherein SEQ ID NO:879 is a clone designated herein as "DNA329213".

Figure 880 shows the amino acid sequence (SEQ ID NO:880) derived from the coding sequence of SEQ ID NO:879 shown in Figure 879.

Figure 881A-B shows a nucleotide sequence (SEQ ID NO:881) of a native sequence PRO84826 cDNA, wherein SEQ ID NO:881 is a clone designated herein as "DNA329214".

Figure 882 shows the amino acid sequence (SEQ ID NO:882) derived from the coding sequence of SEQ ID NO:881 shown in Figure 881A-B.

Figure 883 shows a nucleotide sequence (SEQ ID NO:883) of a native sequence PRO71063 cDNA, wherein SEQ ID NO:883 is a clone designated herein as "DNA304499".

Figure 884 shows the amino acid sequence (SEQ ID NO:884) derived from the coding sequence of SEQ ID NO:883 shown in Figure 883.

Figure 885 shows a nucleotide sequence (SEQ ID NO:885) of a native sequence PRO35991 cDNA, wherein SEQ ID NO:885 is a clone designated herein as "DNA225528".

Figure 886 shows the amino acid sequence (SEQ ID NO:886) derived from the coding sequence of SEQ ID NO:885 shown in Figure 885.

Figure 887 shows a nucleotide sequence (SEQ ID NO:887) of a native sequence PRO7424 cDNA, wherein SEQ ID NO:887 is a clone designated herein as "DNA329215".

Figure 888 shows the amino acid sequence (SEQ ID NO:888) derived from the coding sequence of SEQ ID NO:887 shown in Figure 887.

Figure 889 shows a nucleotide sequence (SEQ ID NO:889) of a native sequence PRO36857 cDNA, wherein SEQ ID NO:889 is a clone designated herein as "DNA226394".

Figure 890 shows the amino acid sequence (SEQ ID NO:890) derived from the coding sequence of SEQ ID NO:889 shown in Figure 889.

Figure 891 shows a nucleotide sequence (SEQ ID NO:891) of a native sequence PRO61638 cDNA, wherein SEQ ID NO:891 is a clone designated herein as "DNA323902".

Figure 892 shows the amino acid sequence (SEQ ID NO:892) derived from the coding sequence of SEQ ID NO:891 shown in Figure 891.

Figure 893 shows a nucleotide sequence (SEQ ID NO:893) of a native sequence PRO84827 cDNA, wherein SEQ ID NO:893 is a clone designated herein as "DNA329216".

Figure 894 shows the amino acid sequence (SEQ ID NO:894) derived from the coding sequence of SEQ ID NO:893 shown in Figure 893.

Figure 895 shows a nucleotide sequence (SEQ ID NO:895) of a native sequence PRO84828 cDNA, wherein SEQ ID NO:895 is a clone designated herein as "DNA329217".

Figure 896 shows the amino acid sequence (SEQ ID NO:896) derived from the coding sequence of SEQ ID NO:895 shown in Figure 895.

Figure 897 shows a nucleotide sequence (SEQ ID NO:897) of a native sequence PRO84829 cDNA, wherein SEQ ID NO:897 is a clone designated herein as "DNA329218".

Figure 898 shows the amino acid sequence (SEQ ID NO:898) derived from the coding sequence of SEQ ID NO:897 shown in Figure 897.

Figure 899 shows a nucleotide sequence (SEQ ID NO:899) of a native sequence PRO83721 cDNA, wherein SEQ ID NO:899 is a clone designated herein as "DNA327747".

Figure 900 shows the amino acid sequence (SEQ ID NO:900) derived from the coding sequence of SEQ ID NO:899 shown in Figure 899.

Figure 901 shows a nucleotide sequence (SEQ ID NO:901) of a native sequence PRO38923 cDNA, wherein SEQ ID NO:901 is a clone designated herein as "DNA237817".

Figure 902 shows the amino acid sequence (SEQ ID NO:902) derived from the coding sequence of SEQ ID NO:901 shown in Figure 901.

Figure 903 shows a nucleotide sequence (SEQ ID NO:903) of a native sequence PRO81278 cDNA, wherein SEQ ID NO:903 is a clone designated herein as "DNA329219".

Figure 904 shows the amino acid sequence (SEQ ID NO:904) derived from the coding sequence of SEQ ID NO:903 shown in Figure 903.

Figure 905A-C shows a nucleotide sequence (SEQ ID NO:905) of a native sequence PRO84830 cDNA, wherein SEQ ID NO:905 is a clone designated herein as "DNA329220".

Figure 906 shows the amino acid sequence (SEQ ID NO:906) derived from the coding sequence of SEQ ID NO:905 shown in Figure 905A-C.

Figure 907 shows a nucleotide sequence (SEQ ID NO:907) of a native sequence PRO50026 cDNA, wherein SEQ ID NO:907 is a clone designated herein as "DNA254936".

Figure 908 shows the amino acid sequence (SEQ ID NO:908) derived from the coding sequence of SEQ ID NO:907 shown in Figure 907.

Figure 909 shows a nucleotide sequence (SEQ ID NO:909) of a native sequence PRO61971 cDNA, wherein SEQ ID NO:909 is a clone designated herein as "DNA274027".

Figure 910 shows the amino acid sequence (SEQ ID NO:910) derived from the coding sequence of SEQ ID NO:909 shown in Figure 909.

Figure 911 shows a nucleotide sequence (SEQ ID NO:911) of a native sequence PRO4555 cDNA, wherein SEQ ID NO:911 is a clone designated herein as "DNA329221".

Figure 912 shows the amino acid sequence (SEQ ID NO:912) derived from the coding sequence of SEQ ID NO:911 shown in Figure 911.

Figure 913 shows a nucleotide sequence (SEQ ID NO:913) of a native sequence PRO61480 cDNA, wherein SEQ ID NO:913 is a clone designated herein as "DNA329222".

Figure 914 shows the amino acid sequence (SEQ ID NO:914) derived from the coding sequence of SEQ ID NO:913 shown in Figure 913.

Figure 915 shows a nucleotide sequence (SEQ ID NO:915) of a native sequence PRO71178 cDNA, wherein SEQ ID NO:915 is a clone designated herein as "DNA304765".

Figure 916 shows the amino acid sequence (SEQ ID NO:916) derived from the coding sequence of SEQ ID NO:915 shown in Figure 915.

Figure 917 shows a nucleotide sequence (SEQ ID NO:917) of a native sequence PRO4723 cDNA, wherein SEQ ID NO:917 is a clone designated herein as "DNA103395".

Figure 918 shows the amino acid sequence (SEQ ID NO:918) derived from the coding sequence of SEQ ID NO:917 shown in Figure 917.

Figure 919A-B shows a nucleotide sequence (SEQ ID NO:919) of a native sequence PRO62786 cDNA, wherein SEQ ID NO:919 is a clone designated herein as "DNA275066".

Figure 920 shows the amino acid sequence (SEQ ID NO:920) derived from the coding sequence of SEQ ID NO:919 shown in Figure 919A-B.

Figure 921 shows a nucleotide sequence (SEQ ID NO:921) of a native sequence PRO83725 cDNA, wherein SEQ ID NO:921 is a clone designated herein as "DNA327755".

Figure 922 shows the amino acid sequence (SEQ ID NO:922) derived from the coding sequence of SEQ ID NO:921 shown in Figure 921.

Figure 923 shows a nucleotide sequence (SEQ ID NO:923) of a native sequence PRO84831 cDNA, wherein SEQ ID NO:923 is a clone designated herein as "DNA329223".

Figure 924 shows the amino acid sequence (SEQ ID NO:924) derived from the coding sequence of SEQ ID NO:923 shown in Figure 923.

Figure 925 shows a nucleotide sequence (SEQ ID NO:925) of a native sequence PRO37041 cDNA, wherein SEQ ID NO:925 is a clone designated herein as "DNA226578".

Figure 926 shows the amino acid sequence (SEQ ID NO:926) derived from the coding sequence of SEQ ID NO:925 shown in Figure 925.

Figure 927 shows a nucleotide sequence (SEQ ID NO:927) of a native sequence PRO84832 cDNA, wherein SEQ ID NO:927 is a clone designated herein as "DNA329224".

Figure 928 shows the amino acid sequence (SEQ ID NO:928) derived from the coding sequence of SEQ ID NO:927 shown in Figure 927.

Figure 929 shows a nucleotide sequence (SEQ ID NO:929) of a native sequence PRO10347 cDNA, wherein SEQ ID NO:929 is a clone designated herein as "DNA328706".

Figure 930 shows the amino acid sequence (SEQ ID NO:930) derived from the coding sequence of SEQ ID NO:929 shown in Figure 929.

Figure 931 shows a nucleotide sequence (SEQ ID NO:931) of a native sequence PRO84833 cDNA, wherein SEQ ID NO:931 is a clone designated herein as "DNA329225".

Figure 932 shows the amino acid sequence (SEQ ID NO:932) derived from the coding sequence of SEQ ID NO:931 shown in Figure 931.

Figure 933A-B shows a nucleotide sequence (SEQ ID NO:933) of a native sequence PRO60388 cDNA, wherein SEQ ID NO:933 is a clone designated herein as "DNA329226".

Figure 934 shows the amino acid sequence (SEQ ID NO:934) derived from the coding sequence of SEQ ID NO:933 shown in Figure 933A-B.

Figure 935 shows a nucleotide sequence (SEQ ID NO:935) of a native sequence PRO2023 cDNA, wherein SEQ ID NO:935 is a clone designated herein as "DNA304473".

Figure 936 shows the amino acid sequence (SEQ ID NO:936) derived from the coding sequence of SEQ ID NO:935 shown in Figure 935.

Figure 937A-B shows a nucleotide sequence (SEQ ID NO:937) of a native sequence PRO34751 cDNA, wherein SEQ ID NO:937 is a clone designated herein as "DNA328685".

Figure 938 shows the amino acid sequence (SEQ ID NO:938) derived from the coding sequence of SEQ ID NO:937 shown in Figure 937A-B.

Figure 939A-B shows a nucleotide sequence (SEQ ID NO:939) of a native sequence PRO81785 cDNA, wherein SEQ ID NO:939 is a clone designated herein as "DNA325227".

Figure 940 shows the amino acid sequence (SEQ ID NO:940) derived from the coding sequence of SEQ ID NO:939 shown in Figure 939A-B.

Figure 941A-B shows a nucleotide sequence (SEQ ID NO:941) of a native sequence cDNA, wherein SEQ ID NO:941 is a clone designated herein as "DNA272195".

Figure 942A-B shows a nucleotide sequence (SEQ ID NO:942) of a native sequence PRO82307 cDNA, wherein SEQ ID NO:942 is a clone designated herein as "DNA329227".

Figure 943 shows the amino acid sequence (SEQ ID NO:943) derived from the coding sequence of SEQ ID NO:942 shown in Figure 942A-B.

Figure 944 shows a nucleotide sequence (SEQ ID NO:944) of a native sequence PRO82388 cDNA, wherein SEQ ID NO:944 is a clone designated herein as "DNA325941".

Figure 945 shows the amino acid sequence (SEQ ID NO:945) derived from the coding sequence of SEQ ID NO:944 shown in Figure 944.

Figure 946 shows a nucleotide sequence (SEQ ID NO:946) of a native sequence PRO69480 cDNA, wherein SEQ ID NO:946 is a clone designated herein as "DNA287194".

Figure 947 shows the amino acid sequence (SEQ ID NO:947) derived from the coding sequence of SEQ ID NO:946 shown in Figure 946.

Figure 948A-C shows a nucleotide sequence (SEQ ID NO:948) of a native sequence PRO84834 cDNA, wherein SEQ ID NO:948 is a clone designated herein as "DNA329228".

Figure 949 shows the amino acid sequence (SEQ ID NO:949) derived from the coding sequence of SEQ ID NO:948 shown in Figure 948A-C.

Figure 950 shows a nucleotide sequence (SEQ ID NO:950) of a native sequence PRO69690 cDNA, wherein SEQ ID NO:950 is a clone designated herein as "DNA287433".

Figure 951 shows the amino acid sequence (SEQ ID NO:951) derived from the coding sequence of SEQ ID NO:950 shown in Figure 950.

Figure 952 shows a nucleotide sequence (SEQ ID NO:952) of a native sequence PRO4710 cDNA, wherein SEQ ID NO:952 is a clone designated herein as "DNA103380".

Figure 953 shows the amino acid sequence (SEQ ID NO:953) derived from the coding sequence of SEQ ID NO:952 shown in Figure 952.

Figure 954A-B shows a nucleotide sequence (SEQ ID NO:954) of a native sequence PRO12560 cDNA, wherein SEQ ID NO:954 is a clone designated herein as "DNA150956".

Figure 955 shows the amino acid sequence (SEQ ID NO:955) derived from the coding sequence of SEQ ID NO:954 shown in Figure 954A-B.

Figure 956A-B shows a nucleotide sequence (SEQ ID NO:956) of a native sequence cDNA, wherein SEQ ID NO:956 is a clone designated herein as "DNA150829".

Figure 957A-B shows a nucleotide sequence (SEQ ID NO:957) of a native sequence PRO84835 cDNA, wherein SEQ ID NO:957 is a clone designated herein as "DNA329229".

Figure 958 shows the amino acid sequence (SEQ ID NO:958) derived from the coding sequence of SEQ ID NO:957 shown in Figure 957A-B.

Figure 959 shows a nucleotide sequence (SEQ ID NO:959) of a native sequence PRO84836 cDNA, wherein SEQ ID NO:959 is a clone designated herein as "DNA329230".

Figure 960 shows the amino acid sequence (SEQ ID NO:960) derived from the coding sequence of SEQ ID NO:959 shown in Figure 959.

Figure 961 shows a nucleotide sequence (SEQ ID NO:961) of a native sequence cDNA, wherein SEQ ID NO:961 is a clone designated herein as "DNA150980".

Figure 962 shows a nucleotide sequence (SEQ ID NO:962) of a native sequence PRO84475 cDNA, wherein SEQ ID NO:962 is a clone designated herein as "DNA328719".

Figure 963 shows the amino acid sequence (SEQ ID NO:963) derived from the coding sequence of SEQ ID NO:962 shown in Figure 962.

Figure 964 shows a nucleotide sequence (SEQ ID NO:964) of a native sequence PRO59425 cDNA, wherein SEQ ID NO:964 is a clone designated herein as "DNA271103".

Figure 965 shows the amino acid sequence (SEQ ID NO:965) derived from the coding sequence of SEQ ID NO:964 shown in Figure 964.

Figure 966 shows a nucleotide sequence (SEQ ID NO:966) of a native sequence cDNA, wherein SEQ ID NO:966 is a clone designated herein as "DNA207620".

Figure 967 shows a nucleotide sequence (SEQ ID NO:967) of a native sequence PRO83141 cDNA, wherein SEQ ID NO:967 is a clone designated herein as "DNA326808".

Figure 968 shows the amino acid sequence (SEQ ID NO:968) derived from the coding sequence of SEQ ID NO:967 shown in Figure 967.

Figure 969A-B shows a nucleotide sequence (SEQ ID NO:969) of a native sequence PRO6323 cDNA, wherein SEQ ID NO:969 is a clone designated herein as "DNA124122".

Figure 970 shows the amino acid sequence (SEQ ID NO:970) derived from the coding sequence of SEQ ID NO:969 shown in Figure 969A-B.

Figure 971A-B shows a nucleotide sequence (SEQ ID NO:971) of a native sequence PRO6323 cDNA, wherein SEQ ID NO:971 is a clone designated herein as "DNA124122".

Figure 972 shows the amino acid sequence (SEQ ID NO:972) derived from the coding sequence of SEQ ID NO:971 shown in Figure 971A-B.

Figure 973 shows a nucleotide sequence (SEQ ID NO:973) of a native sequence PRO69476 cDNA, wherein SEQ ID NO:973 is a clone designated herein as "DNA287190".

Figure 974 shows the amino acid sequence (SEQ ID NO:974) derived from the coding sequence of SEQ ID NO:973 shown in Figure 973.

Figure 975 shows a nucleotide sequence (SEQ ID NO:975) of a native sequence PRO84837 cDNA, wherein SEQ ID NO:975 is a clone designated herein as "DNA329231".

Figure 976 shows the amino acid sequence (SEQ ID NO:976) derived from the coding sequence of SEQ ID NO:975 shown in Figure 975.

Figure 977A-B shows a nucleotide sequence (SEQ ID NO:977) of a native sequence PRO12554 cDNA, wherein SEQ ID NO:977 is a clone designated herein as "DNA150950".

Figure 978 shows the amino acid sequence (SEQ ID NO:978) derived from the coding sequence of SEQ ID NO:977 shown in Figure 977A-B.

Figure 979 shows a nucleotide sequence (SEQ ID NO:979) of a native sequence PRO11708 cDNA, wherein SEQ ID NO:979 is a clone designated herein as "DNA151330".

Figure 980 shows the amino acid sequence (SEQ ID NO:980) derived from the coding sequence of SEQ ID NO:979 shown in Figure 979.

Figure 981 shows a nucleotide sequence (SEQ ID NO:981) of a native sequence cDNA, wherein SEQ ID NO:981 is a clone designated herein as "DNA329232".

Figure 982 shows a nucleotide sequence (SEQ ID NO:982) of a native sequence PRO71082 cDNA, wherein SEQ ID NO:982 is a clone designated herein as "DNA304655".

Figure 983 shows the amino acid sequence (SEQ ID NO:983) derived from the coding sequence of SEQ ID NO:982 shown in Figure 982.

Figure 984 shows a nucleotide sequence (SEQ ID NO:984) of a native sequence PRO84485 cDNA, wherein SEQ ID NO:984 is a clone designated herein as "DNA328732".

Figure 985 shows the amino acid sequence (SEQ ID NO:985) derived from the coding sequence of SEQ ID NO:984 shown in Figure 984.

Figure 986 shows a nucleotide sequence (SEQ ID NO:986) of a native sequence PRO84839 cDNA, wherein SEQ ID NO:986 is a clone designated herein as "DNA329233".

Figure 987 shows the amino acid sequence (SEQ ID NO:987) derived from the coding sequence of SEQ ID NO:986 shown in Figure 986.

Figure 988 shows a nucleotide sequence (SEQ ID NO:988) of a native sequence cDNA, wherein SEQ ID NO:988 is a clone designated herein as "DNA329234".

Figure 989A-D shows a nucleotide sequence (SEQ ID NO:989) of a native sequence PRO84490 cDNA, wherein SEQ ID NO:989 is a clone designated herein as "DNA328737".

Figure 990 shows the amino acid sequence (SEQ ID NO:990) derived from the coding sequence of SEQ ID NO:989 shown in Figure 989A-D.

Figure 991 shows a nucleotide sequence (SEQ ID NO:991) of a native sequence PRO81715 cDNA, wherein SEQ ID NO:991 is a clone designated herein as "DNA329235".

Figure 992 shows the amino acid sequence (SEQ ID NO:992) derived from the coding sequence of SEQ ID NO:991 shown in Figure 991.

Figure 993A-C shows a nucleotide sequence (SEQ ID NO:993) of a native sequence PRO84841 cDNA, wherein SEQ ID NO:993 is a clone designated herein as "DNA329236".

Figure 994 shows the amino acid sequence (SEQ ID NO:994) derived from the coding sequence of SEQ ID NO:993 shown in Figure 993A-C.

Figure 995 shows a nucleotide sequence (SEQ ID NO:995) of a native sequence PRO84841 cDNA, wherein SEQ ID NO:995 is a clone designated herein as "DNA329236".

Figure 996 shows the amino acid sequence (SEQ ID NO:996) derived from the coding sequence of SEQ ID NO:995 shown in Figure 995.

Figure 997 shows a nucleotide sequence (SEQ ID NO:997) of a native sequence PRO11833 cDNA, wherein SEQ ID NO:997 is a clone designated herein as "DNA151487".

Figure 998 shows the amino acid sequence (SEQ ID NO:998) derived from the coding sequence of SEQ ID NO:997 shown in Figure 997.

Figure 999A-B shows a nucleotide sequence (SEQ ID NO:999) of a native sequence PRO84842 cDNA, wherein SEQ ID NO:999 is a clone designated herein as "DNA329237".

Figure 1000 shows the amino acid sequence (SEQ ID NO:1000) derived from the coding sequence of SEQ ID NO:999 shown in Figure 999A-B.

Figure 1001 shows a nucleotide sequence (SEQ ID NO:1001) of a native sequence PRO84843 cDNA, wherein SEQ ID NO:1001 is a clone designated herein as "DNA329238".

Figure 1002 shows the amino acid sequence (SEQ ID NO:1002) derived from the coding sequence of SEQ ID NO:1001 shown in Figure 1001.

Figure 1003A-B shows a nucleotide sequence (SEQ ID NO:1003) of a native sequence cDNA, wherein SEQ ID NO:1003 is a clone designated herein as "DNA327778".

Figure 1004A-B shows a nucleotide sequence (SEQ ID NO:1004) of a native sequence cDNA, wherein SEQ ID NO:1004 is a clone designated herein as "DNA287360".

Figure 1005A-B shows a nucleotide sequence (SEQ ID NO:1005) of a native sequence cDNA, wherein SEQ ID NO:1005 is a clone designated herein as "DNA270118".

Figure 1006A-B shows a nucleotide sequence (SEQ ID NO:1006) of a native sequence PRO 59570 cDNA, wherein SEQ ID NO:1006 is a clone designated herein as "DNA328748".

Figure 1007 shows the amino acid sequence (SEQ ID NO:1007) derived from the coding sequence of SEQ ID NO:1006 shown in Figure 1006A-B.

Figure 1008 shows a nucleotide sequence (SEQ ID NO:1008) of a native sequence PRO84500 cDNA, wherein SEQ ID NO:1008 is a clone designated herein as "DNA328750".

Figure 1009 shows the amino acid sequence (SEQ ID NO:1009) derived from the coding sequence of SEQ ID NO:1008 shown in Figure 1008.

Figure 1010A-B shows a nucleotide sequence (SEQ ID NO:1010) of a native sequence PRO84502 cDNA, wherein SEQ ID NO:1010 is a clone designated herein as "DNA328753".

Figure 1011 shows the amino acid sequence (SEQ ID NO:1011) derived from the coding sequence of SEQ ID NO:1010 shown in Figure1010A-B.

Figure 1012 shows a nucleotide sequence (SEQ ID NO:1012) of a native sequence PRO69549 cDNA, wherein SEQ ID NO:1012 is a clone designated herein as "DNA325596".

Figure 1013 shows the amino acid sequence (SEQ ID NO:1013) derived from the coding sequence of SEQ ID NO:1012 shown in Figure 1012.

Figure 1014 shows a nucleotide sequence (SEQ ID NO:1014) of a native sequence PRO84844 cDNA, wherein SEQ ID NO:1014 is a clone designated herein as "DNA329239".

Figure 1015 shows the amino acid sequence (SEQ ID NO:1015) derived from the coding sequence of SEQ ID NO:1014 shown in Figure 1014.

Figure 1016A-B shows a nucleotide sequence (SEQ ID NO:1016) of a native sequence PRO84845 cDNA, wherein SEQ ID NO:1016 is a clone designated herein as "DNA329240".

Figure 1017 shows the amino acid sequence (SEQ ID NO:1017) derived from the coding sequence of SEQ ID NO:1016 shown in Figure 1016.

Figure 1018 shows a nucleotide sequence (SEQ ID NO:1018) of a native sequence PRO84846 cDNA, wherein SEQ ID NO:1018 is a clone designated herein as "DNA329241".

Figure 1019 shows the amino acid sequence (SEQ ID NO:1019) derived from the coding sequence of SEQ ID NO:1018 shown in Figure 1018.

Figure 1020A-B shows a nucleotide sequence (SEQ ID NO:1020) of a native sequence PRO84847 cDNA, wherein SEQ ID NO:1020 is a clone designated herein as "DNA329242".

Figure 1021 shows the amino acid sequence (SEQ ID NO:1021) derived from the coding sequence of SEQ ID NO:1020 shown in Figure 1020.

Figure 1022 shows a nucleotide sequence (SEQ ID NO:1022) of a native sequence PRO84848 cDNA, wherein SEQ ID NO:1022 is a clone designated herein as "DNA329243".

Figure 1023 shows the amino acid sequence (SEQ ID NO:1023) derived from the coding sequence of SEQ ID NO:1022 shown in Figure 1022.

Figure 1024A-C shows a nucleotide sequence (SEQ ID NO:1024) of a native sequence PRO84849 cDNA, wherein SEQ ID NO:1024 is a clone designated herein as "DNA329244".

Figure 1025 shows the amino acid sequence (SEQ ID NO:1025) derived from the coding sequence of SEQ ID NO:1024 shown in Figure 1024.

Figure 1026A-B shows a nucleotide sequence (SEQ ID NO:1026) of a native sequence cDNA, wherein SEQ ID NO:1026 is a clone designated herein as "DNA328758".

Figure 1027 shows a nucleotide sequence (SEQ ID NO:1027) of a native sequence cDNA, wherein SEQ ID NO:1027 is a clone designated herein as "DNA329245".

Figure 1028A-B shows a nucleotide sequence (SEQ ID NO:1028) of a native sequence cDNA, wherein SEQ ID NO:1028 is a clone designated herein as "DNA329246".

Figure 1029 shows a nucleotide sequence (SEQ ID NO:1029) of a native sequence PRO69509 cDNA, wherein SEQ ID NO:1029 is a clone designated herein as "DNA287230".

Figure 1030 shows the amino acid sequence (SEQ ID NO:1030) derived from the coding sequence of SEQ ID NO:1029 shown in Figure 1029.

Figure 1031 shows a nucleotide sequence (SEQ ID NO:1031) of a native sequence cDNA, wherein SEQ ID NO:1031 is a clone designated herein as "DNA228053".

Figure 1032 shows a nucleotide sequence (SEQ ID NO:1032) of a native sequence PRO69541 cDNA, wherein SEQ ID NO:1032 is a clone designated herein as "DNA287270".

Figure 1033 shows the amino acid sequence (SEQ ID NO:1033) derived from the coding sequence of SEQ ID NO:1032 shown in Figure 1032.

Figure 1034A-C shows a nucleotide sequence (SEQ ID NO:1034) of a native sequence PRO59767 cDNA, wherein SEQ ID NO:1034 is a clone designated herein as "DNA329247".

Figure 1035 shows the amino acid sequence (SEQ ID NO:1035) derived from the coding sequence of SEQ ID NO:1034 shown in Figure 1034.

Figure 1036A-B shows a nucleotide sequence (SEQ ID NO:1036) of a native sequence PRO84850 cDNA, wherein SEQ ID NO:1036 is a clone designated herein as "DNA329248".

Figure 1037 shows the amino acid sequence (SEQ ID NO:1037) derived from the coding sequence of SEQ ID NO:1036 shown in Figure 1036.

FigureA-B 1038 shows a nucleotide sequence (SEQ ID NO:1038) of a native sequence PRO50349 cDNA, wherein SEQ ID NO:1038 is a clone designated herein as "DNA255273".

Figure 1039 shows the amino acid sequence (SEQ ID NO:1039) derived from the coding sequence of SEQ ID NO:1038 shown in Figure 1038.

Figure 1040 shows a nucleotide sequence (SEQ ID NO:1040) of a native sequence PRO10641 cDNA, wherein SEQ ID NO:1040 is a clone designated herein as "DNA329249".

Figure 1041 shows the amino acid sequence (SEQ ID NO:1041) derived from the coding sequence of SEQ ID NO:1040 shown in Figure 1040.

Figure 1042A-B shows a nucleotide sequence (SEQ ID NO:1042) of a native sequence PRO84851 cDNA, wherein SEQ ID NO:1042 is a clone designated herein as "DNA329250".

Figure 1043 shows the amino acid sequence (SEQ ID NO:1043) derived from the coding sequence of SEQ ID NO:1042 shown in Figure 1042.

Figure 1044A-B shows a nucleotide sequence (SEQ ID NO:1044) of a native sequence cDNA, wherein SEQ ID NO:1044 is a clone designated herein as "DNA329251".

Figure 1045 shows a nucleotide sequence (SEQ ID NO:1045) of a native sequence PRO49375 cDNA, wherein SEQ ID NO:1045 is a clone designated herein as "DNA254264".

Figure 1046 shows the amino acid sequence (SEQ ID NO:1046) derived from the coding sequence of SEQ ID NO:1045 shown in Figure 1045.

Figure 1047 shows a nucleotide sequence (SEQ ID NO:1047) of a native sequence PRO83763 cDNA, wherein SEQ ID NO:1047 is a clone designated herein as "DNA327800".

Figure 1048 shows the amino acid sequence (SEQ ID NO:1048) derived from the coding sequence of SEQ ID NO:1047 shown in Figure 1047.

Figure 1049 shows a nucleotide sequence (SEQ ID NO:1049) of a native sequence PRO82188 cDNA, wherein SEQ ID NO:1049 is a clone designated herein as "DNA325704".

Figure 1050 shows the amino acid sequence (SEQ ID NO:1050) derived from the coding sequence of SEQ ID NO:1049 shown in Figure 1049.

Figure 1051 shows a nucleotide sequence (SEQ ID NO:1051) of a native sequence cDNA, wherein SEQ ID NO:1051 is a clone designated herein as "DNA328771".

Figure 1052A-B shows a nucleotide sequence (SEQ ID NO:1052) of a native sequence PRO84852 cDNA, wherein SEQ ID NO:1052 is a clone designated herein as "DNA329252".

Figure 1053 shows the amino acid sequence (SEQ ID NO:1053) derived from the coding sequence of SEQ ID NO:1052 shown in Figure 1052.

Figure 1054 shows a nucleotide sequence (SEQ ID NO:1054) of a native sequence PRO37804 cDNA, wherein SEQ ID NO:1054 is a clone designated herein as "DNA227341".

Figure 1055 shows the amino acid sequence (SEQ ID NO:1055) derived from the coding sequence of SEQ ID NO:1054 shown in Figure 1054.

Figure 1056 shows a nucleotide sequence (SEQ ID NO:1056) of a native sequence PRO60536 cDNA, wherein SEQ ID NO:1056 is a clone designated herein as "DNA328774".

Figure 1057 shows the amino acid sequence (SEQ ID NO:1057) derived from the coding sequence of SEQ ID NO:1056 shown in Figure 1056.

Figure 1058 shows a nucleotide sequence (SEQ ID NO:1058) of a native sequence cDNA, wherein SEQ ID NO:1058 is a clone designated herein as "DNA151041".

Figure 1059 shows a nucleotide sequence (SEQ ID NO:1059) of a native sequence PRO83768 cDNA, wherein SEQ ID NO:1059 is a clone designated herein as "DNA327807".

Figure 1060 shows the amino acid sequence (SEQ ID NO:1060) derived from the coding sequence of SEQ ID NO:1059 shown in Figure 1059.

Figure 1061 shows a nucleotide sequence (SEQ ID NO:1061) of a native sequence PRO2 cDNA, wherein SEQ ID NO:1061 is a clone designated herein as "DNA51782".

Figure 1062 shows the amino acid sequence (SEQ ID NO:1062) derived from the coding sequence of SEQ ID NO:1061 shown in Figure 1061.

Figure 1063 shows a nucleotide sequence (SEQ ID NO:1063) of a native sequence PRO10498 cDNA, wherein SEQ ID NO:1063 is a clone designated herein as "DNA324224".

Figure 1064 shows the amino acid sequence (SEQ ID NO:1064) derived from the coding sequence of SEQ ID NO:1063 shown in Figure 1063.

Figure 1065 shows a nucleotide sequence (SEQ ID NO:1065) of a native sequence PRO84853 cDNA, wherein SEQ ID NO:1065 is a clone designated herein as "DNA329253".

Figure 1066 shows the amino acid sequence (SEQ ID NO:1066) derived from the coding sequence of SEQ ID NO:1065 shown in Figure 1065.

Figure 1067 shows a nucleotide sequence (SEQ ID NO:1067) of a native sequence PRO84854 cDNA, wherein SEQ ID NO:1067 is a clone designated herein as "DNA329254".

Figure 1068 shows the amino acid sequence (SEQ ID NO:1068) derived from the coding sequence of SEQ ID NO:1067 shown in Figure 1067.

Figure 1069A-B shows a nucleotide sequence (SEQ ID NO:1069) of a native sequence PRO60550 cDNA, wherein SEQ ID NO:1069 is a clone designated herein as "DNA272292".

Figure 1070 shows the amino acid sequence (SEQ ID NO:1070) derived from the coding sequence of SEQ ID NO:1069 shown in Figure 1069.

Figure 1071 shows a nucleotide sequence (SEQ ID NO:1071) of a native sequence PRO84855 cDNA, wherein SEQ ID NO:1071 is a clone designated herein as "DNA329255".

Figure 1072 shows the amino acid sequence (SEQ ID NO:1072) derived from the coding sequence of SEQ ID NO:1071 shown in Figure 1071.

Figure 1073A-B shows a nucleotide sequence (SEQ ID NO:1073) of a native sequence PRO84856 cDNA, wherein SEQ ID NO:1073 is a clone designated herein as "DNA329256".

Figure 1074 shows the amino acid sequence (SEQ ID NO:1074) derived from the coding sequence of SEQ ID NO:1073 shown in Figure 1073.

Figure 1075 shows a nucleotide sequence (SEQ ID NO:1075) of a native sequence PRO2398 cDNA, wherein SEQ ID NO:1075 is a clone designated herein as "DNA88530".

Figure 1076 shows the amino acid sequence (SEQ ID NO:1076) derived from the coding sequence of SEQ ID NO:1075 shown in Figure 1075.

Figure 1077 shows a nucleotide sequence (SEQ ID NO:1077) of a native sequence PRO2634 cDNA, wherein SEQ ID NO:1077 is a clone designated herein as "DNA88054".

Figure 1078 shows the amino acid sequence (SEQ ID NO:1078) derived from the coding sequence of SEQ ID NO:1077 shown in Figure 1077.

Figure 1079 shows a nucleotide sequence (SEQ ID NO:1079) of a native sequence PRO83772 cDNA, wherein SEQ ID NO:1079 is a clone designated herein as "DNA327811".

Figure 1080 shows the amino acid sequence (SEQ ID NO:1080) derived from the coding sequence of SEQ ID NO:1079 shown in Figure 1079.

Figure 1081 shows a nucleotide sequence (SEQ ID NO:1081) of a native sequence PRO12564 cDNA, wherein SEQ ID NO:1081 is a clone designated herein as "DNA150971".

Figure 1082 shows the amino acid sequence (SEQ ID NO:1082) derived from the coding sequence of SEQ ID NO:1081 shown in Figure 1081.

Figure 1083A-B shows a nucleotide sequence (SEQ ID NO:1083) of a native sequence PRO84857 cDNA, wherein SEQ ID NO:1083 is a clone designated herein as "DNA329257".

Figure 1084 shows the amino acid sequence (SEQ ID NO:1084) derived from the coding sequence of SEQ ID NO:1083 shown in Figure 1083.

Figure 1085 shows a nucleotide sequence (SEQ ID NO:1085) of a native sequence PRO38069 cDNA, wherein SEQ ID NO:1085 is a clone designated herein as "DNA227606".

Figure 1086 shows the amino acid sequence (SEQ ID NO:1086) derived from the coding sequence of SEQ ID NO:1085 shown in Figure 1085.

Figure 1087 shows a nucleotide sequence (SEQ ID NO:1087) of a native sequence PRO71203 cDNA, wherein SEQ ID NO:1087 is a clone designated herein as "DNA304791".

Figure 1088 shows the amino acid sequence (SEQ ID NO:1088) derived from the coding sequence of SEQ ID NO:1087 shown in Figure 1087.

Figure 1089 shows a nucleotide sequence (SEQ ID NO:1089) of a native sequence PRO10586 cDNA, wherein SEQ ID NO:1089 is a clone designated herein as "DNA329258".

Figure 1090 shows the amino acid sequence (SEQ ID NO:1090) derived from the coding sequence of SEQ ID NO:1089 shown in Figure 1089.

Figure 1091 shows a nucleotide sequence (SEQ ID NO:1091) of a native sequence PRO34267 cDNA, wherein SEQ ID NO:1091 is a clone designated herein as "DNA216515".

Figure 1092 shows the amino acid sequence (SEQ ID NO:1092) derived from the coding sequence of SEQ ID NO:1091 shown in Figure 1091.

Figure 1093A-B shows a nucleotide sequence (SEQ ID NO:1093) of a native sequence PRO85430 cDNA, wherein SEQ ID NO:1093 is a clone designated herein as "DNA328784".

Figure 1094 shows the amino acid sequence (SEQ ID NO:1094) derived from the coding sequence of SEQ ID NO:1093 shown in Figure 1093.

Figure 1095 shows a nucleotide sequence (SEQ ID NO:1095) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:1095 is a clone designated herein as "DNA327817".

Figure 1096 shows the amino acid sequence (SEQ ID NO:1096) derived from the coding sequence of SEQ ID NO:1095 shown in Figure 1095.

Figure 1097 shows a nucleotide sequence (SEQ ID NO:1097) of a native sequence PRO12646 cDNA, wherein SEQ ID NO:1097 is a clone designated herein as "DNA151222".

Figure 1098 shows the amino acid sequence (SEQ ID NO:1098) derived from the coding sequence of SEQ ID NO:1097 shown in Figure 1097.

Figure 1099 shows a nucleotide sequence (SEQ ID NO:1099) of a native sequence cDNA, wherein SEQ ID NO:1099 is a clone designated herein as "DNA329259".

Figure 1100 shows a nucleotide sequence (SEQ ID NO:1100) of a native sequence PRO83851 cDNA, wherein SEQ ID NO:1100 is a clone designated herein as "DNA327916".

Figure 1101 shows the amino acid sequence (SEQ ID NO:1101) derived from the coding sequence of SEQ ID NO:1100 shown in Figure 1100.

Figure 1102A-B shows a nucleotide sequence (SEQ ID NO:1102) of a native sequence PRO84858 cDNA, wherein SEQ ID NO:1102 is a clone designated herein as "DNA329260".

Figure 1103 shows the amino acid sequence (SEQ ID NO:1103) derived from the coding sequence of SEQ ID NO:1102 shown in Figure 1102.

Figure 1104A-B shows a nucleotide sequence (SEQ ID NO:1104) of a native sequence PRO84859 cDNA, wherein SEQ ID NO:1104 is a clone designated herein as "DNA329261".

Figure 1105 shows the amino acid sequence (SEQ ID NO:1105) derived from the coding sequence of SEQ ID NO:1104 shown in Figure 1104.

Figure 1106 shows a nucleotide sequence (SEQ ID NO:1106) of a native sequence PRO1721 cDNA, wherein SEQ ID NO:1106 is a clone designated herein as "DNA328799".

Figure 1107 shows the amino acid sequence (SEQ ID NO:1107) derived from the coding sequence of SEQ ID NO:1106 shown in Figure 1106.

Figure 1108 shows a nucleotide sequence (SEQ ID NO:1108) of a native sequence PRO84860 cDNA, wherein SEQ ID NO:1108 is a clone designated herein as "DNA329262".

Figure 1109 shows the amino acid sequence (SEQ ID NO:1109) derived from the coding sequence of SEQ ID NO:1108 shown in Figure 1108.

Figure 1110 shows a nucleotide sequence (SEQ ID NO:1110) of a native sequence PRO84861 cDNA, wherein SEQ ID NO:1110 is a clone designated herein as "DNA329263".

Figure 1111 shows the amino acid sequence (SEQ ID NO:1111) derived from the coding sequence of SEQ ID NO:1110 shown in Figure 1110.

Figure 1112 shows a nucleotide sequence (SEQ ID NO:1112) of a native sequence PRO60325 cDNA, wherein SEQ ID NO:1112 is a clone designated herein as "DNA326136".

Figure 1113 shows the amino acid sequence (SEQ ID NO:1113) derived from the coding sequence of SEQ ID NO:1112 shown in Figure 1112.

Figure 1114A-B shows a nucleotide sequence (SEQ ID NO:1114) of a native sequence cDNA, wherein SEQ ID NO:1114 is a clone designated herein as "DNA327827".

Figure 1115 shows a nucleotide sequence (SEQ ID NO:1115) of a native sequence PRO2178 cDNA, wherein SEQ ID NO:1115 is a clone designated herein as "DNA88121".

Figure 1116 shows the amino acid sequence (SEQ ID NO:1116) derived from the coding sequence of SEQ ID NO:1115 shown in Figure 1115.

Figure 1117A-B shows a nucleotide sequence (SEQ ID NO:1117) of a native sequence PRO12587 cDNA, wherein SEQ ID NO:1117 is a clone designated herein as "DNA151045".

Figure 1118 shows the amino acid sequence (SEQ ID NO:1118) derived from the coding sequence of SEQ ID NO:1117 shown in Figure 1117.

Figure 1119 shows a nucleotide sequence (SEQ ID NO:1119) of a native sequence PRO9819 cDNA, wherein SEQ ID NO:1119 is a clone designated herein as "DNA325174".

Figure 1120 shows the amino acid sequence (SEQ ID NO:1120) derived from the coding sequence of SEQ ID NO:1119 shown in Figure 1119.

Figure 1121 shows a nucleotide sequence (SEQ ID NO:1121) of a native sequence cDNA, wherein SEQ ID NO:1121 is a clone designated herein as "DNA329264".

Figure 1122 shows a nucleotide sequence (SEQ ID NO:1122) of a native sequence PRO84547 cDNA, wherein SEQ ID NO:1122 is a clone designated herein as "DNA328805".

Figure 1123 shows the amino acid sequence (SEQ ID NO:1123) derived from the coding sequence of SEQ ID NO:1122 shown in Figure 1122.

Figure 1124 shows a nucleotide sequence (SEQ ID NO:1124) of a native sequence PRO66288 cDNA, wherein SEQ ID NO:1124 is a clone designated herein as "DNA281449".

Figure 1125 shows the amino acid sequence (SEQ ID NO:1125) derived from the coding sequence of SEQ ID NO:1124 shown in Figure 1124.

Figure 1126 shows a nucleotide sequence (SEQ ID NO:1126) of a native sequence cDNA, wherein SEQ ID NO:1126 is a clone designated herein as "DNA329265".

Figure 1127 shows a nucleotide sequence (SEQ ID NO:1127) of a native sequence PRO12845 cDNA, wherein SEQ ID NO:1127 is a clone designated herein as "DNA329266".

Figure 1128 shows the amino acid sequence (SEQ ID NO:1128) derived from the coding sequence of SEQ ID NO:1127 shown in Figure 1127.

Figure 1129 shows a nucleotide sequence (SEQ ID NO:1129) of a native sequence PRO69518 cDNA, wherein SEQ ID NO:1129 is a clone designated herein as "DNA287243".

Figure 1130 shows the amino acid sequence (SEQ ID NO:1130) derived from the coding sequence of SEQ ID NO:1129 shown in Figure 1129.

Figure 1131 shows a nucleotide sequence (SEQ ID NO:1131) of a native sequence PRO2274 cDNA, wherein SEQ ID NO:1131 is a clone designated herein as "DNA88296".

Figure 1132 shows the amino acid sequence (SEQ ID NO:1132) derived from the coding sequence of SEQ ID NO:1131 shown in Figure 1131.

Figure 1133 shows a nucleotide sequence (SEQ ID NO:1133) of a native sequence PRO58102 cDNA, wherein SEQ ID NO:1133 is a clone designated herein as "DNA269692".

Figure 1134 shows the amino acid sequence (SEQ ID NO:1134) derived from the coding sequence of SEQ ID NO:1133 shown in Figure 1133.

Figure 1135 shows a nucleotide sequence (SEQ ID NO:1135) of a native sequence PRO21800 cDNA, wherein SEQ ID NO:1135 is a clone designated herein as "DNA188275".

Figure 1136 shows the amino acid sequence (SEQ ID NO:1136) derived from the coding sequence of SEQ ID NO:1135 shown in Figure 1135.

Figure 1137A-B shows a nucleotide sequence (SEQ ID NO:1137) of a native sequence PRO81897 cDNA, wherein SEQ ID NO:1137 is a clone designated herein as "DNA325359".

Figure 1138 shows the amino acid sequence (SEQ ID NO:1138) derived from the coding sequence of SEQ ID NO:1137 shown in Figure 1137.

Figure 1139 shows a nucleotide sequence (SEQ ID NO:1139) of a native sequence cDNA, wherein SEQ ID NO:1139 is a clone designated herein as "DNA329267".

Figure 1140 shows a nucleotide sequence (SEQ ID NO:1140) of a native sequence cDNA, wherein SEQ ID NO:1140 is a clone designated herein as "DNA270839".

Figure 1141 shows a nucleotide sequence (SEQ ID NO:1141) of a native sequence PRO62882 cDNA, wherein SEQ ID NO:1141 is a clone designated herein as "DNA275181".

Figure 1142 shows the amino acid sequence (SEQ ID NO:1142) derived from the coding sequence of SEQ ID NO:1141 shown in Figure 1141.

Figure 1143A-C shows a nucleotide sequence (SEQ ID NO:1143) of a native sequence PRO84864 cDNA, wherein SEQ ID NO:1143 is a clone designated herein as "DNA329268".

Figure 1144 shows the amino acid sequence (SEQ ID NO:1144) derived from the coding sequence of SEQ ID NO:1143 shown in Figure 1143.

Figure 1145A-B shows a nucleotide sequence (SEQ ID NO:1145) of a native sequence PRO84865 cDNA, wherein SEQ ID NO:1145 is a clone designated herein as "DNA329269".

Figure 1146 shows the amino acid sequence (SEQ ID NO:1146) derived from the coding sequence of SEQ ID NO:1145 shown in Figure 1145.

Figure 1147 shows a nucleotide sequence (SEQ ID NO:1147) of a native sequence PRO84866 cDNA, wherein SEQ ID NO:1147 is a clone designated herein as "DNA329270".

Figure 1148 shows the amino acid sequence (SEQ ID NO:1148) derived from the coding sequence of SEQ ID NO:1147 shown in Figure 1147.

Figure 1149 shows a nucleotide sequence (SEQ ID NO:1149) of a native sequence PRO38457 cDNA, wherein SEQ ID NO:1149 is a clone designated herein as "DNA227994".

Figure 1150 shows the amino acid sequence (SEQ ID NO:1150) derived from the coding sequence of SEQ ID NO:1149 shown in Figure 1149.

Figure 1151 shows a nucleotide sequence (SEQ ID NO:1151) of a native sequence PRO84867 cDNA, wherein SEQ ID NO:1151 is a clone designated herein as "DNA329271".

Figure 1152 shows the amino acid sequence (SEQ ID NO:1152) derived from the coding sequence of SEQ ID NO:1151 shown in Figure 1151.

Figure 1153 shows a nucleotide sequence (SEQ ID NO:1153) of a native sequence PRO1869 cDNA, wherein SEQ ID NO:1153 is a clone designated herein as "DNA325832".

Figure 1154 shows the amino acid sequence (SEQ ID NO:1154) derived from the coding sequence of SEQ ID NO:1153 shown in Figure 1153.

Figure 1155A-B shows a nucleotide sequence (SEQ ID NO:1155) of a native sequence PRO2834 cDNA, wherein SEQ ID NO:1155 is a clone designated herein as "DNA327847".

Figure 1156 shows the amino acid sequence (SEQ ID NO:1156) derived from the coding sequence of SEQ ID NO:1155 shown in Figure 1155.

Figure 1157 shows a nucleotide sequence (SEQ ID NO:1157) of a native sequence PRO2834 cDNA, wherein SEQ ID NO:1157 is a clone designated herein as "DNA88541".

Figure 1158 shows the amino acid sequence (SEQ ID NO:1158) derived from the coding sequence of SEQ ID NO:1157 shown in Figure 1157.

Figure 1159 shows a nucleotide sequence (SEQ ID NO:1159) of a native sequence PRO83794 cDNA, wherein SEQ ID NO:1159 is a clone designated herein as "DNA327849".

Figure 1160 shows the amino acid sequence (SEQ ID NO:1160) derived from the coding sequence of SEQ ID NO:1159 shown in Figure 1159.

Figure 1161 shows a nucleotide sequence (SEQ ID NO:1161) of a native sequence PRO82287 cDNA, wherein SEQ ID NO:1161 is a clone designated herein as "DNA325821".

Figure 1162 shows the amino acid sequence (SEQ ID NO:1162) derived from the coding sequence of SEQ ID NO:1161 shown in Figure 1161.

Figure 1163 shows a nucleotide sequence (SEQ ID NO:1163) of a native sequence PRO84557 cDNA, wherein SEQ ID NO:1163 is a clone designated herein as "DNA328819".

Figure 1164 shows the amino acid sequence (SEQ ID NO:1164) derived from the coding sequence of SEQ ID NO:1163 shown in Figure 1163.

Figure 1165 shows a nucleotide sequence (SEQ ID NO:1165) of a native sequence PRO82331 cDNA, wherein SEQ ID NO:1165 is a clone designated herein as "DNA325873".

Figure 1166 shows the amino acid sequence (SEQ ID NO:1166) derived from the coding sequence of SEQ ID NO:1165 shown in Figure 1165.

Figure 1167 shows a nucleotide sequence (SEQ ID NO:1167) of a native sequence PRO84561 cDNA, wherein SEQ ID NO:1167 is a clone designated herein as "DNA328823".

Figure 1168 shows the amino acid sequence (SEQ ID NO:1168) derived from the coding sequence of SEQ ID NO:1167 shown in Figure 1167.

Figure 1169 shows a nucleotide sequence (SEQ ID NO:1169) of a native sequence PRO37635 cDNA, wherein SEQ ID NO:1169 is a clone designated herein as "DNA227172".

Figure 1170 shows the amino acid sequence (SEQ ID NO:1170) derived from the coding sequence of SEQ ID NO:1169 shown in Figure 1169.

Figure 1171 shows a nucleotide sequence (SEQ ID NO:1171) of a native sequence PRO84868 cDNA, wherein SEQ ID NO:1171 is a clone designated herein as "DNA329272".

Figure 1172 shows the amino acid sequence (SEQ ID NO:1172) derived from the coding sequence of SEQ ID NO:1171 shown in Figure 1171

Figure 1173 shows a nucleotide sequence (SEQ ID NO:1173) of a native sequence PRO82223 cDNA, wherein SEQ ID NO:1173 is a clone designated herein as "DNA327853".

Figure 1174 shows the amino acid sequence (SEQ ID NO:1174) derived from the coding sequence of SEQ ID NO:1173 shown in Figure 1173.

Figure 1175 shows a nucleotide sequence (SEQ ID NO:1175) of a native sequence PRO84869 cDNA, wherein SEQ ID NO:1175 is a clone designated herein as "DNA329273".

Figure 1176 shows the amino acid sequence (SEQ ID NO:1176) derived from the coding sequence of SEQ ID NO:1175 shown in Figure 1175.

Figure 1177 shows a nucleotide sequence (SEQ ID NO:1177) of a native sequence PRO84870 cDNA, wherein SEQ ID NO:1177 is a clone designated herein as "DNA329274".

Figure 1178 shows the amino acid sequence (SEQ ID NO:1178) derived from the coding sequence of SEQ ID NO:1177 shown in Figure 1177.

Figure 1179 shows a nucleotide sequence (SEQ ID NO:1179) of a native sequence PRO82813 cDNA, wherein SEQ ID NO:1179 is a clone designated herein as "DNA326428".

Figure 1180 shows the amino acid sequence (SEQ ID NO:1180) derived from the coding sequence of SEQ ID NO:1179 shown in Figure 1179.

Figure 1181 shows a nucleotide sequence (SEQ ID NO:1181) of a native sequence PRO37681 cDNA, wherein SEQ ID NO:1181 is a clone designated herein as "DNA227218".

Figure 1182 shows the amino acid sequence (SEQ ID NO:1182) derived from the coding sequence of SEQ ID NO:1181 shown in Figure 1181.

Figure 1183 shows a nucleotide sequence (SEQ ID NO:1183) of a native sequence PRO233 cDNA, wherein SEQ ID NO:1183 is a clone designated herein as "DNA328831".

Figure 1184 shows the amino acid sequence (SEQ ID NO:1184) derived from the coding sequence of SEQ ID NO:1183 shown in Figure 1183.

Figure 1185 shows a nucleotide sequence (SEQ ID NO:1185) of a native sequence PRO84569 cDNA, wherein SEQ ID NO:1185 is a clone designated herein as "DNA328833".

Figure 1186 shows the amino acid sequence (SEQ ID NO:1186) derived from the coding sequence of SEQ ID NO:1185 shown in Figure 1186.

Figure 1187 shows a nucleotide sequence (SEQ ID NO:) of a native sequence PRO84572 cDNA, wherein SEQ ID NO:1187 is a clone designated herein as "DNA328836".

Figure 1188 shows the amino acid sequence (SEQ ID NO:1188) derived from the coding sequence of SEQ ID NO:1187 shown in Figure 1187.

Figure 1189 shows a nucleotide sequence (SEQ ID NO:1189) of a native sequence PRO12342 cDNA, wherein SEQ ID NO:1189 is a clone designated herein as "DNA329275".

Figure 1190 shows the amino acid sequence (SEQ ID NO:1190) derived from the coding sequence of SEQ ID NO:1189 shown in Figure 1189.

Figure 1191 shows a nucleotide sequence (SEQ ID NO:1191) of a native sequence PRO12104 cDNA, wherein SEQ ID NO:1191 is a clone designated herein as "DNA329276".

Figure 1192 shows the amino acid sequence (SEQ ID NO:1192) derived from the coding sequence of SEQ ID NO:1191 shown in Figure 1191.

Figure 1193 shows a nucleotide sequence (SEQ ID NO:1193) of a native sequence PRO84575 cDNA, wherein SEQ ID NO:1193 is a clone designated herein as "DNA328841".

Figure 1194 shows the amino acid sequence (SEQ ID NO:1194) derived from the coding sequence of SEQ ID NO:1193 shown in Figure 1193.

Figure 1195 shows a nucleotide sequence (SEQ ID NO:1195) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:1195 is a clone designated herein as "DNA329277".

Figure 1196 shows the amino acid sequence (SEQ ID NO:1196) derived from the coding sequence of SEQ ID NO:1195 shown in Figure 1195.

Figure 1197 shows a nucleotide sequence (SEQ ID NO:1197) of a native sequence PRO84871 cDNA, wherein SEQ ID NO:1197 is a clone designated herein as "DNA329278".

Figure 1198 shows the amino acid sequence (SEQ ID NO:1198) derived from the coding sequence of SEQ ID NO:1197 shown in Figure 1197.

Figure 1199 shows a nucleotide sequence (SEQ ID NO:1199) of a native sequence PRO62669 cDNA, wherein SEQ ID NO:1199 is a clone designated herein as "DNA274930".

Figure 1200 shows the amino acid sequence (SEQ ID NO:1200) derived from the coding sequence of SEQ ID NO:1199 shown in Figure 1199.

Figure 1201 shows a nucleotide sequence (SEQ ID NO:1201) of a native sequence PRO84872 cDNA, wherein SEQ ID NO:1201 is a clone designated herein as "DNA329279".

Figure 1202 shows the amino acid sequence (SEQ ID NO:1202) derived from the coding sequence of SEQ ID NO:1201 shown in Figure 1201.

Figure 1203 shows a nucleotide sequence (SEQ ID NO:1203) of a native sequence PRO49837 cDNA, wherein SEQ ID NO:1203 is a clone designated herein as "DNA254739".

Figure 1204 shows the amino acid sequence (SEQ ID NO:1204) derived from the coding sequence of SEQ ID NO:1203 shown in Figure 1203.

Figure 1205 shows a nucleotide sequence (SEQ ID NO:1205) of a native sequence PRO84873 cDNA, wherein SEQ ID NO:1205 is a clone designated herein as "DNA329280".

Figure 1206 shows the amino acid sequence (SEQ ID NO:1206) derived from the coding sequence of SEQ ID NO:1205 shown in Figure 1205.

Figure 1207 shows a nucleotide sequence (SEQ ID NO:1207) of a native sequence PRO83800 cDNA, wherein SEQ ID NO:1207 is a clone designated herein as "DNA327858".

Figure 1208 shows the amino acid sequence (SEQ ID NO:1208) derived from the coding sequence of SEQ ID NO:1207 shown in Figure 1207.

Figure 1209 shows a nucleotide sequence (SEQ ID NO:1209) of a native sequence PRO84581 cDNA, wherein SEQ ID NO:1209 is a clone designated herein as "DNA328850".

Figure 1210 shows the amino acid sequence (SEQ ID NO:1210) derived from the coding sequence of SEQ ID NO:1209 shown in Figure 1209.

Figure 1211 shows a nucleotide sequence (SEQ ID NO:1211) of a native sequence PRO61257 cDNA, wherein SEQ ID NO:1211 is a clone designated herein as "DNA273230".

Figure 1212 shows the amino acid sequence (SEQ ID NO:1212) derived from the coding sequence of SEQ ID NO:1211 shown in Figure 1211.

Figure 1213 shows a nucleotide sequence (SEQ ID NO:1213) of a native sequence PRO82325 cDNA, wherein SEQ ID NO:1213 is a clone designated herein as "DNA325866".

Figure 1214 shows the amino acid sequence (SEQ ID NO:1214) derived from the coding sequence of SEQ ID NO:1213 shown in Figure 1213.

Figure 1215 shows a nucleotide sequence (SEQ ID NO:1215) of a native sequence PRO84874 cDNA, wherein SEQ ID NO:1215 is a clone designated herein as "DNA329281".

Figure 1216 shows the amino acid sequence (SEQ ID NO:1216) derived from the coding sequence of SEQ ID NO:1215 shown in Figure 1215.

Figure 1217 shows a nucleotide sequence (SEQ ID NO:1217) of a native sequence PRO84875 cDNA, wherein SEQ ID NO:1217 is a clone designated herein as "DNA329282".

Figure 1218 shows the amino acid sequence (SEQ ID NO:1218) derived from the coding sequence of SEQ ID NO:1217 shown in Figure 1217.

Figure 1219 shows a nucleotide sequence (SEQ ID NO:1219) of a native sequence PRO61003 cDNA, wherein SEQ ID NO:1219 is a clone designated herein as "DNA272918".

Figure 1220 shows the amino acid sequence (SEQ ID NO:1220) derived from the coding sequence of SEQ ID NO:1219 shown in Figure 1219.

Figure 1221 shows a nucleotide sequence (SEQ ID NO:1221) of a native sequence PRO84876 cDNA, wherein SEQ ID NO:1221 is a clone designated herein as "DNA329283".

Figure 1222 shows the amino acid sequence (SEQ ID NO:1222) derived from the coding sequence of SEQ ID NO:1221 shown in Figure 1221.

Figure 1223A-B shows a nucleotide sequence (SEQ ID NO:1223) of a native sequence PRO84877 cDNA, wherein SEQ ID NO:1223 is a clone designated herein as "DNA329284".

Figure 1224 shows the amino acid sequence (SEQ ID NO:1224) derived from the coding sequence of SEQ ID NO:1223 shown in Figure 1223.

Figure 1225 shows a nucleotide sequence (SEQ ID NO:1225) of a native sequence PRO84878 cDNA, wherein SEQ ID NO:1225 is a clone designated herein as "DNA329285".

Figure 1226 shows the amino acid sequence (SEQ ID NO:1226) derived from the coding sequence of SEQ ID NO:1225 shown in Figure 1225.

Figure 1227 shows a nucleotide sequence (SEQ ID NO:1227) of a native sequence PRO84592 cDNA, wherein SEQ ID NO:1227 is a clone designated herein as "DNA328864".

Figure 1228 shows the amino acid sequence (SEQ ID NO:1228) derived from the coding sequence of SEQ ID NO:1227 shown in Figure 1227.

Figure 1229 shows a nucleotide sequence (SEQ ID NO:1229) of a native sequence PRO224 cDNA, wherein SEQ ID NO:1229 is a clone designated herein as "DNA326550".

Figure 1230 shows the amino acid sequence (SEQ ID NO:1230) derived from the coding sequence of SEQ ID NO:1229 shown in Figure 1229.

Figure 1231 shows a nucleotide sequence (SEQ ID NO:1231) of a native sequence PRO69644 cDNA, wherein SEQ ID NO:1231 is a clone designated herein as "DNA329286".

Figure 1232 shows the amino acid sequence (SEQ ID NO:1232) derived from the coding sequence of SEQ ID NO:1231 shown in Figure 1231.

Figure 1233 shows a nucleotide sequence (SEQ ID NO:1233) of a native sequence PRO4929 cDNA, wherein SEQ ID NO:1233 is a clone designated herein as "DNA93548".

Figure 1234 shows the amino acid sequence (SEQ ID NO:1234) derived from the coding sequence of SEQ ID NO:1233 shown in Figure 1233.

Figure 1235 shows a nucleotide sequence (SEQ ID NO:1235) of a native sequence PRO84879 cDNA, wherein SEQ ID NO:1235 is a clone designated herein as "DNA329287".

Figure 1236 shows the amino acid sequence (SEQ ID NO:1236) derived from the coding sequence of SEQ ID NO:1235 shown in Figure 1235.

Figure 1237 shows a nucleotide sequence (SEQ ID NO:1237) of a native sequence PRO84880 cDNA, wherein SEQ ID NO:1237 is a clone designated herein as "DNA329288".

Figure 1238 shows the amino acid sequence (SEQ ID NO:1238) derived from the coding sequence of SEQ ID NO:1237 shown in Figure 1237.

Figure 1239 shows a nucleotide sequence (SEQ ID NO:1239) of a native sequence PRO38080 cDNA, wherein SEQ ID NO:1239 is a clone designated herein as "DNA227617".

Figure 1240 shows the amino acid sequence (SEQ ID NO:1240) derived from the coding sequence of SEQ ID NO:1239 shown in Figure 1239.

Figure 1241 shows a nucleotide sequence (SEQ ID NO:1241) of a native sequence PRO83216 cDNA, wherein SEQ ID NO:1241 is a clone designated herein as "DNA329289".

Figure 1242 shows the amino acid sequence (SEQ ID NO:1242) derived from the coding sequence of SEQ ID NO:1241 shown in Figure 1241.

Figure 1243 shows a nucleotide sequence (SEQ ID NO:1243) of a native sequence PRO4805 cDNA, wherein SEQ ID NO:1243 is a clone designated herein as "DNA327874".

Figure 1244 shows the amino acid sequence (SEQ ID NO:1244) derived from the coding sequence of SEQ ID NO:1243 shown in Figure 1243.

Figure 1245 shows a nucleotide sequence (SEQ ID NO:1245) of a native sequence PRO37096 cDNA, wherein SEQ ID NO:1245 is a clone designated herein as "DNA226633".

Figure 1246 shows the amino acid sequence (SEQ ID NO:1246) derived from the coding sequence of SEQ ID NO:1245 shown in Figure 1245.

Figure 1247 shows a nucleotide sequence (SEQ ID NO:1247) of a native sequence PRO69889 cDNA, wherein SEQ ID NO:1247 is a clone designated herein as "DNA304780".

Figure 1248 shows the amino acid sequence (SEQ ID NO:1248) derived from the coding sequence of SEQ ID NO:1247 shown in Figure 1247.

Figure 1249 shows a nucleotide sequence (SEQ ID NO:1249) of a native sequence PRO84881 cDNA, wherein SEQ ID NO:1249 is a clone designated herein as "DNA329290".

Figure 1250 shows the amino acid sequence (SEQ ID NO:1250) derived from the coding sequence of SEQ ID NO:1249 shown in Figure 1249.

Figure 1251 shows a nucleotide sequence (SEQ ID NO:1251) of a native sequence PRO1017 cDNA, wherein SEQ ID NO:1251 is a clone designated herein as "DNA329291".

Figure 1252 shows the amino acid sequence (SEQ ID NO:1252) derived from the coding sequence of SEQ ID NO:1251 shown in Figure 1251.

Figure 1253 shows a nucleotide sequence (SEQ ID NO:1253) of a native sequence PRO84712 cDNA, wherein SEQ ID NO:1253 is a clone designated herein as "DNA329050".

Figure 1254 shows the amino acid sequence (SEQ ID NO:1254) derived from the coding sequence of SEQ ID NO:1253 shown in Figure 1253.

Figure 1255 shows a nucleotide sequence (SEQ ID NO:1255) of a native sequence PRO37650 cDNA, wherein SEQ ID NO:1255 is a clone designated herein as "DNA227187".

Figure 1256 shows the amino acid sequence (SEQ ID NO:1256) derived from the coding sequence of SEQ ID NO:1255 shown in Figure 1255.

Figure 1257 shows a nucleotide sequence (SEQ ID NO:1257) of a native sequence PRO84882 cDNA, wherein SEQ ID NO:1257 is a clone designated herein as "DNA329292".

Figure 1258 shows the amino acid sequence (SEQ ID NO:1258) derived from the coding sequence of SEQ ID NO:1257 shown in Figure 1257.

Figure 1259 shows a nucleotide sequence (SEQ ID NO:1259) of a native sequence PRO84883 cDNA, wherein SEQ ID NO:1259 is a clone designated herein as "DNA329293".

Figure 1260 shows the amino acid sequence (SEQ ID NO:1260) derived from the coding sequence of SEQ ID NO:1259 shown in Figure 1259.

Figure 1261 shows a nucleotide sequence (SEQ ID NO:1261) of a native sequence PRO84884 cDNA, wherein SEQ ID NO:1261 is a clone designated herein as "DNA329294".

Figure 1262 shows the amino acid sequence (SEQ ID NO:1262) derived from the coding sequence of SEQ ID NO:1261 shown in Figure 1261.

Figure 1263 shows a nucleotide sequence (SEQ ID NO:1263) of a native sequence PRO69517 cDNA, wherein SEQ ID NO:1263 is a clone designated herein as "DNA287242".

Figure 1264 shows the amino acid sequence (SEQ ID NO:1264) derived from the coding sequence of SEQ ID NO:1263 shown in Figure 1263.

Figure 1265 shows a nucleotide sequence (SEQ ID NO:1265) of a native sequence PRO84885 cDNA, wherein SEQ ID NO:1265 is a clone designated herein as "DNA329295".

Figure 1266 shows the amino acid sequence (SEQ ID NO:1266) derived from the coding sequence of SEQ ID NO:1261 shown in Figure 1261.

Figure 1267 shows a nucleotide sequence (SEQ ID NO:1267) of a native sequence PRO83819 cDNA, wherein SEQ ID NO:1267 is a clone designated herein as "DNA327880".

Figure 1268 shows the amino acid sequence (SEQ ID NO:1268) derived from the coding sequence of SEQ ID NO:1267 shown in Figure 1267.

Figure 1269 shows a nucleotide sequence (SEQ ID NO:1269) of a native sequence PRO84617 cDNA, wherein SEQ ID NO:1269 is a clone designated herein as "DNA328894".

Figure 1270 shows the amino acid sequence (SEQ ID NO:1270) derived from the coding sequence of SEQ ID NO:1269 shown in Figure 1269.

Figure 1271 shows a nucleotide sequence (SEQ ID NO:1271) of a native sequence PRO51682 cDNA, wherein SEQ ID NO:1271 is a clone designated herein as "DNA256749".

Figure 1272 shows the amino acid sequence (SEQ ID NO:1272) derived from the coding sequence of SEQ ID NO:1271 shown in Figure 1271.

Figure 1273 shows a nucleotide sequence (SEQ ID NO:1273) of a native sequence PRO84886 cDNA, wherein SEQ ID NO:1273 is a clone designated herein as "DNA329296".

Figure 1274 shows the amino acid sequence (SEQ ID NO:1274) derived from the coding sequence of SEQ ID NO:1273 shown in Figure 1273.

Figure 1275 shows a nucleotide sequence (SEQ ID NO:1275) of a native sequence PRO82421 cDNA, wherein SEQ ID NO:1275 is a clone designated herein as "DNA325976".

Figure 1276 shows the amino acid sequence (SEQ ID NO:1276) derived from the coding sequence of SEQ ID NO:1275 shown in Figure 1275.

Figure 1277A-C shows a nucleotide sequence (SEQ ID NO:1277) of a native sequence PRO23303 cDNA, wherein SEQ ID NO:1277 is a clone designated herein as "DNA329297".

Figure 1278 shows the amino acid sequence (SEQ ID NO:1278) derived from the coding sequence of SEQ ID NO:1277 shown in Figure 1277.

Figure 1279 shows a nucleotide sequence (SEQ ID NO:1279) of a native sequence PRO50991 cDNA, wherein SEQ ID NO:1279 is a clone designated herein as "DNA255939".

Figure 1280 shows the amino acid sequence (SEQ ID NO:1280) derived from the coding sequence of SEQ ID NO:1279 shown in Figure 1279.

Figure 1281 shows a nucleotide sequence (SEQ ID NO:1281) of a native sequence PRO49625 cDNA, wherein SEQ ID NO:1281 is a clone designated herein as "DNA254518".

Figure 1282 shows the amino acid sequence (SEQ ID NO:1282) derived from the coding sequence of SEQ ID NO:1281 shown in Figure 1281.

Figure 1283A-B shows a nucleotide sequence (SEQ ID NO:1283) of a native sequence PRO84887 cDNA, wherein SEQ ID NO:1283 is a clone designated herein as "DNA329298".

Figure 1284 shows the amino acid sequence (SEQ ID NO:1284) derived from the coding sequence of SEQ ID NO:1283 shown in Figure 1283.

Figure 1285 shows a nucleotide sequence (SEQ ID NO:1285) of a native sequence PRO84622 cDNA, wherein SEQ ID NO:1285 is a clone designated herein as "DNA328901".

Figure 1286 shows the amino acid sequence (SEQ ID NO:1286) derived from the coding sequence of SEQ ID NO:1285 shown in Figure 1285.

Figure 1287A-B shows a nucleotide sequence (SEQ ID NO:1287) of a native sequence PRO37642 cDNA, wherein SEQ ID NO:1287 is a clone designated herein as "DNA227179".

Figure 1288 shows the amino acid sequence (SEQ ID NO:1288) derived from the coding sequence of SEQ ID NO:1287 shown in Figure 1287.

Figure 1289 shows a nucleotide sequence (SEQ ID NO:1289) of a native sequence PRO84888 cDNA, wherein SEQ ID NO:1289 is a clone designated herein as "DNA329299".

Figure 1290 shows the amino acid sequence (SEQ ID NO:1290) derived from the coding sequence of SEQ ID NO:1289 shown in Figure 1289.

Figure 1291 shows a nucleotide sequence (SEQ ID NO:1291) of a native sequence PRO84889 cDNA, wherein SEQ ID NO:1291 is a clone designated herein as "DNA329300".

Figure 1292 shows the amino acid sequence (SEQ ID NO:1292) derived from the coding sequence of SEQ ID NO:1291 shown in Figure 1291.

Figure 1293 shows a nucleotide sequence (SEQ ID NO:1293) of a native sequence PRO51671 cDNA, wherein SEQ ID NO:1293 is a clone designated herein as "DNA256737".

Figure 1294 shows the amino acid sequence (SEQ ID NO:1294) derived from the coding sequence of SEQ ID NO:1293 shown in Figure 1293.

Figure 1295 shows a nucleotide sequence (SEQ ID NO:1295) of a native sequence PRO84890 cDNA, wherein SEQ ID NO:1295 is a clone designated herein as "DNA329301".

Figure 1296 shows the amino acid sequence (SEQ ID NO:1296) derived from the coding sequence of SEQ ID NO:1295 shown in Figure 1295.

Figure 1297A-B shows a nucleotide sequence (SEQ ID NO:1297) of a native sequence PRO84891 cDNA, wherein SEQ ID NO:1297 is a clone designated herein as "DNA329302".

Figure 1298 shows the amino acid sequence (SEQ ID NO:1298) derived from the coding sequence of SEQ ID NO:1297 shown in Figure 1297.

Figure 1299 shows a nucleotide sequence (SEQ ID NO:1299) of a native sequence PRO84634 cDNA, wherein SEQ ID NO:1299 is a clone designated herein as "DNA328915".

Figure 1300 shows the amino acid sequence (SEQ ID NO:1300) derived from the coding sequence of SEQ ID NO:1299 shown in Figure 1299.

Figure 1301A-B shows a nucleotide sequence (SEQ ID NO:1301) of a native sequence PRO61987 cDNA, wherein SEQ ID NO:1301 is a clone designated herein as "DNA274044".

Figure 1302 shows the amino acid sequence (SEQ ID NO:1302) derived from the coding sequence of SEQ ID NO:1301 shown in Figure 1301.

Figure 1303 shows a nucleotide sequence (SEQ ID NO:1303) of a native sequence PRO84892 cDNA, wherein SEQ ID NO:1303 is a clone designated herein as "DNA329303".

Figure 1304 shows the amino acid sequence (SEQ ID NO:1304) derived from the coding sequence of SEQ ID NO:1303 shown in Figure 1303.

Figure 1305 shows a nucleotide sequence (SEQ ID NO:1305) of a native sequence PRO69564 cDNA, wherein SEQ ID NO:1305 is a clone designated herein as "DNA287295".

Figure 1306 shows the amino acid sequence (SEQ ID NO:1306) derived from the coding sequence of SEQ ID NO:1305 shown in Figure 1305.

Figure 1307 shows a nucleotide sequence (SEQ ID NO:1307) of a native sequence PRO84893 cDNA, wherein SEQ ID NO:1307 is a clone designated herein as "DNA329304".

Figure 1308 shows the amino acid sequence (SEQ ID NO:1308) derived from the coding sequence of SEQ ID NO:1307 shown in Figure 1307.

Figure 1309 shows a nucleotide sequence (SEQ ID NO:1309) of a native sequence PRO83839 cDNA, wherein SEQ ID NO:1309 is a clone designated herein as "DNA327904".

Figure 1310 shows the amino acid sequence (SEQ ID NO:1310) derived from the coding sequence of SEQ ID NO:1309 shown in Figure 1309.

Figure 1311 shows a nucleotide sequence (SEQ ID NO:1311) of a native sequence PRO69472 cDNA, wherein SEQ ID NO:1311 is a clone designated herein as "DNA287186".

Figure 1312 shows the amino acid sequence (SEQ ID NO:1312) derived from the coding sequence of SEQ ID NO:1311 shown in Figure 1311.

Figure 1313 shows a nucleotide sequence (SEQ ID NO:1313) of a native sequence PRO84894 cDNA, wherein SEQ ID NO:1313 is a clone designated herein as "DNA329305".

Figure 1314 shows the amino acid sequence (SEQ ID NO:1314) derived from the coding sequence of SEQ ID NO:1313 shown in Figure 1313.

Figure 1315 shows a nucleotide sequence (SEQ ID NO:1315) of a native sequence PRO84895 cDNA, wherein SEQ ID NO:1315 is a clone designated herein as "DNA329306".

Figure 1316 shows the amino acid sequence (SEQ ID NO:1316) derived from the coding sequence of SEQ ID NO:1315 shown in Figure 1315.

Figure 1317 shows a nucleotide sequence (SEQ ID NO:1317) of a native sequence PRO84896 cDNA, wherein SEQ ID NO:1317 is a clone designated herein as "DNA329307".

Figure 1318 shows the amino acid sequence (SEQ ID NO:1318) derived from the coding sequence of SEQ ID NO:1317 shown in Figure 1317.

Figure 1319 shows a nucleotide sequence (SEQ ID NO:1319) of a native sequence PRO80512 cDNA, wherein SEQ ID NO:1319 is a clone designated herein as "DNA323756".

Figure 1320 shows the amino acid sequence (SEQ ID NO:1320) derived from the coding sequence of SEQ ID NO:1319 shown in Figure 1319.

Figure 1321 A-B shows a nucleotide sequence (SEQ ID NO:1321) of a native sequence PRO84897 cDNA, wherein SEQ ID NO:1321 is a clone designated herein as "DNA329308".

Figure 1322 shows the amino acid sequence (SEQ ID NO:1322) derived from the coding sequence of SEQ ID NO:1321 shown in Figure 1321.

Figure 1323 shows a nucleotide sequence (SEQ ID NO:1323) of a native sequence PRO84898 cDNA, wherein SEQ ID NO:1323 is a clone designated herein as "DNA329309".

Figure 1324 shows the amino acid sequence (SEQ ID NO:1324) derived from the coding sequence of SEQ ID NO:1323 shown in Figure 1323.

Figure 1325 shows a nucleotide sequence (SEQ ID NO:1325) of a native sequence PRO70111 cDNA, wherein SEQ ID NO:1325 is a clone designated herein as "DNA288247".

Figure 1326 shows the amino acid sequence (SEQ ID NO:1326) derived from the coding sequence of SEQ ID NO:1325 shown in Figure 1325.

Figure 1327 shows a nucleotide sequence (SEQ ID NO:1327) of a native sequence PRO23253 cDNA, wherein SEQ ID NO:1327 is a clone designated herein as "DNA329078".

Figure 1328 shows the amino acid sequence (SEQ ID NO:1328) derived from the coding sequence of SEQ ID NO:1327 shown in Figure 1327.

Figure 1329 shows a nucleotide sequence (SEQ ID NO:1329) of a native sequence PRO36690 cDNA, wherein SEQ ID NO:1329 is a clone designated herein as "DNA226227".

Figure 1330 shows the amino acid sequence (SEQ ID NO:1330) derived from the coding sequence of SEQ ID NO:1329 shown in Figure 1329.

Figure 1331 shows a nucleotide sequence (SEQ ID NO:1331) of a native sequence PRO34298 cDNA, wherein SEQ ID NO:1331 is a clone designated herein as "DNA217256".

Figure 1332 shows the amino acid sequence (SEQ ID NO:1332) derived from the coding sequence of SEQ ID NO:1331 shown in Figure 1331.

Figure 1333 shows a nucleotide sequence (SEQ ID NO:1333) of a native sequence PRO84899 cDNA, wherein SEQ ID NO:1333 is a clone designated herein as "DNA329310".

Figure 1334 shows the amino acid sequence (SEQ ID NO:1334) derived from the coding sequence of SEQ ID NO:1333 shown in Figure 1333.

Figure 1335 shows a nucleotide sequence (SEQ ID NO:1335) of a native sequence PRO84659 cDNA, wherein SEQ ID NO:1335 is a clone designated herein as "DNA328948".

Figure 1336 shows the amino acid sequence (SEQ ID NO:1336) derived from the coding sequence of SEQ ID NO:1335 shown in Figure 1335.

Figure 1337 shows a nucleotide sequence (SEQ ID NO:1337) of a native sequence PRO52290 cDNA, wherein SEQ ID NO:1337 is a clone designated herein as "DNA257738".

Figure 1338 shows the amino acid sequence (SEQ ID NO:1338) derived from the coding sequence of SEQ ID NO:1337 shown in Figure 1337.

Figure 1339 shows a nucleotide sequence (SEQ ID NO:1339) of a native sequence PRO84900 cDNA, wherein SEQ ID NO:1339 is a clone designated herein as "DNA329311".

Figure 1340 shows the amino acid sequence (SEQ ID NO:1340) derived from the coding sequence of SEQ ID NO:1339 shown in Figure 1339.

Figure 1341 shows a nucleotide sequence (SEQ ID NO:1341) of a native sequence PRO84901 cDNA, wherein SEQ ID NO:1341 is a clone designated herein as "DNA329312".

Figure 1342 shows the amino acid sequence (SEQ ID NO:1342) derived from the coding sequence of SEQ ID NO:1341 shown in Figure 1341.

Figure 1343 shows a nucleotide sequence (SEQ ID NO:1343) of a native sequence PRO70013 cDNA, wherein SEQ ID NO:1343 is a clone designated herein as "DNA288250".

Figure 1344 shows the amino acid sequence (SEQ ID NO:1344) derived from the coding sequence of SEQ ID NO:1343 shown in Figure 1343.

Figure 1345 shows a nucleotide sequence (SEQ ID NO:1345) of a native sequence PRO83944 cDNA, wherein SEQ ID NO:1345 is a clone designated herein as "DNA328027".

Figure 1346 shows the amino acid sequence (SEQ ID NO:1346) derived from the coding sequence of SEQ ID NO:1345 shown in Figure 1345.

Figure 1347 shows a nucleotide sequence (SEQ ID NO:1347) of a native sequence PRO5734 cDNA, wherein SEQ ID NO:1347 is a clone designated herein as "DNA329313".

Figure 1348 shows the amino acid sequence (SEQ ID NO:1348) derived from the coding sequence of SEQ ID NO:1347 shown in Figure 1347.

Figure 1349 A-B shows a nucleotide sequence (SEQ ID NO:1349) of a native sequence PRO84902 cDNA, wherein SEQ ID NO:1349 is a clone designated herein as "DNA329314".

Figure 1350 shows the amino acid sequence (SEQ ID NO:1350) derived from the coding sequence of SEQ ID NO:1349 shown in Figure 1349.

Figure 1351 shows a nucleotide sequence (SEQ ID NO:1351) of a native sequence PRO37766 cDNA, wherein SEQ ID NO:1351 is a clone designated herein as "DNA227303".

Figure 1352 shows the amino acid sequence (SEQ ID NO:1352) derived from the coding sequence of SEQ ID NO:1351 shown in Figure 1351.

Figure 1353 shows a nucleotide sequence (SEQ ID NO:1353) of a native sequence PRO84903 cDNA, wherein SEQ ID NO:1353 is a clone designated herein as "DNA329315".

Figure 1354 shows the amino acid sequence (SEQ ID NO:1354) derived from the coding sequence of SEQ ID NO:1353 shown in Figure 1353.

Figure 1355 A-B shows a nucleotide sequence (SEQ ID NO:1355) of a native sequence PRO84904 cDNA, wherein SEQ ID NO:1355 is a clone designated herein as "DNA329316".

Figure 1356 shows the amino acid sequence (SEQ ID NO:1356) derived from the coding sequence of SEQ ID NO:1355 shown in Figure 1355.

Figure 1357 shows a nucleotide sequence (SEQ ID NO:1357) of a native sequence PRO81157 cDNA, wherein SEQ ID NO:1357 is a clone designated herein as "DNA329317".

Figure 1358 shows the amino acid sequence (SEQ ID NO:1358) derived from the coding sequence of SEQ ID NO:1357 shown in Figure 1357.

Figure 1359 shows a nucleotide sequence (SEQ ID NO:1359) of a native sequence cDNA, wherein SEQ ID NO:1359 is a clone designated herein as "DNA329318".

Figure 1360 shows a nucleotide sequence (SEQ ID NO:1360) of a native sequence PRO1607 cDNA, wherein SEQ ID NO:1360 is a clone designated herein as "DNA329319".

Figure 1361 shows the amino acid sequence (SEQ ID NO:1361) derived from the coding sequence of SEQ ID NO:1360 shown in Figure 1360.

Figure 1362 shows a nucleotide sequence (SEQ ID NO:1362) of a native sequence PRO84667 cDNA, wherein SEQ ID NO:1362 is a clone designated herein as "DNA328961".

Figure 1363 shows the amino acid sequence (SEQ ID NO:1363) derived from the coding sequence of SEQ ID NO:1362 shown in Figure 1362.

Figure 1364 shows a nucleotide sequence (SEQ ID NO:1364) of a native sequence PRO84905 cDNA, wherein SEQ ID NO:1364 is a clone designated herein as "DNA329320".

Figure 1365 shows the amino acid sequence (SEQ ID NO:1365) derived from the coding sequence of SEQ ID NO:1364 shown in Figure 1364.

Figure 1366 shows a nucleotide sequence (SEQ ID NO:1366) of a native sequence PRO84674 cDNA, wherein SEQ ID NO:1366 is a clone designated herein as "DNA328971".

Figure 1367 shows the amino acid sequence (SEQ ID NO:1367) derived from the coding sequence of SEQ ID NO:1366 shown in Figure 1366.

Figure 1368 shows a nucleotide sequence (SEQ ID NO:1368) of a native sequence PRO84906 cDNA, wherein SEQ ID NO:1368 is a clone designated herein as "DNA329321".

Figure 1369 shows the amino acid sequence (SEQ ID NO:1369) derived from the coding sequence of SEQ ID NO:1368 shown in Figure 1368.

Figure 1370 shows a nucleotide sequence (SEQ ID NO:1370) of a native sequence PRO80490 cDNA, wherein SEQ ID NO:1370 is a clone designated herein as "DNA329322".

Figure 1371 shows the amino acid sequence (SEQ ID NO:1371) derived from the coding sequence of SEQ ID NO:1370 shown in Figure 1370.

Figure 1372 shows a nucleotide sequence (SEQ ID NO:1372) of a native sequence PRO47688 cDNA, wherein SEQ ID NO:1372 is a clone designated herein as "DNA328975".

Figure 1373 shows the amino acid sequence (SEQ ID NO:1373) derived from the coding sequence of SEQ ID NO:1372 shown in Figure 1372.

Figure 1374 shows a nucleotide sequence (SEQ ID NO:1374) of a native sequence PRO84677 cDNA, wherein SEQ ID NO:1374 is a clone designated herein as "DNA328976".

Figure 1375 shows the amino acid sequence (SEQ ID NO:1375) derived from the coding sequence of SEQ ID NO:1374 shown in Figure 1374.

Figure 1376 shows a nucleotide sequence (SEQ ID NO:1376) of a native sequence PRO703 cDNA, wherein SEQ ID NO:1376 is a clone designated herein as "DNA323915".

Figure 1377 shows the amino acid sequence (SEQ ID NO:1377) derived from the coding sequence of SEQ ID NO:1376 shown in Figure 1376.

Figure 1378 shows a nucleotide sequence (SEQ ID NO:1378) of a native sequence PRO84907 cDNA, wherein SEQ ID NO:1378 is a clone designated herein as "DNA329323".

Figure 1379 shows the amino acid sequence (SEQ ID NO:1379) derived from the coding sequence of SEQ ID NO:1378 shown in Figure 1378.

Figure 1380 A-B shows a nucleotide sequence (SEQ ID NO:1380) of a native sequence PRO1314 cDNA, wherein SEQ ID NO:1380 is a clone designated herein as "DNA324364".

Figure 1381 shows the amino acid sequence (SEQ ID NO:1381) derived from the coding sequence of SEQ ID NO:1380 shown in Figure 1380.

Figure 1382 shows a nucleotide sequence (SEQ ID NO:1382) of a native sequence PRO84908 cDNA, wherein SEQ ID NO:1382 is a clone designated herein as "DNA329324".

Figure 1383 shows the amino acid sequence (SEQ ID NO:1383) derived from the coding sequence of SEQ ID NO:1382 shown in Figure 1382.

Figure 1384 shows a nucleotide sequence (SEQ ID NO:1384) of a native sequence PRO69560 cDNA, wherein SEQ ID NO:1384 is a clone designated herein as "DNA287290".

Figure 1385 shows the amino acid sequence (SEQ ID NO:1385) derived from the coding sequence of SEQ ID NO:1384 shown in Figure 1384.

Figure 1386 shows a nucleotide sequence (SEQ ID NO:1386) of a native sequence PRO84909 cDNA, wherein SEQ ID NO:1386 is a clone designated herein as "DNA329325".

Figure 1387 shows the amino acid sequence (SEQ ID NO:1387) derived from the coding sequence of SEQ ID NO:1386 shown in Figure 1386.

Figure 1388 shows a nucleotide sequence (SEQ ID NO:1388) of a native sequence PRO37686 cDNA, wherein SEQ ID NO:1388 is a clone designated herein as "DNA227223".

Figure 1389 shows the amino acid sequence (SEQ ID NO:1389) derived from the coding sequence of SEQ ID NO:1388 shown in Figure 1388.

Figure 1390 A-B shows a nucleotide sequence (SEQ ID NO:1390) of a native sequence PRO84910 cDNA, wherein SEQ ID NO:1390 is a clone designated herein as "DNA329326".

Figure 1391 shows the amino acid sequence (SEQ ID NO:1391) derived from the coding sequence of SEQ ID NO:1390 shown in Figure 1390.

Figure 1392 shows a nucleotide sequence (SEQ ID NO:1392) of a native sequence PRO83868 cDNA, wherein SEQ ID NO:1392 is a clone designated herein as "DNA327938".

Figure 1393 shows the amino acid sequence (SEQ ID NO:1393) derived from the coding sequence of SEQ ID NO:1392 shown in Figure 1392.

Figure 1394 shows a nucleotide sequence (SEQ ID NO:1394) of a native sequence PRO83869 cDNA, wherein SEQ ID NO:1394 is a clone designated herein as "DNA327939".

Figure 1395 shows the amino acid sequence (SEQ ID NO:1395) derived from the coding sequence of SEQ ID NO:1394 shown in Figure 1394.

Figure 1396 shows a nucleotide sequence (SEQ ID NO:1396) of a native sequence PRO84911 cDNA, wherein SEQ ID NO:1396 is a clone designated herein as "DNA329327".

Figure 1397 shows the amino acid sequence (SEQ ID NO:1397) derived from the coding sequence of SEQ ID NO:1396 shown in Figure 1396.

Figure 1398 A-B shows a nucleotide sequence (SEQ ID NO:1398) of a native sequence PRO51526 cDNA, wherein SEQ ID NO:1398 is a clone designated herein as "DNA256489".

Figure 1399 shows the amino acid sequence (SEQ ID NO:1399) derived from the coding sequence of SEQ ID NO:1398 shown in Figure 1398.

Figure 1400 shows a nucleotide sequence (SEQ ID NO:1400) of a native sequence PRO4984 cDNA, wherein SEQ ID NO:1400 is a clone designated herein as "DNA304460".

Figure 1401 shows the amino acid sequence (SEQ ID NO:1401) derived from the coding sequence of SEQ ID NO:1400 shown in Figure 1400.

Figure 1402 shows a nucleotide sequence (SEQ ID NO:1402) of a native sequence PRO84912 cDNA, wherein SEQ ID NO:1402 is a clone designated herein as "DNA329328".

Figure 1403 shows the amino acid sequence (SEQ ID NO:1403) derived from the coding sequence of SEQ ID NO:1402 shown in Figure 1402.

Figure 1404 shows a nucleotide sequence (SEQ ID NO:1404) of a native sequence PRO793 cDNA, wherein SEQ ID NO:1404 is a clone designated herein as "DNA304495".

Figure 1405 shows the amino acid sequence (SEQ ID NO:1405) derived from the coding sequence of SEQ ID NO:1404 shown in Figure 1404.

Figure 1406 shows a nucleotide sequence (SEQ ID NO:1406) of a native sequence PRO84913 cDNA, wherein SEQ ID NO:1406 is a clone designated herein as "DNA329329".

Figure 1407 shows the amino acid sequence (SEQ ID NO:1407) derived from the coding sequence of SEQ ID NO:1406 shown in Figure 1406.

Figure 1408 shows a nucleotide sequence (SEQ ID NO:1408) of a native sequence PRO84914 cDNA, wherein SEQ ID NO:1408 is a clone designated herein as "DNA329330".

Figure 1409 shows the amino acid sequence (SEQ ID NO:1409) derived from the coding sequence of SEQ ID NO:1408 shown in Figure 1408.

Figure 1410 shows a nucleotide sequence (SEQ ID NO:1410) of a native sequence PRO865 cDNA, wherein SEQ ID NO:1410 is a clone designated herein as "DNA327943".

Figure 1411 shows the amino acid sequence (SEQ ID NO:1411) derived from the coding sequence of SEQ ID NO:1410 shown in Figure 1410.

Figure 1412 shows a nucleotide sequence (SEQ ID NO:1412) of a native sequence PRO84915 cDNA, wherein SEQ ID NO:1412 is a clone designated herein as "DNA329331".

Figure 1413 shows the amino acid sequence (SEQ ID NO:1413) derived from the coding sequence of SEQ ID NO:1412 shown in Figure 1412.

Figure 1414 shows a nucleotide sequence (SEQ ID NO:1414) of a native sequence PRO80547 cDNA, wherein SEQ ID NO:1414 is a clone designated herein as "DNA323797".

Figure 1415 shows the amino acid sequence (SEQ ID NO:1415) derived from the coding sequence of SEQ ID NO:1414 shown in Figure 1414.

Figure 1416 shows a nucleotide sequence (SEQ ID NO:1416) of a native sequence PRO60967 cDNA, wherein SEQ ID NO:1416 is a clone designated herein as "DNA272874".

Figure 1417 shows the amino acid sequence (SEQ ID NO:1417) derived from the coding sequence of SEQ ID NO:1416 shown in Figure 1416.

Figure 1418 shows a nucleotide sequence (SEQ ID NO:1418) of a native sequence PRO84916 cDNA, wherein SEQ ID NO:1418 is a clone designated herein as "DNA329332".

Figure 1419 shows the amino acid sequence (SEQ ID NO:1419) derived from the coding sequence of SEQ ID NO:1418 shown in Figure 1418.

Figure 1420 shows a nucleotide sequence (SEQ ID NO:1420) of a native sequence PRO84917 cDNA, wherein SEQ ID NO:1420 is a clone designated herein as "DNA329333".

Figure 1421 shows the amino acid sequence (SEQ ID NO:1421) derived from the coding sequence of SEQ ID NO:1420 shown in Figure 1420.

Figure 1422 shows a nucleotide sequence (SEQ ID NO:1422) of a native sequence PRO84918 cDNA, wherein SEQ ID NO:1422 is a clone designated herein as "DNA329334".

Figure 1423 shows the amino acid sequence (SEQ ID NO:1423) derived from the coding sequence of SEQ ID NO:1422 shown in Figure 1422.

Figure 1424 shows a nucleotide sequence (SEQ ID NO:1424) of a native sequence PRO84919 cDNA, wherein SEQ ID NO:1424 is a clone designated herein as "DNA329335".

Figure 1425 shows the amino acid sequence (SEQ ID NO:1425) derived from the coding sequence of SEQ ID NO:1424 shown in Figure 1424.

Figure 1426 shows a nucleotide sequence (SEQ ID NO:1426) of a native sequence PRO84920 cDNA, wherein SEQ ID NO:1426 is a clone designated herein as "DNA329336".

Figure 1427 shows the amino acid sequence (SEQ ID NO:1427) derived from the coding sequence of SEQ ID NO:1426 shown in Figure 1426.

Figure 1428 shows a nucleotide sequence (SEQ ID NO:1428) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:1428 is a clone designated herein as "DNA329337".

Figure 1429 shows the amino acid sequence (SEQ ID NO:1429) derived from the coding sequence of SEQ ID NO:1428 shown in Figure 1428.

Figure 1430 shows a nucleotide sequence (SEQ ID NO:1430) of a native sequence PRO84921 cDNA, wherein SEQ ID NO:1430 is a clone designated herein as "DNA329338".

Figure 1431 shows the amino acid sequence (SEQ ID NO:1431) derived from the coding sequence of SEQ ID NO:1430 shown in Figure 1430.

Figure 1432 A-B shows a nucleotide sequence (SEQ ID NO:1432) of a native sequence PRO84922 cDNA, wherein SEQ ID NO:1432 is a clone designated herein as "DNA329339".

Figure 1433 shows the amino acid sequence (SEQ ID NO:1433) derived from the coding sequence of SEQ ID NO:1432 shown in Figure 1432.

Figure 1434 shows a nucleotide sequence (SEQ ID NO:1434) of a native sequence PRO81805 cDNA, wherein SEQ ID NO:1434 is a clone designated herein as "DNA329340".

Figure 1435 shows the amino acid sequence (SEQ ID NO:1435) derived from the coding sequence of SEQ ID NO:1434 shown in Figure 1434.

Figure 1436 A-B shows a nucleotide sequence (SEQ ID NO:1436) of a native sequence PRO10607 cDNA, wherein SEQ ID NO:1436 is a clone designated herein as "DNA287236".

Figure 1437 shows the amino acid sequence (SEQ ID NO:1437) derived from the coding sequence of SEQ ID NO:1436 shown in Figure 1436.

Figure 1438 shows a nucleotide sequence (SEQ ID NO:1438) of a native sequence PRO84923 cDNA, wherein SEQ ID NO:1438 is a clone designated herein as "DNA329341".

Figure 1439 shows the amino acid sequence (SEQ ID NO:1439) derived from the coding sequence of SEQ ID NO:1438 shown in Figure 1438.

Figure 1440 shows a nucleotide sequence (SEQ ID NO:1440) of a native sequence PRO83133 cDNA, wherein SEQ ID NO:1440 is a clone designated herein as "DNA326800".

Figure 1441 shows the amino acid sequence (SEQ ID NO:1441) derived from the coding sequence of SEQ ID NO:1440 shown in Figure 1440.

Figure 1442 A-B shows a nucleotide sequence (SEQ ID NO:1442) of a native sequence PRO84924 cDNA, wherein SEQ ID NO:1442 is a clone designated herein as "DNA329342".

Figure 1443 shows the amino acid sequence (SEQ ID NO:1443) derived from the coding sequence of SEQ ID NO:1442 shown in Figure 1442.

Figure 1444 A-B shows a nucleotide sequence (SEQ ID NO:1444) of a native sequence PRO84925 cDNA, wherein SEQ ID NO:1444 is a clone designated herein as "DNA329343".

Figure 1445 shows the amino acid sequence (SEQ ID NO:1445) derived from the coding sequence of SEQ ID NO:1444 shown in Figure 1444.

Figure 1446 shows a nucleotide sequence (SEQ ID NO:1446) of a native sequence PRO84926 cDNA, wherein SEQ ID NO:1446 is a clone designated herein as "DNA329344".

Figure 1447 shows the amino acid sequence (SEQ ID NO:1447) derived from the coding sequence of SEQ ID NO:1446 shown in Figure 1446.

Figure 1448 shows a nucleotide sequence (SEQ ID NO:1448) of a native sequence PRO69532 cDNA, wherein SEQ ID NO:1448 is a clone designated herein as "DNA287260".

Figure 1449 shows the amino acid sequence (SEQ ID NO:1449) derived from the coding sequence of SEQ ID NO:1448 shown in Figure 1448.

Figure 1450 shows a nucleotide sequence (SEQ ID NO:1450) of a native sequence PRO37675 cDNA, wherein SEQ ID NO:1450 is a clone designated herein as "DNA324198".

Figure 1451 shows the amino acid sequence (SEQ ID NO:1451) derived from the coding sequence of SEQ ID NO:1450 shown in Figure 1450.

Figure 1452 shows a nucleotide sequence (SEQ ID NO:1452) of a native sequence PRO25349 cDNA, wherein SEQ ID NO:1452 is a clone designated herein as "DNA189412".

Figure 1453 shows the amino acid sequence (SEQ ID NO:1453) derived from the coding sequence of SEQ ID NO:1452 shown in Figure 1452.

Figure 1454 shows a nucleotide sequence (SEQ ID NO:1454) of a native sequence PRO84927 cDNA, wherein SEQ ID NO:1454 is a clone designated herein as "DNA329345".

Figure 1455 shows the amino acid sequence (SEQ ID NO:1455) derived from the coding sequence of SEQ ID NO:1454 shown in Figure 1454.

Figure 1456 shows a nucleotide sequence (SEQ ID NO:1456) of a native sequence PRO12672 cDNA, wherein SEQ ID NO:1456 is a clone designated herein as "DNA151428".

Figure 1457 shows the amino acid sequence (SEQ ID NO:1457) derived from the coding sequence of SEQ ID NO:1456 shown in Figure 1456.

Figure 1458 shows a nucleotide sequence (SEQ ID NO:1458) of a native sequence PRO84928 cDNA, wherein SEQ ID NO:1458 is a clone designated herein as "DNA329346".

Figure 1459 shows the amino acid sequence (SEQ ID NO:1459) derived from the coding sequence of SEQ ID NO:1458 shown in Figure 1458.

Figure 1460 shows a nucleotide sequence (SEQ ID NO:1460) of a native sequence PRO84929 cDNA, wherein SEQ ID NO:1460 is a clone designated herein as "DNA329347".

Figure 1461 shows the amino acid sequence (SEQ ID NO:1461) derived from the coding sequence of SEQ ID NO:1460 shown in Figure 1460.

Figure 1462 shows a nucleotide sequence (SEQ ID NO:1462) of a native sequence PRO80902 cDNA, wherein SEQ ID NO:1462 is a clone designated herein as "DNA324209".

Figure 1463 shows the amino acid sequence (SEQ ID NO:1463) derived from the coding sequence of SEQ ID NO:1462 shown in Figure 1462.

Figure 1464 shows a nucleotide sequence (SEQ ID NO:1464) of a native sequence PRO84930 cDNA, wherein SEQ ID NO:1464 is a clone designated herein as "DNA329348".

Figure 1465 shows the amino acid sequence (SEQ ID NO:1465) derived from the coding sequence of SEQ ID NO:1464 shown in Figure 1464.

Figure 1466 shows a nucleotide sequence (SEQ ID NO:1466) of a native sequence PRO84931 cDNA, wherein SEQ ID NO:1466 is a clone designated herein as "DNA329349".

Figure 1467 shows the amino acid sequence (SEQ ID NO:1467) derived from the coding sequence of SEQ ID NO:1466 shown in Figure 1466.

Figure 1468 shows a nucleotide sequence (SEQ ID NO:1468) of a native sequence PRO83852 cDNA, wherein SEQ ID NO:1468 is a clone designated herein as "DNA327917".

Figure 1469 shows the amino acid sequence (SEQ ID NO:1469) derived from the coding sequence of SEQ ID NO:1468 shown in Figure 1468.

Figure 1470 shows a nucleotide sequence (SEQ ID NO:1470) of a native sequence PRO11732 cDNA, wherein SEQ ID NO:1470 is a clone designated herein as "DNA329350".

Figure 1471 shows the amino acid sequence (SEQ ID NO:1471) derived from the coding sequence of SEQ ID NO:1470 shown in Figure 1470.

Figure 1472 shows a nucleotide sequence (SEQ ID NO:1472) of a native sequence PRO82060 cDNA, wherein SEQ ID NO:1472 is a clone designated herein as "DNA325557".

Figure 1473 shows the amino acid sequence (SEQ ID NO:1473) derived from the coding sequence of SEQ ID NO:1472 shown in Figure 1472.

Figure 1474 shows a nucleotide sequence (SEQ ID NO:1474) of a native sequence PRO81147 cDNA, wherein SEQ ID NO:1474 is a clone designated herein as "DNA329351".

Figure 1475 shows the amino acid sequence (SEQ ID NO:1475) derived from the coding sequence of SEQ ID NO:1474 shown in Figure 1474.

Figure 1476 shows a nucleotide sequence (SEQ ID NO:1476) of a native sequence PRO84932 cDNA, wherein SEQ ID NO:1476 is a clone designated herein as "DNA329352".

Figure 1477 shows the amino acid sequence (SEQ ID NO:1477) derived from the coding sequence of SEQ ID NO:1476 shown in Figure 1476.

Figure 1478 shows a nucleotide sequence (SEQ ID NO:1478) of a native sequence PRO84933 cDNA, wherein SEQ ID NO:1478 is a clone designated herein as "DNA329353".

Figure 1479 shows the amino acid sequence (SEQ ID NO:1479) derived from the coding sequence of SEQ ID NO:1478 shown in Figure 1478.

Figure 1480 shows a nucleotide sequence (SEQ ID NO:1480) of a native sequence PRO83878 cDNA, wherein SEQ ID NO:1480 is a clone designated herein as "DNA327953".

Figure 1481 shows the amino acid sequence (SEQ ID NO:1481) derived from the coding sequence of SEQ ID NO:1480 shown in Figure 1480.

Figure 1482 shows a nucleotide sequence (SEQ ID NO:1482) of a native sequence PRO80542 cDNA, wherein SEQ ID NO:1482 is a clone designated herein as "DNA323792".

Figure 1483 shows the amino acid sequence (SEQ ID NO:1483) derived from the coding sequence of SEQ ID NO:1482 shown in Figure 1482.

Figure 1484 shows a nucleotide sequence (SEQ ID NO:1484) of a native sequence PRO81822 cDNA, wherein SEQ ID NO:1484 is a clone designated herein as "DNA325272".

Figure 1485 shows the amino acid sequence (SEQ ID NO:1485) derived from the coding sequence of SEQ ID NO:1484 shown in Figure 1484.

Figure 1486 shows a nucleotide sequence (SEQ ID NO:1486) of a native sequence PRO71043 cDNA, wherein SEQ ID NO:1486 is a clone designated herein as "DNA304467".

Figure 1487 shows the amino acid sequence (SEQ ID NO:1487) derived from the coding sequence of SEQ ID NO:1486 shown in Figure 1486.

Figure 1488A-B shows a nucleotide sequence (SEQ ID NO:1488) of a native sequence PRO52040 cDNA, wherein SEQ ID NO:1488 is a clone designated herein as "DNA257461".

Figure 1489 shows the amino acid sequence (SEQ ID NO:1489) derived from the coding sequence of SEQ ID NO:1488 shown in Figure 1488.

Figure 1490 shows a nucleotide sequence (SEQ ID NO:1490) of a native sequence PRO84934 cDNA, wherein SEQ ID NO:1490 is a clone designated herein as "DNA329354".

Figure 1491 shows the amino acid sequence (SEQ ID NO:1491) derived from the coding sequence of SEQ ID NO:1490 shown in Figure 1490.

Figure 1492 shows a nucleotide sequence (SEQ ID NO:1492) of a native sequence PRO83881 cDNA, wherein SEQ ID NO:1492 is a clone designated herein as "DNA327956".

Figure 1493 shows the amino acid sequence (SEQ ID NO:1493) derived from the coding sequence of SEQ ID NO:1492 shown in Figure 1492.

Figure 1494 shows a nucleotide sequence (SEQ ID NO:1494) of a native sequence PRO51950 cDNA, wherein SEQ ID NO:1494 is a clone designated herein as "DNA257363".

Figure 1495 shows the amino acid sequence (SEQ ID NO:1495) derived from the coding sequence of SEQ ID NO:1495 shown in Figure

Figure 1496 shows a nucleotide sequence (SEQ ID NO:1496) of a native sequence PRO50434 cDNA, wherein SEQ ID NO:1496 is a clone designated herein as "DNA329355".

Figure 1497 shows the amino acid sequence (SEQ ID NO:1497) derived from the coding sequence of SEQ ID NO:1496 shown in Figure 1496.

Figure 1498 shows a nucleotide sequence (SEQ ID NO:1498) of a native sequence PRO84935 cDNA, wherein SEQ ID NO:1498 is a clone designated herein as "DNA329356".

Figure 1499 shows the amino acid sequence (SEQ ID NO:1499) derived from the coding sequence of SEQ ID NO:1498 shown in Figure 1498.

Figure 1500 shows a nucleotide sequence (SEQ ID NO:1500) of a native sequence PRO84936 cDNA, wherein SEQ ID NO:1500 is a clone designated herein as "DNA329357".

Figure 1501 shows the amino acid sequence (SEQ ID NO:1501) derived from the coding sequence of SEQ ID NO:1500 shown in Figure 1500.

Figure 1502 shows a nucleotide sequence (SEQ ID NO:1502) of a native sequence PRO84937 cDNA, wherein SEQ ID NO:1502 is a clone designated herein as "DNA329358".

Figure 1503 shows the amino acid sequence (SEQ ID NO:1503) derived from the coding sequence of SEQ ID NO:1502 shown in Figure 1502.

Figure 1504 shows a nucleotide sequence (SEQ ID NO:1504) of a native sequence PRO84938 cDNA, wherein SEQ ID NO:1504 is a clone designated herein as "DNA329359".

Figure 1505 shows the amino acid sequence (SEQ ID NO:1505) derived from the coding sequence of SEQ ID NO:1504 shown in Figure 1504.

Figure 1506 shows a nucleotide sequence (SEQ ID NO:1506) of a native sequence PRO84939 cDNA, wherein SEQ ID NO:1506 is a clone designated herein as "DNA329360".

Figure 1507 shows the amino acid sequence (SEQ ID NO:1507) derived from the coding sequence of SEQ ID NO:1506 shown in Figure 1506.

Figure 1508 shows a nucleotide sequence (SEQ ID NO:1508) of a native sequence PRO84940 cDNA, wherein SEQ ID NO:1508 is a clone designated herein as "DNA329361".

Figure 1509 shows the amino acid sequence (SEQ ID NO:1509) derived from the coding sequence of SEQ ID NO:1508 shown in Figure 1508.

Figure 1510 shows a nucleotide sequence (SEQ ID NO:1510) of a native sequence PRO80856 cDNA, wherein SEQ ID NO:1510 is a clone designated herein as "DNA324156".

Figure 1511 shows the amino acid sequence (SEQ ID NO:1511) derived from the coding sequence of SEQ ID NO:1510 shown in Figure 1510.

Figure 1512 shows a nucleotide sequence (SEQ ID NO:1512) of a native sequence PRO84941 cDNA, wherein SEQ ID NO:1512 is a clone designated herein as "DNA329362".

Figure 1513 shows the amino acid sequence (SEQ ID NO:1513) derived from the coding sequence of SEQ ID NO:1512 shown in Figure 1512.

Figure 1514 shows a nucleotide sequence (SEQ ID NO:1514) of a native sequence PRO84942 cDNA, wherein SEQ ID NO:1514 is a clone designated herein as "DNA329363".

Figure 1515 shows the amino acid sequence (SEQ ID NO:1515) derived from the coding sequence of SEQ ID NO:1514 shown in Figure 1514.

Figure 1516 shows a nucleotide sequence (SEQ ID NO:1516) of a native sequence PRO84943 cDNA, wherein SEQ ID NO:1516 is a clone designated herein as "DNA329364".

Figure 1517 shows the amino acid sequence (SEQ ID NO:1517) derived from the coding sequence of SEQ ID NO:1516 shown in Figure 1516.

Figure 1518 shows a nucleotide sequence (SEQ ID NO:1518) of a native sequence PRO84944 cDNA, wherein SEQ ID NO:1518 is a clone designated herein as "DNA329365".

Figure 1519 shows the amino acid sequence (SEQ ID NO:1519) derived from the coding sequence of SEQ ID NO:1518 shown in Figure 1518.

Figure 1520 shows a nucleotide sequence (SEQ ID NO:1520) of a native sequence PRO84945 cDNA, wherein SEQ ID NO:1520 is a clone designated herein as "DNA329366".

Figure 1521 shows the amino acid sequence (SEQ ID NO:1521) derived from the coding sequence of SEQ ID NO:1520 shown in Figure 1520.

Figure 1522 shows a nucleotide sequence (SEQ ID NO:1522) of a native sequence PRO61417 cDNA, wherein SEQ ID NO:1522 is a clone designated herein as "DNA273418".

Figure 1523 shows the amino acid sequence (SEQ ID NO:1523) derived from the coding sequence of SEQ ID NO:1522 shown in Figure 1522.

Figure 1524 shows a nucleotide sequence (SEQ ID NO:1524) of a native sequence PRO81368 cDNA, wherein SEQ ID NO:1524 is a clone designated herein as "DNA324743".

Figure 1525 shows the amino acid sequence (SEQ ID NO:1525) derived from the coding sequence of SEQ ID NO:1524 shown in Figure 1424.

Figure 1526 shows a nucleotide sequence (SEQ ID NO:1526) of a native sequence PRO84946 cDNA, wherein SEQ ID NO:1526 is a clone designated herein as "DNA329367".

Figure 1527 shows the amino acid sequence (SEQ ID NO:1527) derived from the coding sequence of SEQ ID NO:1526 shown in Figure 1526.

Figure 1528 shows a nucleotide sequence (SEQ ID NO:1528) of a native sequence PRO26224 cDNA, wherein SEQ ID NO:1528 is a clone designated herein as "DNA188735".

Figure 1529 shows the amino acid sequence (SEQ ID NO:1529) derived from the coding sequence of SEQ ID NO:1528 shown in Figure 1528.

Figure 1530 shows a nucleotide sequence (SEQ ID NO:1530) of a native sequence PRO69527 cDNA, wherein SEQ ID NO:1530 is a clone designated herein as "DNA287253".

Figure 1531 shows the amino acid sequence (SEQ ID NO:1531) derived from the coding sequence of SEQ ID NO:1530 shown in Figure 1530.

Figure 1532 shows a nucleotide sequence (SEQ ID NO:1532) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:1532 is a clone designated herein as "DNA327200".

Figure 1533 shows the amino acid sequence (SEQ ID NO:1533) derived from the coding sequence of SEQ ID NO:1532 shown in Figure 1532.

Figure 1534 shows a nucleotide sequence (SEQ ID NO:1534) of a native sequence PRO34454 cDNA, wherein SEQ ID NO:1534 is a clone designated herein as "DNA218676".

Figure 1535 shows the amino acid sequence (SEQ ID NO:1535) derived from the coding sequence of SEQ ID NO:1534 shown in Figure 1534.

Figure 1536 shows a nucleotide sequence (SEQ ID NO:1536) of a native sequence PRO84947 cDNA, wherein SEQ ID NO:1536 is a clone designated herein as "DNA329368".

Figure 1537 shows the amino acid sequence (SEQ ID NO:1537) derived from the coding sequence of SEQ ID NO:1536 shown in Figure 1536.

Figure 1538 shows a nucleotide sequence (SEQ ID NO:1538) of a native sequence PRO84948 cDNA, wherein SEQ ID NO:1538 is a clone designated herein as "DNA329369".

Figure 1539 shows the amino acid sequence (SEQ ID NO:1539) derived from the coding sequence of SEQ ID NO:1538 shown in Figure 1538.

Figure 1540 shows a nucleotide sequence (SEQ ID NO:1540) of a native sequence PRO81339 cDNA, wherein SEQ ID NO:1540 is a clone designated herein as "DNA324707".

Figure 1541 shows the amino acid sequence (SEQ ID NO:1541) derived from the coding sequence of SEQ ID NO:1540 shown in Figure 1540.

Figure 1542 shows a nucleotide sequence (SEQ ID NO:1542) of a native sequence PRO84949 cDNA, wherein SEQ ID NO:1542 is a clone designated herein as "DNA329370".

Figure 1543 shows the amino acid sequence (SEQ ID NO:1543) derived from the coding sequence of SEQ ID NO:1542 shown in Figure 1542.

Figure 1544 shows a nucleotide sequence (SEQ ID NO:1544) of a native sequence PRO84950 cDNA, wherein SEQ ID NO:1544 is a clone designated herein as "DNA329371".

Figure 1545 shows the amino acid sequence (SEQ ID NO:1545) derived from the coding sequence of SEQ ID NO:1544 shown in Figure 1544.

Figure 1546 shows a nucleotide sequence (SEQ ID NO:1546) of a native sequence PRO84951 cDNA, wherein SEQ ID NO:1546 is a clone designated herein as "DNA329372".

Figure 1547 shows the amino acid sequence (SEQ ID NO:1547) derived from the coding sequence of SEQ ID NO:1546 shown in Figure 1546.

Figure 1548 shows a nucleotide sequence (SEQ ID NO:1548) of a native sequence PRO84952 cDNA, wherein SEQ ID NO:1548 is a clone designated herein as "DNA329373".

Figure 1549 shows the amino acid sequence (SEQ ID NO:1549) derived from the coding sequence of SEQ ID NO:1548 shown in Figure 1548.

Figure 1550 shows a nucleotide sequence (SEQ ID NO:1550) of a native sequence PRO69574 cDNA, wherein SEQ ID NO:1550 is a clone designated herein as "DNA327976".

Figure 1551 shows the amino acid sequence (SEQ ID NO:1551) derived from the coding sequence of SEQ ID NO:1550 shown in Figure 1550.

Figure 1552 shows a nucleotide sequence (SEQ ID NO:1552) of a native sequence PRO84953 cDNA, wherein SEQ ID NO:1552 is a clone designated herein as "DNA329374".

Figure 1553 shows the amino acid sequence (SEQ ID NO:1553) derived from the coding sequence of SEQ ID NO:1552 shown in Figure 1552.

Figure 1554 shows a nucleotide sequence (SEQ ID NO:1554) of a native sequence PRO51916 cDNA, wherein SEQ ID NO:1554 is a clone designated herein as "DNA329375".

Figure 1555 shows the amino acid sequence (SEQ ID NO:1555) derived from the coding sequence of SEQ ID NO:1554 shown in Figure 1554.

Figure 1556 shows a nucleotide sequence (SEQ ID NO:1556) of a native sequence PRO84954 cDNA, wherein SEQ ID NO:1556 is a clone designated herein as "DNA329376".

Figure 1557 shows the amino acid sequence (SEQ ID NO:1557) derived from the coding sequence of SEQ ID NO:1556 shown in Figure 1556.

Figure 1558 A-B shows a nucleotide sequence (SEQ ID NO:1558) of a native sequence PRO83901 cDNA, wherein SEQ ID NO:1558 is a clone designated herein as "DNA327981".

Figure 1559 shows the amino acid sequence (SEQ ID NO:1559) derived from the coding sequence of SEQ ID NO:1558 shown in Figure 1558.

Figure 1560 shows a nucleotide sequence (SEQ ID NO:1560) of a native sequence PRO84955 cDNA, wherein SEQ ID NO:1560 is a clone designated herein as "DNA329377".

Figure 1561 shows the amino acid sequence (SEQ ID NO:1561) derived from the coding sequence of SEQ ID NO:1560 shown in Figure 1560.

Figure 1562 shows a nucleotide sequence (SEQ ID NO:1562) of a native sequence PRO84956 cDNA, wherein SEQ ID NO:1562 is a clone designated herein as "DNA329378".

Figure 1563 shows the amino acid sequence (SEQ ID NO:1563) derived from the coding sequence of SEQ ID NO:1562 shown in Figure 1562.

Figure 1564 shows a nucleotide sequence (SEQ ID NO:1564) of a native sequence PRO80871 cDNA, wherein SEQ ID NO:1564 is a clone designated herein as "DNA324173".

Figure 1565 shows the amino acid sequence (SEQ ID NO:1565) derived from the coding sequence of SEQ ID NO:1564 shown in Figure 1564.

Figure 1566 shows a nucleotide sequence (SEQ ID NO:1566) of a native sequence PRO69641 cDNA, wherein SEQ ID NO:1566 is a clone designated herein as "DNA287382".

Figure 1567 shows the amino acid sequence (SEQ ID NO:1567) derived from the coding sequence of SEQ ID NO:1566 shown in Figure 1566.

Figure 1568 shows a nucleotide sequence (SEQ ID NO:1568) of a native sequence PRO51940 cDNA, wherein SEQ ID NO:1568 is a clone designated herein as "DNA257352".

Figure 1569 shows the amino acid sequence (SEQ ID NO:1569) derived from the coding sequence of SEQ ID NO:1568 shown in Figure 1568.

Figure 1570 A-B shows a nucleotide sequence (SEQ ID NO:1570) of a native sequence PRO69594 cDNA, wherein SEQ ID NO:1570 is a clone designated herein as "DNA287330".

Figure 1571 shows the amino acid sequence (SEQ ID NO:1571) derived from the coding sequence of SEQ ID NO:1570 shown in Figure 1570.

Figure 1572A-C shows a nucleotide sequence (SEQ ID NO:1572) of a native sequence PRO84957 cDNA, wherein SEQ ID NO:1572 is a clone designated herein as "DNA329379".

Figure 1573 shows the amino acid sequence (SEQ ID NO:1573) derived from the coding sequence of SEQ ID NO:1572 shown in Figure 1572.

Figure 1574 shows a nucleotide sequence (SEQ ID NO:1574) of a native sequence PRO80743 cDNA, wherein SEQ ID NO:1574 is a clone designated herein as "DNA329380".

Figure 1575 shows the amino acid sequence (SEQ ID NO:1575) derived from the coding sequence of SEQ ID NO:1574 shown in Figure 1574.

Figure 1576 shows a nucleotide sequence (SEQ ID NO:1576) of a native sequence cDNA, wherein SEQ ID NO:1576 is a clone designated herein as "DNA329381".

Figure 1577 shows a nucleotide sequence (SEQ ID NO:1577) of a native sequence PRO52338 cDNA, wherein SEQ ID NO:1577 is a clone designated herein as "DNA257789".

Figure 1578 shows the amino acid sequence (SEQ ID NO:1578) derived from the coding sequence of SEQ ID NO:1577 shown in Figure 1577.

Figure 1579 shows a nucleotide sequence (SEQ ID NO:1579) of a native sequence cDNA, wherein SEQ ID NO:1579 is a clone designated herein as "DNA329382".

Figure 1580 shows a nucleotide sequence (SEQ ID NO:1580) of a native sequence PRO23603 cDNA, wherein SEQ ID NO:1580 is a clone designated herein as "DNA194211".

Figure 1581 shows the amino acid sequence (SEQ ID NO:1581) derived from the coding sequence of SEQ ID NO:1580 shown in Figure 1580.

Figure 1582 A-B shows a nucleotide sequence (SEQ ID NO:1582) of a native sequence PRO23253 cDNA, wherein SEQ ID NO:1582 is a clone designated herein as "DNA169523".

Figure 1583 shows the amino acid sequence (SEQ ID NO:1583) derived from the coding sequence of SEQ ID NO:1582 shown in Figure 1582.

Figure 1584 shows a nucleotide sequence (SEQ ID NO:1584) of a native sequence PRO84959 cDNA, wherein SEQ ID NO:1584 is a clone designated herein as "DNA329383".

Figure 1585 shows the amino acid sequence (SEQ ID NO:1585) derived from the coding sequence of SEQ ID NO:1584 shown in Figure 1584.

Figure 1586 shows a nucleotide sequence (SEQ ID NO:1586) of a native sequence PRO84960 cDNA, wherein SEQ ID NO:1586 is a clone designated herein as "DNA329384".

Figure 1587 shows the amino acid sequence (SEQ ID NO:1587) derived from the coding sequence of SEQ ID NO:1586 shown in Figure 1586.

Figure 1588 A-B shows a nucleotide sequence (SEQ ID NO:1588) of a native sequence PRO84961 cDNA, wherein SEQ ID NO:1588 is a clone designated herein as "DNA329385".

Figure 1589 shows the amino acid sequence (SEQ ID NO:1589) derived from the coding sequence of SEQ ID NO:1588 shown in Figure 1588.

Figure 1590 shows a nucleotide sequence (SEQ ID NO:1590) of a native sequence cDNA, wherein SEQ ID NO:1590 is a clone designated herein as "DNA161646".

Figure 1591 shows a nucleotide sequence (SEQ ID NO:1591) of a native sequence PRO84962 cDNA, wherein SEQ ID NO:1591 is a clone designated herein as "DNA329386".

Figure 1592 shows the amino acid sequence (SEQ ID NO:1592) derived from the coding sequence of SEQ ID NO:1592 shown in Figure

Figure 1593 shows a nucleotide sequence (SEQ ID NO:1593) of a native sequence PRO84963 cDNA, wherein SEQ ID NO:1593 is a clone designated herein as "DNA329387".

Figure 1594 shows the amino acid sequence (SEQ ID NO:1594) derived from the coding sequence of SEQ ID NO:1593 shown in Figure 1593.

Figure 1595 shows a nucleotide sequence (SEQ ID NO:1595) of a native sequence PRO84964 cDNA, wherein SEQ ID NO:1595 is a clone designated herein as "DNA329388".

Figure 1596 shows the amino acid sequence (SEQ ID NO:1596) derived from the coding sequence of SEQ ID NO:1595 shown in Figure 1595.

Figure 1597 shows a nucleotide sequence (SEQ ID NO:1597) of a native sequence PRO84965 cDNA, wherein SEQ ID NO:1597 is a clone designated herein as "DNA329389".

Figure 1598 shows the amino acid sequence (SEQ ID NO:1598) derived from the coding sequence of SEQ ID NO:1597 shown in Figure 1597.

Figure 1599A-D shows a nucleotide sequence (SEQ ID NO:1599) of a native sequence PRO84966 cDNA, wherein SEQ ID NO:1599 is a clone designated herein as "DNA329390".

Figure 1600 shows the amino acid sequence (SEQ ID NO:1600) derived from the coding sequence of SEQ ID NO:1600 shown in Figure

Figure 1601A-E shows a nucleotide sequence (SEQ ID NO:1601) of a native sequence PRO84967 cDNA, wherein SEQ ID NO:1601 is a clone designated herein as "DNA329391".

Figure 1602 shows the amino acid sequence (SEQ ID NO:1602) derived from the coding sequence of SEQ ID NO:1601 shown in Figure 1601.

Figure 1603 A-B shows a nucleotide sequence (SEQ ID NO:1603) of a native sequence PRO84968 cDNA, wherein SEQ ID NO:1603 is a clone designated herein as "DNA329392".

Figure 1604 shows the amino acid sequence (SEQ ID NO:1604) derived from the coding sequence of SEQ ID NO:1603 shown in Figure 1603.

Figure 1605 A-B shows a nucleotide sequence (SEQ ID NO:1605) of a native sequence PRO81138 cDNA, wherein SEQ ID NO:1605 is a clone designated herein as "DNA327993".

Figure 1606 shows the amino acid sequence (SEQ ID NO:1606) derived from the coding sequence of SEQ ID NO:1605 shown in Figure 1605.

Figure 1607 shows a nucleotide sequence (SEQ ID NO:1607) of a native sequence cDNA, wherein SEQ ID NO:1607 is a clone designated herein as "DNA155396".

Figure 1608 shows a nucleotide sequence (SEQ ID NO:1608) of a native sequence PRO84969 cDNA, wherein SEQ ID NO:1608 is a clone designated herein as "DNA329393".

Figure 1609 shows the amino acid sequence (SEQ ID NO:1609) derived from the coding sequence of SEQ ID NO:1608 shown in Figure 1608.

Figure 1610 shows a nucleotide sequence (SEQ ID NO:1610) of a native sequence PRO83915 cDNA, wherein SEQ ID NO:1610 is a clone designated herein as "DNA327996".

Figure 1611 shows the amino acid sequence (SEQ ID NO:1611) derived from the coding sequence of SEQ ID NO:1611 shown in Figure

Figure 1612 shows a nucleotide sequence (SEQ ID NO:1612) of a native sequence cDNA, wherein SEQ ID NO:1612 is a clone designated herein as "DNA329394".

Figure 1613 A-B shows a nucleotide sequence (SEQ ID NO:1613) of a native sequence PRO84971 cDNA, wherein SEQ ID NO:1613 is a clone designated herein as "DNA329395".

Figure 1614 shows the amino acid sequence (SEQ ID NO:1614) derived from the coding sequence of SEQ ID NO:1613 shown in Figure 1613.

Figure 1615 shows a nucleotide sequence (SEQ ID NO:1615) of a native sequence cDNA, wherein SEQ ID NO:1615 is a clone designated herein as "DNA228047".

Figure 1616 shows a nucleotide sequence (SEQ ID NO:1616) of a native sequence PRO84972 cDNA, wherein SEQ ID NO:1616 is a clone designated herein as "DNA329396".

Figure 1617 shows the amino acid sequence (SEQ ID NO:1617) derived from the coding sequence of SEQ ID NO:1616 shown in Figure 1616.

Figure 1618 shows a nucleotide sequence (SEQ ID NO:1618) of a native sequence PRO84973 cDNA, wherein SEQ ID NO:1618 is a clone designated herein as "DNA329397".

Figure 1619 shows the amino acid sequence (SEQ ID NO:1619) derived from the coding sequence of SEQ ID NO:1618 shown in Figure 1618.

Figure 1620 A-B shows a nucleotide sequence (SEQ ID NO:1620) of a native sequence PRO4805 cDNA, wherein SEQ ID NO:1620 is a clone designated herein as "DNA329398".

Figure 1621 shows the amino acid sequence (SEQ ID NO:1621) derived from the coding sequence of SEQ ID NO:1620 shown in Figure 1620.

Figure 1622 shows a nucleotide sequence (SEQ ID NO:1622) of a native sequence PRO84974 cDNA, wherein SEQ ID NO:1622 is a clone designated herein as "DNA329399".

Figure 1623 shows the amino acid sequence (SEQ ID NO:1623) derived from the coding sequence of SEQ ID NO:1622 shown in Figure 1622.

Figure 1624 shows a nucleotide sequence (SEQ ID NO:1624) of a native sequence cDNA, wherein SEQ ID NO:1624 is a clone designated herein as "DNA329400".

Figure 1625 shows a nucleotide sequence (SEQ ID NO:1625) of a native sequence PRO28544 cDNA, wherein SEQ ID NO:1625 is a clone designated herein as "DNA199090".

Figure 1626 shows the amino acid sequence (SEQ ID NO:1626) derived from the coding sequence of SEQ ID NO:1625 shown in Figure 1625

Figure 1627 shows a nucleotide sequence (SEQ ID NO:1627) of a native sequence PRO82422 cDNA, wherein SEQ ID NO:1627 is a clone designated herein as "DNA325977".

Figure 1628 shows the amino acid sequence (SEQ ID NO:1628) derived from the coding sequence of SEQ ID NO:1627 shown in Figure 1627.

Figure 1629 shows a nucleotide sequence (SEQ ID NO:1629) of a native sequence PRO84976 cDNA, wherein SEQ ID NO:1629 is a clone designated herein as "DNA329401".

Figure 1630 shows the amino acid sequence (SEQ ID NO:1630) derived from the coding sequence of SEQ ID NO:1629 shown in Figure 1629.

Figure 1631 shows a nucleotide sequence (SEQ ID NO:1631) of a native sequence PRO4845 cDNA, wherein SEQ ID NO:1631 is a clone designated herein as "DNA329402".

Figure 1632 shows the amino acid sequence (SEQ ID NO:1632) derived from the coding sequence of SEQ ID NO:1631 shown in Figure 1631.

Figure 1633 shows a nucleotide sequence (SEQ ID NO:1633) of a native sequence cDNA, wherein SEQ ID NO:1633 is a clone designated herein as "DNA329403".

Figure 1634 shows a nucleotide sequence (SEQ ID NO:1634) of a native sequence cDNA, wherein SEQ ID NO:1634 is a clone designated herein as "DNA195699".

Figure 1635 shows a nucleotide sequence (SEQ ID NO:1635) of a native sequence PRO71212 cDNA, wherein SEQ ID NO:1635 is a clone designated herein as "DNA304802".

Figure 1636 shows the amino acid sequence (SEQ ID NO:1636) derived from the coding sequence of SEQ ID NO:1635 shown in Figure 1635.

Figure 1637 shows a nucleotide sequence (SEQ ID NO:1637) of a native sequence cDNA, wherein SEQ ID NO:1637 is a clone designated herein as "DNA328005".

Figure 1638 shows a nucleotide sequence (SEQ ID NO:1638) of a native sequence PRO82972 cDNA, wherein SEQ ID NO:1638 is a clone designated herein as "DNA329404".

Figure 1639 shows the amino acid sequence (SEQ ID NO:1639) derived from the coding sequence of SEQ ID NO:1638 shown in Figure 1638.

Figure 1640 shows a nucleotide sequence (SEQ ID NO:1640) of a native sequence cDNA, wherein SEQ ID NO:1640 is a clone designated herein as "DNA196561".

Figure 1641 shows a nucleotide sequence (SEQ ID NO:1641) of a native sequence cDNA, wherein SEQ ID NO:1641 is a clone designated herein as "DNA210184".

Figure 1642 shows a nucleotide sequence (SEQ ID NO:1642) of a native sequence cDNA, wherein SEQ ID NO:1642 is a clone designated herein as "DNA329405".

Figure 1643 shows a nucleotide sequence (SEQ ID NO:1643) of a native sequence PRO83926 cDNA, wherein SEQ ID NO:1643 is a clone designated herein as "DNA328008".

Figure 1644 shows the amino acid sequence (SEQ ID NO:1644) derived from the coding sequence of SEQ ID NO:1643 shown in Figure 1643.

Figure 1645 shows a nucleotide sequence (SEQ ID NO:1645) of a native sequence PRO84979 cDNA, wherein SEQ ID NO:1645 is a clone designated herein as "DNA329406".

Figure 1646 shows the amino acid sequence (SEQ ID NO:1646) derived from the coding sequence of SEQ ID NO:1645 shown in Figure 1645.

Figure 1647 A-B shows a nucleotide sequence (SEQ ID NO:1647) of a native sequence PRO84980 cDNA, wherein SEQ ID NO:1647 is a clone designated herein as "DNA329407".

Figure 1648 shows the amino acid sequence (SEQ ID NO:1648) derived from the coding sequence of SEQ ID NO:1647 shown in Figure 1647.

Figure 1649 shows a nucleotide sequence (SEQ ID NO:1649) of a native sequence PRO71045 cDNA, wherein SEQ ID NO:1649 is a clone designated herein as "DNA304469".

Figure 1650 shows the amino acid sequence (SEQ ID NO:1650) derived from the coding sequence of SEQ ID NO:1649 shown in Figure 1649.

Figure 1651 shows a nucleotide sequence (SEQ ID NO:1651) of a native sequence PRO70021 cDNA, wherein SEQ ID NO:1651 is a clone designated herein as "DNA288261".

Figure 1652 shows the amino acid sequence (SEQ ID NO:1652) derived from the coding sequence of SEQ ID NO:1651 shown in Figure 1651.

Figure 1653 shows a nucleotide sequence (SEQ ID NO:1653) of a native sequence PRO38893 cDNA, wherein SEQ ID NO:1653 is a clone designated herein as "DNA329408".

Figure 1654 shows the amino acid sequence (SEQ ID NO:1654) derived from the coding sequence of SEQ ID NO:1653 shown in Figure 1653.

Figure 1655 shows a nucleotide sequence (SEQ ID NO:1655) of a native sequence PRO84981 cDNA, wherein SEQ ID NO:1655 is a clone designated herein as "DNA329409".

Figure 1656 shows the amino acid sequence (SEQ ID NO:1656) derived from the coding sequence of SEQ ID NO:1655 shown in Figure 1655.

Figure 1657 shows a nucleotide sequence (SEQ ID NO:1657) of a native sequence PRO84982 cDNA, wherein SEQ ID NO:1657 is a clone designated herein as "DNA329410".

Figure 1658 shows the amino acid sequence (SEQ ID NO:1658) derived from the coding sequence of SEQ ID NO:1657 shown in Figure 1657.

Figure 1659 shows a nucleotide sequence (SEQ ID NO:1659) of a native sequence PRO84983 cDNA, wherein SEQ ID NO:1659 is a clone designated herein as "DNA329411".

Figure 1660 shows the amino acid sequence (SEQ ID NO:1660) derived from the coding sequence of SEQ ID NO:1659 shown in Figure 1659.

Figure 1661 shows a nucleotide sequence (SEQ ID NO:1661) of a native sequence PRO51958 cDNA, wherein SEQ ID NO:1661 is a clone designated herein as "DNA257371".

Figure 1662 shows the amino acid sequence (SEQ ID NO:1662) derived from the coding sequence of SEQ ID NO:1661 shown in Figure 1661.

Figure 1663 shows a nucleotide sequence (SEQ ID NO:1663) of a native sequence PRO84984 cDNA, wherein SEQ ID NO:1663 is a clone designated herein as "DNA329412".

Figure 1664 shows the amino acid sequence (SEQ ID NO:1664) derived from the coding sequence of SEQ ID NO:1663 shown in Figure 1663.

Figure 1665 shows a nucleotide sequence (SEQ ID NO:1665) of a native sequence PRO84985 cDNA, wherein SEQ ID NO:1665 is a clone designated herein as "DNA329413".

Figure 1666 shows the amino acid sequence (SEQ ID NO:1666) derived from the coding sequence of SEQ ID NO:1665 shown in Figure 1665.

Figure 1667 shows a nucleotide sequence (SEQ ID NO:1667) of a native sequence PRO84986 cDNA, wherein SEQ ID NO:1667 is a clone designated herein as "DNA329414".

Figure 1668 shows the amino acid sequence (SEQ ID NO:1668) derived from the coding sequence of SEQ ID NO:1667 shown in Figure 1667.

Figure 1669 shows a nucleotide sequence (SEQ ID NO:1669) of a native sequence PRO84987 cDNA, wherein SEQ ID NO:1669 is a clone designated herein as "DNA329415".

Figure 1670 shows the amino acid sequence (SEQ ID NO:1670) derived from the coding sequence of SEQ ID NO:1669 shown in Figure 1669.

Figure 1671 shows a nucleotide sequence (SEQ ID NO:1671) of a native sequence PRO84988 cDNA, wherein SEQ ID NO:1671 is a clone designated herein as "DNA329416".

Figure 1672 shows the amino acid sequence (SEQ ID NO:1672) derived from the coding sequence of SEQ ID NO:1671 shown in Figure 1671.

Figure 1673 shows a nucleotide sequence (SEQ ID NO:1673) of a native sequence PRO84989 cDNA, wherein SEQ ID NO:1673 is a clone designated herein as "DNA329417".

Figure 1674 shows the amino acid sequence (SEQ ID NO:1674) derived from the coding sequence of SEQ ID NO:1673 shown in Figure 1673.

Figure 1675 shows a nucleotide sequence (SEQ ID NO:1675) of a native sequence PRO19906 cDNA, wherein SEQ ID NO:1675 is a clone designated herein as "DNA329418".

Figure 1676 shows the amino acid sequence (SEQ ID NO:1676) derived from the coding sequence of SEQ ID NO:1675 shown in Figure 1675.

Figure 1677 shows a nucleotide sequence (SEQ ID NO:1677) of a native sequence PRO69630 cDNA, wherein SEQ ID NO:1677 is a clone designated herein as "DNA287370".

Figure 1678 shows the amino acid sequence (SEQ ID NO:1678) derived from the coding sequence of SEQ ID NO:1677 shown in Figure 1677.

Figure 1679 A-B shows a nucleotide sequence (SEQ ID NO:1679) of a native sequence PRO84990 cDNA, wherein SEQ ID NO:1679 is a clone designated herein as "DNA329419".

Figure 1680 shows the amino acid sequence (SEQ ID NO:1680) derived from the coding sequence of SEQ ID NO:1679 shown in Figure 1679.

Figure 1681 shows a nucleotide sequence (SEQ ID NO:1681) of a native sequence cDNA, wherein SEQ ID NO:1681 is a clone designated herein as "DNA329420".

Figure 1682A-B shows a nucleotide sequence (SEQ ID NO:1682) of a native sequence PRO84992 cDNA, wherein SEQ ID NO:1682 is a clone designated herein as "DNA329421".

Figure 1683 shows the amino acid sequence (SEQ ID NO:1683) derived from the coding sequence of SEQ ID NO:1682 shown in Figure 1682.

Figure 1684 A-B shows a nucleotide sequence (SEQ ID NO:1684) of a native sequence PRO84993 cDNA, wherein SEQ ID NO:1684 is a clone designated herein as "DNA329422".

Figure 1685 shows the amino acid sequence (SEQ ID NO:1685) derived from the coding sequence of SEQ ID NO:1684 shown in Figure 1684.

Figure 1686 A-B shows a nucleotide sequence (SEQ ID NO:1686) of a native sequence PRO84994 cDNA, wherein SEQ ID NO:1686 is a clone designated herein as "DNA329423".

Figure 1687 shows the amino acid sequence (SEQ ID NO:1687) derived from the coding sequence of SEQ ID NO:1686 shown in Figure 1686.

Figure 1688 shows a nucleotide sequence (SEQ ID NO:1688) of a native sequence PRO84995 cDNA, wherein SEQ ID NO:1688 is a clone designated herein as "DNA329424".

Figure 1689 shows the amino acid sequence (SEQ ID NO:1689) derived from the coding sequence of SEQ ID NO:1688 shown in Figure 1688.

Figure 1690 shows a nucleotide sequence (SEQ ID NO:1690) of a native sequence cDNA, wherein SEQ ID NO:1690 is a clone designated herein as "DNA329425".

Figure 1691 shows a nucleotide sequence (SEQ ID NO:1691) of a native sequence PRO84997 cDNA, wherein SEQ ID NO:1691 is a clone designated herein as "DNA329426".

Figure 1692 shows the amino acid sequence (SEQ ID NO:1692) derived from the coding sequence of SEQ ID NO:1691 shown in Figure 1691.

Figure 1693 shows a nucleotide sequence (SEQ ID NO:1693) of a native sequence PRO956 cDNA, wherein SEQ ID NO:1693 is a clone designated herein as "DNA56350".

Figure 1694 shows the amino acid sequence (SEQ ID NO:1694) derived from the coding sequence of SEQ ID NO:1693 shown in Figure 1693.

Figure 1695 shows a nucleotide sequence (SEQ ID NO:1695) of a native sequence PRO84998 cDNA, wherein SEQ ID NO:1695 is a clone designated herein as "DNA329427".

Figure 1696 shows the amino acid sequence (SEQ ID NO:1696) derived from the coding sequence of SEQ ID NO:1695 shown in Figure 1695.

Figure 1697 shows a nucleotide sequence (SEQ ID NO:1697) of a native sequence PRO84999 cDNA, wherein SEQ ID NO:1697 is a clone designated herein as "DNA329428".

Figure 1698 shows the amino acid sequence (SEQ ID NO:1698) derived from the coding sequence of SEQ ID NO:1697 shown in Figure 1697.

Figure 1699 shows a nucleotide sequence (SEQ ID NO:1699) of a native sequence cDNA, wherein SEQ ID NO:1699 is a clone designated herein as "DNA195822".

Figure 1700 shows a nucleotide sequence (SEQ ID NO:1700) of a native sequence PRO23314 cDNA, wherein SEQ ID NO:1700 is a clone designated herein as "DNA193896".

Figure 1701 shows the amino acid sequence (SEQ ID NO:1701) derived from the coding sequence of SEQ ID NO:1700 shown in Figure 1700.

Figure 1702 shows a nucleotide sequence (SEQ ID NO:1702) of a native sequence PRO85000 cDNA, wherein SEQ ID NO:1702 is a clone designated herein as "DNA329429".

Figure 1703 shows the amino acid sequence (SEQ ID NO:1703) derived from the coding sequence of SEQ ID NO:1703 shown in Figure

Figure 1704 shows a nucleotide sequence (SEQ ID NO:1704) of a native sequence PRO83945 cDNA, wherein SEQ ID NO:1704 is a clone designated herein as "DNA328028".

Figure 1705 shows the amino acid sequence (SEQ ID NO:1705) derived from the coding sequence of SEQ ID NO:1704 shown in Figure 1704.

Figure 1706 shows a nucleotide sequence (SEQ ID NO:1706) of a native sequence PRO38524 cDNA, wherein SEQ ID NO:1706 is a clone designated herein as "DNA329430".

Figure 1707 shows the amino acid sequence (SEQ ID NO:1707) derived from the coding sequence of SEQ ID NO:1706 shown in Figure 1706.

Figure 1708A-C shows a nucleotide sequence (SEQ ID NO:1708) of a native sequence PRO12637 cDNA, wherein SEQ ID NO:1708 is a clone designated herein as "DNA151207".

Figure 1709 shows the amino acid sequence (SEQ ID NO:1709) derived from the coding sequence of SEQ ID NO:1708 shown in Figure 1708.

Figure 1710 shows a nucleotide sequence (SEQ ID NO:1710) of a native sequence PRO85001 cDNA, wherein SEQ ID NO:1710 is a clone designated herein as "DNA329431".

Figure 1711 shows the amino acid sequence (SEQ ID NO:1711) derived from the coding sequence of SEQ ID NO:1710 shown in Figure 1710.

Figure 1712 shows a nucleotide sequence (SEQ ID NO:1712) of a native sequence PRO85002 cDNA, wherein SEQ ID NO:1712 is a clone designated herein as "DNA329432".

Figure 1713 shows the amino acid sequence (SEQ ID NO:1713) derived from the coding sequence of SEQ ID NO:1712 shown in Figure 1712.

Figure 1714 shows a nucleotide sequence (SEQ ID NO:1714) of a native sequence PRO85003 cDNA, wherein SEQ ID NO:1714 is a clone designated herein as "DNA329433".

Figure 1715 shows the amino acid sequence (SEQ ID NO:1715) derived from the coding sequence of SEQ ID NO:1714 shown in Figure 1714.

Figure 1716 shows a nucleotide sequence (SEQ ID NO:1716) of a native sequence PRO85004 cDNA, wherein SEQ ID NO:1716 is a clone designated herein as "DNA329434".

Figure 1717 shows the amino acid sequence (SEQ ID NO:1717) derived from the coding sequence of SEQ ID NO:1716 shown in Figure 1716.

Figure 1718 shows a nucleotide sequence (SEQ ID NO:1718) of a native sequence PRO52418 cDNA, wherein SEQ ID NO:1718 is a clone designated herein as "DNA257884".

Figure 1719 shows the amino acid sequence (SEQ ID NO:1719) derived from the coding sequence of SEQ ID NO:1718 shown in Figure 1718.

Figure 1720A-C shows a nucleotide sequence (SEQ ID NO:1720) of a native sequence PRO84288 cDNA, wherein SEQ ID NO:1720 is a clone designated herein as "DNA328462".

Figure 1721 shows the amino acid sequence (SEQ ID NO:1721) derived from the coding sequence of SEQ ID NO:1720 shown in Figure 1720

Figure 1722 shows a nucleotide sequence (SEQ ID NO:1722) of a native sequence PRO85005 cDNA, wherein SEQ ID NO:1722 is a clone designated herein as "DNA329435".

Figure 1723 shows the amino acid sequence (SEQ ID NO:1723) derived from the coding sequence of SEQ ID NO:1722 shown in Figure 1722.

Figure 1724A-B shows a nucleotide sequence (SEQ ID NO:1724) of a native sequence PRO85006 cDNA, wherein SEQ ID NO:1724 is a clone designated herein as "DNA329436".

Figure 1725 shows the amino acid sequence (SEQ ID NO:1725) derived from the coding sequence of SEQ ID NO:1724 shown in Figure 1724

Figure 1726 shows a nucleotide sequence (SEQ ID NO:1726) of a native sequence PRO85007 cDNA, wherein SEQ ID NO:1726 is a clone designated herein as "DNA329437".

Figure 1727 shows the amino acid sequence (SEQ ID NO:1727) derived from the coding sequence of SEQ ID NO:1726 shown in Figure 1726.

Figure 1728A-B shows a nucleotide sequence (SEQ ID NO:1728) of a native sequence PRO85008 cDNA, wherein SEQ ID NO:1728 is a clone designated herein as "DNA329438".

Figure 1729 shows the amino acid sequence (SEQ ID NO:1729) derived from the coding sequence of SEQ ID NO:1728 shown in Figure 1728.

Figure 1730 shows a nucleotide sequence (SEQ ID NO:1730) of a native sequence cDNA, wherein SEQ ID NO:1730 is a clone designated herein as "DNA329439".

Figure 1731 shows a nucleotide sequence (SEQ ID NO:1731) of a native sequence PRO12626 cDNA, wherein SEQ ID NO:1731 is a clone designated herein as "DNA151170".

Figure 1732 shows the amino acid sequence (SEQ ID NO:1732) derived from the coding sequence of SEQ ID NO:1731 shown in Figure 1731.

Figure 1733 shows a nucleotide sequence (SEQ ID NO:1733) of a native sequence PRO85009 cDNA, wherein SEQ ID NO:1733 is a clone designated herein as "DNA329440".

Figure 1734 shows the amino acid sequence (SEQ ID NO:1734) derived from the coding sequence of SEQ ID NO:1733 shown in Figure 1733

Figure 1735 shows a nucleotide sequence (SEQ ID NO:1735) of a native sequence PRO83963 cDNA, wherein SEQ ID NO:1735 is a clone designated herein as "DNA328049".

Figure 1736 shows the amino acid sequence (SEQ ID NO:1736) derived from the coding sequence of SEQ ID NO:1735 shown in Figure 1735

Figure 1737 shows a nucleotide sequence (SEQ ID NO:1737) of a native sequence PRO85010 cDNA, wherein SEQ ID NO:1737 is a clone designated herein as "DNA329441".

Figure 1738 shows the amino acid sequence (SEQ ID NO:1738) derived from the coding sequence of SEQ ID NO:1737 shown in Figure 1737.

Figure 1739 shows a nucleotide sequence (SEQ ID NO:1739) of a native sequence cDNA, wherein SEQ ID NO:1739 is a clone designated herein as "DNA329442".

Figure 1740 shows a nucleotide sequence (SEQ ID NO:1740) of a native sequence PRO85011 cDNA, wherein SEQ ID NO:1740 is a clone designated herein as "DNA329443".

Figure 1741 shows the amino acid sequence (SEQ ID NO:1741) derived from the coding sequence of SEQ ID NO:1740 shown in Figure 1740.

Figure 1742 shows a nucleotide sequence (SEQ ID NO:1742) of a native sequence PRO85012 cDNA, wherein SEQ ID NO:1742 is a clone designated herein as "DNA329444".

Figure 1743 shows the amino acid sequence (SEQ ID NO:1743) derived from the coding sequence of SEQ ID NO:1742 shown in Figure 1742.

Figure 1744 shows a nucleotide sequence (SEQ ID NO:1744) of a native sequence PRO85013 cDNA, wherein SEQ ID NO:1744 is a clone designated herein as "DNA329445".

Figure 1745 shows the amino acid sequence (SEQ ID NO:1745) derived from the coding sequence of SEQ ID NO:1744 shown in Figure 1744.

Figure 1746 shows a nucleotide sequence (SEQ ID NO:1746) of a native sequence PRO85014 cDNA, wherein SEQ ID NO:1746 is a clone designated herein as "DNA329446".

Figure 1747 shows the amino acid sequence (SEQ ID NO:1747) derived from the coding sequence of SEQ ID NO:1746 shown in Figure 1746.

Figure 1748 shows a nucleotide sequence (SEQ ID NO:1748) of a native sequence PRO61074 cDNA, wherein SEQ ID NO:1748 is a clone designated herein as "DNA273002".

Figure 1749 shows the amino acid sequence (SEQ ID NO:1749) derived from the coding sequence of SEQ ID NO:1748 shown in Figure 1748.

Figure 1750 shows a nucleotide sequence (SEQ ID NO:1750) of a native sequence PRO85015 cDNA, wherein SEQ ID NO:1750 is a clone designated herein as "DNA329447".

Figure 1751 shows the amino acid sequence (SEQ ID NO:1751) derived from the coding sequence of SEQ ID NO:1750 shown in Figure 1750.

Figure 1752A-B shows a nucleotide sequence (SEQ ID NO:1752) of a native sequence PRO83968 cDNA, wherein SEQ ID NO:1752 is a clone designated herein as "DNA328054".

Figure 1753 shows the amino acid sequence (SEQ ID NO:1753) derived from the coding sequence of SEQ ID NO:1752 shown in Figure 1752.

Figure 1754 shows a nucleotide sequence (SEQ ID NO:1754) of a native sequence PRO85016 cDNA, wherein SEQ ID NO:1754 is a clone designated herein as "DNA329448".

Figure 1755 shows the amino acid sequence (SEQ ID NO:1755) derived from the coding sequence of SEQ ID NO:1754 shown in Figure 1754.

Figure 1756 shows a nucleotide sequence (SEQ ID NO:1756) of a native sequence PRO85017 cDNA, wherein SEQ ID NO:1756 is a clone designated herein as "DNA329449".

Figure 1757 shows the amino acid sequence (SEQ ID NO:1757) derived from the coding sequence of SEQ ID NO:1756 shown in Figure 1756.

Figure 1758 shows a nucleotide sequence (SEQ ID NO:1758) of a native sequence cDNA, wherein SEQ ID NO:1758 is a clone designated herein as "DNA161163".

Figure 1759 shows a nucleotide sequence (SEQ ID NO:1759) of a native sequence PRO80483 cDNA, wherein SEQ ID NO:1759 is a clone designated herein as "DNA323723".

Figure 1760 shows the amino acid sequence (SEQ ID NO:1760) derived from the coding sequence of SEQ ID NO:1759 shown in Figure 1759.

Figure 1761 shows a nucleotide sequence (SEQ ID NO:1761) of a native sequence PRO85018 cDNA, wherein SEQ ID NO:1761 is a clone designated herein as "DNA329450".

Figure 1762 shows the amino acid sequence (SEQ ID NO:1762) derived from the coding sequence of SEQ ID NO:1761 shown in Figure 1761.

Figure 1763 shows a nucleotide sequence (SEQ ID NO:1763) of a native sequence PRO85019 cDNA, wherein SEQ ID NO:1763 is a clone designated herein as "DNA329451".

Figure 1764 shows the amino acid sequence (SEQ ID NO:1764) derived from the coding sequence of SEQ ID NO:1763 shown in Figure 1763.

Figure 1765 shows a nucleotide sequence (SEQ ID NO:1765) of a native sequence PRO85020 cDNA, wherein SEQ ID NO:1765 is a clone designated herein as "DNA329452".

Figure 1766 shows the amino acid sequence (SEQ ID NO:1766) derived from the coding sequence of SEQ ID NO:1765 shown in Figure 1765.

Figure 1767 shows a nucleotide sequence (SEQ ID NO:1767) of a native sequence cDNA, wherein SEQ ID NO:1767 is a clone designated herein as "DNA329453".

Figure 1768 shows a nucleotide sequence (SEQ ID NO:1768) of a native sequence PRO85022 cDNA, wherein SEQ ID NO:1768 is a clone designated herein as "DNA329454".

Figure 1769 shows the amino acid sequence (SEQ ID NO:1769) derived from the coding sequence of SEQ ID NO:1768 shown in Figure 1768.

Figure 1770 shows a nucleotide sequence (SEQ ID NO:1770) of a native sequence PRO82968 cDNA, wherein SEQ ID NO:1770 is a clone designated herein as "DNA329455".

Figure 1771 shows the amino acid sequence (SEQ ID NO:1771) derived from the coding sequence of SEQ ID NO:1771 shown in Figure

Figure 1772 shows a nucleotide sequence (SEQ ID NO:1772) of a native sequence PRO11849 cDNA, wherein SEQ ID NO:1772 is a clone designated herein as "DNA151503".

Figure 1773 shows the amino acid sequence (SEQ ID NO:1773) derived from the coding sequence of SEQ ID NO:1772 shown in Figure 1772.

Figure 1774 shows a nucleotide sequence (SEQ ID NO:1774) of a native sequence PRO85023 cDNA, wherein SEQ ID NO:1774 is a clone designated herein as "DNA329456".

Figure 1775 shows the amino acid sequence (SEQ ID NO:1775) derived from the coding sequence of SEQ ID NO:1774 shown in Figure 1774.

Figure 1776 shows a nucleotide sequence (SEQ ID NO:1776) of a native sequence PRO11901 cDNA, wherein SEQ ID NO:1776 is a clone designated herein as "DNA151580".

Figure 1777 shows the amino acid sequence (SEQ ID NO:1777) derived from the coding sequence of SEQ ID NO:1777 shown in Figure

Figure 1778 shows a nucleotide sequence (SEQ ID NO:1778) of a native sequence PRO85024 cDNA, wherein SEQ ID NO:1778 is a clone designated herein as "DNA329457".

Figure 1779 shows the amino acid sequence (SEQ ID NO:1779) derived from the coding sequence of SEQ ID NO:1778 shown in Figure 1778.

Figure 1780 shows a nucleotide sequence (SEQ ID NO:1780) of a native sequence PRO12397 cDNA, wherein SEQ ID NO:1780 is a clone designated herein as "DNA150660".

Figure 1781 shows the amino acid sequence (SEQ ID NO:1781) derived from the coding sequence of SEQ ID NO:1780 shown in Figure 1780.

Figure 1782 shows a nucleotide sequence (SEQ ID NO:1782) of a native sequence PRO85025 cDNA, wherein SEQ ID NO:1782 is a clone designated herein as "DNA329458".

Figure 1783 shows the amino acid sequence (SEQ ID NO:1783) derived from the coding sequence of SEQ ID NO:1782 shown in Figure 1782.

Figure 1784 shows a nucleotide sequence (SEQ ID NO:1784) of a native sequence PRO85026 cDNA, wherein SEQ ID NO:1784 is a clone designated herein as "DNA329459".

Figure 1785 shows the amino acid sequence (SEQ ID NO:1785) derived from the coding sequence of SEQ ID NO:1784 shown in Figure 1784.

Figure 1786 shows a nucleotide sequence (SEQ ID NO:1786) of a native sequence PRO85027 cDNA, wherein SEQ ID NO:1786 is a clone designated herein as "DNA329460".

Figure 1787 shows the amino acid sequence (SEQ ID NO:1787) derived from the coding sequence of SEQ ID NO:1786 shown in Figure 1786.

Figure 1788 shows a nucleotide sequence (SEQ ID NO:1788) of a native sequence PRO85028 cDNA, wherein SEQ ID NO:1788 is a clone designated herein as "DNA329461".

Figure 1789 shows the amino acid sequence (SEQ ID NO:1789) derived from the coding sequence of SEQ ID NO:1788 shown in Figure 1788.

Figure 1790 shows a nucleotide sequence (SEQ ID NO:1790) of a native sequence cDNA, wherein SEQ ID NO:1790 is a clone designated herein as "DNA153924".

Figure 1791 shows a nucleotide sequence (SEQ ID NO:1791) of a native sequence PRO37992 cDNA, wherein SEQ ID NO:1791 is a clone designated herein as "DNA227529".

Figure 1792 shows the amino acid sequence (SEQ ID NO:1792) derived from the coding sequence of SEQ ID NO:1791 shown in Figure 1791.

Figure 1793 shows a nucleotide sequence (SEQ ID NO:1793) of a native sequence cDNA, wherein SEQ ID NO:1793 is a clone designated herein as "DNA328074".

Figure 1794 shows a nucleotide sequence (SEQ ID NO:1794) of a native sequence PRO85029 cDNA, wherein SEQ ID NO:1794 is a clone designated herein as "DNA329462".

Figure 1795 shows the amino acid sequence (SEQ ID NO:1795) derived from the coding sequence of SEQ ID NO:1794 shown in Figure 1794.

Figure 1796 shows a nucleotide sequence (SEQ ID NO:1796) of a native sequence PRO85030 cDNA, wherein SEQ ID NO:1796 is a clone designated herein as "DNA329463".

Figure 1797 shows the amino acid sequence (SEQ ID NO:1797) derived from the coding sequence of SEQ ID NO:1797 shown in Figure

Figure 1798 shows a nucleotide sequence (SEQ ID NO:1798) of a native sequence PRO83994 cDNA, wherein SEQ ID NO:1798 is a clone designated herein as "DNA328082".

Figure 1799 shows the amino acid sequence (SEQ ID NO:1799) derived from the coding sequence of SEQ ID NO:1798 shown in Figure 1798.

Figure 1800 shows a nucleotide sequence (SEQ ID NO:1800) of a native sequence cDNA, wherein SEQ ID NO:1800 is a clone designated herein as "DNA260010".

Figure 1801 shows a nucleotide sequence (SEQ ID NO:1801) of a native sequence PRO85031 cDNA, wherein SEQ ID NO:1801 is a clone designated herein as "DNA329464".

Figure 1802 shows the amino acid sequence (SEQ ID NO:1802) derived from the coding sequence of SEQ ID NO:1801 shown in Figure 1801.

Figure 1803 shows a nucleotide sequence (SEQ ID NO:1803) of a native sequence cDNA, wherein SEQ ID NO:1803 is a clone designated herein as "DNA257575".

Figure 1804 shows a nucleotide sequence (SEQ ID NO:1804) of a native sequence PRO69678 cDNA, wherein SEQ ID NO:1804 is a clone designated herein as "DNA287421".

Figure 1805 shows the amino acid sequence (SEQ ID NO:1805) derived from the coding sequence of SEQ ID NO:1804 shown in Figure 1804.

Figure 1806 shows a nucleotide sequence (SEQ ID NO:1806) of a native sequence PRO84001 cDNA, wherein SEQ ID NO:1806 is a clone designated herein as "DNA328090".

Figure 1807 shows the amino acid sequence (SEQ ID NO:1807) derived from the coding sequence of SEQ ID NO:1806 shown in Figure 1806.

Figure 1808 shows a nucleotide sequence (SEQ ID NO:1808) of a native sequence PRO85032 cDNA, wherein SEQ ID NO:1808 is a clone designated herein as "DNA329465".

Figure 1809 shows the amino acid sequence (SEQ ID NO:1809) derived from the coding sequence of SEQ ID NO:1808 shown in Figure 1808.

Figure 1810 shows a nucleotide sequence (SEQ ID NO:1810) of a native sequence PRO83478 cDNA, wherein SEQ ID NO:1810 is a clone designated herein as "DNA327205".

Figure 1811 shows the amino acid sequence (SEQ ID NO:1811) derived from the coding sequence of SEQ ID NO:1810 shown in Figure 1810.

Figure 1812A-B shows a nucleotide sequence (SEQ ID NO:1812) of a native sequence PRO38448 cDNA, wherein SEQ ID NO:1812 is a clone designated herein as "DNA227985".

Figure 1813 shows the amino acid sequence (SEQ ID NO:1813) derived from the coding sequence of SEQ ID NO:1812 shown in Figure 1812.

Figure 1814 shows a nucleotide sequence (SEQ ID NO:1814) of a native sequence PRO84003 cDNA, wherein SEQ ID NO:1814 is a clone designated herein as "DNA328092".

Figure 1815 shows the amino acid sequence (SEQ ID NO:1815) derived from the coding sequence of SEQ ID NO:1814 shown in Figure 1814.

Figure 1816 shows a nucleotide sequence (SEQ ID NO:1816) of a native sequence PRO81900 cDNA, wherein SEQ ID NO:1816 is a clone designated herein as "DNA325363".

Figure 1817 shows the amino acid sequence (SEQ ID NO:1817) derived from the coding sequence of SEQ ID NO:1817 shown in Figure

Figure 1818 shows a nucleotide sequence (SEQ ID NO:1818) of a native sequence PRO23814 cDNA, wherein SEQ ID NO:1818 is a clone designated herein as "DNA329466".

Figure 1819 shows the amino acid sequence (SEQ ID NO:1819) derived from the coding sequence of SEQ ID NO:1818 shown in Figure 1818.

Figure 1820 shows a nucleotide sequence (SEQ ID NO:1820) of a native sequence PRO85033 cDNA, wherein SEQ ID NO:1820 is a clone designated herein as "DNA329467".

Figure 1821 shows the amino acid sequence (SEQ ID NO:1821) derived from the coding sequence of SEQ ID NO:1820 shown in Figure 1820.

Figure 1822 shows a nucleotide sequence (SEQ ID NO:1822) of a native sequence PRO88 cDNA, wherein SEQ ID NO:1822 is a clone designated herein as "DNA329468".

Figure 1823 shows the amino acid sequence (SEQ ID NO:1823) derived from the coding sequence of SEQ ID NO:1822 shown in Figure 1822.

Figure 1824A-B shows a nucleotide sequence (SEQ ID NO:1824) of a native sequence PRO24061 cDNA, wherein SEQ ID NO:1824 is a clone designated herein as "DNA194784".

Figure 1825 shows the amino acid sequence (SEQ ID NO:1825) derived from the coding sequence of SEQ ID NO:1824 shown in Figure 1824.

Figure 1826 shows a nucleotide sequence (SEQ ID NO:1826) of a native sequence PRO85034 cDNA, wherein SEQ ID NO:1826 is a clone designated herein as "DNA329469".

Figure 1827 shows the amino acid sequence (SEQ ID NO:1827) derived from the coding sequence of SEQ ID NO:1826 shown in Figure 1826.

Figure 1828 shows a nucleotide sequence (SEQ ID NO:1828) of a native sequence PRO85035 cDNA, wherein SEQ ID NO:1828 is a clone designated herein as "DNA329470".

Figure 1829 shows the amino acid sequence (SEQ ID NO:1829) derived from the coding sequence of SEQ ID NO:1828 shown in Figure 1828.

Figure 1830 shows a nucleotide sequence (SEQ ID NO:1830) of a native sequence PRO85036 cDNA, wherein SEQ ID NO:1830 is a clone designated herein as "DNA329471".

Figure 1831 shows the amino acid sequence (SEQ ID NO:1831) derived from the coding sequence of SEQ ID NO:1831 shown in Figure

Figure 1832 shows a nucleotide sequence (SEQ ID NO:1832) of a native sequence PRO85037 cDNA, wherein SEQ ID NO:1832 is a clone designated herein as "DNA329472".

Figure 1833 shows the amino acid sequence (SEQ ID NO:1833) derived from the coding sequence of SEQ ID NO:1832 shown in Figure 1832.

Figure 1834 shows a nucleotide sequence (SEQ ID NO:1834) of a native sequence cDNA, wherein SEQ ID NO:1834 is a clone designated herein as "DNA136927".

Figure 1835 shows a nucleotide sequence (SEQ ID NO:1835) of a native sequence PRO1265 cDNA, wherein SEQ ID NO:1835 is a clone designated herein as "DNA304827".

Figure 1836 shows the amino acid sequence (SEQ ID NO:1836) derived from the coding sequence of SEQ ID NO:1835 shown in Figure 1835.

Figure 1837 shows a nucleotide sequence (SEQ ID NO:1837) of a native sequence PRO85038 cDNA, wherein SEQ ID NO:1837 is a clone designated herein as "DNA329473".

Figure 1838 shows the amino acid sequence (SEQ ID NO:1838) derived from the coding sequence of SEQ ID NO:1837 shown in Figure 1837.

Figure 1839 shows a nucleotide sequence (SEQ ID NO:1839) of a native sequence cDNA, wherein SEQ ID NO:1839 is a clone designated herein as "DNA195707".

Figure 1840 shows a nucleotide sequence (SEQ ID NO:1840) of a native sequence PRO38893 cDNA, wherein SEQ ID NO: is a clone designated herein as "DNA329474".

Figure 1841 shows the amino acid sequence (SEQ ID NO:1841) derived from the coding sequence of SEQ ID NO:1840 shown in Figure 1840.

Figure 1842 shows a nucleotide sequence (SEQ ID NO:1842) of a native sequence PRO85039 cDNA, wherein SEQ ID NO:1842 is a clone designated herein as "DNA329475".

Figure 1843 shows the amino acid sequence (SEQ ID NO:1843) derived from the coding sequence of SEQ ID NO:1843 shown in Figure

Figure 1844A-B shows a nucleotide sequence (SEQ ID NO:1844) of a native sequence PRO85040 cDNA, wherein SEQ ID NO:1844 is a clone designated herein as "DNA329476".

Figure 1845 shows the amino acid sequence (SEQ ID NO:1845) derived from the coding sequence of SEQ ID NO:1845 shown in Figure

Figure 1846 shows a nucleotide sequence (SEQ ID NO:1846) of a native sequence PRO51137 cDNA, wherein SEQ ID NO:1846 is a clone designated herein as "DNA256087".

Figure 1847 shows the amino acid sequence (SEQ ID NO:1847) derived from the coding sequence of SEQ ID NO:1846 shown in Figure 1846.

Figure 1848A-B shows a nucleotide sequence (SEQ ID NO:1848) of a native sequence PRO85041 cDNA, wherein SEQ ID NO:1848 is a clone designated herein as "DNA329477".

Figure 1849 shows the amino acid sequence (SEQ ID NO:1849) derived from the coding sequence of SEQ ID NO:1848 shown in Figure 1848.

Figure 1850 shows a nucleotide sequence (SEQ ID NO:1850) of a native sequence PRO10720 cDNA, wherein SEQ ID NO:1850 is a clone designated herein as "DNA329478".

Figure 1851 shows the amino acid sequence (SEQ ID NO:1851) derived from the coding sequence of SEQ ID NO:1850 shown in Figure 1850.

Figure 1852 shows a nucleotide sequence (SEQ ID NO:1852) of a native sequence cDNA, wherein SEQ ID NO:1852 is a clone designated herein as "DNA329479".

Figure 1853A-B shows a nucleotide sequence (SEQ ID NO:1853) of a native sequence PRO85043 cDNA, wherein SEQ ID NO:1853 is a clone designated herein as "DNA329480".

Figure 1854 shows the amino acid sequence (SEQ ID NO:1854) derived from the coding sequence of SEQ ID NO:1853 shown in Figure 1853.

Figure 1855 shows a nucleotide sequence (SEQ ID NO:1855) of a native sequence PRO60949 cDNA, wherein SEQ ID NO:1855 is a clone designated herein as "DNA329481".

Figure 1856 shows the amino acid sequence (SEQ ID NO:1856) derived from the coding sequence of SEQ ID NO:1855 shown in Figure 1855.

Figure 1857 shows a nucleotide sequence (SEQ ID NO:1857) of a native sequence PRO85044 cDNA, wherein SEQ ID NO:1857 is a clone designated herein as "DNA329482".

Figure 1858 shows the amino acid sequence (SEQ ID NO:1858) derived from the coding sequence of SEQ ID NO:1857 shown in Figure 1857.

Figure 1859 shows a nucleotide sequence (SEQ ID NO:1859) of a native sequence PRO20110 cDNA, wherein SEQ ID NO:1859 is a clone designated herein as "DNA329483".

Figure 1860 shows the amino acid sequence (SEQ ID NO:1860) derived from the coding sequence of SEQ ID NO:1859 shown in Figure 1859.

Figure 1861 shows a nucleotide sequence (SEQ ID NO:1861) of a native sequence cDNA, wherein SEQ ID NO:1861 is a clone designated herein as "DNA329484".

Figure 1862A-B shows a nucleotide sequence (SEQ ID NO:1862) of a native sequence PRO85046 cDNA, wherein SEQ ID NO:1862 is a clone designated herein as "DNA329485".

Figure 1863 shows the amino acid sequence (SEQ ID NO:1863) derived from the coding sequence of SEQ ID NO:1862 shown in Figure 1862.

Figure 1864 shows a nucleotide sequence (SEQ ID NO:1864) of a native sequence PRO84051 cDNA, wherein SEQ ID NO:1864 is a clone designated herein as "DNA328146".

Figure 1865 shows the amino acid sequence (SEQ ID NO:1865) derived from the coding sequence of SEQ ID NO:1864 shown in Figure 1864.

Figure 1866 shows a nucleotide sequence (SEQ ID NO:1866) of a native sequence PRO85047 cDNA, wherein SEQ ID NO:1866 is a clone designated herein as "DNA329486".

Figure 1867 shows the amino acid sequence (SEQ ID NO:1867) derived from the coding sequence of SEQ ID NO:1866 shown in Figure 1866.

Figure 1868A-B shows a nucleotide sequence (SEQ ID NO:1868) of a native sequence PRO85048 cDNA, wherein SEQ ID NO:1868 is a clone designated herein as "DNA329487".

Figure 1869 shows the amino acid sequence (SEQ ID NO:1869) derived from the coding sequence of SEQ ID NO:1868 shown in Figure 1868

Figure 1870 shows a nucleotide sequence (SEQ ID NO:1870) of a native sequence PRO85049 cDNA, wherein SEQ ID NO:1870 is a clone designated herein as "DNA329488".

Figure 1871 shows the amino acid sequence (SEQ ID NO:1871) derived from the coding sequence of SEQ ID NO:1871 shown in Figure

Figure 1872 shows a nucleotide sequence (SEQ ID NO:1872) of a native sequence PRO85050 cDNA, wherein SEQ ID NO:1872 is a clone designated herein as "DNA329489".

Figure 1873 shows the amino acid sequence (SEQ ID NO:1873) derived from the coding sequence of SEQ ID NO:1872 shown in Figure 1872.

Figure 1874 shows a nucleotide sequence (SEQ ID NO:1874) of a native sequence PRO70016 cDNA, wherein SEQ ID NO:1874 is a clone designated herein as "DNA288255".

Figure 1875 shows the amino acid sequence (SEQ ID NO:1875) derived from the coding sequence of SEQ ID NO:1874 shown in Figure 1874.

Figure 1876 shows a nucleotide sequence (SEQ ID NO:1876) of a native sequence PRO85051 cDNA, wherein SEQ ID NO:1876 is a clone designated herein as "DNA329490".

Figure 1877 shows the amino acid sequence (SEQ ID NO:1877) derived from the coding sequence of SEQ ID NO:1876 shown in Figure 1876.

Figure 1878 shows a nucleotide sequence (SEQ ID NO:1878) of a native sequence cDNA, wherein SEQ ID NO:1878 is a clone designated herein as "DNA259903".

Figure 1879 shows a nucleotide sequence (SEQ ID NO:1879) of a native sequence cDNA, wherein SEQ ID NO:1879 is a clone designated herein as "DNA259749".

Figure 1880 shows a nucleotide sequence (SEQ ID NO:1880) of a native sequence PRO85052 cDNA, wherein SEQ ID NO:1880 is a clone designated herein as "DNA329491".

Figure 1881 shows the amino acid sequence (SEQ ID NO:1881) derived from the coding sequence of SEQ ID NO:1880 shown in Figure 1880.

Figure 1882 shows a nucleotide sequence (SEQ ID NO:1882) of a native sequence PRO85053 cDNA, wherein SEQ ID NO:1882 is a clone designated herein as "DNA329492".

Figure 1883 shows the amino acid sequence (SEQ ID NO:1883) derived from the coding sequence of SEQ ID NO:1882 shown in Figure 1882.

Figure 1884 shows a nucleotide sequence (SEQ ID NO:1884) of a native sequence PRO85054 cDNA, wherein SEQ ID NO:1884 is a clone designated herein as "DNA329493".

Figure 1885 shows the amino acid sequence (SEQ ID NO:1885) derived from the coding sequence of SEQ ID NO:1884 shown in Figure 1884.

Figure 1886A-B shows a nucleotide sequence (SEQ ID NO:1886) of a native sequence PRO85055 cDNA, wherein SEQ ID NO:1886 is a clone designated herein as "DNA329494".

Figure 1887 shows the amino acid sequence (SEQ ID NO:1887) derived from the coding sequence of SEQ ID NO:1886 shown in Figure 1886.

Figure 1888 shows a nucleotide sequence (SEQ ID NO:1888) of a native sequence PRO52486 cDNA, wherein SEQ ID NO:1888 is a clone designated herein as "DNA257959".

Figure 1889 shows the amino acid sequence (SEQ ID NO:1889) derived from the coding sequence of SEQ ID NO:1888 shown in Figure 1888.

Figure 1890 shows a nucleotide sequence (SEQ ID NO:1890) of a native sequence PRO85056 cDNA, wherein SEQ ID NO:1890 is a clone designated herein as "DNA329495".

Figure 1891 shows the amino acid sequence (SEQ ID NO:1891) derived from the coding sequence of SEQ ID NO:1890 shown in Figure 1890.

Figure 1892 shows a nucleotide sequence (SEQ ID NO:1892) of a native sequence PRO85057 cDNA, wherein SEQ ID NO:1892 is a clone designated herein as "DNA329496".

Figure 1893 shows the amino acid sequence (SEQ ID NO:1893) derived from the coding sequence of SEQ ID NO:1892 shown in Figure 1892.

Figure 1894 shows a nucleotide sequence (SEQ ID NO:1894) of a native sequence PRO85058 cDNA, wherein SEQ ID NO:1894 is a clone designated herein as "DNA329497".

Figure 1895 shows the amino acid sequence (SEQ ID NO:1895) derived from the coding sequence of SEQ ID NO:1894 shown in Figure 1894.

Figure 1896 shows a nucleotide sequence (SEQ ID NO:1896) of a native sequence PRO85059 cDNA, wherein SEQ ID NO:1896 is a clone designated herein as "DNA329498".

Figure 1897 shows the amino acid sequence (SEQ ID NO:1897) derived from the coding sequence of SEQ ID NO:1896 shown in Figure 1896.

Figure 1898A-B shows a nucleotide sequence (SEQ ID NO:1898) of a native sequence PRO85060 cDNA, wherein SEQ ID NO:1898 is a clone designated herein as "DNA329499".

Figure 1899 shows the amino acid sequence (SEQ ID NO:1899) derived from the coding sequence of SEQ ID NO:1898 shown in Figure 1898.

Figure 1900 shows a nucleotide sequence (SEQ ID NO:1900) of a native sequence PRO85061 cDNA, wherein SEQ ID NO:1900 is a clone designated herein as "DNA329500".

Figure 1901 shows the amino acid sequence (SEQ ID NO:1901) derived from the coding sequence of SEQ ID NO:1900 shown in Figure 1900.

Figure 1902 shows a nucleotide sequence (SEQ ID NO:1902) of a native sequence PRO85062 cDNA, wherein SEQ ID NO:1902 is a clone designated herein as "DNA329501".

Figure 1903 shows the amino acid sequence (SEQ ID NO:1903) derived from the coding sequence of SEQ ID NO:1902 shown in Figure 1902.

Figure 1904 shows a nucleotide sequence (SEQ ID NO:1904) of a native sequence PRO85063 cDNA, wherein SEQ ID NO:1904 is a clone designated herein as "DNA329502".

Figure 1905 shows the amino acid sequence (SEQ ID NO:1905) derived from the coding sequence of SEQ ID NO:1904 shown in Figure 1904.

Figure 1906A-B shows a nucleotide sequence (SEQ ID NO:1906) of a native sequence cDNA, wherein SEQ ID NO:1906 is a clone designated herein as "DNA329503".

Figure 1907 shows a nucleotide sequence (SEQ ID NO:1907) of a native sequence PRO69635 cDNA, wherein SEQ ID NO:1907 is a clone designated herein as "DNA325417".

Figure 1908 shows the amino acid sequence (SEQ ID NO:1908) derived from the coding sequence of SEQ ID NO:1907 shown in Figure 1907.

Figure 1909 shows a nucleotide sequence (SEQ ID NO:1909) of a native sequence PRO85065 cDNA, wherein SEQ ID NO:1909 is a clone designated herein as "DNA329504".

Figure 1910 shows the amino acid sequence (SEQ ID NO:1910) derived from the coding sequence of SEQ ID NO:1909 shown in Figure 1909.

Figure 1911 shows a nucleotide sequence (SEQ ID NO:1911) of a native sequence cDNA, wherein SEQ ID NO:1911 is a clone designated herein as "DNA329505".

Figure 1912 shows a nucleotide sequence (SEQ ID NO:1912) of a native sequence PRO85067 cDNA, wherein SEQ ID NO:1912 is a clone designated herein as "DNA329506".

Figure 1913 shows the amino acid sequence (SEQ ID NO:1913) derived from the coding sequence of SEQ ID NO:1912 shown in Figure 1912.

Figure 1914 shows a nucleotide sequence (SEQ ID NO:1914) of a native sequence PRO85068 cDNA, wherein SEQ ID NO:1914 is a clone designated herein as "DNA329507".

Figure 1915 shows the amino acid sequence (SEQ ID NO:1915) derived from the coding sequence of SEQ ID NO:1914 shown in Figure 1914.

Figure 1916A-B shows a nucleotide sequence (SEQ ID NO:1916) of a native sequence PRO85069 cDNA, wherein SEQ ID NO:1916 is a clone designated herein as "DNA329508".

Figure 1917 shows the amino acid sequence (SEQ ID NO:1917) derived from the coding sequence of SEQ ID NO:1916 shown in Figure 1916.

Figure 1918 shows a nucleotide sequence (SEQ ID NO:1918) of a native sequence PRO85070 cDNA, wherein SEQ ID NO:1918 is a clone designated herein as "DNA329509".

Figure 1919 shows the amino acid sequence (SEQ ID NO:1919) derived from the coding sequence of SEQ ID NO:1918 shown in Figure 1918.

Figure 1920A-B shows a nucleotide sequence (SEQ ID NO:1920) of a native sequence cDNA, wherein SEQ ID NO:1920 is a clone designated herein as "DNA258863".

Figure 1921 shows a nucleotide sequence (SEQ ID NO:1921) of a native sequence PRO85071 cDNA, wherein SEQ ID NO:1921 is a clone designated herein as "DNA329510".

Figure 1922 shows the amino acid sequence (SEQ ID NO:1922) derived from the coding sequence of SEQ ID NO:1921 shown in Figure 1921.

Figure 1923 shows a nucleotide sequence (SEQ ID NO:1923) of a native sequence PRO23576 cDNA, wherein SEQ ID NO:1923 is a clone designated herein as "DNA194184".

Figure 1924 shows the amino acid sequence (SEQ ID NO:1924) derived from the coding sequence of SEQ ID NO:1923 shown in Figure 1923.

Figure 1925 shows a nucleotide sequence (SEQ ID NO:1925) of a native sequence PRO85072 cDNA, wherein SEQ ID NO:1925 is a clone designated herein as "DNA329511".

Figure 1926 shows the amino acid sequence (SEQ ID NO:1926) derived from the coding sequence of SEQ ID NO:1925 shown in Figure 1925.

Figure 1927 shows a nucleotide sequence (SEQ ID NO:1927) of a native sequence PRO84141 cDNA, wherein SEQ ID NO:1927 is a clone designated herein as "DNA328238".

Figure 1928 shows the amino acid sequence (SEQ ID NO:1928) derived from the coding sequence of SEQ ID NO:1927 shown in Figure 1927.

Figure 1929 shows a nucleotide sequence (SEQ ID NO:1929) of a native sequence PRO85073 cDNA, wherein SEQ ID NO:1929 is a clone designated herein as "DNA329512".

Figure 1930 shows the amino acid sequence (SEQ ID NO:1930) derived from the coding sequence of SEQ ID NO:1929 shown in Figure 1929.

Figure 1931 shows a nucleotide sequence (SEQ ID NO:1931) of a native sequence PRO85074 cDNA, wherein SEQ ID NO:1931 is a clone designated herein as "DNA329513".

Figure 1932 shows the amino acid sequence (SEQ ID NO:1932) derived from the coding sequence of SEQ ID NO:1931 shown in Figure 1931.

Figure 1933 shows a nucleotide sequence (SEQ ID NO:1933) of a native sequence PRO85075 cDNA, wherein SEQ ID NO:1933 is a clone designated herein as "DNA329514".

Figure 1934 shows the amino acid sequence (SEQ ID NO:1934) derived from the coding sequence of SEQ ID NO:1933 shown in Figure 1933.

Figure 1935 shows a nucleotide sequence (SEQ ID NO:1935) of a native sequence PRO4404 cDNA, wherein SEQ ID NO:1935 is a clone designated herein as "DNA84142".

Figure 1936 shows the amino acid sequence (SEQ ID NO:1936) derived from the coding sequence of SEQ ID NO:1935 shown in Figure 1935.

Figure 1937 shows a nucleotide sequence (SEQ ID NO:1937) of a native sequence PRO4348 cDNA, wherein SEQ ID NO:1937 is a clone designated herein as "DNA325654".

Figure 1938 shows the amino acid sequence (SEQ ID NO:1938) derived from the coding sequence of SEQ ID NO:1937 shown in Figure 1937.

Figure 1939 shows a nucleotide sequence (SEQ ID NO:1939) of a native sequence PRO4347 cDNA, wherein SEQ ID NO:1939 is a clone designated herein as "DNA329515".

Figure 1940 shows the amino acid sequence (SEQ ID NO:1940) derived from the coding sequence of SEQ ID NO:1940 shown in Figure

Figure 1941 shows a nucleotide sequence (SEQ ID NO:1941) of a native sequence PRO220 cDNA, wherein SEQ ID NO:1941 is a clone designated herein as "DNA329516".

Figure 1942 shows the amino acid sequence (SEQ ID NO:1942) derived from the coding sequence of SEQ ID NO:1941 shown in Figure 1941.

Figure 1943 shows a nucleotide sequence (SEQ ID NO:1943) of a native sequence PRO85076 cDNA, wherein SEQ ID NO:1943 is a clone designated herein as "DNA329517".

Figure 1944 shows the amino acid sequence (SEQ ID NO:1944) derived from the coding sequence of SEQ ID NO:1943 shown in Figure 1943.

Figure 1945 shows a nucleotide sequence (SEQ ID NO:1945) of a native sequence PRO329 cDNA, wherein SEQ ID NO:1945 is a clone designated herein as "DNA323978".

Figure 1946 shows the amino acid sequence (SEQ ID NO:1946) derived from the coding sequence of SEQ ID NO:1945 shown in Figure 1945.

Figure 1947 shows a nucleotide sequence (SEQ ID NO:1947) of a native sequence PRO85077 cDNA, wherein SEQ ID NO:1947 is a clone designated herein as "DNA329518".

Figure 1948 shows the amino acid sequence (SEQ ID NO:1948) derived from the coding sequence of SEQ ID NO:1947 shown in Figure 1947.

Figure 1949 shows a nucleotide sequence (SEQ ID NO:1949) of a native sequence PRO38838 cDNA, wherein SEQ ID NO:1949 is a clone designated herein as "DNA233283".

Figure 1950 shows the amino acid sequence (SEQ ID NO:1950) derived from the coding sequence of SEQ ID NO:1949 shown in Figure 1949.

Figure 1951 shows a nucleotide sequence (SEQ ID NO:1951) of a native sequence PRO941 cDNA, wherein SEQ ID NO:1951 is a clone designated herein as "DNA329519".

Figure 1952 shows the amino acid sequence (SEQ ID NO:1952) derived from the coding sequence of SEQ ID NO:1951 shown in Figure 1951.

Figure 1953 shows a nucleotide sequence (SEQ ID NO:1953) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:1953 is a clone designated herein as "DNA58853".

Figure 1954 shows the amino acid sequence (SEQ ID NO:1954) derived from the coding sequence of SEQ ID NO:1954 shown in Figure

Figure 1955 shows a nucleotide sequence (SEQ ID NO:1955) of a native sequence PRO85078 cDNA, wherein SEQ ID NO:1955 is a clone designated herein as "DNA329520".

Figure 1956 shows the amino acid sequence (SEQ ID NO:1956) derived from the coding sequence of SEQ ID NO:1955 shown in Figure 1955.

Figure 1957 shows a nucleotide sequence (SEQ ID NO:1957) of a native sequence PRO6517 cDNA, wherein SEQ ID NO:1957 is a clone designated herein as "DNA109234".

Figure 1958 shows the amino acid sequence (SEQ ID NO:1958) derived from the coding sequence of SEQ ID NO:1957 shown in Figure 1957.

Figure 1959 shows a nucleotide sequence (SEQ ID NO:1959) of a native sequence PRO85079 cDNA, wherein SEQ ID NO:1959 is a clone designated herein as "DNA329521".

Figure 1960 shows the amino acid sequence (SEQ ID NO:1960) derived from the coding sequence of SEQ ID NO:1959 shown in Figure 1959.

Figure 1961 shows a nucleotide sequence (SEQ ID NO:1961) of a native sequence PRO12810 cDNA, wherein SEQ ID NO:1961 is a clone designated herein as "DNA150823".

Figure 1962 shows the amino acid sequence (SEQ ID NO:1962) derived from the coding sequence of SEQ ID NO:1961 shown in Figure 1961.

Figure 1963A-B shows a nucleotide sequence (SEQ ID NO:1963) of a native sequence PRO2598 cDNA, wherein SEQ ID NO:1963 is a clone designated herein as "DNA83118".

Figure 1964 shows the amino acid sequence (SEQ ID NO:1964) derived from the coding sequence of SEQ ID NO:1963 shown in Figure 1963.

Figure 1965 shows a nucleotide sequence (SEQ ID NO:1965) of a native sequence PRO2844 cDNA, wherein SEQ ID NO:1965 is a clone designated herein as "DNA88567".

Figure 1966 shows the amino acid sequence (SEQ ID NO:1966) derived from the coding sequence of SEQ ID NO:1965 shown in Figure 1965.

Figure 1967 shows a nucleotide sequence (SEQ ID NO:1967) of a native sequence PRO2852 cDNA, wherein SEQ ID NO:1967 is a clone designated herein as "DNA88583".

Figure 1968 shows the amino acid sequence (SEQ ID NO:1968) derived from the coding sequence of SEQ ID NO:1967 shown in Figure 1967.

Figure 1969 shows a nucleotide sequence (SEQ ID NO:1969) of a native sequence PRO24845 cDNA, wherein SEQ ID NO:1969 is a clone designated herein as "DNA196337".

Figure 1970 shows the amino acid sequence (SEQ ID NO:1970) derived from the coding sequence of SEQ ID NO:1969 shown in Figure 1969.

Figure 1971 shows a nucleotide sequence (SEQ ID NO:1971) of a native sequence PRO85080 cDNA, wherein SEQ ID NO:1971 is a clone designated herein as "DNA329522".

Figure 1972 shows the amino acid sequence (SEQ ID NO:1972) derived from the coding sequence of SEQ ID NO:1971 shown in Figure 1971.

Figure 1973 shows a nucleotide sequence (SEQ ID NO:1973) of a native sequence PRO2155 cDNA, wherein SEQ ID NO:1973 is a clone designated herein as "DNA329523".

Figure 1974 shows the amino acid sequence (SEQ ID NO:1974) derived from the coding sequence of SEQ ID NO:1973 shown in Figure 1973.

Figure 1975 shows a nucleotide sequence (SEQ ID NO:1975) of a native sequence PRO36996 cDNA, wherein SEQ ID NO:1975 is a clone designated herein as "DNA329524".

Figure 1976 shows the amino acid sequence (SEQ ID NO:1976) derived from the coding sequence of SEQ ID NO:1975 shown in Figure 1975.

Figure 1977 shows a nucleotide sequence (SEQ ID NO:1977) of a native sequence PRO2663 cDNA, wherein SEQ ID NO:1977 is a clone designated herein as "DNA88119".

Figure 1978 shows the amino acid sequence (SEQ ID NO:1978) derived from the coding sequence of SEQ ID NO:1977 shown in Figure 1977.

Figure 1979 shows a nucleotide sequence (SEQ ID NO:1979) of a native sequence PRO21942 cDNA, wherein SEQ ID NO:1979 is a clone designated herein as "DNA188234".

Figure 1980 shows the amino acid sequence (SEQ ID NO:1980) derived from the coding sequence of SEQ ID NO:1979 shown in Figure 1979.

Figure 1981 shows a nucleotide sequence (SEQ ID NO:1981) of a native sequence PRO36456 cDNA, wherein SEQ ID NO:1981 is a clone designated herein as "DNA225993".

Figure 1982 shows the amino acid sequence (SEQ ID NO:1982) derived from the coding sequence of SEQ ID NO:1981 shown in Figure 1981.

Figure 1983 shows a nucleotide sequence (SEQ ID NO:1983) of a native sequence PRO2590 cDNA, wherein SEQ ID NO:1983 is a clone designated herein as "DNA83101".

Figure 1984 shows the amino acid sequence (SEQ ID NO:1984) derived from the coding sequence of SEQ ID NO:1983 shown in Figure 1983.

Figure 1985 shows a nucleotide sequence (SEQ ID NO:1985) of a native sequence PRO69 cDNA, wherein SEQ ID NO:1985 is a clone designated herein as "DNA36714".

Figure 1986 shows the amino acid sequence (SEQ ID NO:1986) derived from the coding sequence of SEQ ID NO:1985 shown in Figure 1985.

Figure 1987 shows a nucleotide sequence (SEQ ID NO:1987) of a native sequence PRO36659 cDNA, wherein SEQ ID NO:1987 is a clone designated herein as "DNA226196".

Figure 1988 shows the amino acid sequence (SEQ ID NO:1988) derived from the coding sequence of SEQ ID NO:1987 shown in Figure 1987.

Figure 1989 shows a nucleotide sequence (SEQ ID NO:1989) of a native sequence PRO20139 cDNA, wherein SEQ ID NO:1989 is a clone designated herein as "DNA246375".

Figure 1990 shows the amino acid sequence (SEQ ID NO:1990) derived from the coding sequence of SEQ ID NO:1989 shown in Figure 1989.

Figure 1991 shows a nucleotide sequence (SEQ ID NO:1991) of a native sequence PRO2691 cDNA, wherein SEQ ID NO:1991 is a clone designated herein as "DNA88191".

Figure 1992 shows the amino acid sequence (SEQ ID NO:1992) derived from the coding sequence of SEQ ID NO:1991 shown in Figure 1991.

Figure 1993 shows a nucleotide sequence (SEQ ID NO:1993) of a native sequence PRO85081 cDNA, wherein SEQ ID NO:1993 is a clone designated herein as "DNA329525".

Figure 1994 shows the amino acid sequence (SEQ ID NO:1994) derived from the coding sequence of SEQ ID NO:1993 shown in Figure 1993.

Figure 1995 shows a nucleotide sequence (SEQ ID NO:1995) of a native sequence PRO4940 cDNA, wherein SEQ ID NO:1995 is a clone designated herein as "DNA328576".

Figure 1996 shows the amino acid sequence (SEQ ID NO:1996) derived from the coding sequence of SEQ ID NO:1995 shown in Figure 1995.

Figure 1997 shows a nucleotide sequence (SEQ ID NO:1997) of a native sequence PRO37421 cDNA, wherein SEQ ID NO:1997 is a clone designated herein as "DNA226958".

Figure 1998 shows the amino acid sequence (SEQ ID NO:1998) derived from the coding sequence of SEQ ID NO:1997 shown in Figure 1997.

Figure 1999 shows a nucleotide sequence (SEQ ID NO:1999) of a native sequence PRO81141 cDNA, wherein SEQ ID NO:1999 is a clone designated herein as "DNA324480".

Figure 2000 shows the amino acid sequence (SEQ ID NO:2000) derived from the coding sequence of SEQ ID NO:1999 shown in Figure 1999.

Figure 2001 shows a nucleotide sequence (SEQ ID NO:2001) of a native sequence PRO1718 cDNA, wherein SEQ ID NO:2001 is a clone designated herein as "DNA82362".

Figure 2002 shows the amino acid sequence (SEQ ID NO:2002) derived from the coding sequence of SEQ ID NO:2001 shown in Figure 2001.

Figure 2003 shows a nucleotide sequence (SEQ ID NO:2003) of a native sequence PRO37476 cDNA, wherein SEQ ID NO:2003 is a clone designated herein as "DNA227013".

Figure 2004 shows the amino acid sequence (SEQ ID NO:2004) derived from the coding sequence of SEQ ID NO:2003 shown in Figure 2003.

Figure 2005A-B shows a nucleotide sequence (SEQ ID NO:2005) of a native sequence PRO36827 cDNA, wherein SEQ ID NO:2005 is a clone designated herein as "DNA226364".

Figure 2006 shows the amino acid sequence (SEQ ID NO:2006) derived from the coding sequence of SEQ ID NO:2005 shown in Figure 2005.

Figure 2007 shows a nucleotide sequence (SEQ ID NO:2007) of a native sequence PRO2640 cDNA, wherein SEQ ID NO:2007 is a clone designated herein as "DNA88076".

Figure 2008 shows the amino acid sequence (SEQ ID NO:2008) derived from the coding sequence of SEQ ID NO:2007 shown in Figure 2007.

Figure 2009 shows a nucleotide sequence (SEQ ID NO:2009) of a native sequence PRO2013 cDNA, wherein SEQ ID NO:2009 is a clone designated herein as "DNA75526".

Figure 2010 shows the amino acid sequence (SEQ ID NO:2010) derived from the coding sequence of SEQ ID NO:2009 shown in Figure 2009.

Figure 2011 shows a nucleotide sequence (SEQ ID NO:2011) of a native sequence PRO2177 cDNA, wherein SEQ ID NO:2011 is a clone designated herein as "DNA88116".

Figure 2012 shows the amino acid sequence (SEQ ID NO:2012) derived from the coding sequence of SEQ ID NO:2011 shown in Figure 2011.

Figure 2013 shows a nucleotide sequence (SEQ ID NO:2013) of a native sequence PRO4695 cDNA, wherein SEQ ID NO:2013 is a clone designated herein as "DNA226380".

Figure 2014 shows the amino acid sequence (SEQ ID NO:2014) derived from the coding sequence of SEQ ID NO:2013 shown in Figure 2013.

Figure 2015 shows a nucleotide sequence (SEQ ID NO:2015) of a native sequence PRO80473 cDNA, wherein SEQ ID NO:2015 is a clone designated herein as "DNA329526".

Figure 2016 shows the amino acid sequence (SEQ ID NO:2016) derived from the coding sequence of SEQ ID NO:2015 shown in Figure 2015.

Figure 2017A-B shows a nucleotide sequence (SEQ ID NO:2017) of a native sequence PRO2249 cDNA, wherein SEQ ID NO:2017 is a clone designated herein as "DNA88251".

Figure 2018 shows the amino acid sequence (SEQ ID NO:2018) derived from the coding sequence of SEQ ID NO:2017 shown in Figure 2017.

Figure 2019A-B shows a nucleotide sequence (SEQ ID NO:2019) of a native sequence PRO25018 cDNA, wherein SEQ ID NO:2019 is a clone designated herein as "DNA196533".

Figure 2020 shows the amino acid sequence (SEQ ID NO:2020) derived from the coding sequence of SEQ ID NO:2019 shown in Figure 2019.

Figure 2021 shows a nucleotide sequence (SEQ ID NO:2021) of a native sequence PRO36124 cDNA, wherein SEQ ID NO:2021 is a clone designated herein as "DNA225661".

Figure 2022 shows the amino acid sequence (SEQ ID NO:2022) derived from the coding sequence of SEQ ID NO:2021 shown in Figure 2021.

Figure 2023 shows a nucleotide sequence (SEQ ID NO:2023) of a native sequence PRO2868 cDNA, wherein SEQ ID NO:2023 is a clone designated herein as "DNA329527".

Figure 2024 shows the amino acid sequence (SEQ ID NO:2024) derived from the coding sequence of SEQ ID NO:2023 shown in Figure 2023.

Figure 2025 shows a nucleotide sequence (SEQ ID NO:2025) of a native sequence PRO85082 cDNA, wherein SEQ ID NO:2025 is a clone designated herein as "DNA329528".

Figure 2026 shows the amino acid sequence (SEQ ID NO:2026) derived from the coding sequence of SEQ ID NO:2025 shown in Figure 2025.

Figure 2027 shows a nucleotide sequence (SEQ ID NO:2027) of a native sequence PRO85083 cDNA, wherein SEQ ID NO:2027 is a clone designated herein as "DNA329529".

Figure 2028 shows the amino acid sequence (SEQ ID NO:2028) derived from the coding sequence of SEQ ID NO:2028 shown in Figure

Figure 2029 shows a nucleotide sequence (SEQ ID NO:2029) of a native sequence PRO82739 cDNA, wherein SEQ ID NO:2029 is a clone designated herein as "DNA326343".

Figure 2030 shows the amino acid sequence (SEQ ID NO:2030) derived from the coding sequence of SEQ ID NO:2029 shown in Figure 2029.

Figure 2031 shows a nucleotide sequence (SEQ ID NO:2031) of a native sequence PRO2809 cDNA, wherein SEQ ID NO:2031 is a clone designated herein as "DNA88472".

Figure 2032 shows the amino acid sequence (SEQ ID NO:2032) derived from the coding sequence of SEQ ID NO:2031 shown in Figure 2031.

Figure 2033 shows a nucleotide sequence (SEQ ID NO:2033) of a native sequence PRO11604 cDNA, wherein SEQ ID NO:2033 is a clone designated herein as "DNA329530".

Figure 2034 shows the amino acid sequence (SEQ ID NO:2034) derived from the coding sequence of SEQ ID NO:2033 shown in Figure 2033.

Figure 2035 shows a nucleotide sequence (SEQ ID NO:2035) of a native sequence PRO12452 cDNA, wherein SEQ ID NO:2035 is a clone designated herein as "DNA150757".

Figure 2036 shows the amino acid sequence (SEQ ID NO:2036) derived from the coding sequence of SEQ ID NO:2035 shown in Figure 2035.

Figure 2037 shows a nucleotide sequence (SEQ ID NO:2037) of a native sequence PRO21783 cDNA, wherein SEQ ID NO:2037 is a clone designated herein as "DNA188330".

Figure 2038 shows the amino acid sequence (SEQ ID NO:2038) derived from the coding sequence of SEQ ID NO:2037 shown in Figure 2037.

Figure 2039 shows a nucleotide sequence (SEQ ID NO:2039) of a native sequence PRO84151 cDNA, wherein SEQ ID NO:2039 is a clone designated herein as "DNA328258".

Figure 2040 shows the amino acid sequence (SEQ ID NO:2040) derived from the coding sequence of SEQ ID NO:2039 shown in Figure 2039.

Figure 2041 shows a nucleotide sequence (SEQ ID NO:2041) of a native sequence PRO85084 cDNA, wherein SEQ ID NO:2041 is a clone designated herein as "DNA329531".

Figure 2042 shows the amino acid sequence (SEQ ID NO:2042) derived from the coding sequence of SEQ ID NO:2041 shown in Figure 2041.

Figure 2043 shows a nucleotide sequence (SEQ ID NO:2043) of a native sequence PRO37029 cDNA, wherein SEQ ID NO:2043 is a clone designated herein as "DNA329007".

Figure 2044 shows the amino acid sequence (SEQ ID NO:2044) derived from the coding sequence of SEQ ID NO:2043 shown in Figure 2043.

Figure 2045 shows a nucleotide sequence (SEQ ID NO:2045) of a native sequence PRO36606 cDNA, wherein SEQ ID NO:2045 is a clone designated herein as "DNA226143".

Figure 2046 shows the amino acid sequence (SEQ ID NO:2046) derived from the coding sequence of SEQ ID NO:2045 shown in Figure 2045.

Figure 2047 shows a nucleotide sequence (SEQ ID NO:2047) of a native sequence PRO24862 cDNA, wherein SEQ ID NO:2047 is a clone designated herein as "DNA196357".

Figure 2048 shows the amino acid sequence (SEQ ID NO:2048) derived from the coding sequence of SEQ ID NO:2047 shown in Figure 2047.

Figure 2049A-B shows a nucleotide sequence (SEQ ID NO:2049) of a native sequence PRO37968 cDNA, wherein SEQ ID NO:2049 is a clone designated herein as "DNA227505".

Figure 2050 shows the amino acid sequence (SEQ ID NO:2050) derived from the coding sequence of SEQ ID NO:2049 shown in Figure 2049.

Figure 2051 shows a nucleotide sequence (SEQ ID NO:2051) of a native sequence PRO12658 cDNA, wherein SEQ ID NO:2051 is a clone designated herein as "DNA329532".

Figure 2052 shows the amino acid sequence (SEQ ID NO:2052) derived from the coding sequence of SEQ ID NO:2051 shown in Figure 2051.

Figure 2053 shows a nucleotide sequence (SEQ ID NO:2053) of a native sequence PRO85085 cDNA, wherein SEQ ID NO:2053 is a clone designated herein as "DNA329533".

Figure 2054 shows the amino acid sequence (SEQ ID NO:2054) derived from the coding sequence of SEQ ID NO:2053 shown in Figure 2053.

Figure 2055A-B shows a nucleotide sequence (SEQ ID NO:2055) of a native sequence PRO36420 cDNA, wherein SEQ ID NO:2055 is a clone designated herein as "DNA225957".

Figure 2056 shows the amino acid sequence (SEQ ID NO:2056) derived from the coding sequence of SEQ ID NO:2055 shown in Figure 2055.

Figure 2057 shows a nucleotide sequence (SEQ ID NO:2057) of a native sequence PRO84153 cDNA, wherein SEQ ID NO:2057 is a clone designated herein as "DNA328262".

Figure 2058 shows the amino acid sequence (SEQ ID NO:2058) derived from the coding sequence of SEQ ID NO:2057 shown in Figure 2057.

Figure 2059 shows a nucleotide sequence (SEQ ID NO:2059) of a native sequence PRO2904 cDNA, wherein SEQ ID NO:2059 is a clone designated herein as "DNA329534".

Figure 2060 shows the amino acid sequence (SEQ ID NO:2060) derived from the coding sequence of SEQ ID NO:2059 shown in Figure 2059.

Figure 2061 shows a nucleotide sequence (SEQ ID NO:2061) of a native sequence PRO85086 cDNA, wherein SEQ ID NO:2061 is a clone designated herein as "DNA329535".

Figure 2062 shows the amino acid sequence (SEQ ID NO:2062) derived from the coding sequence of SEQ ID NO:2061 shown in Figure 2061.

Figure 2063 shows a nucleotide sequence (SEQ ID NO:2063) of a native sequence PRO2733 cDNA, wherein SEQ ID NO:2063 is a clone designated herein as "DNA325039".

Figure 2064 shows the amino acid sequence (SEQ ID NO:2064) derived from the coding sequence of SEQ ID NO:2063 shown in Figure 2063.

Figure 2065 shows a nucleotide sequence (SEQ ID NO:2065) of a native sequence PRO23370 cDNA, wherein SEQ ID NO:2065 is a clone designated herein as "DNA329010".

Figure 2066 shows the amino acid sequence (SEQ ID NO:2066) derived from the coding sequence of SEQ ID NO:2065 shown in Figure 2065.

Figure 2067 shows a nucleotide sequence (SEQ ID NO:2067) of a native sequence PRO2602 cDNA, wherein SEQ ID NO:2067 is a clone designated herein as "DNA83134".

Figure 2068 shows the amino acid sequence (SEQ ID NO:2068) derived from the coding sequence of SEQ ID NO:2067 shown in Figure 2067.

Figure 2069 shows a nucleotide sequence (SEQ ID NO:2069) of a native sequence PRO4599 cDNA, wherein SEQ ID NO:2069 is a clone designated herein as "DNA103269".

Figure 2070 shows the amino acid sequence (SEQ ID NO:2070) derived from the coding sequence of SEQ ID NO:2069 shown in Figure 2069.

Figure 2071A-B shows a nucleotide sequence (SEQ ID NO:2071) of a native sequence PRO22775 cDNA, wherein SEQ ID NO:2071 is a clone designated herein as "DNA329536".

Figure 2072 shows the amino acid sequence (SEQ ID NO:2072) derived from the coding sequence of SEQ ID NO:2072 shown in Figure 2072.

Figure 2073 shows a nucleotide sequence (SEQ ID NO:2073) of a native sequence PRO85087 cDNA, wherein SEQ ID NO:2073 is a clone designated herein as "DNA329537".

Figure 2074 shows the amino acid sequence (SEQ ID NO:2074) derived from the coding sequence of SEQ ID NO:2073 shown in Figure 2073.

Figure 2075 shows a nucleotide sequence (SEQ ID NO:2075) of a native sequence PRO36963 cDNA, wherein SEQ ID NO:2075 is a clone designated herein as "DNA226500".

Figure 2076 shows the amino acid sequence (SEQ ID NO:2076) derived from the coding sequence of SEQ ID NO:2075 shown in Figure 2075.

Figure 2077 shows a nucleotide sequence (SEQ ID NO:2077) of a native sequence PRO20128 cDNA, wherein SEQ ID NO:2077 is a clone designated herein as "DNA329013".

Figure 2078 shows the amino acid sequence (SEQ ID NO:2078) derived from the coding sequence of SEQ ID NO:2077 shown in Figure 2077.

Figure 2079 shows a nucleotide sequence (SEQ ID NO:2079) of a native sequence PRO38443 cDNA, wherein SEQ ID NO:2079 is a clone designated herein as "DNA227980".

Figure 2080 shows the amino acid sequence (SEQ ID NO:2080) derived from the coding sequence of SEQ ID NO:2079 shown in Figure 2079.

Figure 2081 shows a nucleotide sequence (SEQ ID NO:2081) of a native sequence PRO85088 cDNA, wherein SEQ ID NO:2081 is a clone designated herein as "DNA329538".

Figure 2082 shows the amino acid sequence (SEQ ID NO:2082) derived from the coding sequence of SEQ ID NO:2081 shown in Figure 2081.

Figure 2083 shows a nucleotide sequence (SEQ ID NO:2083) of a native sequence PRO6180 cDNA, wherein SEQ ID NO:2083 is a clone designated herein as "DNA287376".

Figure 2084 shows the amino acid sequence (SEQ ID NO:2084) derived from the coding sequence of SEQ ID NO:2083 shown in Figure 2083.

Figure 2085 shows a nucleotide sequence (SEQ ID NO:2085) of a native sequence PRO85089 cDNA, wherein SEQ ID NO:2085 is a clone designated herein as "DNA329539".

Figure 2086 shows the amino acid sequence (SEQ ID NO:2086) derived from the coding sequence of SEQ ID NO:2085 shown in Figure 2085.

Figure 2087 shows a nucleotide sequence (SEQ ID NO:2087) of a native sequence PRO2520 cDNA, wherein SEQ ID NO:2087 is a clone designated herein as "DNA28759".

Figure 2088 shows the amino acid sequence (SEQ ID NO:2088) derived from the coding sequence of SEQ ID NO:2087 shown in Figure 2087.

Figure 2089 shows a nucleotide sequence (SEQ ID NO:2089) of a native sequence PRO4887 cDNA, wherein SEQ ID NO:2089 is a clone designated herein as "DNA329016".

Figure 2090 shows the amino acid sequence (SEQ ID NO:2090) derived from the coding sequence of SEQ ID NO:2089 shown in Figure 2089.

Figure 2091 shows a nucleotide sequence (SEQ ID NO:2091) of a native sequence PRO85090 cDNA, wherein SEQ ID NO:2091 is a clone designated herein as "DNA329540".

Figure 2092 shows the amino acid sequence (SEQ ID NO:2092) derived from the coding sequence of SEQ ID NO:2091 shown in Figure 2091.

Figure 2093 shows a nucleotide sequence (SEQ ID NO:2093) of a native sequence PRO4515 cDNA, wherein SEQ ID NO:2093 is a clone designated herein as "DNA93439".

Figure 2094 shows the amino acid sequence (SEQ ID NO:2094) derived from the coding sequence of SEQ ID NO:2093 shown in Figure 2093.

Figure 2095 shows a nucleotide sequence (SEQ ID NO:2095) of a native sequence PRO12358 cDNA, wherein SEQ ID NO:2095 is a clone designated herein as "DNA329541".

Figure 2096 shows the amino acid sequence (SEQ ID NO:2096) derived from the coding sequence of SEQ ID NO:2095 shown in Figure 2095.

Figure 2097 shows a nucleotide sequence (SEQ ID NO:2097) of a native sequence PRO37975 cDNA, wherein SEQ ID NO:2097 is a clone designated herein as "DNA227512".

Figure 2098 shows the amino acid sequence (SEQ ID NO:2098) derived from the coding sequence of SEQ ID NO:2097 shown in Figure 2097

Figure 2099 shows a nucleotide sequence (SEQ ID NO:2099) of a native sequence PRO12468 cDNA, wherein SEQ ID NO:2099 is a clone designated herein as "DNA324897".

Figure 2100 shows the amino acid sequence (SEQ ID NO:2100) derived from the coding sequence of SEQ ID NO:2099 shown in Figure 2099.

Figure 2101 shows a nucleotide sequence (SEQ ID NO:2101) of a native sequence PRO4767 cDNA, wherein SEQ ID NO:2101 is a clone designated herein as "DNA103440".

Figure 2102 shows the amino acid sequence (SEQ ID NO:2102) derived from the coding sequence of SEQ ID NO:2101 shown in Figure 2101.

Figure 2103 shows a nucleotide sequence (SEQ ID NO:2103) of a native sequence PRO4735 cDNA, wherein SEQ ID NO:2103 is a clone designated herein as "DNA329542".

Figure 2104 shows the amino acid sequence (SEQ ID NO:2104) derived from the coding sequence of SEQ ID NO:2103 shown in Figure 2103.

Figure 2105 shows a nucleotide sequence (SEQ ID NO:2105) of a native sequence PRO36506 cDNA, wherein SEQ ID NO:2105 is a clone designated herein as "DNA226043".

Figure 2106 shows the amino acid sequence (SEQ ID NO:2106) derived from the coding sequence of SEQ ID NO:2105 shown in Figure 2105.

Figure 2107 shows a nucleotide sequence (SEQ ID NO:2107) of a native sequence PRO2690 cDNA, wherein SEQ ID NO:2107 is a clone designated herein as "DNA88189".

Figure 2108 shows the amino acid sequence (SEQ ID NO:2108) derived from the coding sequence of SEQ ID NO:2107 shown in Figure 2107.

Figure 2109 shows a nucleotide sequence (SEQ ID NO:2109) of a native sequence PRO4808 cDNA, wherein SEQ ID NO:2109 is a clone designated herein as "DNA103481".

Figure 2110 shows the amino acid sequence (SEQ ID NO:2110) derived from the coding sequence of SEQ ID NO:2109 shown in Figure 2109.

Figure 2111 shows a nucleotide sequence (SEQ ID NO:2111) of a native sequence PRO4419 cDNA, wherein SEQ ID NO:2111 is a clone designated herein as "DNA329543".

Figure 2112 shows the amino acid sequence (SEQ ID NO:2112) derived from the coding sequence of SEQ ID NO:2111 shown in Figure 2111.

Figure 2113 shows a nucleotide sequence (SEQ ID NO:2113) of a native sequence PRO619 cDNA, wherein SEQ ID NO:2113 is a clone designated herein as "DNA329544".

Figure 2114 shows the amino acid sequence (SEQ ID NO:2114) derived from the coding sequence of SEQ ID NO:2113 shown in Figure 2113.

Figure 2115 shows a nucleotide sequence (SEQ ID NO:2115) of a native sequence PRO85091 cDNA, wherein SEQ ID NO:2115 is a clone designated herein as "DNA329545".

Figure 2116 shows the amino acid sequence (SEQ ID NO:2116) derived from the coding sequence of SEQ ID NO:2115 shown in Figure 2115.

Figure 2117 shows a nucleotide sequence (SEQ ID NO:2117) of a native sequence PRO23859 cDNA, wherein SEQ ID NO:2117 is a clone designated herein as "DNA328957".

Figure 2118 shows the amino acid sequence (SEQ ID NO:2118) derived from the coding sequence of SEQ ID NO:2117 shown in Figure 2117.

Figure 2119 shows a nucleotide sequence (SEQ ID NO:2119) of a native sequence PRO37696 cDNA, wherein SEQ ID NO:2119 is a clone designated herein as "DNA227233".

Figure 2120 shows the amino acid sequence (SEQ ID NO:2120) derived from the coding sequence of SEQ ID NO:2119 shown in Figure 2119.

Figure 2121 shows a nucleotide sequence (SEQ ID NO:2121) of a native sequence PRO296 cDNA, wherein SEQ ID NO:2121 is a clone designated herein as "DNA329546".

Figure 2122 shows the amino acid sequence (SEQ ID NO:2122) derived from the coding sequence of SEQ ID NO:2123 shown in Figure 2123.

Figure 2123 shows a nucleotide sequence (SEQ ID NO:2123) of a native sequence PRO34477 cDNA, wherein SEQ ID NO:2123 is a clone designated herein as "DNA218845".

Figure 2124 shows the amino acid sequence (SEQ ID NO:2124) derived from the coding sequence of SEQ ID NO:2123 shown in Figure 2123.

Figure 2125 shows a nucleotide sequence (SEQ ID NO:2125) of a native sequence PRO85092 cDNA, wherein SEQ ID NO:2125 is a clone designated herein as "DNA329547".

Figure 2126 shows the amino acid sequence (SEQ ID NO:2126) derived from the coding sequence of SEQ ID NO:2125 shown in Figure 2125.

Figure 2127 shows a nucleotide sequence (SEQ ID NO:2127) of a native sequence PRO24955 cDNA, wherein SEQ ID NO:2127 is a clone designated herein as "DNA196460".

Figure 2128 shows the amino acid sequence (SEQ ID NO:2128) derived from the coding sequence of SEQ ID NO:2127 shown in Figure 2127.

Figure 2129 shows a nucleotide sequence (SEQ ID NO:2129) of a native sequence PRO33679 cDNA, wherein SEQ ID NO:2129 is a clone designated herein as "DNA210134".

Figure 2130 shows the amino acid sequence (SEQ ID NO:2130) derived from the coding sequence of SEQ ID NO:2129 shown in Figure 2129.

Figure 2131 shows a nucleotide sequence (SEQ ID NO:2131) of a native sequence PRO36002 cDNA, wherein SEQ ID NO:2131 is a clone designated herein as "DNA225539".

Figure 2132 shows the amino acid sequence (SEQ ID NO:2132) derived from the coding sequence of SEQ ID NO:2131 shown in Figure 2131.

Figure 2133 shows a nucleotide sequence (SEQ ID NO:2133) of a native sequence PRO85093 cDNA, wherein SEQ ID NO:2133 is a clone designated herein as "DNA329548".

Figure 2134 shows the amino acid sequence (SEQ ID NO:2134) derived from the coding sequence of SEQ ID NO:2133 shown in Figure 2133.

Figure 2135 shows a nucleotide sequence (SEQ ID NO:2135) of a native sequence PRO71042 cDNA, wherein SEQ ID NO:2135 is a clone designated herein as "DNA304464".

Figure 2136 shows the amino acid sequence (SEQ ID NO:2136) derived from the coding sequence of SEQ ID NO:2135 shown in Figure 2135.

Figure 2137 shows a nucleotide sequence (SEQ ID NO:2137) of a native sequence PRO85094 cDNA, wherein SEQ ID NO:2137 is a clone designated herein as "DNA329549".

Figure 2138 shows the amino acid sequence (SEQ ID NO:2138) derived from the coding sequence of SEQ ID NO:2137 shown in Figure 2137.

Figure 2139 shows a nucleotide sequence (SEQ ID NO:2139) of a native sequence PRO36113 cDNA, wherein SEQ ID NO:2139 is a clone designated herein as "DNA225650".

Figure 2140 shows the amino acid sequence (SEQ ID NO:2140) derived from the coding sequence of SEQ ID NO:2139 shown in Figure 2139.

Figure 2141 shows a nucleotide sequence (SEQ ID NO:2141) of a native sequence PRO85095 cDNA, wherein SEQ ID NO:2141 is a clone designated herein as "DNA329550".

Figure 2142 shows the amino acid sequence (SEQ ID NO:2142) derived from the coding sequence of SEQ ID NO:2141 shown in Figure 2141.

Figure 2143 shows a nucleotide sequence (SEQ ID NO:2143) of a native sequence PRO9891 cDNA, wherein SEQ ID NO:2143 is a clone designated herein as "DNA328933".

Figure 2144 shows the amino acid sequence (SEQ ID NO:2144) derived from the coding sequence of SEQ ID NO:2143 shown in Figure 2143.

Figure 2145A-B shows a nucleotide sequence (SEQ ID NO:2145) of a native sequence PRO4330 cDNA, wherein SEQ ID NO:2145 is a clone designated herein as "DNA328454".

Figure 2146 shows the amino acid sequence (SEQ ID NO:2146) derived from the coding sequence of SEQ ID NO:2145 shown in Figure 2145.

Figure 2147 shows a nucleotide sequence (SEQ ID NO:2147) of a native sequence PRO34297 cDNA, wherein SEQ ID NO:2147 is a clone designated herein as "DNA217255".

Figure 2148 shows the amino acid sequence (SEQ ID NO:2148) derived from the coding sequence of SEQ ID NO:2147 shown in Figure 2147.

Figure 2149 shows a nucleotide sequence (SEQ ID NO:2149) of a native sequence PRO85096 cDNA, wherein SEQ ID NO:2149 is a clone designated herein as "DNA329551".

Figure 2150 shows the amino acid sequence (SEQ ID NO:2150) derived from the coding sequence of SEQ ID NO:2149 shown in Figure 2149.

Figure 2151 shows a nucleotide sequence (SEQ ID NO:2151) of a native sequence PRO85097 cDNA, wherein SEQ ID NO:2151 is a clone designated herein as "DNA329552".

Figure 2152 shows the amino acid sequence (SEQ ID NO:2152) derived from the coding sequence of SEQ ID NO:2151 shown in Figure 2151.

Figure 2153 shows a nucleotide sequence (SEQ ID NO:2153) of a native sequence PRO38313 cDNA, wherein SEQ ID NO:2153 is a clone designated herein as "DNA329553".

Figure 2154 shows the amino acid sequence (SEQ ID NO:2154) derived from the coding sequence of SEQ ID NO:2153 shown in Figure 2153.

Figure 2155 shows a nucleotide sequence (SEQ ID NO:2155) of a native sequence PRO85098 cDNA, wherein SEQ ID NO:2155 is a clone designated herein as "DNA329554".

Figure 2156 shows the amino acid sequence (SEQ ID NO:2156) derived from the coding sequence of SEQ ID NO:2155 shown in Figure 2155.

Figure 2157 shows a nucleotide sequence (SEQ ID NO:2157) of a native sequence PRO85099 cDNA, wherein SEQ ID NO:2157 is a clone designated herein as "DNA329555".

Figure 2158 shows the amino acid sequence (SEQ ID NO:2158) derived from the coding sequence of SEQ ID NO:2157 shown in Figure 2157.

Figure 2159 shows a nucleotide sequence (SEQ ID NO:2159) of a native sequence PRO12916 cDNA, wherein SEQ ID NO:2159 is a clone designated herein as "DNA151893".

Figure 2160 shows the amino acid sequence (SEQ ID NO:2160) derived from the coding sequence of SEQ ID NO:2159 shown in Figure 2159.

Figure 2161A-B shows a nucleotide sequence (SEQ ID NO:2161) of a native sequence cDNA, wherein SEQ ID NO:2161 is a clone designated herein as "DNA329556".

Figure 2162 shows a nucleotide sequence (SEQ ID NO:2162) of a native sequence PRO7250 cDNA, wherein SEQ ID NO:2162 is a clone designated herein as "DNA329557".

Figure 2163 shows the amino acid sequence (SEQ ID NO:2163) derived from the coding sequence of SEQ ID NO:2162 shown in Figure 2162.

Figure 2164 shows a nucleotide sequence (SEQ ID NO:2164) of a native sequence PRO38486 cDNA, wherein SEQ ID NO:2164 is a clone designated herein as "DNA228023".

Figure 2165 shows the amino acid sequence (SEQ ID NO:2165) derived from the coding sequence of SEQ ID NO:2164 shown in Figure 2164.

Figure 2166A-B shows a nucleotide sequence (SEQ ID NO:2166) of a native sequence PRO85100 cDNA, wherein SEQ ID NO:2166 is a clone designated herein as "DNA329558".

Figure 2167 shows the amino acid sequence (SEQ ID NO:2167) derived from the coding sequence of SEQ ID NO:2166 shown in Figure 2166.

Figure 2168 shows a nucleotide sequence (SEQ ID NO:2168) of a native sequence cDNA, wherein SEQ ID NO:2168 is a clone designated herein as "DNA150552".

Figure 2169 shows a nucleotide sequence (SEQ ID NO:2169) of a native sequence PRO80622 cDNA, wherein SEQ ID NO:2169 is a clone designated herein as "DNA323879".

Figure 2170 shows the amino acid sequence (SEQ ID NO:2170) derived from the coding sequence of SEQ ID NO:2169 shown in Figure 2169.

Figure 2171A-B shows a nucleotide sequence (SEQ ID NO:2171) of a native sequence PRO12843 cDNA, wherein SEQ ID NO:2171 is a clone designated herein as "DNA151027".

Figure 2172 shows the amino acid sequence (SEQ ID NO:2172) derived from the coding sequence of SEQ ID NO:2171 shown in Figure 2171.

Figure 2173 shows a nucleotide sequence (SEQ ID NO:2173) of a native sequence PRO85101 cDNA, wherein SEQ ID NO:2173 is a clone designated herein as "DNA329559".

Figure 2174 shows the amino acid sequence (SEQ ID NO:2174) derived from the coding sequence of SEQ ID NO:2173 shown in Figure 2173.

Figure 2175A-B shows a nucleotide sequence (SEQ ID NO:2175) of a native sequence PRO85102 cDNA, wherein SEQ ID NO:2175 is a clone designated herein as "DNA329560".

Figure 2176 shows the amino acid sequence (SEQ ID NO:2176) derived from the coding sequence of SEQ ID NO:2175 shown in Figure 2175.

Figure 2177 shows a nucleotide sequence (SEQ ID NO:2177) of a native sequence PRO85103 cDNA, wherein SEQ ID NO:2177 is a clone designated herein as "DNA329561".

Figure 2178 shows the amino acid sequence (SEQ ID NO:2178) derived from the coding sequence of SEQ ID NO:2177 shown in Figure 2177.

Figure 2179 shows a nucleotide sequence (SEQ ID NO:2179) of a native sequence PRO85104 cDNA, wherein SEQ ID NO:2179 is a clone designated herein as "DNA329562".

Figure 2180 shows the amino acid sequence (SEQ ID NO:2180) derived from the coding sequence of SEQ ID NO:2179 shown in Figure 2179.

Figure 2181 shows a nucleotide sequence (SEQ ID NO:2181) of a native sequence PRO84160 cDNA, wherein SEQ ID NO:2181 is a clone designated herein as "DNA328284".

Figure 2182 shows the amino acid sequence (SEQ ID NO:2182) derived from the coding sequence of SEQ ID NO:2181 shown in Figure 2181.

Figure 2183 shows a nucleotide sequence (SEQ ID NO:2183) of a native sequence PRO81947 cDNA, wherein SEQ ID NO:2183 is a clone designated herein as "DNA325421".

Figure 2184 shows the amino acid sequence (SEQ ID NO:2184) derived from the coding sequence of SEQ ID NO:2183 shown in Figure 2183.

Figure 2185A-B shows a nucleotide sequence (SEQ ID NO:2185) of a native sequence PRO1920 cDNA, wherein SEQ ID NO:2185 is a clone designated herein as "DNA329563".

Figure 2186 shows the amino acid sequence (SEQ ID NO:2186) derived from the coding sequence of SEQ ID NO:2185 shown in Figure 2185.

Figure 2187 shows a nucleotide sequence (SEQ ID NO:2187) of a native sequence PRO85105 cDNA, wherein SEQ ID NO:2187 is a clone designated herein as "DNA329564".

Figure 2188 shows the amino acid sequence (SEQ ID NO:2188) derived from the coding sequence of SEQ ID NO:2187 shown in Figure 2187.

Figure 2189 shows a nucleotide sequence (SEQ ID NO:2189) of a native sequence cDNA, wherein SEQ ID NO:2189 is a clone designated herein as "DNA196002".

Figure 2190A-B shows a nucleotide sequence (SEQ ID NO:2190) of a native sequence PRO84476 cDNA, wherein SEQ ID NO:2190 is a clone designated herein as "DNA328720".

Figure 2191 shows the amino acid sequence (SEQ ID NO:2191) derived from the coding sequence of SEQ ID NO:2190 shown in Figure 2190.

Figure 2192 shows a nucleotide sequence (SEQ ID NO:2192) of a native sequence PRO23880 cDNA, wherein SEQ ID NO:2192 is a clone designated herein as "DNA194522".

Figure 2193 shows the amino acid sequence (SEQ ID NO:2193) derived from the coding sequence of SEQ ID NO:2192 shown in Figure 2192.

Figure 2194 shows a nucleotide sequence (SEQ ID NO:2194) of a native sequence PRO85106 cDNA, wherein SEQ ID NO:2194 is a clone designated herein as "DNA329565".

Figure 2195 shows the amino acid sequence (SEQ ID NO:2195) derived from the coding sequence of SEQ ID NO:2194 shown in Figure 2194.

Figure 2196 shows a nucleotide sequence (SEQ ID NO:2196) of a native sequence PRO85107 cDNA, wherein SEQ ID NO:2196 is a clone designated herein as "DNA329566".

Figure 2197 shows the amino acid sequence (SEQ ID NO:2197) derived from the coding sequence of SEQ ID NO:2196 shown in Figure 2196.

Figure 2198 shows a nucleotide sequence (SEQ ID NO:2198) of a native sequence PRO69876 cDNA, wherein SEQ ID NO:2198 is a clone designated herein as "DNA328288".

Figure 2199 shows the amino acid sequence (SEQ ID NO:2199) derived from the coding sequence of SEQ ID NO:2198 shown in Figure 2198.

Figure 2200 shows a nucleotide sequence (SEQ ID NO:2200) of a native sequence PRO33775 cDNA, wherein SEQ ID NO:2200 is a clone designated herein as "DNA210241".

Figure 2201 shows the amino acid sequence (SEQ ID NO:2201) derived from the coding sequence of SEQ ID NO:2200 shown in Figure 2200.

Figure 2202 shows a nucleotide sequence (SEQ ID NO:2202) of a native sequence cDNA, wherein SEQ ID NO:2202 is a clone designated herein as "DNA33782".

Figure 2203 shows a nucleotide sequence (SEQ ID NO:2203) of a native sequence PRO85109 cDNA, wherein SEQ ID NO:2203 is a clone designated herein as "DNA329568".

Figure 2204 shows the amino acid sequence (SEQ ID NO:2204) derived from the coding sequence of SEQ ID NO:2203 shown in Figure 2203.

Figure 2205 shows a nucleotide sequence (SEQ ID NO:2205) of a native sequence cDNA, wherein SEQ ID NO:2205 is a clone designated herein as "DNA196162".

Figure 2206A-B shows a nucleotide sequence (SEQ ID NO:2206) of a native sequence PRO85110 cDNA, wherein SEQ ID NO:2206 is a clone designated herein as "DNA329569".

Figure 2207 shows the amino acid sequence (SEQ ID NO:2207) derived from the coding sequence of SEQ ID NO:2206 shown in Figure 2206.

Figure 2208 shows a nucleotide sequence (SEQ ID NO:2208) of a native sequence PRO7367 cDNA, wherein SEQ ID NO:2208 is a clone designated herein as "DNA90840".

Figure 2209 shows the amino acid sequence (SEQ ID NO:2209) derived from the coding sequence of SEQ ID NO:2208 shown in Figure 2208.

Figure 2210 shows a nucleotide sequence (SEQ ID NO:2210) of a native sequence cDNA, wherein SEQ ID NO:2210 is a clone designated herein as "DNA329570".

Figure 2211 shows a nucleotide sequence (SEQ ID NO:2211) of a native sequence PRO2391 cDNA, wherein SEQ ID NO:2211 is a clone designated herein as "DNA88516".

Figure 2212 shows the amino acid sequence (SEQ ID NO:2212) derived from the coding sequence of SEQ ID NO:2211 shown in Figure 2211.

Figure 2213 shows a nucleotide sequence (SEQ ID NO:2213) of a native sequence PRO50208 cDNA, wherein SEQ ID NO:2213 is a clone designated herein as "DNA255127".

Figure 2214 shows the amino acid sequence (SEQ ID NO:2214) derived from the coding sequence of SEQ ID NO:2213 shown in Figure 2213.

Figure 2215 shows a nucleotide sequence (SEQ ID NO:2215) of a native sequence PRO50791 cDNA, wherein SEQ ID NO:2215 is a clone designated herein as "DNA255734".

Figure 2216 shows the amino acid sequence (SEQ ID NO:2216) derived from the coding sequence of SEQ ID NO:2215 shown in Figure 2215.

Figure 2217 shows a nucleotide sequence (SEQ ID NO:2217) of a native sequence PRO51662 cDNA, wherein SEQ ID NO:2217 is a clone designated herein as "DNA329571".

Figure 2218 shows the amino acid sequence (SEQ ID NO:2218) derived from the coding sequence of SEQ ID NO:2217 shown in Figure 2217.

Figure 2219 shows a nucleotide sequence (SEQ ID NO:2219) of a native sequence PRO51611 cDNA, wherein SEQ ID NO:2219 is a clone designated herein as "DNA256608".

Figure 2220 shows the amino acid sequence (SEQ ID NO:2220) derived from the coding sequence of SEQ ID NO:2219 shown in Figure 2219.

Figure 2221 shows a nucleotide sequence (SEQ ID NO:2221) of a native sequence PRO85111 cDNA, wherein SEQ ID NO:2221 is a clone designated herein as "DNA329572".

Figure 2222 shows the amino acid sequence (SEQ ID NO:2222) derived from the coding sequence of SEQ ID NO:2221 shown in Figure 2221.

Figure 2223 shows a nucleotide sequence (SEQ ID NO:2223) of a native sequence PRO50241 cDNA, wherein SEQ ID NO:2223 is a clone designated herein as "DNA255161".

Figure 2224 shows the amino acid sequence (SEQ ID NO:2224) derived from the coding sequence of SEQ ID NO:2223 shown in Figure 2223.

Figure 2225 shows a nucleotide sequence (SEQ ID NO:2225) of a native sequence PRO62346 cDNA, wherein SEQ ID NO:2225 is a clone designated herein as "DNA274437".

Figure 2226 shows the amino acid sequence (SEQ ID NO:2226) derived from the coding sequence of SEQ ID NO:2225 shown in Figure 2225.

Figure 2227 shows a nucleotide sequence (SEQ ID NO:2227) of a native sequence PRO49615 cDNA, wherein SEQ ID NO:2227 is a clone designated herein as "DNA254508".

Figure 2228 shows the amino acid sequence (SEQ ID NO:2228) derived from the coding sequence of SEQ ID NO:2227 shown in Figure 2227.

Figure 2229 shows a nucleotide sequence (SEQ ID NO:2229) of a native sequence PRO2386 cDNA, wherein SEQ ID NO:2229 is a clone designated herein as "DNA88511".

Figure 2230 shows the amino acid sequence (SEQ ID NO:2230) derived from the coding sequence of SEQ ID NO:2229 shown in Figure 2229.

Figure 2231 shows a nucleotide sequence (SEQ ID NO:2231) of a native sequence PRO51556 cDNA, wherein SEQ ID NO:2231 is a clone designated herein as "DNA256521".

Figure 2232 shows the amino acid sequence (SEQ ID NO:2232) derived from the coding sequence of SEQ ID NO:2231 shown in Figure 2231.

Figure 2233 shows a nucleotide sequence (SEQ ID NO:2233) of a native sequence PRO51565 cDNA, wherein SEQ ID NO:2233 is a clone designated herein as "DNA256533".

Figure 2234 shows the amino acid sequence (SEQ ID NO:2234) derived from the coding sequence of SEQ ID NO:2233 shown in Figure 2233.

Figure 2235 shows a nucleotide sequence (SEQ ID NO:2235) of a native sequence PRO85112 cDNA, wherein SEQ ID NO:2235 is a clone designated herein as "DNA329573".

Figure 2236 shows the amino acid sequence (SEQ ID NO:2236) derived from the coding sequence of SEQ ID NO:2235 shown in Figure 2235.

Figure 2237 shows a nucleotide sequence (SEQ ID NO:2237) of a native sequence PRO59409 cDNA, wherein SEQ ID NO:2237 is a clone designated herein as "DNA271085".

Figure 2238 shows the amino acid sequence (SEQ ID NO:2238) derived from the coding sequence of SEQ ID NO:2237 shown in Figure 2237.

Figure 2239 shows a nucleotide sequence (SEQ ID NO:2239) of a native sequence PRO85113 cDNA, wherein SEQ ID NO:2239 is a clone designated herein as "DNA329574".

Figure 2240 shows the amino acid sequence (SEQ ID NO:) derived from the coding sequence of SEQ ID NO: shown in Figure

Figure 2241 shows a nucleotide sequence (SEQ ID NO:2241) of a native sequence PRO61403 cDNA, wherein SEQ ID NO:2241 is a clone designated herein as "DNA329575".

Figure 2242 shows the amino acid sequence (SEQ ID NO:2242) derived from the coding sequence of SEQ ID NO:2241 shown in Figure 2241.

Figure 2243 shows a nucleotide sequence (SEQ ID NO:2243) of a native sequence PRO64127 cDNA, wherein SEQ ID NO:2243 is a clone designated herein as "DNA329576".

Figure 2244 shows the amino acid sequence (SEQ ID NO:2244) derived from the coding sequence of SEQ ID NO:2243 shown in Figure 2243.

Figure 2245 shows a nucleotide sequence (SEQ ID NO:2245) of a native sequence PRO61623 cDNA, wherein SEQ ID NO:2245 is a clone designated herein as "DNA273653".

Figure 2246 shows the amino acid sequence (SEQ ID NO:2246) derived from the coding sequence of SEQ ID NO:2245 shown in Figure 2245.

Figure 2247 shows a nucleotide sequence (SEQ ID NO:2247) of a native sequence PRO50191 cDNA, wherein SEQ ID NO:2247 is a clone designated herein as "DNA329577".

Figure 2248 shows the amino acid sequence (SEQ ID NO:2248) derived from the coding sequence of SEQ ID NO:2247 shown in Figure 2247.

Figure 2249 shows a nucleotide sequence (SEQ ID NO:2249) of a native sequence PRO51820 cDNA, wherein SEQ ID NO:2249 is a clone designated herein as "DNA329578".

Figure 2250 shows the amino acid sequence (SEQ ID NO:2250) derived from the coding sequence of SEQ ID NO:2249 shown in Figure 2249.

Figure 2251 shows a nucleotide sequence (SEQ ID NO:2251) of a native sequence PRO69609 cDNA, wherein SEQ ID NO:2251 is a clone designated herein as "DNA329579".

Figure 2252 shows the amino acid sequence (SEQ ID NO:2252) derived from the coding sequence of SEQ ID NO:2251 shown in Figure 2251.

Figure 2253 shows a nucleotide sequence (SEQ ID NO:2253) of a native sequence PRO57311 cDNA, wherein SEQ ID NO:2253 is a clone designated herein as "DNA327927".

Figure 2254 shows the amino acid sequence (SEQ ID NO:2254) derived from the coding sequence of SEQ ID NO:2253 shown in Figure 2253.

Figure 2255 shows a nucleotide sequence (SEQ ID NO:2255) of a native sequence PRO58197 cDNA, wherein SEQ ID NO:2255 is a clone designated herein as "DNA269791".

Figure 2256 shows the amino acid sequence (SEQ ID NO:2256) derived from the coding sequence of SEQ ID NO:2255 shown in Figure 2255.

Figure 2257 shows a nucleotide sequence (SEQ ID NO:2257) of a native sequence PRO85114 cDNA, wherein SEQ ID NO:2257 is a clone designated herein as "DNA329580".

Figure 2258 shows the amino acid sequence (SEQ ID NO:2258) derived from the coding sequence of SEQ ID NO:2257 shown in Figure 2257.

Figure 2259 shows a nucleotide sequence (SEQ ID NO:2259) of a native sequence PRO85115 cDNA, wherein SEQ ID NO:2259 is a clone designated herein as "DNA329581".

Figure 2260 shows the amino acid sequence (SEQ ID NO:2260) derived from the coding sequence of SEQ ID NO:2259 shown in Figure 2259.

Figure 2261 shows a nucleotide sequence (SEQ ID NO:2261) of a native sequence PRO51602 cDNA, wherein SEQ ID NO:2261 is a clone designated herein as "DNA256578".

Figure 2262 shows the amino acid sequence (SEQ ID NO:2262) derived from the coding sequence of SEQ ID NO:2261 shown in Figure 2261.

Figure 2263 shows a nucleotide sequence (SEQ ID NO:2263) of a native sequence PRO49368 cDNA, wherein SEQ ID NO:2263 is a clone designated herein as "DNA254256".

Figure 2264 shows the amino acid sequence (SEQ ID NO:2264) derived from the coding sequence of SEQ ID NO:2263 shown in Figure 2263.

Figure 2265 shows a nucleotide sequence (SEQ ID NO:2265) of a native sequence PRO50216 cDNA, wherein SEQ ID NO:2265 is a clone designated herein as "DNA255135".

Figure 2266 shows the amino acid sequence (SEQ ID NO:2266) derived from the coding sequence of SEQ ID NO:2265 shown in Figure 2265.

Figure 2267 shows a nucleotide sequence (SEQ ID NO:2267) of a native sequence PRO50365 cDNA, wherein SEQ ID NO:2267 is a clone designated herein as "DNA255292".

Figure 2268 shows the amino acid sequence (SEQ ID NO:2268) derived from the coding sequence of SEQ ID NO:2267 shown in Figure 2267.

Figure 2269 shows a nucleotide sequence (SEQ ID NO:2269) of a native sequence PRO85116 cDNA, wherein SEQ ID NO:2269 is a clone designated herein as "DNA329582".

Figure 2270 shows the amino acid sequence (SEQ ID NO:2270) derived from the coding sequence of SEQ ID NO:2269 shown in Figure 2269.

Figure 2271 shows a nucleotide sequence (SEQ ID NO:2271) of a native sequence PRO50544 cDNA, wherein SEQ ID NO:2271 is a clone designated herein as "DNA255477".

Figure 2272 shows the amino acid sequence (SEQ ID NO:2272) derived from the coding sequence of SEQ ID NO:2271 shown in Figure 2271.

Figure 2273 shows a nucleotide sequence (SEQ ID NO:2273) of a native sequence PRO85117 cDNA, wherein SEQ ID NO:2273 is a clone designated herein as "DNA329583".

Figure 2274 shows the amino acid sequence (SEQ ID NO:2274) derived from the coding sequence of SEQ ID NO:2273 shown in Figure 2273.

Figure 2275 shows a nucleotide sequence (SEQ ID NO:2275) of a native sequence PRO85118 cDNA, wherein SEQ ID NO:2275 is a clone designated herein as "DNA329584".

Figure 2276 shows the amino acid sequence (SEQ ID NO:2276) derived from the coding sequence of SEQ ID NO:2275 shown in Figure 2275.

Figure 2277 shows a nucleotide sequence (SEQ ID NO:2277) of a native sequence PRO59911 cDNA, wherein SEQ ID NO:2277 is a clone designated herein as "DNA271624".

Figure 2278 shows the amino acid sequence (SEQ ID NO:2278) derived from the coding sequence of SEQ ID NO:2277 shown in Figure 2277.

Figure 2279 shows a nucleotide sequence (SEQ ID NO:2279) of a native sequence PRO69503 cDNA, wherein SEQ ID NO:2279 is a clone designated herein as "DNA287224".

Figure 2280 shows the amino acid sequence (SEQ ID NO:2280) derived from the coding sequence of SEQ ID NO:2279 shown in Figure 2279.

Figure 2281 shows a nucleotide sequence (SEQ ID NO:2281) of a native sequence PRO59278 cDNA, wherein SEQ ID NO:2281 is a clone designated herein as "DNA270947".

Figure 2282 shows the amino acid sequence (SEQ ID NO:2282) derived from the coding sequence of SEQ ID NO:2281 shown in Figure 2281.

Figure 2283 shows a nucleotide sequence (SEQ ID NO:2283) of a native sequence PRO85119 cDNA, wherein SEQ ID NO:2283 is a clone designated herein as "DNA329585".

Figure 2284 shows the amino acid sequence (SEQ ID NO:2284) derived from the coding sequence of SEQ ID NO:2283 shown in Figure 2283.

Figure 2285 shows a nucleotide sequence (SEQ ID NO:2285) of a native sequence PRO85120 cDNA, wherein SEQ ID NO:2285 is a clone designated herein as "DNA329586".

Figure 2286 shows the amino acid sequence (SEQ ID NO:2286) derived from the coding sequence of SEQ ID NO:2285 shown in Figure 2285.

Figure 2287 shows a nucleotide sequence (SEQ ID NO:2287) of a native sequence PRO51584 cDNA, wherein SEQ ID NO:2287 is a clone designated herein as "DNA256553".

Figure 2288 shows the amino acid sequence (SEQ ID NO:2288) derived from the coding sequence of SEQ ID NO:2287 shown in Figure 2287.

Figure 2289 shows a nucleotide sequence (SEQ ID NO:2289) of a native sequence PRO61504 cDNA, wherein SEQ ID NO:2289 is a clone designated herein as "DNA273523".

Figure 2290 shows the amino acid sequence (SEQ ID NO:2290) derived from the coding sequence of SEQ ID NO:2289 shown in Figure 2289.

Figure 2291 shows a nucleotide sequence (SEQ ID NO:2291) of a native sequence PRO58541 cDNA, wherein SEQ ID NO:2291 is a clone designated herein as "DNA270152".

Figure 2292 shows the amino acid sequence (SEQ ID NO:2292) derived from the coding sequence of SEQ ID NO:2291 shown in Figure 2291.

Figure 2293 shows a nucleotide sequence (SEQ ID NO:2293) of a native sequence PRO85121 cDNA, wherein SEQ ID NO:2293 is a clone designated herein as "DNA329587".

Figure 2294 shows the amino acid sequence (SEQ ID NO:2294) derived from the coding sequence of SEQ ID NO:2293 shown in Figure 2293

Figure 2295 shows a nucleotide sequence (SEQ ID NO:2295) of a native sequence PRO50682 cDNA, wherein SEQ ID NO:2295 is a clone designated herein as "DNA255619".

Figure 2296 shows the amino acid sequence (SEQ ID NO:2296) derived from the coding sequence of SEQ ID NO:2295 shown in Figure 2295.

Figure 2297 shows a nucleotide sequence (SEQ ID NO:2297) of a native sequence PRO85122 cDNA, wherein SEQ ID NO:2297 is a clone designated herein as "DNA329588".

Figure 2298 shows the amino acid sequence (SEQ ID NO:2298) derived from the coding sequence of SEQ ID NO:2297 shown in Figure 2297

Figure 2299 shows a nucleotide sequence (SEQ ID NO:2299) of a native sequence cDNA, wherein SEQ ID NO:2299 is a clone designated herein as "DNA256110".

Figure 2300 shows a nucleotide sequence (SEQ ID NO:2300) of a native sequence PRO85123 cDNA, wherein SEQ ID NO:2300 is a clone designated herein as "DNA329589".

Figure 2301 shows the amino acid sequence (SEQ ID NO:2301) derived from the coding sequence of SEQ ID NO:2300 shown in Figure 2300.

Figure 2302A-B shows a nucleotide sequence (SEQ ID NO:2302) of a native sequence PRO84706 cDNA, wherein SEQ ID NO:2302 is a clone designated herein as "DNA329039".

Figure 2303 shows the amino acid sequence (SEQ ID NO:2303) derived from the coding sequence of SEQ ID NO:2302 shown in Figure 2302.

Figure 2304 shows a nucleotide sequence (SEQ ID NO:2304) of a native sequence PRO57996 cDNA, wherein SEQ ID NO:2304 is a clone designated herein as "DNA328509".

Figure 2305 shows the amino acid sequence (SEQ ID NO:2305) derived from the coding sequence of SEQ ID NO:2304 shown in Figure 2304.

Figure 2306 shows a nucleotide sequence (SEQ ID NO:2306) of a native sequence PRO50614 cDNA, wherein SEQ ID NO:2306 is a clone designated herein as "DNA329590".

Figure 2307 shows the amino acid sequence (SEQ ID NO:2307) derived from the coding sequence of SEQ ID NO:2306 shown in Figure 2306.

Figure 2308 shows a nucleotide sequence (SEQ ID NO:2308) of a native sequence cDNA, wherein SEQ ID NO:2308 is a clone designated herein as "DNA329591".

Figure 2309 shows a nucleotide sequence (SEQ ID NO:2309) of a native sequence PRO85124 cDNA, wherein SEQ ID NO:2309 is a clone designated herein as "DNA329592".

Figure 2310 shows the amino acid sequence (SEQ ID NO:2310) derived from the coding sequence of SEQ ID NO:2309 shown in Figure 2309.

Figure 2311 shows a nucleotide sequence (SEQ ID NO:2311) of a native sequence PRO51777 cDNA, wherein SEQ ID NO:2311 is a clone designated herein as "DNA256846".

Figure 2312 shows the amino acid sequence (SEQ ID NO:2312) derived from the coding sequence of SEQ ID NO:2311 shown in Figure 2311.

Figure 2313 shows a nucleotide sequence (SEQ ID NO:2313) of a native sequence PRO85125 cDNA, wherein SEQ ID NO:2313 is a clone designated herein as "DNA329593".

Figure 2314 shows the amino acid sequence (SEQ ID NO:2314) derived from the coding sequence of SEQ ID NO:2313 shown in Figure 2313.

Figure 2315 shows a nucleotide sequence (SEQ ID NO:2315) of a native sequence PRO50261 cDNA, wherein SEQ ID NO:2315 is a clone designated herein as "DNA255181".

Figure 2316 shows the amino acid sequence (SEQ ID NO:2316) derived from the coding sequence of SEQ ID NO:2315 shown in Figure 2315.

Figure 2317 shows a nucleotide sequence (SEQ ID NO:2317) of a native sequence cDNA, wherein SEQ ID NO:2317 is a clone designated herein as "DNA329594".

Figure 2318 shows a nucleotide sequence (SEQ ID NO:2318) of a native sequence PRO85127 cDNA, wherein SEQ ID NO:2318 is a clone designated herein as "DNA329595".

Figure 2319 shows the amino acid sequence (SEQ ID NO:2319) derived from the coding sequence of SEQ ID NO:2318 shown in Figure 2318.

Figure 2320A-B shows a nucleotide sequence (SEQ ID NO:2320) of a native sequence PRO85128 cDNA, wherein SEQ ID NO:2320 is a clone designated herein as "DNA329596".

Figure 2321 shows the amino acid sequence (SEQ ID NO:2321) derived from the coding sequence of SEQ ID NO:2320 shown in Figure 2320.

Figure 2322 shows a nucleotide sequence (SEQ ID NO:2322) of a native sequence PRO85129 cDNA, wherein SEQ ID NO:2322 is a clone designated herein as "DNA329597".

Figure 2323 shows the amino acid sequence (SEQ ID NO:2323) derived from the coding sequence of SEQ ID NO:2322 shown in Figure 2322.

Figure 2324 shows a nucleotide sequence (SEQ ID NO:2324) of a native sequence PRO23253 cDNA, wherein SEQ ID NO:2324 is a clone designated herein as "DNA329078".

Figure 2325 shows the amino acid sequence (SEQ ID NO:2325) derived from the coding sequence of SEQ ID NO:2324 shown in Figure 2324.

Figure 2326 shows a nucleotide sequence (SEQ ID NO:2326) of a native sequence PRO85130 cDNA, wherein SEQ ID NO:2326 is a clone designated herein as "DNA329598".

Figure 2327 shows the amino acid sequence (SEQ ID NO:2327) derived from the coding sequence of SEQ ID NO:2326 shown in Figure 2326.

Figure 2328 shows a nucleotide sequence (SEQ ID NO:2328) of a native sequence PRO60456 cDNA, wherein SEQ ID NO:2328 is a clone designated herein as "DNA272191".

Figure 2329 shows the amino acid sequence (SEQ ID NO:2329) derived from the coding sequence of SEQ ID NO:2328 shown in Figure 2328.

Figure 2330A-B shows a nucleotide sequence (SEQ ID NO:2330) of a native sequence PRO85131 cDNA, wherein SEQ ID NO:2330 is a clone designated herein as "DNA329599".

Figure 2331 shows the amino acid sequence (SEQ ID NO:2331) derived from the coding sequence of SEQ ID NO:2230 shown in Figure 2230.

Figure 2332 shows a nucleotide sequence (SEQ ID NO:2332) of a native sequence PRO81261 cDNA, wherein SEQ ID NO:2332 is a clone designated herein as "DNA324612".

Figure 2333 shows the amino acid sequence (SEQ ID NO:2333) derived from the coding sequence of SEQ ID NO:2332 shown in Figure 2332

Figure 2334 shows a nucleotide sequence (SEQ ID NO:2334) of a native sequence PRO59570 cDNA, wherein SEQ ID NO:2334 is a clone designated herein as "DNA329600".

Figure 2335 shows the amino acid sequence (SEQ ID NO:2335) derived from the coding sequence of SEQ ID NO:2334 shown in Figure 2334.

Figure 2336A-B shows a nucleotide sequence (SEQ ID NO:2336) of a native sequence PRO50357 cDNA, wherein SEQ ID NO:2336 is a clone designated herein as "DNA255281".

Figure 2337 shows the amino acid sequence (SEQ ID NO:2337) derived from the coding sequence of SEQ ID NO:2336 shown in Figure 2336.

Figure 2338 shows a nucleotide sequence (SEQ ID NO:2338) of a native sequence PRO58933 cDNA, wherein SEQ ID NO:2338 is a clone designated herein as "DNA270558".

Figure 2339 shows the amino acid sequence (SEQ ID NO:2339) derived from the coding sequence of SEQ ID NO:2338 shown in Figure 2338.

Figure 2340 shows a nucleotide sequence (SEQ ID NO:2340) of a native sequence PRO82373 cDNA, wherein SEQ ID NO:2340 is a clone designated herein as "DNA325920".

Figure 2341 shows the amino acid sequence (SEQ ID NO:2341) derived from the coding sequence of SEQ ID NO:2340 shown in Figure 2340.

Figure 2342 shows a nucleotide sequence (SEQ ID NO:2342) of a native sequence PRO58993 cDNA, wherein SEQ ID NO:2342 is a clone designated herein as "DNA324690".

Figure 2343 shows the amino acid sequence (SEQ ID NO:2343) derived from the coding sequence of SEQ ID NO:2342 shown in Figure 2342.

Figure 2344 shows a nucleotide sequence (SEQ ID NO:2344) of a native sequence PRO57930 cDNA, wherein SEQ ID NO:2344 is a clone designated herein as "DNA269514".

Figure 2345 shows the amino acid sequence (SEQ ID NO:2345) derived from the coding sequence of SEQ ID NO:2344 shown in Figure 2344.

Figure 2346 shows a nucleotide sequence (SEQ ID NO:2346) of a native sequence PRO85132 cDNA, wherein SEQ ID NO:2346 is a clone designated herein as "DNA329601".

Figure 2347 shows the amino acid sequence (SEQ ID NO:2347) derived from the coding sequence of SEQ ID NO:2346 shown in Figure 2346.

Figure 2348 shows a nucleotide sequence (SEQ ID NO:2348) of a native sequence PRO49288 cDNA, wherein SEQ ID NO:2348 is a clone designated herein as "DNA254175".

Figure 2349 shows the amino acid sequence (SEQ ID NO:2349) derived from the coding sequence of SEQ ID NO:2348 shown in Figure 2348.

Figure 2350 shows a nucleotide sequence (SEQ ID NO:2350) of a native sequence PRO58175 cDNA, wherein SEQ ID NO:2350 is a clone designated herein as "DNA269766".

Figure 2351 shows the amino acid sequence (SEQ ID NO:2351) derived from the coding sequence of SEQ ID NO:2350 shown in Figure 2350.

Figure 2352 shows a nucleotide sequence (SEQ ID NO:2352) of a native sequence PRO85133 cDNA, wherein SEQ ID NO:2352 is a clone designated herein as "DNA329602".

Figure 2353 shows the amino acid sequence (SEQ ID NO:2353) derived from the coding sequence of SEQ ID NO:2352 shown in Figure 2352.

Figure 2354A-B shows a nucleotide sequence (SEQ ID NO:2354) of a native sequence PRO59246 cDNA, wherein SEQ ID NO:2354 is a clone designated herein as "DNA329603".

Figure 2355 shows the amino acid sequence (SEQ ID NO:2355) derived from the coding sequence of SEQ ID NO:2354 shown in Figure 2354.

Figure 2356 shows a nucleotide sequence (SEQ ID NO:2356) of a native sequence PRO85134 cDNA, wherein SEQ ID NO:2356 is a clone designated herein as "DNA329604".

Figure 2357 shows the amino acid sequence (SEQ ID NO:2357) derived from the coding sequence of SEQ ID NO:2356 shown in Figure 2356.

Figure 2358 shows a nucleotide sequence (SEQ ID NO:2358) of a native sequence PRO85135 cDNA, wherein SEQ ID NO:2358 is a clone designated herein as "DNA329605".

Figure 2359 shows the amino acid sequence (SEQ ID NO:2359) derived from the coding sequence of SEQ ID NO:2358 shown in Figure 2358.

Figure 2360 shows a nucleotide sequence (SEQ ID NO:2360) of a native sequence PRO58219 cDNA, wherein SEQ ID NO:2360 is a clone designated herein as "DNA269816".

Figure 2361 shows the amino acid sequence (SEQ ID NO:2361) derived from the coding sequence of SEQ ID NO:2360 shown in Figure 2360.

Figure 2362 shows a nucleotide sequence (SEQ ID NO:2362) of a native sequence PRO58754 cDNA, wherein SEQ ID NO:2362 is a clone designated herein as "DNA270369".

Figure 2363 shows the amino acid sequence (SEQ ID NO:2363) derived from the coding sequence of SEQ ID NO:2362 shown in Figure 2362.

Figure 2364 shows a nucleotide sequence (SEQ ID NO:2364) of a native sequence PRO85136 cDNA, wherein SEQ ID NO:2364 is a clone designated herein as "DNA329606".

Figure 2365 shows the amino acid sequence (SEQ ID NO:2365) derived from the coding sequence of SEQ ID NO:2364 shown in Figure 2364.

Figure 2366 shows a nucleotide sequence (SEQ ID NO:2366) of a native sequence PRO81893 cDNA, wherein SEQ ID NO:2366 is a clone designated herein as "DNA325355".

Figure 2367 shows the amino acid sequence (SEQ ID NO:2367) derived from the coding sequence of SEQ ID NO:2366 shown in Figure 2366.

Figure 2368 shows a nucleotide sequence (SEQ ID NO:2368) of a native sequence PRO85137 cDNA, wherein SEQ ID NO:2368 is a clone designated herein as "DNA329607".

Figure 2369 shows the amino acid sequence (SEQ ID NO:2369) derived from the coding sequence of SEQ ID NO:2368 shown in Figure 2368.

Figure 2370 shows a nucleotide sequence (SEQ ID NO:2370) of a native sequence PRO70699 cDNA, wherein SEQ ID NO:2370 is a clone designated herein as "DNA293243".

Figure 2371 shows the amino acid sequence (SEQ ID NO:2371) derived from the coding sequence of SEQ ID NO:2370 shown in Figure 2370.

Figure 2372 shows a nucleotide sequence (SEQ ID NO:2372) of a native sequence PRO2388 cDNA, wherein SEQ ID NO:2372 is a clone designated herein as "DNA88513".

Figure 2373 shows the amino acid sequence (SEQ ID NO:2373) derived from the coding sequence of SEQ ID NO:2372 shown in Figure 2372.

Figure 2374 shows a nucleotide sequence (SEQ ID NO:2374) of a native sequence PRO85138 cDNA, wherein SEQ ID NO:2374 is a clone designated herein as "DNA329608".

Figure 2375 shows the amino acid sequence (SEQ ID NO:2375) derived from the coding sequence of SEQ ID NO:2374 shown in Figure 2374.

Figure 2376A-B shows a nucleotide sequence (SEQ ID NO:2376) of a native sequence cDNA, wherein SEQ ID NO:2376 is a clone designated herein as "DNA329051".

Figure 2377 shows a nucleotide sequence (SEQ ID NO:2377) of a native sequence PRO85139 cDNA, wherein SEQ ID NO:2377 is a clone designated herein as "DNA329609".

Figure 2378 shows the amino acid sequence (SEQ ID NO:2378) derived from the coding sequence of SEQ ID NO:2378 shown in Figure

Figure 2379 shows a nucleotide sequence (SEQ ID NO:2379) of a native sequence PRO84183 cDNA, wherein SEQ ID NO:2379 is a clone designated herein as "DNA328315".

Figure 2380 shows the amino acid sequence (SEQ ID NO:2380) derived from the coding sequence of SEQ ID NO:2379 shown in Figure 2379.

Figure 2381 shows a nucleotide sequence (SEQ ID NO:2381) of a native sequence cDNA, herein SEQ ID NO:2381 is a clone designated herein as "DNA329610".

Figure 2382 shows a nucleotide sequence (SEQ ID NO:2382) of a native sequence PRO85141 cDNA, wherein SEQ ID NO:2382 is a clone designated herein as "DNA329611".

Figure 2383 shows the amino acid sequence (SEQ ID NO:2383) derived from the coding sequence of SEQ ID NO:2382 shown in Figure 2382.

Figure 2384 shows a nucleotide sequence (SEQ ID NO:2384) of a native sequence cDNA, wherein SEQ ID NO:2384 is a clone designated herein as "DNA256198".

Figure 2385 shows a nucleotide sequence (SEQ ID NO:2385) of a native sequence PRO85142 cDNA, wherein SEQ ID NO:2385 is a clone designated herein as "DNA329612".

Figure 2386 shows the amino acid sequence (SEQ ID NO:2386) derived from the coding sequence of SEQ ID NO:2385 shown in Figure 2385.

Figure 2387 shows a nucleotide sequence (SEQ ID NO:2387) of a native sequence PRO85143 cDNA, wherein SEQ ID NO:2387 is a clone designated herein as "DNA329613".

Figure 2388 shows the amino acid sequence (SEQ ID NO:2388) derived from the coding sequence of SEQ ID NO:2387 shown in Figure 2387.

Figure 2389 shows a nucleotide sequence (SEQ ID NO:2389) of a native sequence cDNA, wherein SEQ ID NO:2389 is a clone designated herein as "DNA329614".

Figure 2390 shows a nucleotide sequence (SEQ ID NO:2390) of a native sequence PRO50379 cDNA, wherein SEQ ID NO:2390 is a clone designated herein as "DNA255306".

Figure 2391 shows the amino acid sequence (SEQ ID NO:2391) derived from the coding sequence of SEQ ID NO:2390 shown in Figure 2390.

Figure 2392 shows a nucleotide sequence (SEQ ID NO:2392) of a native sequence PRO70559 cDNA, wherein SEQ ID NO:2392 is a clone designated herein as "DNA290812".

Figure 2393 shows the amino acid sequence (SEQ ID NO:2393) derived from the coding sequence of SEQ ID NO:2392 shown in Figure 2392.

Figure 2394 shows a nucleotide sequence (SEQ ID NO:2394) of a native sequence cDNA, wherein SEQ ID NO:2394 is a clone designated herein as "DNA256085".

Figure 2395A-B shows a nucleotide sequence (SEQ ID NO:2395) of a native sequence PRO84584 cDNA, wherein SEQ ID NO:2395 is a clone designated herein as "DNA328853".

Figure 2396 shows the amino acid sequence (SEQ ID NO:2396) derived from the coding sequence of SEQ ID NO:2395 shown in Figure 2395.

Figure 2397 shows a nucleotide sequence (SEQ ID NO:2397) of a native sequence PRO85144 cDNA, wherein SEQ ID NO:2397 is a clone designated herein as "DNA329615".

Figure 2398 shows the amino acid sequence (SEQ ID NO:2398) derived from the coding sequence of SEQ ID NO:2397 shown in Figure 2397.

Figure 2399 shows a nucleotide sequence (SEQ ID NO:2399) of a native sequence cDNA, wherein SEQ ID NO:2399 is a clone designated herein as "DNA329616".

Figure 2400 shows a nucleotide sequence (SEQ ID NO:2400) of a native sequence cDNA, wherein SEQ ID NO:2400 is a clone designated herein as "DNA257960".

Figure 2401 shows a nucleotide sequence (SEQ ID NO:2401) of a native sequence PRO85146 cDNA, wherein SEQ ID NO:2401 is a clone designated herein as "DNA329617".

Figure 2402 shows the amino acid sequence (SEQ ID NO:2402) derived from the coding sequence of SEQ ID NO:2401 shown in Figure 2401.

Figure 2403 shows a nucleotide sequence (SEQ ID NO:2403) of a native sequence PRO52682 cDNA, wherein SEQ ID NO:2403 is a clone designated herein as "DNA258747".

Figure 2404 shows the amino acid sequence (SEQ ID NO:2404) derived from the coding sequence of SEQ ID NO:2403 shown in Figure 2403.

Figure 2405 shows a nucleotide sequence (SEQ ID NO:2405) of a native sequence cDNA, wherein SEQ ID NO:2405 is a clone designated herein as "DNA258793".

Figure 2406 shows a nucleotide sequence (SEQ ID NO:2406) of a native sequence cDNA, wherein SEQ ID NO:2406 is a clone designated herein as "DNA258683".

Figure 2407 shows a nucleotide sequence (SEQ ID NO:2407) of a native sequence PRO85147 cDNA, wherein SEQ ID NO:2407 is a clone designated herein as "DNA329618".

Figure 2408 shows the amino acid sequence (SEQ ID NO:2408) derived from the coding sequence of SEQ ID NO:2407 shown in Figure 2407.

Figure 2409 shows a nucleotide sequence (SEQ ID NO:2409) of a native sequence PRO85148 cDNA, wherein SEQ ID NO:2409 is a clone designated herein as "DNA329619".

Figure 2410 shows the amino acid sequence (SEQ ID NO:2410) derived from the coding sequence of SEQ ID NO:2409 shown in Figure 2409.

Figure 2411 shows a nucleotide sequence (SEQ ID NO:2411) of a native sequence PRO85149 cDNA, wherein SEQ ID NO:2411 is a clone designated herein as "DNA329620".

Figure 2412 shows the amino acid sequence (SEQ ID NO:2412) derived from the coding sequence of SEQ ID NO:2411 shown in Figure 2411.

Figure 2413 shows a nucleotide sequence (SEQ ID NO:2413) of a native sequence cDNA, wherein SEQ ID NO:2413 is a clone designated herein as "DNA258763".

Figure 2414 shows a nucleotide sequence (SEQ ID NO:2414) of a native sequence PRO85150 cDNA, wherein SEQ ID NO:2414 is a clone designated herein as "DNA329621".

Figure 2415 shows the amino acid sequence (SEQ ID NO:2415) derived from the coding sequence of SEQ ID NO:2414 shown in Figure 2414.

Figure 2416 shows a nucleotide sequence (SEQ ID NO:2416) of a native sequence cDNA, wherein SEQ ID NO:2416 is a clone designated herein as "DNA259435".

Figure 2417 shows a nucleotide sequence (SEQ ID NO:2417) of a native sequence PRO53966 cDNA, wherein SEQ ID NO:2417 is a clone designated herein as "DNA260036".

Figure 2418 shows the amino acid sequence (SEQ ID NO:2418) derived from the coding sequence of SEQ ID NO:2417 shown in Figure 2417.

Figure 2419 shows a nucleotide sequence (SEQ ID NO:2419) of a native sequence PRO85151 cDNA, wherein SEQ ID NO:2419 is a clone designated herein as "DNA329622".

Figure 2420 shows the amino acid sequence (SEQ ID NO:2420) derived from the coding sequence of SEQ ID NO:2419 shown in Figure 2419.

Figure 2421 shows a nucleotide sequence (SEQ ID NO:2421) of a native sequence PRO85152 cDNA, wherein SEQ ID NO:2421 is a clone designated herein as "DNA329623".

Figure 2422 shows the amino acid sequence (SEQ ID NO:2422) derived from the coding sequence of SEQ ID NO:2421 shown in Figure 2421.

Figure 2423 shows a nucleotide sequence (SEQ ID NO:2423) of a native sequence PRO85153 cDNA, wherein SEQ ID NO:2423 is a clone designated herein as "DNA329624".

Figure 2424 shows the amino acid sequence (SEQ ID NO:2424) derived from the coding sequence of SEQ ID NO:2423 shown in Figure 2423.

Figure 2425 shows a nucleotide sequence (SEQ ID NO:2425) of a native sequence PRO85154 cDNA, wherein SEQ ID NO:2425 is a clone designated herein as "DNA329625".

Figure 2426 shows the amino acid sequence (SEQ ID NO:2426) derived from the coding sequence of SEQ ID NO:2424 shown in Figure 2425.

Figure 2427 shows a nucleotide sequence (SEQ ID NO:2427) of a native sequence cDNA, wherein SEQ ID NO:2427 is a clone designated herein as "DNA258637".

Figure 2428 shows a nucleotide sequence (SEQ ID NO:2428) of a native sequence cDNA, wherein SEQ ID NO:2428 is a clone designated herein as "DNA262810".

Figure 2429 shows a nucleotide sequence (SEQ ID NO:2429) of a native sequence PRO51901 cDNA, wherein SEQ ID NO:2429 is a clone designated herein as "DNA257309".

Figure 2430 shows the amino acid sequence (SEQ ID NO:2430) derived from the coding sequence of SEQ ID NO:2429 shown in Figure 2429.

Figure 2431 shows a nucleotide sequence (SEQ ID NO:2431) of a native sequence PRO85155 cDNA, wherein SEQ ID NO:2431 is a clone designated herein as "DNA329626".

Figure 2432 shows the amino acid sequence (SEQ ID NO:2432) derived from the coding sequence of SEQ ID NO:2431 shown in Figure 2431.

Figure 2433 shows a nucleotide sequence (SEQ ID NO:2433) of a native sequence PRO85156 cDNA, wherein SEQ ID NO:2433 is a clone designated herein as "DNA329627".

Figure 2434 shows the amino acid sequence (SEQ ID NO:2434) derived from the coding sequence of SEQ ID NO:2433 shown in Figure 2433.

Figure 2435 shows a nucleotide sequence (SEQ ID NO:2435) of a native sequence PRO53004 cDNA, wherein SEQ ID NO:2435 is a clone designated herein as "DNA259071".

Figure 2436 shows the amino acid sequence (SEQ ID NO:2436) derived from the coding sequence of SEQ ID NO:2435 shown in Figure 2435.

Figure 2437 shows a nucleotide sequence (SEQ ID NO:2437) of a native sequence PRO85157 cDNA, wherein SEQ ID NO:2437 is a clone designated herein as "DNA329628".

Figure 2438 shows the amino acid sequence (SEQ ID NO:2438) derived from the coding sequence of SEQ ID NO:2437 shown in Figure 2437.

Figure 2439 shows a nucleotide sequence (SEQ ID NO:2439) of a native sequence PRO85158 cDNA, wherein SEQ ID NO:2439 is a clone designated herein as "DNA329629".

Figure 2440 shows the amino acid sequence (SEQ ID NO:2440) derived from the coding sequence of SEQ ID NO:2439 shown in Figure 2439.

Figure 2441 shows a nucleotide sequence (SEQ ID NO:2441) of a native sequence PRO52822 cDNA, wherein SEQ ID NO:2441 is a clone designated herein as "DNA258889".

Figure 2442 shows the amino acid sequence (SEQ ID NO:2442) derived from the coding sequence of SEQ ID NO:2441 shown in Figure 2441.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length,

alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-

BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid

sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence

D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a

solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhésin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those

in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains

bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass

(e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

The term "immune related disease" means a disease in which a component of the immune system of a mammal causes, mediates or otherwise contributes to a morbidity in the mammal. Also included are diseases in which stimulation or intervention of the immune response has an ameliorative effect on progression of the disease. Included within this term are immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*

The term "T cell mediated disease" means a disease in which T cells directly or indirectly mediate or otherwise contribute to a morbidity in a mammal. The T cell mediated disease may be associated with cell mediated effects, lymphokine mediated effects, *etc.*, and even effects associated with B cells if the B cells are stimulated, for example, by the lymphokines secreted by T cells.

Examples of immune-related and inflammatory diseases, some of which are immune or T cell mediated, which can be treated according to the invention include systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease. Infectious diseases including viral diseases such as AIDS (HIV infection), hepatitis A, B, C, D, and E, herpes, *etc.*, bacterial infections, fungal infections, protozoal infections and parasitic infections.

The term "effective amount" is a concentration or amount of a PRO polypeptide and/or

agonist/antagonist which results in achieving a particular stated purpose. An "effective amount" of a PRO polypeptide or agonist or antagonist thereof may be determined empirically. Furthermore, a "therapeutically effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which is effective for achieving a stated therapeutic effect. This amount may also be determined empirically.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (*e.g.*, I^{131}, I^{125}, Y^{90} and Re^{186}), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxin, taxoids, *e.g.*, paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere, Rhône-Poulenc Rorer, Antony, France), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p. 13.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-α and -β; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-β; platelet-growth factor; transforming growth factors (TGFs) such as TGF-α and TGF-β; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-α, -β, and -γ; colony stimulating factors (CSFs) such as

macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1α, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF-α or TNF-β; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (*i.e.*, is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

As used herein, the term “inflammatory cells” designates cells that enhance the inflammatory response such as mononuclear cells, eosinophils, macrophages, and polymorphonuclear neutrophils (PMN).

Table 1

```
/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define  _M        -8          /* value of a match with a stop */
int       _day[26][26] = {
/*      A  B  C  D  E  F  G  H  I  J  K  L  M  N  O  P  Q  R  S  T  U  V  W  X  Y  Z */
/* A */    { 2, 0,-2, 0, 0,-4, 1,-1,-1, 0,-1,-2,-1, 0,_M, 1, 0,-2, 1, 1, 0, 0,-6, 0,-3, 0},
/* B */    { 0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2,_M,-1, 1, 0, 0, 0, 0,-2,-5, 0,-3, 1},
/* C */    {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
/* D */    { 0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2},
/* E */    { 0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
/* F */    {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4,_M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
/* G */    { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0,_M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
/* H */    {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2,_M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
/* I */    {-1,-2,-2,-2,-2, 1,-3,-2, 5, 0,-2, 2, 2,-2,_M,-2,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
/* J */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */    {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1,_M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
/* L */    {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-3,-1, 0, 2,-2, 0,-1,-2},
/* M */    {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2,_M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1},
/* N */    { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2,_M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
/* O */    {_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M, 0,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M},
/* P */    { 1,-1,-3,-1,-1,-5,-1, 0,-2, 0,-1,-3,-2,-1,_M, 6, 0, 0, 1, 0, 0,-1,-6, 0,-5, 0},
/* Q */    { 0, 1,-5, 2, 2,-5,-1, 3,-2, 0, 1,-2,-1, 1,_M, 0, 4, 1,-1,-1, 0,-2,-5, 0,-4, 3},
/* R */    {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0,_M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
/* S */    { 1, 0, 0, 0, 0,-3, 1,-1,-1, 0, 0,-3,-2, 1,_M, 1,-1, 0, 2, 1, 0,-1,-2, 0,-3, 0},
/* T */    { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0,_M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
/* U */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */    { 0,-2,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2,_M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2},
/* W */    {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4,_M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
/* X */    { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */    {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2,_M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
/* Z */    { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1,_M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
};
```

Table 1 (cont')

```
/*
 */
#include <stdio.h>
#include <ctype.h>

#define  MAXJMP      16      /* max jumps in a diag */
#define  MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define  JMPS        1024    /* max jmps in an path */
#define  MX          4       /* save if there's at least MX-1 bases since last jmp */

#define  DMAT        3       /* value of matching bases */
#define  DMIS        0       /* penalty for mismatched bases */
#define  DINS0       8       /* penalty for a gap */
#define  DINS1       1       /* penalty per base */
#define  PINS0       8       /* penalty for a gap */
#define  PINS1       4       /* penalty per residue */

struct jmp {
        short           n[MAXJMP];      /* size of jmp (neg for dely) */
        unsigned short  x[MAXJMP];      /* base no. of jmp in seq x */
};                                      /* limits seq to 2^16 -1 */

struct diag {
        int             score;          /* score at last jmp */
        long            offset;         /* offset of prev block */
        short           ijmp;           /* current jmp index */
        struct jmp      jp;             /* list of jmps */
};

struct path {
        int     spc;            /* number of leading spaces */
        short   n[JMPS];/* size of jmp (gap) */
        int     x[JMPS];/* loc of jmp (last elem before gap) */
};

char            *ofile;         /* output file name */
char            *namex[2];      /* seq names: getseqs() */
char            *prog;          /* prog name for err msgs */
char            *seqx[2];       /* seqs: getseqs() */
int             dmax;           /* best diag: nw() */
int             dmax0;          /* final diag */
int             dna;            /* set if dna: main() */
int             endgaps;        /* set if penalizing end gaps */
int             gapx, gapy;     /* total gaps in seqs */
int             len0, len1;     /* seq lens */
int             ngapx, ngapy;   /* total size of gaps */
int             smax;           /* max score: nw() */
int             *xbm;           /* bitmap for matching */
long            offset;         /* current offset in jmp file */
struct  diag    *dx;            /* holds diagonals */
struct  path    pp[2];          /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();
```

Table 1 (cont')

```
/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 *   The sequences can be in upper- or lower-case an may contain ambiguity
 *   Any lines beginning with ';', '>' or '<' are ignored
 *   Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *   Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static    _dbval[26] = {
          1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static    _pbval[26] = {
          1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
          128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
          1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
          1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
          main
          int       ac;
          char      *av[ ];
{
          prog = av[0];
          if (ac != 3) {
                    fprintf(stderr,"usage: %s file1 file2\n", prog);
                    fprintf(stderr,"where file1 and file2 are two dna or two protein sequences.\n");
                    fprintf(stderr,"The sequences can be in upper- or lower-case\n");
                    fprintf(stderr,"Any lines beginning with ';' or '<' are ignored\n");
                    fprintf(stderr,"Output is in the file \"align.out\"\n");
                    exit(1);
          }
          namex[0] = av[1];
          namex[1] = av[2];
          seqx[0] = getseq(namex[0], &len0);
          seqx[1] = getseq(namex[1], &len1);
          xbm = (dna)? _dbval : _pbval;

          endgaps = 0;                              /* 1 to penalize endgaps */
          ofile = "align.out";              /* output file */

          nw();                     /* fill in the matrix, get the possible jmps */
          readjmps();               /* get the actual jmps */
          print();                  /* print stats, alignment */

          cleanup(0);               /* unlink any tmp files */
}
```

Table 1 (cont')

```
/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
        nw
{
        char            *px, *py;       /* seqs and ptrs */
        int             *ndely, *dely;  /* keep track of dely */
        int             ndelx, delx;    /* keep track of delx */
        int             *tmp;           /* for swapping row0, row1 */
        int             mis;            /* score for each type */
        int             ins0, ins1;     /* insertion penalties */
        register        id;             /* diagonal index */
        register        ij;             /* jmp index */
        register        *col0, *col1;   /* score for curr, last row */
        register        xx, yy;         /* index into seqs */

        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
        col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

        smax = -10000;
        if (endgaps) {
                for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                        col0[yy] = dely[yy] = col0[yy-1] - ins1;
                        ndely[yy] = yy;
                }
                col0[0] = 0;            /* Waterman Bull Math Biol 84 */
        }
        else
                for (yy = 1; yy <= len1; yy++)
                        dely[yy] = -ins0;

        /* fill in match matrix
         */
        for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
                /* initialize first entry in col
                 */
                if (endgaps) {
                        if (xx == 1)
                                col1[0] = delx = -(ins0+ins1);
                        else
                                col1[0] = delx = col0[0] - ins1;
                        ndelx = xx;
                }
                else {
                        col1[0] = 0;
                        delx = -ins0;
                        ndelx = 0;
                }
```

Table 1 (cont')

...nw

```
for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
                mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
                mis += _day[*px-'A'][*py-'A'];

        /* update penalty for del in x seq;
         * favor new del over ongong del
         * ignore MAXGAP if weighting endgaps
         */
        if (endgaps || ndely[yy] < MAXGAP) {
                if (col0[yy] - ins0 >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else {
                        dely[yy] -= ins1;
                        ndely[yy]++;
                }
        } else {
                if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else
                        ndely[yy]++;
        }

        /* update penalty for del in y seq;
         * favor new del over ongong del
         */
        if (endgaps || ndelx < MAXGAP) {
                if (col1[yy-1] - ins0 >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else {
                        delx -= ins1;
                        ndelx++;
                }
        } else {
                if (col1[yy-1] - (ins0+ins1) >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else
                        ndelx++;
        }

        /* pick the maximum score; we're favoring
         * mis over any del and delx over dely
         */
```

Table 1 (cont')

...nw

```
id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
        col1[yy] = mis;
else if (delx >= dely[yy]) {
        col1[yy] = delx;
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
                        ij = dx[id].ijmp = 0;
                        dx[id].offset = offset;
                        offset += sizeof(struct jmp) + sizeof(offset);
                }
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
}
else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                dx[id].ijmp++;
                if (++ij >= MAXJMP) {
                        writejmps(id);
                        ij = dx[id].ijmp = 0;
                        dx[id].offset = offset;
                        offset += sizeof(struct jmp) + sizeof(offset);
                }
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
}
if (xx == len0 && yy < len1) {
        /* last col
         */
        if (endgaps)
                col1[yy] -= ins0+ins1*(len1-yy);
        if (col1[yy] > smax) {
                smax = col1[yy];
                dmax = id;
        }
}
}
if (endgaps && xx < len0)
        col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
        smax = col1[yy-1];
        dmax = id;
}
tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);                    }
```

Table 1 (cont')

```
/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[ ]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() - -put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC     3
#define P_LINE  256     /* maximum output line */
#define P_SPC   3       /* space between name or num and seq */

extern  _day[26][26];
int     olen;           /* set output line length */
FILE    *fx;            /* output file */

print()
        print
{
        int     lx, ly, firstgap, lastgap;      /* overlap */

        if ((fx = fopen(ofile, "w")) == 0) {
                fprintf(stderr,"%s: can't write %s\n", prog, ofile);
                cleanup(1);
        }
        fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
        fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
        olen = 60;
        lx = len0;
        ly = len1;
        firstgap = lastgap = 0;
        if (dmax < len1 - 1) {          /* leading gap in x */
                pp[0].spc = firstgap = len1 - dmax - 1;
                ly -= pp[0].spc;
        }
        else if (dmax > len1 - 1) {     /* leading gap in y */
                pp[1].spc = firstgap = dmax - (len1 - 1);
                lx -= pp[1].spc;
        }
        if (dmax0 < len0 - 1) {         /* trailing gap in x */
                lastgap = len0 - dmax0 -1;
                lx -= lastgap;
        }
        else if (dmax0 > len0 - 1) {    /* trailing gap in y */
                lastgap = dmax0 - (len0 - 1);
                ly -= lastgap;
        }
        getmat(lx, ly, firstgap, lastgap);
        pr_align();
}
```

Table 1 (cont')

getmat

```
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
        int     lx, ly;                 /* "core" (minus endgaps) */
        int     firstgap, lastgap;      /* leading trailing overlap */
{
        int             nm, i0, i1, siz0, siz1;
        char            outx[32];
        double          pct;
        register        n0, n1;
        register char   *p0, *p1;

        /* get total matches, score
         */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
        p1 = seqx[1] + pp[0].spc;
        n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;

        nm = 0;
        while ( *p0 && *p1 ) {
                if (siz0) {
                        p1++;
                        n1++;
                        siz0--;
                }
                else if (siz1) {
                        p0++;
                        n0++;
                        siz1--;
                }
                else {
                        if (xbm[*p0-'A']&xbm[*p1-'A'])
                                nm++;
                        if (n0++ == pp[0].x[i0])
                                siz0 = pp[0].n[i0++];
                        if (n1++ == pp[1].x[i1])
                                siz1 = pp[1].n[i1++];
                        p0++;
                        p1++;
                }
        }

        /* pct homology:
         * if penalizing endgaps, base is the shorter seq
         * else, knock off overhangs and take shorter core
         */
        if (endgaps)
                lx = (len0 < len1)? len0 : len1;
        else
                lx = (lx < ly)? lx : ly;
        pct = 100.*(double)nm/(double)lx;
        fprintf(fx, "\n");
        fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
                nm, (nm == 1)? "" : "es", lx, pct);
```

Table 1 (cont')

...getmat

```
fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
        (void) sprintf(outx, " (%d %s%s)",
                ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
        fprintf(fx,"%s", outx);

fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
                ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
        fprintf(fx,"%s", outx);
}
if (dna)
        fprintf(fx,
        "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
        fprintf(fx,
        "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINS0, PINS1);
if (endgaps)
        fprintf(fx,
        "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
        lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
else
        fprintf(fx, "<endgaps not penalized\n");
}
static          nm;             /* matches in core -- for checking */
static          lmax;           /* lengths of stripped file names */
static          ij[2];          /* jmp index for a path */
static          nc[2];          /* number at start of current line */
static          ni[2];          /* current elem number -- for gapping */
static          siz[2];
static char     *ps[2];         /* ptr to current element */
static char     *po[2];         /* ptr to next output char slot */
static char     out[2][P_LINE]; /* output line */
static char     star[P_LINE];   /* set by stars() */

/*
 * print alignment of described in struct path pp[ ]
 */
static
pr_align()
```

pr_align

```
{
        int             nn;     /* char count */
        int             more;
        register        i;

        for (i =  0, lmax = 0; i < 2; i++) {
                nn = stripname(namex[i]);
                if (nn > lmax)
                        lmax = nn;

                nc[i] = 1;
                ni[i] = 1;
                siz[i] = ij[i] = 0;
                ps[i] = seqx[i];
                po[i] = out[i];                 }
```

Table 1 (cont')

...pr_align

```
for (nn = nm = 0, more = 1; more; ) {
        for (i = more = 0; i < 2; i++) {
                /*
                 * do we have more of this sequence?
                 */
                if (!*ps[i])
                        continue;

                more++;

                if (pp[i].spc) {        /* leading space */
                        *po[i]++ = ' ';
                        pp[i].spc--;
                }
                else if (siz[i]) {      /* in a gap */
                        *po[i]++ = '-';
                        siz[i]--;
                }
                else {                  /* we're putting a seq element
                                         */
                        *po[i] = *ps[i];
                        if (islower(*ps[i]))
                                *ps[i] = toupper(*ps[i]);
                        po[i]++;
                        ps[i]++;

                        /*
                         * are we at next gap for this seq?
                         */
                        if (ni[i] == pp[i].x[ij[i]]) {
                                /*
                                 * we need to merge all gaps
                                 * at this location
                                 */
                                siz[i] = pp[i].n[ij[i]++];
                                while (ni[i] == pp[i].x[ij[i]])
                                        siz[i] += pp[i].n[ij[i]++];
                        }
                        ni[i]++;
                }
        }
        if (++nn == olen || !more && nn) {
                dumpblock();
                for (i = 0; i < 2; i++)
                        po[i] = out[i];
                nn = 0;
        }
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
```

dumpblock

```
{
        register   i;
        for (i = 0; i < 2; i++)
                *po[i]-- = \0';
```

Table 1 (cont')

...dumpblock

```
        (void) putc('\n', fx);
        for (i = 0; i < 2; i++) {
                if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
                        if (i == 0)
                                nums(i);
                        if (i == 0 && *out[1])
                                stars();
                        putline(i);
                        if (i == 0 && *out[1])
                                fprintf(fx, star);
                        if (i == 1)
                                nums(i);
                }
        }
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
        int     ix;     /* index in out[ ] holding seq line */
{
        char            nline[P_LINE];
        register        i, j;
        register char   *pn, *px, *py;

        for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
                *pn = ' ';
        for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
                if (*py == ' ' || *py == '-')
                        *pn = ' ';
                else {
                        if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                                j = (i < 0)? -i : i;
                                for (px = pn; j; j /= 10, px--)
                                        *px = j%10 + '0';
                                if (i < 0)
                                        *px = '-';
                        }
                        else
                                *pn = ' ';
                        i++;
                }
        }
        *pn = '\0';
        nc[ix] = i;
        for (pn = nline; *pn; pn++)
                (void) putc(*pn, fx);
        (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
        int     ix;                     {
```

nums

putline

Table 1 (cont')

...putline

```
        int             i;
        register char   *px;

        for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
                (void) putc(*px, fx);
        for (; i < lmax+P_SPC; i++)
                (void) putc(' ', fx);

        /* these count from 1:
         * ni[ ] is current element (from 1)
         * nc[ ] is number at start of current line
         */
        for (px = out[ix]; *px; px++)
                (void) putc(*px&0x7F, fx);
        (void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
        stars
{
        int             i;
        register char   *p0, *p1, cx, *px;

        if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
            !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
                return;
        px = star;
        for (i = lmax+P_SPC; i; i--)
                *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
                if (isalpha(*p0) && isalpha(*p1)) {

                        if (xbm[*p0-'A']&xbm[*p1-'A']) {
                                cx = '*';
                                nm++;
                        }
                        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                                cx = '.';
                        else
                                cx = ' ';
                }
                else
                        cx = ' ';
                *px++ = cx;
        }
        *px++ = '\n';
        *px = '\0';
}
```

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
        stripname
        char    *pn;    /* file name (may be path) */
{
        register char   *px, *py;

        py = 0;
        for (px = pn; *px; px++)
                if (*px == '/')
                        py = px + 1;
        if (py)
                (void) strcpy(pn, py);
        return(strlen(pn));
}
```

Table 1 (cont')

```
/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";             /* tmp file for jmps */
FILE    *fj;

int     cleanup();                              /* cleanup tmp file */
long    lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)                                                          cleanup
        int     i;
{
        if (fj)
                (void) unlink(jname);
        exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)                                                   getseq
        char    *file;      /* file name */
        int     *len;       /* seq len */
{
        char            line[1024], *pseq;
        register char   *px, *py;
        int             natgc, tlen;
        FILE            *fp;

        if ((fp = fopen(file,"r")) == 0) {
                fprintf(stderr,"%s: can't read %s\n", prog, file);
                exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++)
                        if (isupper(*px) || islower(*px))
                                tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
                fprintf(stderr,"%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
                exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

Table 1 (cont')

...getseq

```
        py = pseq + 4;
        *len = tlen;
        rewind(fp);

        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++) {
                        if (isupper(*px))
                                *py++ = *px;
                        else if (islower(*px))
                                *py++ = toupper(*px);
                        if (index("ATGCU",*(py-1)))
                                natgc++;
                }
        }
        *py++ = '\0';
        *py = '\0';
        (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
}

char    *
g_calloc(msg, nx, sz)
        char    *msg;           /* program, calling routine */
        int     nx, sz;         /* number and size of elements */
{
        char            *px, *calloc();

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
                if (*msg) {
                        fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                        exit(1);
                }
        }
        return(px);
}

/*
 * get final jmps from dx[ ] or tmp file, set pp[ ], reset dmax: main()
 */
readjmps()
        readjmps
{
        int             fd = -1;
        int             siz, i0, i1;
        register  i, j, xx;

        if (fj) {
                (void) fclose(fj);
                if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                        fprintf(stderr, "%s: can't open() %s\n", prog, jname);
                        cleanup(1);
                }
        }
        for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
                while (1) {
                        for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                                ;
```

g_calloc

Table 1 (cont')

...readjmps

```
                if (j < 0 && dx[dmax].offset && fj) {
                        (void) lseek(fd, dx[dmax].offset, 0);
                        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                        dx[dmax].ijmp = MAXJMP-1;
                }
                else
                        break;
        }
        if (i >= JMPS) {
                fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                cleanup(1);
        }
        if (j >= 0) {
                siz = dx[dmax].jp.n[j];
                xx = dx[dmax].jp.x[j];
                dmax += siz;
                if (siz < 0) {                  /* gap in second seq */
                        pp[1].n[i1] = -siz;
                        xx += siz;
                        /* id = xx - yy + len1 - 1
                         */
                        pp[1].x[i1] = xx - dmax + len1 - 1;
                        gapy++;
                        ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
                        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
                        i1++;
                }
                else if (siz > 0) {     /* gap in first seq */
                        pp[0].n[i0] = siz;
                        pp[0].x[i0] = xx;
                        gapx++;
                        ngapx += siz;
/* ignore MAXGAP when doing endgaps */
                        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
                        i0++;
                }
        }
        else
                break;
}

/* reverse the order of jmps
 */
for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
        (void) close(fd);
if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
}                                       }
```

Table 1 (cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejmps(ix)
        writejmps
        int     ix;
{
        char    *mktemp();

        if (!fj) {
                if (mktemp(jname) < 0) {
                        fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                        cleanup(1);
                }
                if ((fj = fopen(jname, "w")) == 0) {
                        fprintf(stderr, "%s: can't write %s\n", prog, jname);
                        exit(1);
                }
        }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
        }
```

Table 2

PRO	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
5 divided by 10 = 50%

Table 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
6 divided by 14 = 42.9%

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been disclosed. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native

protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an alpha-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, $CaCl_2$, $CaPO_4$, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan*^{r}; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan*^{r}; *E. coli* W3110 strain 40B4, which is strain

37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,* and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination

sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be

employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Tissue Distribution

The location of tissues expressing the PRO can be identified by determining mRNA expression in various human tissues. The location of such genes provides information about which tissues are most likely to be affected by the stimulating and inhibiting activities of the PRO polypeptides. The location of a gene in a specific tissue also provides sample tissue for the activity blocking assays discussed below.

As noted before, gene expression in various tissues may be measured by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA (Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 [1980]), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

Gene expression in various tissues, alternatively, may be measured by immunological methods, such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining

and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence of a PRO polypeptide or against a synthetic peptide based on the DNA sequences encoding the PRO polypeptide or against an exogenous sequence fused to a DNA encoding a PRO polypeptide and encoding a specific antibody epitope. General techniques for generating antibodies, and special protocols for Northern blotting and *in situ* hybridization are provided below.

F. Antibody Binding Studies

The activity of the PRO polypeptides can be further verified by antibody binding studies, in which the ability of anti-PRO antibodies to inhibit the effect of the PRO polypeptides, respectively, on tissue cells is tested. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies, the preparation of which will be described hereinbelow.

Antibody binding studies may be carried out in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158 (CRC Press, Inc., 1987).

Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of antibody. The amount of target protein in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies preferably are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex. See, *e.g.*, US Pat No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

For immunohistochemistry, the tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin, for example.

G. Cell-Based Assays

Cell-based assays and animal models for immune related diseases can be used to further understand the relationship between the genes and polypeptides identified herein and the development and pathogenesis of immune related disease.

In a different approach, cells of a cell type known to be involved in a particular immune related disease are transfected with the cDNAs described herein, and the ability of these cDNAs to stimulate or inhibit immune function is analyzed. Suitable cells can be transfected with the desired gene, and monitored for immune function activity. Such transfected cell lines can then be used to test the ability of poly- or monoclonal antibodies or antibody compositions to inhibit or stimulate immune function, for example to modulate T-cell proliferation or inflammatory cell infiltration. Cells transfected with the coding sequences of the genes identified herein can further be used to identify drug candidates for the treatment of immune

related diseases.

In addition, primary cultures derived from transgenic animals (as described below) can be used in the cell-based assays herein, although stable cell lines are preferred. Techniques to derive continuous cell lines from transgenic animals are well known in the art (see, *e.g.,* Small *et al., Mol. Cell. Biol.* 5: 642-648 [1985]).

One suitable cell based assay is the mixed lymphocyte reaction (MLR). *Current Protocols in Immunology*, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc. In this assay, the ability of a test compound to stimulate or inhibit the proliferation of activated T cells is assayed. A suspension of responder T cells is cultured with allogeneic stimulator cells and the proliferation of T cells is measured by uptake of tritiated thymidine. This assay is a general measure of T cell reactivity. Since the majority of T cells respond to and produce IL-2 upon activation, differences in responsiveness in this assay in part reflect differences in IL-2 production by the responding cells. The MLR results can be verified by a standard lymphokine (IL-2) detection assay. *Current Protocols in Immunology*, above, 3.15, 6.3.

A proliferative T cell response in an MLR assay may be due to direct mitogenic properties of an assayed molecule or to external antigen induced activation. Additional verification of the T cell stimulatory activity of the PRO polypeptides can be obtained by a costimulation assay. T cell activation requires an antigen specific signal mediated through the T-cell receptor (TCR) and a costimulatory signal mediated through a second ligand binding interaction, for example, the B7 (CD80, CD86)/CD28 binding interaction. CD28 crosslinking increases lymphokine secretion by activated T cells. T cell activation has both negative and positive controls through the binding of ligands which have a negative or positive effect. CD28 and CTLA-4 are related glycoproteins in the Ig superfamily which bind to B7. CD28 binding to B7 has a positive costimulation effect of T cell activation; conversely, CTLA-4 binding to B7 has a T cell deactivating effect. Chambers, C. A. and Allison, *J. P., Curr. Opin. Immunol.* (1997) 9:396. Schwartz, R. H., *Cell* (1992) 71:1065; Linsey, P. S. and Ledbetter, J. A., *Annu. Rev. Immunol.* (1993) 11:191; June, C. H. *et al, Immunol. Today* (1994) 15:321; Jenkins, M. K., *Immunity* (1994) 1:405. In a costimulation assay, the PRO polypeptides are assayed for T cell costimulatory or inhibitory activity.

Direct use of a stimulating compound as in the invention has been validated in experiments with 4-1BB glycoprotein, a member of the tumor necrosis factor receptor family, which binds to a ligand (4-1BBL) expressed on primed T cells and signals T cell activation and growth. Alderson, M. E. *et al., J. Immunol.* (1994) 24:2219.

The use of an agonist stimulating compound has also been validated experimentally. Activation of 4-1BB by treatment with an agonist anti-4-1BB antibody enhances eradication of tumors. Hellstrom, I. and Hellstrom, K. E., *Crit. Rev. Immunol.* (1998) 18:1. Immunoadjuvant therapy for treatment of tumors, described in more detail below, is another example of the use of the stimulating compounds of the invention.

Alternatively, an immune stimulating or enhancing effect can also be achieved by administration of a PRO which has vascular permeability enhancing properties. Enhanced vascular permeability would be beneficial to disorders which can be attenuated by local infiltration of immune cells (*e.g.*, monocytes, eosinophils, PMNs) and inflammation.

On the other hand, PRO polypeptides, as well as other compounds of the invention, which are direct inhibitors of T cell proliferation/activation, lymphokine secretion, and/or vascular permeability can be directly used to suppress the immune response. These compounds are useful to reduce the degree of the immune response and to treat immune related diseases characterized by a hyperactive, superoptimal, or autoimmune response. This use of the compounds of the invention has been validated by the experiments described above in which CTLA-4 binding to receptor B7 deactivates T cells. The direct inhibitory compounds of the invention function in an analogous manner. The use of compound which suppress vascular permeability would be expected to reduce inflammation. Such uses would be beneficial in treating conditions associated with excessive inflammation.

Alternatively, compounds, *e.g.,* antibodies, which bind to stimulating PRO polypeptides and block the stimulating effect of these molecules produce a net inhibitory effect and can be used to suppress the T cell mediated immune response by inhibiting T cell proliferation/activation and/or lymphokine secretion. Blocking the stimulating effect of the polypeptides suppresses the immune response of the mammal. This use has been validated in experiments using an anti-IL2 antibody. In these experiments, the antibody binds to IL2 and blocks binding of IL2 to its receptor thereby achieving a T cell inhibitory effect.

H. Animal Models

The results of the cell based in vitro assays can be further verified using *in vivo* animal models and assays for T-cell function. A variety of well known animal models can be used to further understand the role of the genes identified herein in the development and pathogenesis of immune related disease, and to test the efficacy of candidate therapeutic agents, including antibodies, and other antagonists of the native polypeptides, including small molecule antagonists. The *in vivo* nature of such models makes them predictive of responses in human patients. Animal models of immune related diseases include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, *e.g.,* murine models. Such models can be generated by introducing cells into syngeneic mice using standard techniques, *e.g.,* subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, implantation under the renal capsule, *etc.*

Graft-versus-host disease occurs when immunocompetent cells are transplanted into immunosuppressed or tolerant patients. The donor cells recognize and respond to host antigens. The response can vary from life threatening severe inflammation to mild cases of diarrhea and weight loss. Graft-versus-host disease models provide a means of assessing T cell reactivity against MHC antigens and minor transplant antigens. A suitable procedure is described in detail in Current Protocols in Immunology, above, unit 4.3.

An animal model for skin allograft rejection is a means of testing the ability of T cells to mediate *in vivo* tissue destruction and a measure of their role in transplant rejection. The most common and accepted models use murine tail-skin grafts. Repeated experiments have shown that skin allograft rejection is mediated by T cells, helper T cells and killer-effector T cells, and not antibodies. Auchincloss, H. Jr. and Sachs, D. H., *Fundamental Immunology*, 2nd ed., W. E. Paul ed., Raven Press, NY, 1989, 889-992. A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.4. Other transplant rejection models which can be used to test the compounds of the invention are the allogeneic heart

transplant models described by Tanabe, M. *et al, Transplantation* (1994) 58:23 and Tinubu, S. A. *et al, J. Immunol.* (1994) 4330-4338.

Animal models for delayed type hypersensitivity provides an assay of cell mediated immune function as well. Delayed type hypersensitivity reactions are a T cell mediated *in vivo* immune response characterized by inflammation which does not reach a peak until after a period of time has elapsed after challenge with an antigen. These reactions also occur in tissue specific autoimmune diseases such as multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE, a model for MS). A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.5.

EAE is a T cell mediated autoimmune disease characterized by T cell and mononuclear cell inflammation and subsequent demyelination of axons in the central nervous system. EAE is generally considered to be a relevant animal model for MS in humans. Bolton, C., *Multiple Sclerosis* (1995) 1:143. Both acute and relapsing-remitting models have been developed. The compounds of the invention can be tested for T cell stimulatory or inhibitory activity against immune mediated demyelinating disease using the protocol described in *Current Protocols in Immunology*, above, units 15.1 and 15.2. See also the models for myelin disease in which oligodendrocytes or Schwann cells are grafted into the central nervous system as described in Duncan, I. D. *et al, Molec. Med. Today* (1997) 554-561.

Contact hypersensitivity is a simple delayed type hypersensitivity *in vivo* assay of cell mediated immune function. In this procedure, cutaneous exposure to exogenous haptens which gives rise to a delayed type hypersensitivity reaction which is measured and quantitated. Contact sensitivity involves an initial sensitizing phase followed by an elicitation phase. The elicitation phase occurs when the T lymphocytes encounter an antigen to which they have had previous contact. Swelling and inflammation occur, making this an excellent model of human allergic contact dermatitis. A suitable procedure is described in detail in *Current Protocols in Immunology*, Eds. J. E. Cologan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach and W. Strober, John Wiley & Sons, Inc., 1994, unit 4.2. See also Grabbe, S. and Schwarz, T, *Immun. Today* 19 (1): 37-44 (1998) .

An animal model for arthritis is collagen-induced arthritis. This model shares clinical, histological and immunological characteristics of human autoimmune rheumatoid arthritis and is an acceptable model for human autoimmune arthritis. Mouse and rat models are characterized by synovitis, erosion of cartilage and subchondral bone. The compounds of the invention can be tested for activity against autoimmune arthritis using the protocols described in *Current Protocols in Immunology*, above, units 15.5. See also the model using a monoclonal antibody to CD18 and VLA-4 integrins described in Issekutz, A.C. *et al., Immunology* (1996) 88:569.

A model of asthma has been described in which antigen-induced airway hyper-reactivity, pulmonary eosinophilia and inflammation are induced by sensitizing an animal with ovalbumin and then challenging the animal with the same protein delivered by aerosol. Several animal models (guinea pig, rat, non-human primate) show symptoms similar to atopic asthma in humans upon challenge with aerosol antigens. Murine models have many of the features of human asthma. Suitable procedures to test the compounds of the invention for activity and effectiveness in the treatment of asthma are described by Wolyniec, W. W. *et al, Am. J. Respir. Cell Mol. Biol.* (1998) 18:777 and the references cited therein.

Additionally, the compounds of the invention can be tested on animal models for psoriasis like diseases. Evidence suggests a T cell pathogenesis for psoriasis. The compounds of the invention can be tested in the scid/scid mouse model described by Schon, M. P. *et al, Nat. Med.* (1997) 3:183, in which the mice demonstrate histopathologic skin lesions resembling psoriasis. Another suitable model is the human skin/scid mouse chimera prepared as described by Nickoloff, B. J. *et al, Am. J. Path.* (1995) 146:580.

Recombinant (transgenic) animal models can be engineered by introducing the coding portion of the genes identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, *e.g.*, baboons, chimpanzees and monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (Hoppe and Wanger, U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (*e.g.*, Van der Putten *et al., Proc. Natl. Acad. Sci. USA* 82, 6148-615 [1985]); gene targeting in embryonic stem cells (Thompson *et al., Cell* 56, 313-321 [1989]); electroporation of embryos (Lo, *Mol. Cel. Biol.* 3, 1803-1814 [1983]); sperm-mediated gene transfer (Lavitrano *et al., Cell* 57, 717-73 [1989]). For review, see, for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, *e.g.*, head-to-head or head-to-tail tandems. Selective introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko *et al., Proc. Natl. Acad. Sci. USA* 89, 6232-636 (1992).

The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry.

The animals may be further examined for signs of immune disease pathology, for example by histological examination to determine infiltration of immune cells into specific tissues. Blocking experiments can also be performed in which the transgenic animals are treated with the compounds of the invention to determine the extent of the T cell proliferation stimulation or inhibition of the compounds. In these experiments, blocking antibodies which bind to the PRO polypeptide, prepared as described above, are administered to the animal and the effect on immune function is determined.

Alternatively, "knock out" animals can be constructed which have a defective or altered gene encoding a polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular polypeptide can be used to clone genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see *e.g.*, Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA

has homologously recombined with the endogenous DNA are selected [see *e.g.*, Li *et al.*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse or rat) to form aggregation chimeras [see *e.g.*, Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the polypeptide.

I. ImmunoAdjuvant Therapy

In one embodiment, the immunostimulating compounds of the invention can be used in immunoadjuvant therapy for the treatment of tumors (cancer). It is now well established that T cells recognize human tumor specific antigens. One group of tumor antigens, encoded by the MAGE, BAGE and GAGE families of genes, are silent in all adult normal tissues , but are expressed in significant amounts in tumors, such as melanomas, lung tumors, head and neck tumors, and bladder carcinomas. DeSmet, C. *et al.*, (1996) *Proc. Natl. Acad. Sci. USA*, 93:7149. It has been shown that costimulation of T cells induces tumor regression and an antitumor response both *in vitro* and *in vivo*. Melero, I. *et al.*, *Nature Medicine* (1997) 3:682; Kwon, E. D. *et al.*, *Proc. Natl. Acad. Sci. USA* (1997) 94: 8099; Lynch, D. H. *et al, Nature Medicine* (1997) 3:625; Finn, O. J. and Lotze, M. T., *J. Immunol.* (1998) 21:114. The stimulatory compounds of the invention can be administered as adjuvants, alone or together with a growth regulating agent, cytotoxic agent or chemotherapeutic agent, to stimulate T cell proliferation/activation and an antitumor response to tumor antigens. The growth regulating, cytotoxic, or chemotherapeutic agent may be administered in conventional amounts using known administration regimes. Immunostimulating activity by the compounds of the invention allows reduced amounts of the growth regulating, cytotoxic, or chemotherapeutic agents thereby potentially lowering the toxicity to the patient.

J. Screening Assays for Drug Candidates

Screening assays for drug candidates are designed to identify compounds that bind to or complex with the polypeptides encoded by the genes identified herein or a biologically active fragment thereof, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds, including peptides, preferably soluble peptides, (poly)peptide-immunoglobulin fusions, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art. All assays are common in that they call for contacting the drug candidate with a polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to

interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, *e.g.,* on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the polypeptide and drying. Alternatively, an immobilized antibody, *e.g.,* a monoclonal antibody, specific for the polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, *e.g.,* the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, *e.g.,* by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labelled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular protein encoded by a gene identified herein, its interaction with that protein can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers [Fields and Song, *Nature (London)* 340, 245-246 (1989); Chien *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 9578-9582 (1991)] as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA* 89, 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, while the other one functioning as the transcription activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lac*Z reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

In order to find compounds that interfere with the interaction of a gene identified herein and other intra- or extracellular components can be tested, a reaction mixture is usually prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a test compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described above.

The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

K. Compositions and Methods for the Treatment of Immune Related Diseases

The compositions useful in the treatment of immune related diseases include, without limitation, proteins, antibodies, small organic molecules, peptides, phosphopeptides, antisense and ribozyme molecules, triple helix molecules, *etc.* that inhibit or stimulate immune function, for example, T cell proliferation/activation, lymphokine release, or immune cell infiltration.

For example, antisense RNA and RNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation initiation site, *e.g.,* between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, *e.g.,* Rossi, *Current Biology* 4, 469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, *e.g.,* PCT publication No. WO 97/33551, *supra.*

These molecules can be identified by any or any combination of the screening assays discussed above and/or by any other screening techniques well known for those skilled in the art.

L. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology 10, 779-783 (1992); Lonberg *et al.*, Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild *et al.*, Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by

affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form

the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al* ., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

M. Pharmaceutical Compositions

The active PRO molecules of the invention (*e.g.*, PRO polypeptides, anti-PRO antibodies, and/or variants of each) as well as other molecules identified by the screening assays disclosed above, can be administered for the treatment of immune related diseases, in the form of pharmaceutical compositions.

Therapeutic formulations of the active PRO molecule, preferably a polypeptide or antibody of the invention, are prepared for storage by mixing the active molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

Compounds identified by the screening assays disclosed herein can be formulated in an analogous manner, using standard techniques well known in the art.

Lipofections or liposomes can also be used to deliver the PRO molecule into cells. Where antibody fragments are used, the smallest inhibitory fragment which specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable region sequences of an antibody, peptide molecules can be designed which retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (see, *e.g.*, Marasco *et al.*, *Proc. Natl. Acad. Sci. USA* 90, 7889-7893 [1993]).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine or growth inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active PRO molecules may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980).

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished

by filtration through sterile filtration membranes.

Sustained-release preparations or the PRO molecules may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

N. Methods of Treatment

It is contemplated that the polypeptides, antibodies and other active compounds of the present invention may be used to treat various immune related diseases and conditions, such as T cell mediated diseases, including those characterized by infiltration of inflammatory cells into a tissue, stimulation of T-cell proliferation, inhibition of T-cell proliferation, increased or decreased vascular permeability or the inhibition thereof.

Exemplary conditions or disorders to be treated with the polypeptides, antibodies and other compounds of the invention, include, but are not limited to systemic lupus erythematosis, rheumatoid arthritis, juvenile chronic arthritis, osteoarthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic

diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In systemic lupus erythematosus, the central mediator of disease is the production of auto-reactive antibodies to self proteins/tissues and the subsequent generation of immune-mediated inflammation. Antibodies either directly or indirectly mediate tissue injury. Though T lymphocytes have not been shown to be directly involved in tissue damage, T lymphocytes are required for the development of auto-reactive antibodies. The genesis of the disease is thus T lymphocyte dependent. Multiple organs and systems are affected clinically including kidney, lung, musculoskeletal system, mucocutaneous, eye, central nervous system, cardiovascular system, gastrointestinal tract, bone marrow and blood.

Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease that mainly involves the synovial membrane of multiple joints with resultant injury to the articular cartilage. The pathogenesis is T lymphocyte dependent and is associated with the production of rheumatoid factors, auto-antibodies directed against self IgG, with the resultant formation of immune complexes that attain high levels in joint fluid and blood. These complexes in the joint may induce the marked infiltrate of lymphocytes and monocytes into the synovium and subsequent marked synovial changes; the joint space/fluid if infiltrated by similar cells with the addition of numerous neutrophils. Tissues affected are primarily the joints, often in symmetrical pattern. However, extra-articular disease also occurs in two major forms. One form is the development of extra-articular lesions with ongoing progressive joint disease and typical lesions of pulmonary fibrosis, vasculitis, and cutaneous ulcers. The second form of extra-articular disease is the so called Felty's syndrome which occurs late in the RA disease course, sometimes after joint disease has become quiescent, and involves the presence of neutropenia, thrombocytopenia and splenomegaly. This can be accompanied by vasculitis in multiple organs with formations of infarcts, skin ulcers and gangrene. Patients often also develop rheumatoid nodules in the subcutis tissue overlying affected joints; the nodules late stage have necrotic centers surrounded by a mixed inflammatory cell infiltrate. Other manifestations which can occur in RA include: pericarditis, pleuritis, coronary arteritis, intestitial pneumonitis with pulmonary fibrosis, keratoconjunctivitis sicca, and rhematoid nodules.

Juvenile chronic arthritis is a chronic idiopathic inflammatory disease which begins often at less than 16 years of age. Its phenotype has some similarities to RA; some patients which are rhematoid factor positive are classified as juvenile rheumatoid arthritis. The disease is sub-classified into three major categories: pauciarticular, polyarticular, and systemic. The arthritis can be severe and is typically destructive and leads to joint ankylosis and retarded growth. Other manifestations can include chronic anterior uveitis and systemic amyloidosis.

Spondyloarthropathies are a group of disorders with some common clinical features and the common association with the expression of HLA-B27 gene product. The disorders include: ankylosing sponylitis, Reiter's syndrome (reactive arthritis), arthritis associated with inflammatory bowel disease, spondylitis associated with psoriasis, juvenile onset spondyloarthropathy and undifferentiated spondyloarthropathy. Distinguishing features include sacroileitis with or without spondylitis; inflammatory asymmetric arthritis; association with HLA-B27 (a serologically defined allele of the HLA-B locus of class I MHC); ocular inflammation, and absence of autoantibodies associated with other rheumatoid disease. The cell most implicated as key to induction of the disease is the CD8+ T lymphocyte, a cell which targets

antigen presented by class I MHC molecules. CD8+ T cells may react against the class I MHC allele HLA-B27 as if it were a foreign peptide expressed by MHC class I molecules. It has been hypothesized that an epitope of HLA-B27 may mimic a bacterial or other microbial antigenic epitope and thus induce a CD8+ T cells response.

Systemic sclerosis (scleroderma) has an unknown etiology. A hallmark of the disease is induration of the skin; likely this is induced by an active inflammatory process. Scleroderma can be localized or systemic; vascular lesions are common and endothelial cell injury in the microvasculature is an early and important event in the development of systemic sclerosis; the vascular injury may be immune mediated. An immunologic basis is implied by the presence of mononuclear cell infiltrates in the cutaneous lesions and the presence of anti-nuclear antibodies in many patients. ICAM-1 is often upregulated on the cell surface of fibroblasts in skin lesions suggesting that T cell interaction with these cells may have a role in the pathogenesis of the disease. Other organs involved include: the gastrointestinal tract: smooth muscle atrophy and fibrosis resulting in abnormal peristalsis/motility; kidney: concentric subendothelial intimal proliferation affecting small arcuate and interlobular arteries with resultant reduced renal cortical blood flow, results in proteinuria, azotemia and hypertension; skeletal muscle: atrophy, interstitial fibrosis; inflammation; lung: interstitial pneumonitis and interstitial fibrosis; and heart: contraction band necrosis, scarring/fibrosis.

Idiopathic inflammatory myopathies including dermatomyositis, polymyositis and others are disorders of chronic muscle inflammation of unknown etiology resulting in muscle weakness. Muscle injury/inflammation is often symmetric and progressive. Autoantibodies are associated with most forms. These myositis-specific autoantibodies are directed against and inhibit the function of components, proteins and RNA's, involved in protein synthesis.

Sjögren's syndrome is due to immune-mediated inflammation and subsequent functional destruction of the tear glands and salivary glands. The disease can be associated with or accompanied by inflammatory connective tissue diseases. The disease is associated with autoantibody production against Ro and La antigens, both of which are small RNA-protein complexes. Lesions result in keratoconjunctivitis sicca, xerostomia, with other manifestations or associations including bilary cirrhosis, peripheral or sensory neuropathy, and palpable purpura.

Systemic vasculitis are diseases in which the primary lesion is inflammation and subsequent damage to blood vessels which results in ischemia/necrosis/degeneration to tissues supplied by the affected vessels and eventual end-organ dysfunction in some cases. Vasculitides can also occur as a secondary lesion or sequelae to other immune-inflammatory mediated diseases such as rheumatoid arthritis, systemic sclerosis, *etc.*, particularly in diseases also associated with the formation of immune complexes. Diseases in the primary systemic vasculitis group include: systemic necrotizing vasculitis: polyarteritis nodosa, allergic angiitis and granulomatosis, polyangiitis; Wegener's granulomatosis; lymphomatoid granulomatosis; and giant cell arteritis. Miscellaneous vasculitides include: mucocutaneous lymph node syndrome (MLNS or Kawasaki's disease), isolated CNS vasculitis, Behet's disease, thromboangiitis obliterans (Buerger's disease) and cutaneous necrotizing venulitis. The pathogenic mechanism of most of the types of vasculitis listed is believed to be primarily due to the deposition of immunoglobulin complexes in the vessel wall and subsequent induction of an inflammatory response either via ADCC, complement activation, or both.

Sarcoidosis is a condition of unknown etiology which is characterized by the presence of epithelioid granulomas in nearly any tissue in the body; involvement of the lung is most common. The pathogenesis involves the persistence of activated macrophages and lymphoid cells at sites of the disease with subsequent chronic sequelae resultant from the release of locally and systemically active products released by these cell types.

Autoimmune hemolytic anemia including autoimmune hemolytic anemia, immune pancytopenia, and paroxysmal noctural hemoglobinuria is a result of production of antibodies that react with antigens expressed on the surface of red blood cells (and in some cases other blood cells including platelets as well) and is a reflection of the removal of those antibody coated cells via complement mediated lysis and/or ADCC/Fc-receptor-mediated mechanisms.

In autoimmune thrombocytopenia including thrombocytopenic purpura, and immune-mediated thrombocytopenia in other clinical settings, platelet destruction/removal occurs as a result of either antibody or complement attaching to platelets and subsequent removal by complement lysis, ADCC or FC-receptor mediated mechanisms.

Thyroiditis including Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, and atrophic thyroiditis, are the result of an autoimmune response against thyroid antigens with production of antibodies that react with proteins present in and often specific for the thyroid gland. Experimental models exist including spontaneous models: rats (BUF and BB rats) and chickens (obese chicken strain); inducible models: immunization of animals with either thyroglobulin, thyroid microsomal antigen (thyroid peroxidase).

Type I diabetes mellitus or insulin-dependent diabetes is the autoimmune destruction of pancreatic islet β cells; this destruction is mediated by auto-antibodies and auto-reactive T cells. Antibodies to insulin or the insulin receptor can also produce the phenotype of insulin-non-responsiveness.

Immune mediated renal diseases, including glomerulonephritis and tubulointerstitial nephritis, are the result of antibody or T lymphocyte mediated injury to renal tissue either directly as a result of the production of autoreactive antibodies or T cells against renal antigens or indirectly as a result of the deposition of antibodies and/or immune complexes in the kidney that are reactive against other, non-renal antigens. Thus other immune-mediated diseases that result in the formation of immune-complexes can also induce immune mediated renal disease as an indirect sequelae. Both direct and indirect immune mechanisms result in inflammatory response that produces/induces lesion development in renal tissues with resultant organ function impairment and in some cases progression to renal failure. Both humoral and cellular immune mechanisms can be involved in the pathogenesis of lesions.

Demyelinating diseases of the central and peripheral nervous systems, including Multiple Sclerosis; idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome; and Chronic Inflammatory Demyelinating Polyneuropathy, are believed to have an autoimmune basis and result in nerve demyelination as a result of damage caused to oligodendrocytes or to myelin directly. In MS there is evidence to suggest that disease induction and progression is dependent on T lymphocytes. Multiple Sclerosis is a demyelinating disease that is T lymphocyte-dependent and has either a relapsing-remitting course or a chronic progressive course. The etiology is unknown; however, viral infections, genetic predisposition, environment, and autoimmunity all contribute. Lesions contain infiltrates of predominantly T lymphocyte mediated,

microglial cells and infiltrating macrophages; CD4+ T lymphocytes are the predominant cell type at lesions. The mechanism of oligodendrocyte cell death and subsequent demyelination is not known but is likely T lymphocyte driven.

Inflammatory and Fibrotic Lung Disease, including Eosinophilic Pneumonias; Idiopathic Pulmonary Fibrosis, and Hypersensitivity Pneumonitis may involve a disregulated immune-inflammatory response. Inhibition of that response would be of therapeutic benefit.

Autoimmune or Immune-mediated Skin Disease including Bullous Skin Diseases, Erythema Multiforme, and Contact Dermatitis are mediated by auto-antibodies, the genesis of which is T lymphocyte-dependent.

Psoriasis is a T lymphocyte-mediated inflammatory disease. Lesions contain infiltrates of T lymphocytes, macrophages and antigen processing cells, and some neutrophils.

Allergic diseases, including asthma; allergic rhinitis; atopic dermatitis; food hypersensitivity; and urticaria are T lymphocyte dependent. These diseases are predominantly mediated by T lymphocyte induced inflammation, IgE mediated-inflammation or a combination of both.

Transplantation associated diseases, including Graft rejection and Graft-Versus-Host-Disease (GVHD) are T lymphocyte-dependent; inhibition of T lymphocyte function is ameliorative.

Other diseases in which intervention of the immune and/or inflammatory response have benefit are infectious disease including but not limited to viral infection (including but not limited to AIDS, hepatitis A, B, C, D, E and herpes) bacterial infection, fungal infections, and protozoal and parasitic infections (molecules (or derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response to infectious agents), diseases of immunodeficiency (molecules/derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response for conditions of inherited, acquired, infectious induced (as in HIV infection), or iatrogenic (*i.e.,* as from chemotherapy) immunodeficiency, and neoplasia.

It has been demonstrated that some human cancer patients develop an antibody and/or T lymphocyte response to antigens on neoplastic cells. It has also been shown in animal models of neoplasia that enhancement of the immune response can result in rejection or regression of that particular neoplasm. Molecules that enhance the T lymphocyte response in the MLR have utility *in vivo* in enhancing the immune response against neoplasia. Molecules which enhance the T lymphocyte proliferative response in the MLR (or small molecule agonists or antibodies that affected the same receptor in an agonistic fashion) can be used therapeutically to treat cancer. Molecules that inhibit the lymphocyte response in the MLR also function *in vivo* during neoplasia to suppress the immune response to a neoplasm; such molecules can either be expressed by the neoplastic cells themselves or their expression can be induced by the neoplasm in other cells. Antagonism of such inhibitory molecules (either with antibody, small molecule antagonists or other means) enhances immune-mediated tumor rejection.

Additionally, inhibition of molecules with proinflammatory properties may have therapeutic benefit in reperfusion injury; stroke; myocardial infarction; atherosclerosis; acute lung injury; hemorrhagic shock; burn; sepsis/septic shock; acute tubular necrosis; endometriosis; degenerative joint disease and pancreatis.

The compounds of the present invention, *e.g.,* polypeptides or antibodies, are administered to a mammal, preferably a human, in accord with known methods, such as intravenous administration as a bolus

or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation (intranasal, intrapulmonary) routes. Intravenous or inhaled administration of polypeptides and antibodies is preferred.

In immunoadjuvant therapy, other therapeutic regimens, such administration of an anti-cancer agent, may be combined with the administration of the proteins, antibodies or compounds of the instant invention. For example, the patient to be treated with a the immunoadjuvant of the invention may also receive an anti-cancer agent (chemotherapeutic agent) or radiation therapy. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in *Chemotherapy Service* Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992). The chemotherapeutic agent may precede, or follow administration of the immunoadjuvant or may be given simultaneously therewith. Additionally, an anti-estrogen compound such as tamoxifen or an anti-progesterone such as onapristone (see, EP 616812) may be given in dosages known for such molecules.

It may be desirable to also administer antibodies against other immune disease associated or tumor associated antigens, such as antibodies which bind to CD20, CD11a, CD18, ErbB2, EGFR, ErbB3, ErbB4, or vascular endothelial factor (VEGF). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be coadministered to the patient. Sometimes, it may be beneficial to also administer one or more cytokines to the patient. In one embodiment, the PRO polypeptides are coadministered with a growth inhibitory agent. For example, the growth inhibitory agent may be administered first, followed by a PRO polypeptide. However, simultaneous administration or administration first is also contemplated. Suitable dosages for the growth inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth inhibitory agent and the PRO polypeptide.

For the treatment or reduction in the severity of immune related disease, the appropriate dosage of an a compound of the invention will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the compound, and the discretion of the attending physician. The compound is suitably administered to the patient at one time or over a series of treatments.

For example, depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (*e.g.*, 0.1-20 mg/kg) of polypeptide or antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

O. Articles of Manufacture

In another embodiment of the invention, an article of manufacture containing materials (*e.g.*, comprising a PRO molecule) useful for the diagnosis or treatment of the disorders described above is provided. The article of manufacture comprises a container and an instruction. Suitable containers include,

for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for diagnosing or treating the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is usually a polypeptide or an antibody of the invention. An instruction or label on, or associated with, the container indicates that the composition is used for diagnosing or treating the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

P. Diagnosis and Prognosis of Immune Related Disease

Cell surface proteins, such as proteins which are overexpressed in certain immune related diseases, are excellent targets for drug candidates or disease treatment. The same proteins along with secreted proteins encoded by the genes amplified in immune related disease states find additional use in the diagnosis and prognosis of these diseases. For example, antibodies directed against the protein products of genes amplified in multiple sclerosis, rheumatoid arthritis, or another immune related disease, can be used as diagnostics or prognostics.

For example, antibodies, including antibody fragments, can be used to qualitatively or quantitatively detect the expression of proteins encoded by amplified or overexpressed genes ("marker gene products"). The antibody preferably is equipped with a detectable, *e.g.*, fluorescent label, and binding can be monitored by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. These techniques are particularly suitable, if the overexpressed gene encodes a cell surface protein Such binding assays are performed essentially as described above.

In situ detection of antibody binding to the marker gene products can be performed, for example, by immunofluorescence or immunoelectron microscopy. For this purpose, a histological specimen is removed from the patient, and a labeled antibody is applied to it, preferably by overlaying the antibody on a biological sample. This procedure also allows for determining the distribution of the marker gene product in the tissue examined. It will be apparent for those skilled in the art that a wide variety of histological methods are readily available for *in situ* detection.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Microarray analysis of stimulated T-cells

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (in this instance, activated CD4+ T cells) sample is greater than hybridization signal of a probe from a control (in this instance, non-stimulated CD4 + T cells) sample, the gene or genes overexpressed in the test tissue are identified. The implication of this result is that an overexpressed protein in a test tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In one example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in PCT Patent Application Serial No. PCT/US01/10482, filed on March 30, 2001 and which is herein incorporated by reference.

The specific conditions for this set of experiments began by collecting 100 ml of fresh blood from donors. Peripheral blood mononuclear cells (PBMC) were isolated with LSM (ficol) (ICN Biomedicals) by step gradient separation. Monocytes were depleted by adherence to culture flask. CD45 RA and CD45 RO high cells were sorted by FACS with additional gating on lymphocytes by forward and side scatter. Cells of intermediate expression of either CD45RA or CD45 RO were not collected. Sorting was verified by re-FACS of samples of the sorted population and found to be approximately 99% correctly sorted. Cells were cultured for 16 hours in RPMI 1640,10% heat inactivated FBS, 100 units/mL of Penicillin, 100 mg/mL of streptomycin, 2 mM L-glutamine and IL-2 (100U/ml) and in the presence or absence of plate bound anti-CD3 (10 ug/ml) and soluble anti-CD28 (10 ug/ml). The activation status of the cells was monitored by FACS for cell surface expression of CD69 and CD25. Cells were then pelleted and RNA isolated by Qiagen miniprep and analysis run on Affimax™ (Affymetrix Inc. Santa Clara, CA) microarray chips. Non-stimulated (resting) cells were harvested immediately after purification, and subjected to the same analysis. Genes were compared whose expression was upregulated at either of the two timepoints in activated vs. resting cells

Below are the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly differentially expressed in isolated CD45RO activated by anti-CD3/anti-CD28 as compared to: isolated resting CD45RO, isolated resting CD45RA and isolated CD45RA activated by anti-CD3/anti-CD28 cells. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more immune disorders, but also serve as therapeutic targets for the treatment of those immune disorders. The Figures 1-2442 show the nucleic acids of the invention and their encoded PRO polypeptides. The nucleic acids and encoded proteins of Figure 533, Figure 539, Figure 674, Figure 877, Figure 885, Figure

1135, Figure 1428, Figure 1651 and Figure 1859 are significantly overexpressed in activated CD45RO compared to matched isolated resting CD45RO, isolated resting CD45RA cells and activated CD45RA cells.

EXAMPLE 2: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate•2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8

with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 4: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ^{35}S-cysteine and 200 µCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of PRO polypeptide, the culture medium

may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 promoter/enhancer containing vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 promoter/enhancer containing vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^{-7} cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mL of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35%

polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μl of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 5: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 6: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His_{10}-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB

Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 9: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the

aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 10: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as

limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

What is claimed:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID

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NO:2062), Figure 2064 (SEQ ID NO:2064), Figure 2066 (SEQ ID NO:2066), Figure 2068 (SEQ ID NO:2068), Figure 2070 (SEQ ID NO:2070), Figure 2072 (SEQ ID NO:2072), Figure 2074 (SEQ ID NO:2074), Figure 2076 (SEQ ID NO:2076), Figure 2078 (SEQ ID NO:2078), Figure 2080 (SEQ ID NO:2080), Figure 2082 (SEQ ID NO:2082), Figure 2084 (SEQ ID NO:2084), Figure 2086 (SEQ ID NO:2086), Figure 2088 (SEQ ID NO:2088), Figure 2090 (SEQ ID NO:2090), Figure 2092 (SEQ ID NO:2092), Figure 2094 (SEQ ID NO:2094), Figure 2096 (SEQ ID NO:2096), Figure 2098 (SEQ ID NO:2098), Figure 2100 (SEQ ID NO:2100), Figure 2102 (SEQ ID NO:2102), Figure 2104 (SEQ ID NO:2104), Figure 2106 (SEQ ID NO:2106), Figure 2108 (SEQ ID NO:2108), Figure 2110 (SEQ ID NO:2110), Figure 2112 (SEQ ID NO:2112), Figure 2114 (SEQ ID NO:2114), Figure 2116 (SEQ ID NO:2116), Figure 2118 (SEQ ID NO:2118), Figure 2120 (SEQ ID NO:2120), Figure 2122 (SEQ ID NO:2122), Figure 2124 (SEQ ID NO:2124), Figure 2126 (SEQ ID NO:2126), Figure 2128 (SEQ ID NO:2128), Figure 2130 (SEQ ID NO:2130), Figure 2132 (SEQ ID NO:2132), Figure 2134 (SEQ ID NO:2134), Figure 2136 (SEQ ID NO:2136), Figure 2138 (SEQ ID NO:2138), Figure 2140 (SEQ ID NO:2140), Figure 2142 (SEQ ID NO:2142), Figure 2144 (SEQ ID NO:2144), Figure 2146 (SEQ ID NO:2146), Figure 2148 (SEQ ID NO:2148), Figure 2150 (SEQ ID NO:2150), Figure 2152 (SEQ ID NO:2152), Figure 2154 (SEQ ID NO:2154), Figure 2156 (SEQ ID NO:2156), Figure 2158 (SEQ ID NO:2158), Figure 2160 (SEQ ID NO:2160), Figure 2163 (SEQ ID NO:2163), Figure 2165 (SEQ ID NO:2165), Figure 2167 (SEQ ID NO:2167), Figure 2170 (SEQ ID NO:2170), Figure 2172 (SEQ ID NO:2172), Figure 2174 (SEQ ID NO:2174), Figure 2176 (SEQ ID NO:2176), Figure 2178 (SEQ ID NO:2178), Figure 2180 (SEQ ID NO:2180), Figure 2182 (SEQ ID NO:2182), Figure 2184 (SEQ ID NO:2184), Figure 2186 (SEQ ID NO:2186), Figure 2188 (SEQ ID NO:2188), Figure 2191 (SEQ ID NO:2191), Figure 2193 (SEQ ID NO:2193), Figure 2195 (SEQ ID NO:2195), Figure 2197 (SEQ ID NO:2197), Figure 2199 (SEQ ID NO:2199), Figure 2201 (SEQ ID NO:2201), Figure 2204 (SEQ ID NO:2204), Figure 2207 (SEQ ID NO:2207), Figure 2209 (SEQ ID NO:2209), Figure 2212 (SEQ ID NO:2212), Figure 2214 (SEQ ID NO:2214), Figure 2216 (SEQ ID NO:2216), Figure 2218 (SEQ ID NO:2218), Figure 2220 (SEQ ID NO:2220), Figure 2222 (SEQ ID NO:2222), Figure 2224 (SEQ ID NO:2224), Figure 2226 (SEQ ID NO:2226), Figure 2228 (SEQ ID NO:2228), Figure 2230 (SEQ ID NO:2230), Figure 2232 (SEQ ID NO:2232), Figure 2234 (SEQ ID NO:2234), Figure 2236 (SEQ ID NO:2236), Figure 2238 (SEQ ID NO:2238), Figure 2240 (SEQ ID NO:2240), Figure 2242 (SEQ ID NO:2242), Figure 2244 (SEQ ID NO:2244), Figure 2246 (SEQ ID NO:2246), Figure 2248 (SEQ ID NO:2248), Figure 2250 (SEQ ID NO:2250), Figure 2252 (SEQ ID NO:2252), Figure 2254 (SEQ ID NO:2254), Figure 2256 (SEQ ID NO:2256), Figure 2258 (SEQ ID NO:2258), Figure 2260 (SEQ ID NO:2260), Figure 2262 (SEQ ID NO:2262), Figure 2264 (SEQ ID NO:2264), Figure 2266 (SEQ ID NO:2266), Figure 2268 (SEQ ID NO:2268), Figure 2270 (SEQ ID NO:2270), Figure 2272 (SEQ ID NO:2272), Figure 2274 (SEQ ID NO:2274), Figure 2276 (SEQ ID NO:2276), Figure 2278 (SEQ ID NO:2278), Figure 2280 (SEQ ID NO:2280), Figure 2282 (SEQ ID NO:2282), Figure 2284 (SEQ ID NO:2284), Figure 2286 (SEQ ID NO:2286), Figure 2288 (SEQ ID NO:2288), Figure 2290 (SEQ ID NO:2290), Figure 2292 (SEQ ID NO:2292), Figure 2294 (SEQ ID NO:2294), Figure 2296 (SEQ ID NO:2296), Figure 2298 (SEQ ID NO:2298), Figure 2301 (SEQ ID NO:2301), Figure 2303 (SEQ ID NO:2303), Figure 2305 (SEQ ID NO:2305), Figure 2307 (SEQ ID NO:2307), Figure 2310 (SEQ ID

NO:2310), Figure 2312 (SEQ ID NO:2312), Figure 2314 (SEQ ID NO:2314), Figure 2316 (SEQ ID NO:2316), Figure 2319 (SEQ ID NO:2319), Figure 2321 (SEQ ID NO:2321), Figure 2323 (SEQ ID NO:2323), Figure 2325 (SEQ ID NO:2325), Figure 2327 (SEQ ID NO:2327), Figure 2329 (SEQ ID NO:2329), Figure 2331 (SEQ ID NO:2331), Figure 2333 (SEQ ID NO:2333), Figure 2335 (SEQ ID NO:2335), Figure 2337 (SEQ ID NO:2337), Figure 2339 (SEQ ID NO:2339), Figure 2341 (SEQ ID NO:2341), Figure 2343 (SEQ ID NO:2343), Figure 2345 (SEQ ID NO:2345), Figure 2347 (SEQ ID NO:2347), Figure 2349 (SEQ ID NO:2349), Figure 2351 (SEQ ID NO:2351), Figure 2353 (SEQ ID NO:2353), Figure 2355 (SEQ ID NO:2355), Figure 2357 (SEQ ID NO:2357), Figure 2359 (SEQ ID NO:2359), Figure 2361 (SEQ ID NO:2361), Figure 2363 (SEQ ID NO:2363), Figure 2365 (SEQ ID NO:2365), Figure 2367 (SEQ ID NO:2367), Figure 2369 (SEQ ID NO:2369), Figure 2371 (SEQ ID NO:2371), Figure 2373 (SEQ ID NO:2373), Figure 2375 (SEQ ID NO:2375), Figure 2378 (SEQ ID NO:2378), Figure 2380 (SEQ ID NO:2380), Figure 2383 (SEQ ID NO:2383), Figure 2386 (SEQ ID NO:2386), Figure 2388 (SEQ ID NO:2388), Figure 2391 (SEQ ID NO:2391), Figure 2393 (SEQ ID NO:2393), Figure 2396 (SEQ ID NO:2396), Figure 2398 (SEQ ID NO:2398), Figure 2402 (SEQ ID NO:2402), Figure 2404 (SEQ ID NO:2404), Figure 2408 (SEQ ID NO:2408), Figure 2410 (SEQ ID NO:2410), Figure 2412 (SEQ ID NO:2412), Figure 2415 (SEQ ID NO:2415), Figure 2418 (SEQ ID NO:2418), Figure 2420 (SEQ ID NO:2420), Figure 2422 (SEQ ID NO:2422), Figure 2424 (SEQ ID NO:2424), Figure 2426 (SEQ ID NO:2426), Figure 2430 (SEQ ID NO:2430), Figure 2432 (SEQ ID NO:2432), Figure 2434 (SEQ ID NO:2434), Figure 2436 (SEQ ID NO:2436), Figure 2438 (SEQ ID NO:2438), Figure 2440 (SEQ ID NO:2440), or Figure 2442 (SEQ ID NO:2442).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119

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NO:2302), Figure 2304 (SEQ ID NO:2304), Figure 2306 (SEQ ID NO:2306), Figure 2308 (SEQ ID NO:2308), Figure 2309 (SEQ ID NO:2309), Figure 2311 (SEQ ID NO:2311), Figure 2313 (SEQ ID NO:2313), Figure 2315 (SEQ ID NO:2315), Figure 2317 (SEQ ID NO:2317), Figure 2318 (SEQ ID NO:2318), Figure 2320A-B (SEQ ID NO:2320), Figure 2322 (SEQ ID NO:2322), Figure 2324 (SEQ ID NO:2324), Figure 2326 (SEQ ID NO:2326), Figure 2328 (SEQ ID NO:2328), Figure 2330A-B (SEQ ID NO:2330), Figure 2332 (SEQ ID NO:2332), Figure 2334 (SEQ ID NO:2334), Figure 2336A-B (SEQ ID NO:2336), Figure 2338 (SEQ ID NO:2338), Figure 2340 (SEQ ID NO:2340), Figure 2342 (SEQ ID NO:2342), Figure 2344 (SEQ ID NO:2344), Figure 2346 (SEQ ID NO:2346), Figure 2348 (SEQ ID NO:2348), Figure 2350 (SEQ ID NO:2350), Figure 2352 (SEQ ID NO:2352), Figure 2354A-B (SEQ ID NO:2354), Figure 2356 (SEQ ID NO:2356), Figure 2358 (SEQ ID NO:2358), Figure 2360 (SEQ ID NO:2360), Figure 2362 (SEQ ID NO:2362), Figure 2364 (SEQ ID NO:2364), Figure 2366 (SEQ ID NO:2366), Figure 2368 (SEQ ID NO:2368), Figure 2370 (SEQ ID NO:2370), Figure 2372 (SEQ ID NO:2372), Figure 2374 (SEQ ID NO:2374), Figure 2376A-B (SEQ ID NO:2376), Figure 2377 (SEQ ID NO:2377), Figure 2379 (SEQ ID NO:2379), Figure 2381 (SEQ ID NO:2381), Figure 2382 (SEQ ID NO:2382), Figure 2384 (SEQ ID NO:2384), Figure 2385 (SEQ ID NO:2385), Figure 2387 (SEQ ID NO:2387), Figure 2389 (SEQ ID NO:2389), Figure 2390 (SEQ ID NO:2390), Figure 2392 (SEQ ID NO:2392), Figure 2394 (SEQ ID NO:2394), Figure 2395A-B (SEQ ID NO:2395), Figure 2397 (SEQ ID NO:2397), Figure 2399 (SEQ ID NO:2399), Figure 2400 (SEQ ID NO:2400), Figure 2401 (SEQ ID NO:2401), Figure 2403 (SEQ ID NO:2403), Figure 2405 (SEQ ID NO:2405), Figure 2406 (SEQ ID NO:2406), Figure 2407 (SEQ ID NO:2407), Figure 2409 (SEQ ID NO:2409), Figure 2411 (SEQ ID NO:2411), Figure 2413 (SEQ ID NO:2413), Figure 2414 (SEQ ID NO:2414), Figure 2416 (SEQ ID NO:2416), Figure 2417 (SEQ ID NO:2417), Figure 2419 (SEQ ID NO:2419), Figure 2421 (SEQ ID NO:2421), Figure 2423 (SEQ ID NO:2423), Figure 2425 (SEQ ID NO:2425), Figure 2427 (SEQ ID NO:2427), Figure 2428 (SEQ ID NO:2428), Figure 2429 (SEQ ID NO:2429), Figure 2431 (SEQ ID NO:2431), Figure 2433 (SEQ ID NO:2433), Figure 2435 (SEQ ID NO:2435), Figure 2437 (SEQ ID NO:2437), Figure 2439 (SEQ ID NO:2439) or Figure 2441 (SEQ ID NO:2441).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID

NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:231), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figure 289 (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figure 311 (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347),

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4. A vector comprising the nucleic acid of Claim 1.

5. The vector of Claim 4 operably linked to control sequences recognized by a host cell transformed with the vector.

6. A host cell comprising the vector of Claim 4.

7. The host cell of Claim 6, wherein said cell is a CHO cell, an *E.coli* cell or a yeast cell.

8. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

9. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID

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NO:2290), Figure 2292 (SEQ ID NO:2292), Figure 2294 (SEQ ID NO:2294), Figure 2296 (SEQ ID NO:2296), Figure 2298 (SEQ ID NO:2298), Figure 2301 (SEQ ID NO:2301), Figure 2303 (SEQ ID NO:2303), Figure 2305 (SEQ ID NO:2305), Figure 2307 (SEQ ID NO:2307), Figure 2310 (SEQ ID NO:2310), Figure 2312 (SEQ ID NO:2312), Figure 2314 (SEQ ID NO:2314), Figure 2316 (SEQ ID NO:2316), Figure 2319 (SEQ ID NO:2319), Figure 2321 (SEQ ID NO:2321), Figure 2323 (SEQ ID NO:2323), Figure 2325 (SEQ ID NO:2325), Figure 2327 (SEQ ID NO:2327), Figure 2329 (SEQ ID NO:2329), Figure 2331 (SEQ ID NO:2331), Figure 2333 (SEQ ID NO:2333), Figure 2335 (SEQ ID NO:2335), Figure 2337 (SEQ ID NO:2337), Figure 2339 (SEQ ID NO:2339), Figure 2341 (SEQ ID NO:2341), Figure 2343 (SEQ ID NO:2343), Figure 2345 (SEQ ID NO:2345), Figure 2347 (SEQ ID NO:2347), Figure 2349 (SEQ ID NO:2349), Figure 2351 (SEQ ID NO:2351), Figure 2353 (SEQ ID NO:2353), Figure 2355 (SEQ ID NO:2355), Figure 2357 (SEQ ID NO:2357), Figure 2359 (SEQ ID NO:2359), Figure 2361 (SEQ ID NO:2361), Figure 2363 (SEQ ID NO:2363), Figure 2365 (SEQ ID NO:2365), Figure 2367 (SEQ ID NO:2367), Figure 2369 (SEQ ID NO:2369), Figure 2371 (SEQ ID NO:2371), Figure 2373 (SEQ ID NO:2373), Figure 2375 (SEQ ID NO:2375), Figure 2378 (SEQ ID NO:2378), Figure 2380 (SEQ ID NO:2380), Figure 2383 (SEQ ID NO:2383), Figure 2386 (SEQ ID NO:2386), Figure 2388 (SEQ ID NO:2388), Figure 2391 (SEQ ID NO:2391), Figure 2393 (SEQ ID NO:2393), Figure 2396 (SEQ ID NO:2396), Figure 2398 (SEQ ID NO:2398), Figure 2402 (SEQ ID NO:2402), Figure 2404 (SEQ ID NO:2404), Figure 2408 (SEQ ID NO:2408), Figure 2410 (SEQ ID NO:2410), Figure 2412 (SEQ ID NO:2412), Figure 2415 (SEQ ID NO:2415), Figure 2418 (SEQ ID NO:2418), Figure 2420 (SEQ ID NO:2420), Figure 2422 (SEQ ID NO:2422), Figure 2424 (SEQ ID NO:2424), Figure 2426 (SEQ ID NO:2426), Figure 2430 (SEQ ID NO:2430), Figure 2432 (SEQ ID NO:2432), Figure 2434 (SEQ ID NO:2434), Figure 2436 (SEQ ID NO:2436), Figure 2438 (SEQ ID NO:2438), Figure 2440 (SEQ ID NO:2440) or Figure 2442 (SEQ ID NO:2442).

10. A chimeric molecule comprising a polypeptide according to Claim 9 fused to a heterologous amino acid sequence.

11. The chimeric molecule of Claim 10, wherein said heterologous amino acid sequence is an epitope tag sequence or an Fc region of an immunoglobulin.

12. An antibody which specifically binds to a polypeptide according to Claim 9.

13. The antibody of Claim 12, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

14. A composition of matter comprising (a) a polypeptide of Claim 9, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, in combination with a carrier.

15. The composition of matter of Claim 14, wherein said carrier is a pharmaceutically acceptable carrier.

16. The composition of matter of Claim 15 comprising a therapeutically effective amount of (a), (b), (c) or (d).

17. An article of manufacture, comprising:

a container;

a label on said container; and

a composition of matter comprising (a) a polypeptide of Claim 9, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, contained within said container, wherein label on said container indicates that said composition of matter can be used for treating an immune related disease.

18. A method of treating an immune related disorder in a mammal in need thereof comprising administering to said mammal a therapeutically effective amount of (a) a polypeptide of Claim 9, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide.

19. The method of Claim 18, wherein the immune related disorder is systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barré syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host-disease.

20. A method for determining the presence of a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46

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NO:2373), Figure 2375 (SEQ ID NO:2375), Figure 2378 (SEQ ID NO:2378), Figure 2380 (SEQ ID NO:2380), Figure 2383 (SEQ ID NO:2383), Figure 2386 (SEQ ID NO:2386), Figure 2388 (SEQ ID NO:2388), Figure 2391 (SEQ ID NO:2391), Figure 2393 (SEQ ID NO:2393), Figure 2396 (SEQ ID NO:2396), Figure 2398 (SEQ ID NO:2398), Figure 2402 (SEQ ID NO:2402), Figure 2404 (SEQ ID NO:2404), Figure 2408 (SEQ ID NO:2408), Figure 2410 (SEQ ID NO:2410), Figure 2412 (SEQ ID NO:2412), Figure 2415 (SEQ ID NO:2415), Figure 2418 (SEQ ID NO:2418), Figure 2420 (SEQ ID NO:2420), Figure 2422 (SEQ ID NO:2422), Figure 2424 (SEQ ID NO:2424), Figure 2426 (SEQ ID NO:2426), Figure 2430 (SEQ ID NO:2430), Figure 2432 (SEQ ID NO:2432), Figure 2434 (SEQ ID NO:2434), Figure 2436 (SEQ ID NO:2436), Figure 2438 (SEQ ID NO:2438), Figure 2440 (SEQ ID NO:2440), or Figure 2442 (SEQ ID NO:2442), in a sample suspected of containing said polypeptide, said method comprising exposing said sample to an anti-PRO antibody, and determining binding of said antibody to a component of said sample.

21. A method of diagnosing an immune related disease in a mammal, said method comprising detecting the level of expression of a gene encoding a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177),

Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446

(SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), Figure 609 (SEQ ID NO:609), Figure 611 (SEQ ID NO:611), Figure 613 (SEQ ID NO:613), Figure 615 (SEQ ID NO:615), Figure 617 (SEQ ID NO:617), Figure 619 (SEQ ID NO:619), Figure 621 (SEQ ID NO:621), Figure 623 (SEQ ID NO:623), Figure 625 (SEQ ID NO:625), Figure 627 (SEQ ID NO:627), Figure 629 (SEQ ID NO:629), Figure 631 (SEQ ID NO:631), Figure 633 (SEQ ID NO:633), Figure 635 (SEQ ID NO:635), Figure 637 (SEQ ID NO:637), Figure 639 (SEQ ID NO:639), Figure 641 (SEQ ID NO:641), Figure 643 (SEQ ID NO:643), Figure 645 (SEQ ID NO:645), Figure 647 (SEQ ID NO:647), Figure 649 (SEQ ID NO:649), Figure 651 (SEQ ID NO:651), Figure 653 (SEQ ID NO:653), Figure 655 (SEQ ID NO:655), Figure 657 (SEQ ID NO:657), Figure 659 (SEQ ID NO:659), Figure 661 (SEQ ID NO:661), Figure 663 (SEQ ID NO:663), Figure 665 (SEQ ID NO:665), Figure 667 (SEQ ID NO:667), Figure 669 (SEQ ID NO:669), Figure 671 (SEQ ID NO:671), Figure 673 (SEQ ID NO:673), Figure 675 (SEQ ID NO:675), Figure 677 (SEQ ID NO:377), Figure 679 (SEQ ID NO:679), Figure 681 (SEQ ID NO:681), Figure 683 (SEQ ID NO:683), Figure 685 (SEQ ID NO:685), Figure 687 (SEQ ID NO:687), Figure 689 (SEQ ID NO:689), Figure 691 (SEQ ID NO:691), Figure 693 (SEQ ID NO:693), Figure 695 (SEQ ID NO:695), Figure 697 (SEQ ID NO:697), Figure 699 (SEQ ID NO:699), Figure 701 (SEQ ID NO:701), Figure 703 (SEQ ID NO:703), Figure 705 (SEQ ID NO:705), Figure 707 (SEQ ID NO:707), Figure 709 (SEQ ID NO:709), Figure 711 (SEQ ID NO:711), Figure 713 (SEQ ID

NO:713), Figure 715 (SEQ ID NO:715), Figure 717 (SEQ ID NO:717), Figure 719 (SEQ ID NO:719), Figure 721 (SEQ ID NO:721), Figure 723 (SEQ ID NO:723), Figure 725 (SEQ ID NO:725), Figure 727 (SEQ ID NO:727), Figure 729 (SEQ ID NO:729), Figure 731 (SEQ ID NO:731), Figure 733 (SEQ ID NO:733), Figure 735 (SEQ ID NO:735), Figure 737 (SEQ ID NO:737), Figure 739 (SEQ ID NO:739), Figure 741 (SEQ ID NO:741), Figure 743 (SEQ ID NO:743), Figure 745 (SEQ ID NO:745), Figure 747 (SEQ ID NO:747), Figure 749 (SEQ ID NO:749), Figure 751 (SEQ ID NO:751), Figure 753 (SEQ ID NO:753), Figure 755 (SEQ ID NO:755), Figure 757 (SEQ ID NO:757), Figure 759 (SEQ ID NO:759), Figure 761 (SEQ ID NO:761), Figure 763 (SEQ ID NO:763), Figure 765 (SEQ ID NO:765), Figure 767 (SEQ ID NO:767), Figure 769 (SEQ ID NO:769), Figure 771 (SEQ ID NO:771), Figure 773 (SEQ ID NO:773), Figure 775 (SEQ ID NO:775), Figure 777 (SEQ ID NO:777), Figure 779 (SEQ ID NO:779), Figure 781 (SEQ ID NO:781), Figure 783 (SEQ ID NO:783), Figure 785 (SEQ ID NO:785), Figure 787 (SEQ ID NO:787), Figure 789 (SEQ ID NO:789), Figure 791 (SEQ ID NO:791), Figure 793 (SEQ ID NO:793), Figure 795 (SEQ ID NO:795), Figure 797 (SEQ ID NO:797), Figure 799 (SEQ ID NO:799), Figure 801 (SEQ ID NO:801), Figure 803 (SEQ ID NO:803), Figure 805 (SEQ ID NO:805), Figure 807 (SEQ ID NO:807), Figure 809 (SEQ ID NO:809), Figure 811 (SEQ ID NO:811), Figure 813 (SEQ ID NO:813), Figure 815 (SEQ ID NO:815), Figure 817 (SEQ ID NO:817), Figure 819 (SEQ ID NO:819), Figure 821 (SEQ ID NO:821), Figure 823 (SEQ ID NO:823), Figure 825 (SEQ ID NO:825), Figure 827 (SEQ ID NO:827), Figure 829 (SEQ ID NO:829), Figure 831 (SEQ ID NO:831), Figure 833 (SEQ ID NO:833), Figure 835 (SEQ ID NO:835), Figure 837 (SEQ ID NO:837), Figure 839 (SEQ ID NO:839), Figure 841 (SEQ ID NO:841), Figure 843 (SEQ ID NO:843), Figure 845 (SEQ ID NO:845), Figure 847 (SEQ ID NO:847), Figure 849 (SEQ ID NO:849), Figure 851 (SEQ ID NO:851), Figure 853 (SEQ ID NO:853), Figure 855 (SEQ ID NO:855), Figure 858 (SEQ ID NO:858), Figure 860 (SEQ ID NO:860), Figure 862 (SEQ ID NO:862), Figure 864 (SEQ ID NO:864), Figure 866 (SEQ ID NO:866), Figure 868 (SEQ ID NO:868), Figure 870 (SEQ ID NO:870), Figure 872 (SEQ ID NO:872), Figure 874 (SEQ ID NO:874), Figure 876 (SEQ ID NO:876), Figure 878 (SEQ ID NO:878), Figure 880 (SEQ ID NO:880), Figure 882 (SEQ ID NO:882), Figure 884 (SEQ ID NO:884), Figure 886 (SEQ ID NO:886), Figure 888 (SEQ ID NO:888), Figure 890 (SEQ ID NO:890), Figure 892 (SEQ ID NO:892), Figure 894 (SEQ ID NO:894), Figure 896 (SEQ ID NO:896), Figure 898 (SEQ ID NO:898), Figure 900 (SEQ ID NO:900), Figure 902 (SEQ ID NO:902), Figure 904 (SEQ ID NO:904), Figure 906 (SEQ ID NO:906), Figure 908 (SEQ ID NO:908), Figure 910 (SEQ ID NO:910), Figure 912 (SEQ ID NO:912), Figure 914 (SEQ ID NO:914), Figure 916 (SEQ ID NO:916), Figure 918 (SEQ ID NO:918), Figure 920 (SEQ ID NO:920), Figure 922 (SEQ ID NO:922), Figure 924 (SEQ ID NO:924), Figure 926 (SEQ ID NO:926), Figure 928 (SEQ ID NO:928), Figure 930 (SEQ ID NO:930), Figure 932 (SEQ ID NO:932), Figure 934 (SEQ ID NO:934), Figure 936 (SEQ ID NO:936), Figure 938 (SEQ ID NO:938), Figure 940 (SEQ ID NO:940), Figure 943 (SEQ ID NO:943), Figure 945 (SEQ ID NO:945), Figure 947 (SEQ ID NO:947), Figure 949 (SEQ ID NO:949), Figure 951 (SEQ ID NO:951), Figure 953 (SEQ ID NO:953), Figure 955 (SEQ ID NO:955), Figure 958 (SEQ ID NO:958), Figure 960 (SEQ ID NO:960), Figure 963 (SEQ ID NO:963), Figure 965 (SEQ ID NO:965), Figure 968 (SEQ ID NO:968), Figure 970 (SEQ ID NO:970), Figure 972 (SEQ ID NO:972), Figure 974 (SEQ ID NO:974), Figure 976 (SEQ ID NO:976), Figure 978 (SEQ ID NO:978), Figure 980 (SEQ ID NO:980), Figure 983 (SEQ ID NO:983), Figure 985 (SEQ ID NO:985),

Figure 987 (SEQ ID NO:987), Figure 990 (SEQ ID NO:990), Figure 992 (SEQ ID NO:992), Figure 994 (SEQ ID NO:994), Figure 996 (SEQ ID NO:996), Figure 998 (SEQ ID NO:998), Figure 1000 (SEQ ID NO:1000), Figure 1002 (SEQ ID NO:1002), Figure 1007 (SEQ ID NO:1007), Figure 1009 (SEQ ID NO:1009), Figure 1011 (SEQ ID NO:1011), Figure 1013 (SEQ ID NO:1013), Figure 1015 (SEQ ID NO:1015), Figure 1017 (SEQ ID NO:1017), Figure 1019 (SEQ ID NO:1019), Figure 1021 (SEQ ID NO:1021), Figure 1023 (SEQ ID NO:1023), Figure 1025 (SEQ ID NO:1025), Figure 1030 (SEQ ID NO:1030), Figure 1033 (SEQ ID NO:1033), Figure 1035 (SEQ ID NO:1035), Figure 1037 (SEQ ID NO:1037), Figure 1039 (SEQ ID NO:1039), Figure 1041 (SEQ ID NO:1041), Figure 1043 (SEQ ID NO:1043), Figure 1046 (SEQ ID NO:1046), Figure 1048 (SEQ ID NO:1048), Figure 1050 (SEQ ID NO:1050), Figure 1053 (SEQ ID NO:1053), Figure 1055 (SEQ ID NO:1055), Figure 1057 (SEQ ID NO:1057), Figure 1060 (SEQ ID NO:1060), Figure 1062 (SEQ ID NO:1062), Figure 1064 (SEQ ID NO:1064), Figure 1066 (SEQ ID NO:1066), Figure 1068 (SEQ ID NO:1068), Figure 1070 (SEQ ID NO:1070), Figure 1072 (SEQ ID NO:1072), Figure 1074 (SEQ ID NO:1074), Figure 1076 (SEQ ID NO:1076), Figure 1078 (SEQ ID NO:1078), Figure 1080 (SEQ ID NO:1080), Figure 1082 (SEQ ID NO:1082), Figure 1084 (SEQ ID NO:1084), Figure 1086 (SEQ ID NO:1086), Figure 1088 (SEQ ID NO:1088), Figure 1090 (SEQ ID NO:1090), Figure 1092 (SEQ ID NO:1092), Figure 1094 (SEQ ID NO:1094), Figure 1096 (SEQ ID NO:1096), Figure 1098 (SEQ ID NO:1098), Figure 1101 (SEQ ID NO:1101), Figure 1103 (SEQ ID NO:1103), Figure 1105 (SEQ ID NO:1105), Figure 1107 (SEQ ID NO:1107), Figure 1109 (SEQ ID NO:1109), Figure 1111 (SEQ ID NO:1111), Figure 1113 (SEQ ID NO:1113), Figure 1116 (SEQ ID NO:1116), Figure 1118 (SEQ ID NO:1118), Figure 1120 (SEQ ID NO:1120), Figure 1123 (SEQ ID NO:1123), Figure 1125 (SEQ ID NO:1125), Figure 1128 (SEQ ID NO:1128), Figure 1130 (SEQ ID NO:1130), Figure 1132 (SEQ ID NO:1132), Figure 1134 (SEQ ID NO:1134), Figure 1136 (SEQ ID NO:1136), Figure 1138 (SEQ ID NO:1138), Figure 1142 (SEQ ID NO:1142), Figure 1144 (SEQ ID NO:1144), Figure 1146 (SEQ ID NO:1146), Figure 1148 (SEQ ID NO:1148), Figure 1150 (SEQ ID NO:1150), Figure 1152 (SEQ ID NO:1152), Figure 1154 (SEQ ID NO:1154), Figure 1156 (SEQ ID NO:1156), Figure 1158 (SEQ ID NO:1158), Figure 1160 (SEQ ID NO:1160), Figure 1162 (SEQ ID NO:1162), Figure 1164 (SEQ ID NO:1164), Figure 1166 (SEQ ID NO:1166), Figure 1168 (SEQ ID NO:1168), Figure 1170 (SEQ ID NO:1170), Figure 1172 (SEQ ID NO:1172), Figure 1174 (SEQ ID NO:1174), Figure 1176 (SEQ ID NO:1176), Figure 1178 (SEQ ID NO:1178), Figure 1180 (SEQ ID NO:1180), Figure 1182 (SEQ ID NO:1182), Figure 1184 (SEQ ID NO:1184), Figure 1186 (SEQ ID NO:1186), Figure 1188 (SEQ ID NO:1188), Figure 1190 (SEQ ID NO:1190), Figure 1192 (SEQ ID NO:1192), Figure 1194 (SEQ ID NO:1194), Figure 1196 (SEQ ID NO:1196), Figure 1198 (SEQ ID NO:1198), Figure 1200 (SEQ ID NO:1200), Figure 1202 (SEQ ID NO:1202), Figure 1204 (SEQ ID NO:1204), Figure 1206 (SEQ ID NO:1206), Figure 1208 (SEQ ID NO:1208), Figure 1210 (SEQ ID NO:1210), Figure 1212 (SEQ ID NO:1212), Figure 1214 (SEQ ID NO:1214), Figure 1216 (SEQ ID NO:1216), Figure 1218 (SEQ ID NO:1218), Figure 1220 (SEQ ID NO:1220), Figure 1222 (SEQ ID NO:1222), Figure 1224 (SEQ ID NO:1224), Figure 1226 (SEQ ID NO:1226), Figure 1228 (SEQ ID NO:1228), Figure 1230 (SEQ ID NO:1230), Figure 1232 (SEQ ID NO:1232), Figure 1234 (SEQ ID NO:1234), Figure 1236 (SEQ ID NO:1236), Figure 1238 (SEQ ID NO:1238), Figure 1240 (SEQ ID NO:1240), Figure 1242 (SEQ ID NO:1242), Figure 1244 (SEQ ID

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22. A method of diagnosing an immune related disease in a mammal, said method comprising (a) contacting a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID

NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302

(SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID

NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), Figure 609 (SEQ ID NO:609), Figure 611 (SEQ ID NO:611), Figure 613 (SEQ ID NO:613), Figure 615 (SEQ ID NO:615), Figure 617 (SEQ ID NO:617), Figure 619 (SEQ ID NO:619), Figure 621 (SEQ ID NO:621), Figure 623 (SEQ ID NO:623), Figure 625 (SEQ ID NO:625), Figure 627 (SEQ ID NO:627), Figure 629 (SEQ ID NO:629), Figure 631 (SEQ ID NO:631), Figure 633 (SEQ ID NO:633), Figure 635 (SEQ ID NO:635), Figure 637 (SEQ ID NO:637), Figure 639 (SEQ ID NO:639), Figure 641 (SEQ ID NO:641), Figure 643 (SEQ ID NO:643), Figure 645 (SEQ ID NO:645), Figure 647 (SEQ ID NO:647), Figure 649 (SEQ ID NO:649), Figure 651 (SEQ ID NO:651), Figure 653 (SEQ ID NO:653), Figure 655 (SEQ ID NO:655), Figure 657 (SEQ ID NO:657), Figure 659 (SEQ ID NO:659), Figure 661 (SEQ ID NO:661), Figure 663 (SEQ ID NO:663), Figure 665 (SEQ ID NO:665), Figure 667 (SEQ ID NO:667), Figure 669 (SEQ ID NO:669), Figure 671 (SEQ ID NO:671), Figure 673 (SEQ ID NO:673), Figure 675 (SEQ ID NO:675), Figure 677 (SEQ ID NO:377), Figure 679 (SEQ ID NO:679), Figure 681 (SEQ ID NO:681), Figure 683 (SEQ ID NO:683), Figure 685 (SEQ ID NO:685), Figure 687 (SEQ ID NO:687), Figure 689 (SEQ ID NO:689), Figure 691 (SEQ ID NO:691), Figure 693 (SEQ ID NO:693), Figure 695 (SEQ ID NO:695), Figure 697 (SEQ ID NO:697), Figure 699 (SEQ ID NO:699), Figure 701 (SEQ ID NO:701), Figure 703 (SEQ ID NO:703), Figure 705 (SEQ ID NO:705), Figure 707 (SEQ ID NO:707), Figure 709 (SEQ ID NO:709), Figure 711 (SEQ ID NO:711), Figure 713 (SEQ ID NO:713), Figure 715 (SEQ ID NO:715), Figure 717 (SEQ ID NO:717), Figure 719 (SEQ ID NO:719), Figure 721 (SEQ ID NO:721), Figure 723 (SEQ ID NO:723), Figure 725 (SEQ ID NO:725), Figure 727 (SEQ ID NO:727), Figure 729 (SEQ ID NO:729), Figure 731 (SEQ ID NO:731), Figure 733 (SEQ ID NO:733), Figure 735 (SEQ ID NO:735), Figure 737 (SEQ ID NO:737), Figure 739 (SEQ ID NO:739), Figure 741 (SEQ ID NO:741), Figure 743 (SEQ ID NO:743), Figure 745 (SEQ ID NO:745), Figure 747 (SEQ ID NO:747), Figure 749 (SEQ ID NO:749), Figure 751 (SEQ ID NO:751), Figure 753 (SEQ ID NO:753), Figure 755 (SEQ ID NO:755), Figure 757 (SEQ ID NO:757), Figure 759 (SEQ ID NO:759), Figure 761 (SEQ ID NO:761), Figure 763 (SEQ ID NO:763), Figure 765 (SEQ ID NO:765), Figure 767 (SEQ ID NO:767), Figure 769 (SEQ ID NO:769), Figure 771 (SEQ ID NO:771), Figure 773 (SEQ ID NO:773), Figure 775 (SEQ ID NO:775), Figure 777 (SEQ ID NO:777), Figure 779 (SEQ ID NO:779), Figure 781 (SEQ ID NO:781), Figure 783 (SEQ ID NO:783), Figure 785 (SEQ ID NO:785), Figure 787 (SEQ ID NO:787), Figure 789 (SEQ ID NO:789), Figure 791 (SEQ ID NO:791), Figure 793 (SEQ ID NO:793), Figure 795 (SEQ ID NO:795), Figure 797 (SEQ ID NO:797), Figure 799 (SEQ ID NO:799), Figure 801 (SEQ ID NO:801), Figure 803 (SEQ ID NO:803), Figure 805 (SEQ ID NO:805), Figure 807 (SEQ ID NO:807), Figure 809 (SEQ ID NO:809), Figure 811 (SEQ ID NO:811), Figure 813 (SEQ ID NO:813), Figure 815 (SEQ ID NO:815), Figure 817 (SEQ ID NO:817), Figure 819 (SEQ ID NO:819), Figure 821 (SEQ ID NO:821), Figure 823 (SEQ ID NO:823), Figure 825 (SEQ ID NO:825), Figure 827 (SEQ ID NO:827), Figure 829 (SEQ ID NO:829), Figure 831 (SEQ ID NO:831), Figure 833 (SEQ ID NO:833), Figure 835 (SEQ ID NO:835),

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23. A method of identifying a compound that inhibits the activity of a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149),

Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418

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NO:2220), Figure 2222 (SEQ ID NO:2222), Figure 2224 (SEQ ID NO:2224), Figure 2226 (SEQ ID NO:2226), Figure 2228 (SEQ ID NO:2228), Figure 2230 (SEQ ID NO:2230), Figure 2232 (SEQ ID NO:2232), Figure 2234 (SEQ ID NO:2234), Figure 2236 (SEQ ID NO:2236), Figure 2238 (SEQ ID NO:2238), Figure 2240 (SEQ ID NO:2240), Figure 2242 (SEQ ID NO:2242), Figure 2244 (SEQ ID NO:2244), Figure 2246 (SEQ ID NO:2246), Figure 2248 (SEQ ID NO:2248), Figure 2250 (SEQ ID NO:2250), Figure 2252 (SEQ ID NO:2252), Figure 2254 (SEQ ID NO:2254), Figure 2256 (SEQ ID NO:2256), Figure 2258 (SEQ ID NO:2258), Figure 2260 (SEQ ID NO:2260), Figure 2262 (SEQ ID NO:2262), Figure 2264 (SEQ ID NO:2264), Figure 2266 (SEQ ID NO:2266), Figure 2268 (SEQ ID NO:2268), Figure 2270 (SEQ ID NO:2270), Figure 2272 (SEQ ID NO:2272), Figure 2274 (SEQ ID NO:2274), Figure 2276 (SEQ ID NO:2276), Figure 2278 (SEQ ID NO:2278), Figure 2280 (SEQ ID NO:2280), Figure 2282 (SEQ ID NO:2282), Figure 2284 (SEQ ID NO:2284), Figure 2286 (SEQ ID NO:2286), Figure 2288 (SEQ ID NO:2288), Figure 2290 (SEQ ID NO:2290), Figure 2292 (SEQ ID NO:2292), Figure 2294 (SEQ ID NO:2294), Figure 2296 (SEQ ID NO:2296), Figure 2298 (SEQ ID NO:2298), Figure 2301 (SEQ ID NO:2301), Figure 2303 (SEQ ID NO:2303), Figure 2305 (SEQ ID NO:2305), Figure 2307 (SEQ ID NO:2307), Figure 2310 (SEQ ID NO:2310), Figure 2312 (SEQ ID NO:2312), Figure 2314 (SEQ ID NO:2314), Figure 2316 (SEQ ID NO:2316), Figure 2319 (SEQ ID NO:2319), Figure 2321 (SEQ ID NO:2321), Figure 2323 (SEQ ID NO:2323), Figure 2325 (SEQ ID NO:2325), Figure 2327 (SEQ ID NO:2327), Figure 2329 (SEQ ID NO:2329), Figure 2331 (SEQ ID NO:2331), Figure 2333 (SEQ ID NO:2333), Figure 2335 (SEQ ID NO:2335), Figure 2337 (SEQ ID NO:2337), Figure 2339 (SEQ ID NO:2339), Figure 2341 (SEQ ID NO:2341), Figure 2343 (SEQ ID NO:2343), Figure 2345 (SEQ ID NO:2345), Figure 2347 (SEQ ID NO:2347), Figure 2349 (SEQ ID NO:2349), Figure 2351 (SEQ ID NO:2351), Figure 2353 (SEQ ID NO:2353), Figure 2355 (SEQ ID NO:2355), Figure 2357 (SEQ ID NO:2357), Figure 2359 (SEQ ID NO:2359), Figure 2361 (SEQ ID NO:2361), Figure 2363 (SEQ ID NO:2363), Figure 2365 (SEQ ID NO:2365), Figure 2367 (SEQ ID NO:2367), Figure 2369 (SEQ ID NO:2369), Figure 2371 (SEQ ID NO:2371), Figure 2373 (SEQ ID NO:2373), Figure 2375 (SEQ ID NO:2375), Figure 2378 (SEQ ID NO:2378), Figure 2380 (SEQ ID NO:2380), Figure 2383 (SEQ ID NO:2383), Figure 2386 (SEQ ID NO:2386), Figure 2388 (SEQ ID NO:2388), Figure 2391 (SEQ ID NO:2391), Figure 2393 (SEQ ID NO:2393), Figure 2396 (SEQ ID NO:2396), Figure 2398 (SEQ ID NO:2398), Figure 2402 (SEQ ID NO:2402), Figure 2404 (SEQ ID NO:2404), Figure 2408 (SEQ ID NO:2408), Figure 2410 (SEQ ID NO:2410), Figure 2412 (SEQ ID NO:2412), Figure 2415 (SEQ ID NO:2415), Figure 2418 (SEQ ID NO:2418), Figure 2420 (SEQ ID NO:2420), Figure 2422 (SEQ ID NO:2422), Figure 2424 (SEQ ID NO:2424), Figure 2426 (SEQ ID NO:2426), Figure 2430 (SEQ ID NO:2430), Figure 2432 (SEQ ID NO:2432), Figure 2434 (SEQ ID NO:2434), Figure 2436 (SEQ ID NO:2436), Figure 2438 (SEQ ID NO:2438), Figure 2440 (SEQ ID NO:2440), or Figure 2442 (SEQ ID NO:2442) said method comprising contacting cells which normally respond to said polypeptide with (a) said polypeptide and (b) a candidate compound, and determining the lack responsiveness by said cell to (a).

24. A method of identifying a compound that inhibits the expression of a gene encoding a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4),

Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID

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25. The method of Claim 24, wherein said candidate compound is an antisense nucleic acid.

26. A method of identifying a compound that mimics the activity of a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137

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NO:1962), Figure 1964 (SEQ ID NO:1964), Figure 1966 (SEQ ID NO:1966), Figure 1968 (SEQ ID NO:1968), Figure 1970 (SEQ ID NO:1970), Figure 1972 (SEQ ID NO:1972), Figure 1974 (SEQ ID NO:1974), Figure 1976 (SEQ ID NO:1976), Figure 1978 (SEQ ID NO:1978), Figure 1980 (SEQ ID NO:1980), Figure 1982 (SEQ ID NO:1982), Figure 1984 (SEQ ID NO:1984), Figure 1986 (SEQ ID NO:1986), Figure 1988 (SEQ ID NO:1988), Figure 1990 (SEQ ID NO:1990), Figure 1992 (SEQ ID NO:1992), Figure 1994 (SEQ ID NO:1994), Figure 1996 (SEQ ID NO:1996), Figure 1998 (SEQ ID NO:1998), Figure 2000 (SEQ ID NO:2000), Figure 2002 (SEQ ID NO:2002), Figure 2004 (SEQ ID NO:2004), Figure 2006 (SEQ ID NO:2006), Figure 2008 (SEQ ID NO:2008), Figure 2010 (SEQ ID NO:2010), Figure 2012 (SEQ ID NO:2012), Figure 2014 (SEQ ID NO:2014), Figure 2016 (SEQ ID NO:2016), Figure 2018 (SEQ ID NO:2018), Figure 2020 (SEQ ID NO:2020), Figure 2022 (SEQ ID NO:2022), Figure 2024 (SEQ ID NO:2024), Figure 2026 (SEQ ID NO:2026), Figure 2028 (SEQ ID NO:2028), Figure 2030 (SEQ ID NO:2030), Figure 2032 (SEQ ID NO:2032), Figure 2034 (SEQ ID NO:2034), Figure 2036 (SEQ ID NO:2036), Figure 2038 (SEQ ID NO:2038), Figure 2040 (SEQ ID NO:2040), Figure 2042 (SEQ ID NO:2042), Figure 2044 (SEQ ID NO:2044), Figure 2046 (SEQ ID NO:2046), Figure 2048 (SEQ ID NO:2048), Figure 2050 (SEQ ID NO:2050), Figure 2052 (SEQ ID NO:2052), Figure 2054 (SEQ ID NO:2054), Figure 2056 (SEQ ID NO:2056), Figure 2058 (SEQ ID NO:2058), Figure 2060 (SEQ ID NO:2060), Figure 2062 (SEQ ID NO:2062), Figure 2064 (SEQ ID NO:2064), Figure 2066 (SEQ ID NO:2066), Figure 2068 (SEQ ID NO:2068), Figure 2070 (SEQ ID NO:2070), Figure 2072 (SEQ ID NO:2072), Figure 2074 (SEQ ID NO:2074), Figure 2076 (SEQ ID NO:2076), Figure 2078 (SEQ ID NO:2078), Figure 2080 (SEQ ID NO:2080), Figure 2082 (SEQ ID NO:2082), Figure 2084 (SEQ ID NO:2084), Figure 2086 (SEQ ID NO:2086), Figure 2088 (SEQ ID NO:2088), Figure 2090 (SEQ ID NO:2090), Figure 2092 (SEQ ID NO:2092), Figure 2094 (SEQ ID NO:2094), Figure 2096 (SEQ ID NO:2096), Figure 2098 (SEQ ID NO:2098), Figure 2100 (SEQ ID NO:2100), Figure 2102 (SEQ ID NO:2102), Figure 2104 (SEQ ID NO:2104), Figure 2106 (SEQ ID NO:2106), Figure 2108 (SEQ ID NO:2108), Figure 2110 (SEQ ID NO:2110), Figure 2112 (SEQ ID NO:2112), Figure 2114 (SEQ ID NO:2114), Figure 2116 (SEQ ID NO:2116), Figure 2118 (SEQ ID NO:2118), Figure 2120 (SEQ ID NO:2120), Figure 2122 (SEQ ID NO:2122), Figure 2124 (SEQ ID NO:2124), Figure 2126 (SEQ ID NO:2126), Figure 2128 (SEQ ID NO:2128), Figure 2130 (SEQ ID NO:2130), Figure 2132 (SEQ ID NO:2132), Figure 2134 (SEQ ID NO:2134), Figure 2136 (SEQ ID NO:2136), Figure 2138 (SEQ ID NO:2138), Figure 2140 (SEQ ID NO:2140), Figure 2142 (SEQ ID NO:2142), Figure 2144 (SEQ ID NO:2144), Figure 2146 (SEQ ID NO:2146), Figure 2148 (SEQ ID NO:2148), Figure 2150 (SEQ ID NO:2150), Figure 2152 (SEQ ID NO:2152), Figure 2154 (SEQ ID NO:2154), Figure 2156 (SEQ ID NO:2156), Figure 2158 (SEQ ID NO:2158), Figure 2160 (SEQ ID NO:2160), Figure 2163 (SEQ ID NO:2163), Figure 2165 (SEQ ID NO:2165), Figure 2167 (SEQ ID NO:2167), Figure 2170 (SEQ ID NO:2170), Figure 2172 (SEQ ID NO:2172), Figure 2174 (SEQ ID NO:2174), Figure 2176 (SEQ ID NO:2176), Figure 2178 (SEQ ID NO:2178), Figure 2180 (SEQ ID NO:2180), Figure 2182 (SEQ ID NO:2182), Figure 2184 (SEQ ID NO:2184), Figure 2186 (SEQ ID NO:2186), Figure 2188 (SEQ ID NO:2188), Figure 2191 (SEQ ID NO:2191), Figure 2193 (SEQ ID NO:2193), Figure 2195 (SEQ ID NO:2195), Figure 2197 (SEQ ID NO:2197), Figure 2199 (SEQ ID NO:2199), Figure 2201 (SEQ ID NO:2201), Figure 2204 (SEQ ID NO:2204), Figure 2207 (SEQ ID

NO:2207), Figure 2209 (SEQ ID NO:2209), Figure 2212 (SEQ ID NO:2212), Figure 2214 (SEQ ID NO:2214), Figure 2216 (SEQ ID NO:2216), Figure 2218 (SEQ ID NO:2218), Figure 2220 (SEQ ID NO:2220), Figure 2222 (SEQ ID NO:2222), Figure 2224 (SEQ ID NO:2224), Figure 2226 (SEQ ID NO:2226), Figure 2228 (SEQ ID NO:2228), Figure 2230 (SEQ ID NO:2230), Figure 2232 (SEQ ID NO:2232), Figure 2234 (SEQ ID NO:2234), Figure 2236 (SEQ ID NO:2236), Figure 2238 (SEQ ID NO:2238), Figure 2240 (SEQ ID NO:2240), Figure 2242 (SEQ ID NO:2242), Figure 2244 (SEQ ID NO:2244), Figure 2246 (SEQ ID NO:2246), Figure 2248 (SEQ ID NO:2248), Figure 2250 (SEQ ID NO:2250), Figure 2252 (SEQ ID NO:2252), Figure 2254 (SEQ ID NO:2254), Figure 2256 (SEQ ID NO:2256), Figure 2258 (SEQ ID NO:2258), Figure 2260 (SEQ ID NO:2260), Figure 2262 (SEQ ID NO:2262), Figure 2264 (SEQ ID NO:2264), Figure 2266 (SEQ ID NO:2266), Figure 2268 (SEQ ID NO:2268), Figure 2270 (SEQ ID NO:2270), Figure 2272 (SEQ ID NO:2272), Figure 2274 (SEQ ID NO:2274), Figure 2276 (SEQ ID NO:2276), Figure 2278 (SEQ ID NO:2278), Figure 2280 (SEQ ID NO:2280), Figure 2282 (SEQ ID NO:2282), Figure 2284 (SEQ ID NO:2284), Figure 2286 (SEQ ID NO:2286), Figure 2288 (SEQ ID NO:2288), Figure 2290 (SEQ ID NO:2290), Figure 2292 (SEQ ID NO:2292), Figure 2294 (SEQ ID NO:2294), Figure 2296 (SEQ ID NO:2296), Figure 2298 (SEQ ID NO:2298), Figure 2301 (SEQ ID NO:2301), Figure 2303 (SEQ ID NO:2303), Figure 2305 (SEQ ID NO:2305), Figure 2307 (SEQ ID NO:2307), Figure 2310 (SEQ ID NO:2310), Figure 2312 (SEQ ID NO:2312), Figure 2314 (SEQ ID NO:2314), Figure 2316 (SEQ ID NO:2316), Figure 2319 (SEQ ID NO:2319), Figure 2321 (SEQ ID NO:2321), Figure 2323 (SEQ ID NO:2323), Figure 2325 (SEQ ID NO:2325), Figure 2327 (SEQ ID NO:2327), Figure 2329 (SEQ ID NO:2329), Figure 2331 (SEQ ID NO:2331), Figure 2333 (SEQ ID NO:2333), Figure 2335 (SEQ ID NO:2335), Figure 2337 (SEQ ID NO:2337), Figure 2339 (SEQ ID NO:2339), Figure 2341 (SEQ ID NO:2341), Figure 2343 (SEQ ID NO:2343), Figure 2345 (SEQ ID NO:2345), Figure 2347 (SEQ ID NO:2347), Figure 2349 (SEQ ID NO:2349), Figure 2351 (SEQ ID NO:2351), Figure 2353 (SEQ ID NO:2353), Figure 2355 (SEQ ID NO:2355), Figure 2357 (SEQ ID NO:2357), Figure 2359 (SEQ ID NO:2359), Figure 2361 (SEQ ID NO:2361), Figure 2363 (SEQ ID NO:2363), Figure 2365 (SEQ ID NO:2365), Figure 2367 (SEQ ID NO:2367), Figure 2369 (SEQ ID NO:2369), Figure 2371 (SEQ ID NO:2371), Figure 2373 (SEQ ID NO:2373), Figure 2375 (SEQ ID NO:2375), Figure 2378 (SEQ ID NO:2378), Figure 2380 (SEQ ID NO:2380), Figure 2383 (SEQ ID NO:2383), Figure 2386 (SEQ ID NO:2386), Figure 2388 (SEQ ID NO:2388), Figure 2391 (SEQ ID NO:2391), Figure 2393 (SEQ ID NO:2393), Figure 2396 (SEQ ID NO:2396), Figure 2398 (SEQ ID NO:2398), Figure 2402 (SEQ ID NO:2402), Figure 2404 (SEQ ID NO:2404), Figure 2408 (SEQ ID NO:2408), Figure 2410 (SEQ ID NO:2410), Figure 2412 (SEQ ID NO:2412), Figure 2415 (SEQ ID NO:2415), Figure 2418 (SEQ ID NO:2418), Figure 2420 (SEQ ID NO:2420), Figure 2422 (SEQ ID NO:2422), Figure 2424 (SEQ ID NO:2424), Figure 2426 (SEQ ID NO:2426), Figure 2430 (SEQ ID NO:2430), Figure 2432 (SEQ ID NO:2432), Figure 2434 (SEQ ID NO:2434), Figure 2436 (SEQ ID NO:2436), Figure 2438 (SEQ ID NO:2438), Figure 2440 (SEQ ID NO:2440), or Figure 2442 (SEQ ID NO:2442) said method comprising contacting cells which normally respond to said polypeptide with a candidate compound, and determining the responsiveness by said cell to said candidate compound.

27. A method of stimulating the immune response in a mammal, said method comprising administering to said mammal an effective amount of a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266),

Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534

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28. A method of diagnosing an inflammatory immune response in a mammal, said method comprising detecting the level of expression of a gene encoding a PRO polypeptide of the invention as described in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137),

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presence of an inflammatory immune response in the mammal from which the test tissue cells were obtained.

DEMANDE OU BREVET VOLUMINEUX

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FIGURE 1A

GCGGCCTCTTGTGTGAGGGCCTGTGGGATTCTCCGGAT**ATG**GCCGGAGTGTTTCCTTATCGAGGGCCGGGTAACC
CGGTGCCTGGCCCTCTAGCCCCGCTACCGGACTACATGTCGGAGGAGAAGCTGCAGGAGAAAGCTCGAAAATGGC
AGCAATTGCAGGCCAAGCGCTATGCAGAAAAGCGGAAGTTTGGGTTTGTGGATGCCCAGAAGGAAGACATGCCCC
CAGAACATGTCAGGGAGATCATTCGAGACCATGGAGACATGACCAACAGGAAGTTCCGCCATGACAAAAGGGTTT
ACTTGGGTGCCCTAAAGTACATGCCCCACGCAGTCCTCAAACTCCTGGAGAACATGCCTATGCCTTGGGAGCAGA
TTCGGGATGTGCCCGTGCTGTACCACATCACTGGAGCCATTTCCTTCGTCAATGAGATTCCCTGGGTCATTGAAC
CTGTCTACATCTCCCAGTGGGGGTCAATGTGGATTATGATGCGCCGAGAAAAAAGAGATAGGAGGCATTTCAAGA
GAATGCGTTTTCCCCCTTTTGATGATGAGGAGCCGCCCTTGGACTATGCTGACAACATCCTAAATGTTGAGCCAC
TGGAGGCCATTCAGCTAGAGCTGGACCCTGAGGAGGACGCCCCTGTGTTGGACTGGTTCTATGACCACCAGCCGT
TGAGGGACAGCAGGAAGTATGTAAATGGCTCCACTTACCAGCGCTGGCAGTTCACACTACCTATGATGTCAACTC
TCTACCGCCTGGCTAATCAGCTCCTGACAGACTTGGTGGATGACAACTACTTCTACCTGTTTGATTTGAAGGCCT
TCTTTACGTCCAAGGCACTCAATATGGCCATTCCTGGAGGCCCCAAATTTGAACCTCTTGTTCGAGACATCAACC
TACAGGATGAAGACTGGAATGAATTCAATGATATTAACAAGATTATCATCCGGCAGCCTATCCGGACTGAGTACA
AGATTGCTTTTCCTTACTTGTACAACAATCTTCCACACCATGTCCACCTCACCTGGTACCATACTCCCAATGTTG
TATTCATCAAAACTGAAGATCCTGACTTGCCAGCTTTCTACTTTGACCCTTTGATCAACCCAATCTCCCATAGGC
ACTCAGTCAAGAGCCAGGAACCATTGCCGGATGATGATGAGGAATTTGAGCTCCCGGAGTTTGTGGAGCCCTTCC
TGAAGGACACACCCCTCTATACAGACAATACAGCCAATGGCATTGCCCTGCTCTGGGCCCCGCGGCCCTTCAACC
TACGCTCTGGTCGCACCCGTCGGGCCCTGGACATACCCCTTGTCAAGAACTGGTATCGGGAGCATTGTCCTGCCG
GGCAGCCTGTGAAAGTGAGGGTCTCCTACCAGAAGCTGCTTAAGTACTATGTGCTGAATGCCCTGAAGCATCGGC
CCCCTAAGGCTCAAAAGAAGAGGTATTTGTTCCGCTCCTTCAAAGCCACCAAATTCTTTCAGTCCACAAAGCTGG
ACTGGGTGGAGGGTTGGCTCCAGGTTTGCCGCCAGGGCTACAACATGCTCAACCTTCTCATTCACCGCAAAAACC
TCAACTACCTGCACCTGGACTACAACTTCAACCTCAAGCCTGTGAAAACGCTCACCACCAAGGAAAGAAAGAAAT
CTCGTTTTGGGAATGCTTTCCACCTGTGTCGGGAAGTTCTGCGTTTGACTAAGCTGGTGGTGGATAGTCACGTGC
AGTATCGGCTGGGCAATGTGGATGCCTTCCAGCTGGCAGATGGATTGCAGTATATATTTGCCCATGTTGGGCAGT
TGACGGGCATGTATCGATACAAATACAAGCTGATGCGACAGATTCGCGTGTGCAAGGACCTGAAGCATCTCATCT
ATTATCGTTTCAACACAGGCCCTGTAGGGAAGGGTCCTGGCTGTGGCTTCTGGGCTGCCGGTTGGCGAGTCTGGC
TCTTTTTCATGCGTGGCATTACCCCTTTATTAGAGCGATGGCTTGGCAACCTCCTGGCCCGGCAGTTTGAAGGTC
GACACTCAAAGGGGGTGGCAAAGACAGTAACAAAGCAGCGAGTGGAGTCACATTTTGACCTTGAGCTGCGGGCAG
CTGTGATGCATGATATTCTGGACATGATGCCTGAGGGGATCAAGCAGAACAAGGCCCGGACAATCCTGCAGCACC
TCAGTGAAGCCTGGCGCTGCTGGAAAGCCAACATTCCCTGGAAGGTCCCTGGGCTGCCGACGCCCATAGAGAATA
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GAGGGGCCACTGTGGACAAGACTGTTTGTAAAAAGAATCTGGGCCGCCTCACCCGGCTCTATCTGAAGGCAGAAC
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CAGTGCATTGGTTGGAAAGCCGCAGGTTTTCACCCATCCCATTCCCCCCACTCTCCTATAAGCATGACACCAAGT
TGCTCATCTTGGCATTGGAGCGGCTCAAGGAAGCTTATAGTGTGAAGTCTCGGTTGAACCAGTCTCAGAGGGAGG
AGCTAGGTCTGATCGAGCAGGCCTACGATAACCTCCACGAGGCGCTGTCCCGCATAAAGCGTCACCTCCTCACAC
AGAGAGCCTTCAAAGAGGTGGGCATTGAGTTCATGGATCTGTATAGCCACCTCGTTCCAGTATATGATGTTGAGC
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CCTGGATTAAGCCTGCAGACACAGAACCACCTCCACTGCTTGTTTACAAGTGGTGTCAAGGCATCAATAACCTGC
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TCGACTTGACTCTGCTCAACAGGCTCGTGCGCCTCATCGTGGACCACAACATAGCCGACTACATGACAGCCAAGA
ACAACGTCGTCATCAACTATAAGGACATGAACCATACGAATTCATATGGGATCATCAGAGGCCTGCAGTTTGCCT
CATTCATAGTGCAGTATTATGGCCTGGTGATGGATTTGCTTGTATTGGGATTGCACCGGGCCAGTGAGATGGCTG
GGCCCCCTCAGATGCCAAATGACTTTCTCAGTTTCCAGGACATAGCCACTGAGGCTGCCCACCCCATCCGTCTCT
TCTGCAGATACATTGATCGCATCCATATTTTTTTCAGGTTCACAGCAGATGAGGCTCGGGACCTGATTCAACGTT
ACCTGACAGAGCACCCTGACCCCAATAATGAAAACATCGTTGGCTATAATAACAAGAAGTGCTGGCCCCGAGATG
CCCGCATGCGCCTCATGAAACATGATGTTAACTTAGGCCGGGCGGTATTCTGGGACATCAAGAACCGCTTGCCAC
GGTCAGTGACTACAGTTCAGTGGGAGAACAGCTTCGTGTCTGTGTACAGTAAGGACAACCCCAACCTGCTGTTCA

FIGURE 1B

ACATGTGTGGCTTCGAGTGCCGCATCCTGCCTAAGTGCCGCACCAGCTATGAGGAGTTCACCCACAAGGACGGGG
TCTGGAACCTGCAGAATGAGGTTACTAAGGAGCGCACAGCTCAGTGTTTCCTGCGTGTGGACGATGAGTCAATGC
AGCGCTTCCACAACCGCGTGCGTCAGATTCTCATGGCCTCTGGGTCCACCACCTTCACCAAGATTGTGAATAAGT
GGAATACAGCTCTCATTGGCCTTATGACATACTTTCGGGAGGCTGTGGTGAACACCCAAGAGCTCTTGGACTTAC
TGGTGAAGTGTGAGAACAAAATCCAGACACGTATCAAGATTGGACTCAACTCCAAGATGCCAAGTCGGTTCCCCC
CGGTTGTGTTCTACACCCCTAAGGAGTTGGGTGGACTCGGCATGCTCTCAATGGGCCATGTGCTCATCCCCCAAT
CCGACCTCAGGTGGTCCAAACAGACAGATGTAGGTATCACACACTTTCGTTCAGGAATGAGCCATGAAGAAGACC
AGCTCATTCCCAACTTGTACCGCTACATACAGCCATGGGAGAGCGAGTTCATTGATTCTCAGCGGGTCTGGGCTG
AGTACGCACTCAAGAGGCAAGAGGCCATTGCTCAGAACAGACGCCTGACTTTAGAAGACCTAGAAGATTCATGGG
ATCGTGGCATTCCTCGAATCAATACCCTCTTCCAGAAGGACCGGCACACACTGGCTTATGATAAGGGCTGGCGTG
TCAGAACTGACTTTAAGCAGTATCAGGTTTTGAAGCAGAATCCGTTCTGGTGGACACACCAGCGGCATGATGGGA
AGCTCTGGAACCTGAACAACTACCGTACAGACATGATCCAGGCCCTGGGCGGTGTGGAAGGCATTCTGGAACACA
CACTCTTTAAGGGCACTTACTTCCCTACCTGGGAGGGGCTTTTCTGGGAGAAGGCCAGTGGCTTTGAGGAATCTA
TGAAGTGGAAGAAGCTAACTAATGCTCAGCGATCAGGACTGAACCAGATTCCCAATCGTAGATTCACCCTCTGGT
GGTCCCCGACCATTAATCGAGCCAATGTATATGTAGGCTTTCAGGTGCAGCTAGACCTGACGGGTATCTTCATGC
ACGGCAAGATCCCCACGCTGAAGATCTCTCTCATCCAGATCTTCCGAGCTCACTTGTGGCAGAAGATCCATGAGA
GCATTGTTATGGACTTATGTCAGGTGTTTGACCAGGAACTTGATGCACTGGAAATTGAGACAGTACAAAAGGAGA
CAATCCATCCCCGAAAGTCATATAAGATGAACTCTTCCTGTGCAGATATCCTGCTCTTTGCCTCCTATAAGTGGA
ATGTCTCCCGGCCCTCATTGCTGGCTGACTCCAAGGATGTGATGGACAGCACCACCACCCAGAAATACTGGATTG
ACATCCAGTTGCGCTGGGGGGACTATGATTCCCACGACATTGAGCGCTACGCCCGGGCCAAGTTCCTGGACTACA
CCACCGACAACATGAGTATCTACCCTTCGCCCACAGGTGTACTCATCGCCATTGACCTGGCCTATAACTTGCACA
GTGCCTATGGAAACTGGTTCCCAGGCAGCAAGCCTCTCATACAACAGGCCATGGCCAAGATCATGAAGGCAAACC
CTGCCCTGTATGTGTTACGTGAACGGATCCGCAAGGGGCTACAGCTCTATTCATCTGAACCCACTGAGCCTTATT
TGTCTTCTCAGAACTATGGTGAGCTCTTCTCCAACCAGATTATCTGGTTTGTGGATGACACCAACGTCTACAGAG
TGACTATTCACAAGACCTTTGAAGGGAACTTGACAACCAAGCCCATCAACGGAGCCATCTTCATCTTCAACCCAC
GCACAGGGCAGCTGTTCCTCAAGATAATCCACACGTCCGTGTGGGCGGGACAGAAGCGTTTGGGGCAGTTGGCTA
AGTGGAAGACAGCTGAGGAGGTGGCCGCCCTGATCCGATCTCTGCCTGTGGAGGAGCAGCCCAAGCAGATCATTG
TCACCAGGAAGGGCATGCTGGACCCACTGGAGGTGCACTTACTGGACTTCCCCAATATTGTCATCAAAGGATCGG
AGCTCCAACTCCCTTTCCAGGCGTGTCTCAAGGTGGAAAAATTCGGGGATCTCATCCTTAAAGCCACTGAGCCCC
AGATGGTTCTCTTCAACCTCTATGACGACTGGCTCAAGACTATTTCATCTTACACGGCCTTCTCCCGTCTCATCC
TGATTCTGCGTGCCCTACATGTGAACAACGATCGGGCAAAAGTGATCCTGAAGCCAGACAAGACTACTATTACAG
AACCACACCACATCTGGCCCACTCTGACTGACGAAGAATGGATCAAGGTCGAGGTGCAGCTCAAGGATCTGATCT
TGGCTGACTACGGCAAGAAAAACAATGTGAACGTGGCATCACTGACACAATCAGAAATTCGAGACATCATCCTGG
GTATGGAGATCTCGGCACCGTCACAGCAGCGGCAGCAGATCGCTGAGATCGAGAAGCAGACCAAGGAACAATCGC
AGCTGACGGCAACACAGACTCGCACTGTCAACAAGCATGGCGATGAGATCATCACCTCCACCACCAGCAACTATG
AGACCCAGACTTTCTCATCCAAGACTGAGTGGAGGGTCAGGGCCATCTCTGCTGCCAACCTGCACCTAAGGACCA
ATCACATCTATGTTTCATCTGACGACATCAAGGAGACTGGCTACACCTACATCCTTCCCAAGAATGTGCTTAAGA
AGTTCATCTGCATATCTGACCTTCGGGCCCAAATTGCAGGATACCTATATGGGGTGAGCCCACCAGATAACCCCC
AGGTGAAGGAGATCCGCTGCATTGTGATGGTGCCGCAGTGGGGCACTCACCAGACCGTGCACCTGCCTGGCCAGC
TGCCCCAGCATGAGTACCTCAAGGAGATGGAACCCTTAGGTTGGATCCACACTCAGCCCAATGAGTCCCCGCAGT
TATCACCCCAGGATGTCACCACCCATGCCAAGATCATGGCTGACAACCCATCTTGGGATGGCGAGAAGACCATTA
TCATCACATGCAGCTTCACGCCAGGCTCCTGTACACTGACGGCCTACAAGCTGACCCCCAGTGGCTACGAATGGG
GCCGCCAGAACACAGACAAGGGCAACAACCCCAAGGGCTACCTGCCTTCACACTATGAGAGGGTGCAGATGCTGC
TGTCGGACCGTTTCCTTGGCTTCTTCATGGTCCCTGCCCAGTCCTCGTGGAACTACAACTTCATGGGTGTTCGGC
ATGACCCCAACATGAAATATGAGCTACAGCTGGCGAACCCCAAAGAGTTCTACCACGAGGTGCACAGGCCCTCTC
ACTTCCTCAACTTTGCTCTCCTGCAGGAGGGGGAGGTTTACTCTGCGGATCGGGAGGACCTGTATGCCTGACCGT
TTCCCTGCCTCCTGCTTCAGCCTCCCGAGGCCGAAGCCTCAGCCCCTCCAGACAGGCCGCTGACATTCAGCAGTT
TGGCCTCTTTCCCTCTGTCTGTGCTTGTGTTGTTGACCTCCTGATGGCTTGTCATCCTGAATAAAATATAATAAT

FIGURE 1C

AAATTTTGTATAAATAGG

FIGURE 2

MAGVFPYRGPGNPVPGPLAPLPDYMSEEKLQEKARKWQQLQAKRYAEKRKFGFVDAQKEDMPPEHVREIIRDHGD
MTNRKFRHDKRVYLGALKYMPHAVLKLLENMPMPWEQIRDVPVLYHITGAISFVNEIPWVIEPVYISQWGSMWIM
MRREKRDRRHFKRMRFPPFDDEEPPLDYADNILNVEPLEAIQLELDPEEDAPVLDWFYDHQPLRDSRKYVNGSTY
QRWQFTLPMMSTLYRLANQLLTDLVDDNYFYLFDLKAFFTSKALNMAIPGGPKFEPLVRDINLQDEDWNEFNDIN
KIIIRQPIRTEYKIAFPYLYNNLPHHVHLTWYHTPNVVFIKTEDPDLPAFYFDPLINPISHRHSVKSQEPLPDDD
EEFELPEFVEPFLKDTPLYTDNTANGIALLWAPRPFNLRSGRTRRALDIPLVKNWYREHCPAGQPVKVRVSYQKL
LKYYVLNALKHRPPKAQKKRYLFRSFKATKFFQSTKLDWVEGWLQVCRQGYNMLNLLIHRKNLNYLHLDYNFNLK
PVKTLTTKERKKSRFGNAFHLCREVLRLTKLVVDSHVQYRLGNVDAFQLADGLQYIFAHVGQLTGMYRYKYKLMR
QIRVCKDLKHLIYYRFNTGPVGKGPGCGFWAAGWRVWLFFMRGITPLLERWLGNLLARQFEGRHSKGVAKTVTKQ
RVESHFDLELRAAVMHDILDMMPEGIKQNKARTILQHLSEAWRCWKANIPWKVPGLPTPIENMILRYVKAKADWW
TNTAHYNRERIRRGATVDKTVCKKNLGRLTRLYLKAEQERQHNYLKDGPYITAEETVAVYTTTVHWLESRRFSPI
PFPPLSYKHDTKLLILALERLKEAYSVKSRLNQSQREELGLIEQAYDNLHEALSRIKRHLLTQRAFKEVGIEFMD
LYSHLVPVYDVEPLEKITDAYLDQYLWYEADKRRLFPPWIKPADTEPPPLLVYKWCQGINNLQDVWETSEGECNV
MLESRFEKMYEKIDLTLLNRLVRLIVDHNIADYMTAKNNVVINYKDMNHTNSYGIIRGLQFASFIVQYYGLVMDL
LVLGLHRASEMAGPPQMPNDFLSFQDIATEAAHPIRLFCRYIDRIHIFFRFTADEARDLIQRYLTEHPDPNNENI
VGYNNKKCWPRDARMRLMKHDVNLGRAVFWDIKNRLPRSVTTVQWENSFVSVYSKDNPNLLFNMCGFECRILPKC
RTSYEEFTHKDGVWNLQNEVTKERTAQCFLRVDDESMQRFHNRVRQILMASGSTTFTKIVNKWNTALIGLMTYFR
EAVVNTQELLDLLVKCENKIQTRIKIGLNSKMPSRFPPVVFYTPKELGGLGMLSMGHVLIPQSDLRWSKQTDVGI
THFRSGMSHEEDQLIPNLYRYIQPWESEFIDSQRVWAEYALKRQEAIAQNRRLTLEDLEDSWDRGIPRINTLFQK
DRHTLAYDKGWRVRTDFKQYQVLKQNPFWWTHQRHDGKLWNLNNYRTDMIQALGGVEGILEHTLFKGTYFPTWEG
LFWEKASGFEESMKWKKLTNAQRSGLNQIPNRRFTLWWSPTINRANVYVGFQVQLDLTGIFMHGKIPTLKISLIQ
IFRAHLWQKIHESIVMDLCQVFDQELDALEIETVQKETIHPRKSYKMNSSCADILLFASYKWNVSRPSLLADSKD
VMDSTTTQKYWIDIQLRWGDYDSHDIERYARAKFLDYTTDNMSIYPSPTGVLIAIDLAYNLHSAYGNWFPGSKPL
IQQAMAKIMKANPALYVLRERIRKGLQLYSSEPTEPYLSSQNYGELFSNQIIWFVDDTNVYRVTIHKTFEGNLTT
KPINGAIFIFNPRTGQLFLKIIHTSVWAGQKRLGQLAKWKTAEEVAALIRSLPVEEQPKQIIVTRKGMLDPLEVH
LLDFPNIVIKGSELQLPFQACLKVEKFGDLILKATEPQMVLFNLYDDWLKTISSYTAFSRLILILRALHVNNDRA
KVILKPDKTTITEPHHIWPTLTDEEWIKVEVQLKDLILADYGKKNNVNVA

FIGURE 3

GAATTCGGCACGAGATAAAA**ATG**GCTTCCAAAAGAGCTCTGGTCATCCTGGCTAAAGGAGCAGAGGAAATGGAGA
CGGTCATCCCTGTAGATGTCATGAGGCGAGCTGGGATTAAGGTCACCGTTGCAGGCCTGGCTGGAAAAGACCCAG
TACAGTGTAGCCGTGATGTGGTCATTTGTCCTGATGCCAGCCTTGAAGATGCAAAAAAAGAGGGACCATATGATG
TGGTGGTTCTACCAGGAGGTAATCTGGGCGCACAGAATTTATCTGAGTCTGCTGCTGTGAAGGAGATACTGAAGG
AGCAGGAAAACCGGAAGGGCCTGATAGCCGCCATCTGTGCAGGTCCTACTGCTCTGTTGGCTCATGAAATAGGTT
GTGGAAGTAAAGTTACAACACACCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCTACTCTGAGA
ATCGTGTGGAAAAAGACGGCCTGATTCTTACAAGCCGGGGGCCTGGGACCAGCTTCGAGTTTGCGCTTGCAATTG
TTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTCCACTTGTTCTTAAAGAC**TAG**AGCAGCGAAC
TGCGACGATCACTTAGAGAAACAGGCCGTTAGGAATCCATTCTCACTGTGTTCGCTCTAAACAAAACAGTGGTAG
GTTAATGTGTTCAGAAGTCGCTGTCCTTACTACTTTTGCGGAAGTATGGAAGTCACAACTACACAGAGATTTCTC
AGCCTACAAATTGTGTCTATACATTTCTAAGCCTTGTTTGCAGAATAAACAGGGCATTTAGCAAACTAAAAAAAA
AAAAAAAAAAACTCGAG

FIGURE 4

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLEDAKKEGPYDVVVLPGG
NLGAQNLSESAAVKEILKEQENRKGLIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGGHYTYSENRVEKDG
LILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD

FIGURE 5

TTTTGTGAAGAGACGAAGACTGAGCGGTTGTGGCCGCGTTGCCGACCTCCAGCAGCAGTCGGCATTCTCTAACGC
AGAAACCCGGGAGTAGGAGACTCAGAATCGAATCTCTTCTCCCTCCCCTTCTTGTGAGATTTTTTTGATCTTCAG
CTACATTTTCGGCTTTGTGAGAAACCTTACCATCAAACACG**ATG**GCCAGCAACGTTACCAACAAGACAGATCCTC
GCTCCATGAACTCCCGTGTATTCATTGGGAATCTCAACACTCTTGTGGTCAAGAAATCTGATGTGGAGGCAATCT
TTTCGAAGTATGGCAAAATTGTGGGCTGCTCTGTTCATAAGGGCTTTGCCTTCGTTCAGTATGTTAATGAGAGAA
ATGCCCGGGCTGCTGTAGCAGGAGAGGATGGCAGAATGATTGCTGGCCAGGTTTTAGATATTAACCTGGCTGCAG
AGCCAAAAGTGAACCGAGGAAAAGCAGGTGTGAAACGATCTGCAGCGGAGATGTACGGGTCAGTAACAGAACACC
CTTCTCCGTCCCCTCTACTCAGCTCCTCTTTTGACTTGGACTATGACTTTCAACGGGACTATTATGATAGGATGT
ACAGTTACCCAGCACGTGTACCTCCTCCTCCTCCTATTGCTCGGGCTGTAGTGCCCTCGAAACGTCAGCGTGTAT
CAGGAAACACTTCACGAAGGGGCAAAAGTGGCTTCAATTCTAAGAGTGGACAGCGGGGATCTTCCAAGTCTGGAA
AGTTGAAAGGAGATGACCTTCAGGCCATTAAGAAGGAGCTGACCCAGATAAAACAAAAAGTGGATTCTCTCCTGG
AAAACCTGGAAAAAATGGAAAAGGAACAGAGCAAACAAGCAGTAGAGATGAAGAATGATAAGTCAGAAGAGGAGC
AGAGCAGCAGCTCCGTGAAGAAAGATGAGACTAATGTGAAGATGGAGTCTGAGGGGGGTGCAGATGACTCTGCTG
AGGAGGGGGACCTACTGGATGATGATGATAATGAAGATCGGGGGGATGACCAGCTGGAGTTGATCAAGGATGATG
AAAAAGAGGCTGAGGAAGGAGAGGATGACAGAGACAGCGCCAATGGAGGA**TGA**CTCTTAAGCACATAGTGGGGTT
TAGAAATCTTATCCCATTATTTCTTTACCTAGGCGCTTGTCTAAGATCAAATTTTTCACCAGATCCTCTCCCCTA
GTATCTTCAGCACATGCTCACTGTTCTCCCCATCCTTGTCCTTCCCATGTTCATTAATTCATATTGCCCCGCGCC
TAGTCCCATTTTCACTTCCTTTGACGCTCCTAGTAGTTTTGTTAAGTCTTACCCTGTAATTTTTGCTTTTAATTT
TGATACCTCTTTATGACTTAACAATAAAAAGGATGTATGGTTTTTATCAACTGTCTCCAAAATAATCTCTTGTTA
TGCAGGGAGTACAGTTCTTTTCATTCATACATAAGTTCAGTAGTTGCTTCCCTAACTGCAAAGGCAATCTCATTT
AGTTGAGTAGCTCTTGAAAGCAGCTTTGAGTTAGAAGTATGTGTGTTACACCCTCACATTAGTGTGCTGTGTGGG
GCAGTTCAACACAAATGTAACAATTATTTTTGTGAATGAGAGTTGGCATGTCAAATGCATCCTCTAGAAAAATAA
TTAGTGTTATAGTCTTAAGATTTGTTTTCTAAAGTTGATACTGTGGGATTTTTGTGAACAGCCTGATGTTTGGGA
CCTTTTTTTCCTCAAAATAAACAAGTCCTTATTAAACCAGGAATTTGGAG

FIGURE 6

MASNVTNKTDPRSMNSRVFIGNLNTLVVKKSDVEAIFSKYGKIVGCSVHKGFAFVQYVNERNARAAVAGEDGRMI
AGQVLDINLAAEPKVNRGKAGVKRSAAEMYGSVTEHPSPSPLLSSSFDLDYDFQRDYYDRMYSYPARVPPPPPIA
RAVVPSKRQRVSGNTSRRGKSGFNSKSGQRGSSKSGKLKGDDLQAIKKELTQIKQKVDSLLENLEKMEKEQSKQA
VEMKNDKSEEEQSSSSVKKDETNVKMESEGGADDSAEEGDLLDDDDNEDRGDDQLELIKDDEKEAEEGEDDRDSA
NGG

FIGURE 7

CCGACATGTTGAGTCATAAGACGCGTCGGTGTTGCAGTCTGTGTCCTTGGAGGTGACCAGGGCCACTGCAGGCAT
GGTGCTAGCAGAGCTGTACGTCTCTGACCGAGAGGGAAGCGATGCCACGGGAGATGGAACCAAGGAGAAACCATT
TAAAACAGGTCTAAAGGCTTTGATGACAGTAGGGAAAGAACCATTTCCTACCATTTACGTAGATTCACAAAAAGA
AAATGAGAGGTGGAATGTTATTTCTAAATCACAGTTGAAGAACATTAAAAAGATGTGGCATAGGGAACAAATGAA
GAGTGAATCCCGGGAAAAGAAAGAGGCAGAAGATAGTTTACGAAGAGAAAAGAACCTGGAAGAAGCAAAGAAGAT
TACCATTAAAAATGATCCAAGTCTCCCAGAGCCAAAATGTGTGAAGATTGGTGCGTTAGAAGGATATAGAGGCCA
AAGAGTAAAGGTGTTTGGCTGGGTCCACAGGCTGCGCAGGCAAGGAAAGAATTTAATGTTTCTGGTGTTGCGAGA
TGGTACAGGTTATCTTCAGTGTGTCTTGGCGGATGAGTTGTGTCAGTGCTACAATGGAGTTCTCTTGTCCACGGA
GAGCAGTGTTGCAGTGTATGGAATGCTAAATCTTACCCCAAAGGGCAAGCAGGCTCCAGGTGGCCATGAGCTGAG
TTGTGACTTCTGGGAACTAATTGGGTTGGCCCCTGCTGGAGGAGCTGACAACCTGATCAATGAGGAGTCTGACGT
TGATGTCCAGCTCAACAACAGACACATGATGATCCGAGGAGAAAACATGTCCAAAATCCTAAAAGCACGATCCAT
GGTCACCAGGTGCTTTAGAGATCACTTCTTTGATAGGGGGTACTATGAAGTTACTCCTCCAACATTAGTGCAAAC
ACAAGTAGAAGGTGGTGCCACACTCTTCAAGCTTGACTATTTTGGGGAAGAGGCATTTTTGACTCAATCCTCTCA
GTTGTACTTGGAGACCTGCCTCCCAGCCCTGGGAGATGTTTTTTGTATTGCTCAGTCATACCGGGCAGAGCAGTC
CAGAACACGAAGGCACCTGGCTGAGTACACTCACGTGGAAGCTGAGTGTCCTTTCCTGACTTTTGACGACCTCCT
GAACCGGTTGGAGGACTTGGTTTGTGATGTGGTAGATCGAATATTGAAGTCACCTGCAGGGAGCATAGTGCATGA
GCTCAACCCGAACTTTCAGCCCCCCAAACGGCCTTTCAAACGGATGAACTATTCAGATGCTATCGTTTGGCTAAA
AGAACATGATGTAAAGAAAGAAGATGGAACTTTCTATGAATTTGGAGAAGATATCCCAGAAGCTCCTGAGAGACT
GATGACAGACACCATTAATGAACCAATCTTGCTGTGTCGATTTCCTGTGGAGATCAAGTCCTTCTACATGCAGCG
ATGTCCTGAGGATTCCCGTCTTACTGAATCTGTCGACGTGTTGATGCCCAATGTTGGTGAGATTGTGGGAGGCTC
AATGCGTATCTTTGATAGTGAAGAAATACTGGCAGGTTATAAAAGGGAAGGGATTGACCCCACTCCCTATTACTG
GTATACGGATCAGAGAAAATACGGTACATGTCCCCATGGAGGATATGGCTTGGGCTTGGAACGATTCTTAACGTG
GATTCTGAATAGGTATCACATCCGAGACGTGTGCTTATACCCTCGATTTGTCCAGCGTTGCACGCCATAACCATT
TTCTCCAGAAGCGTGGAGGAAAGATTATGAAAGGAACAGGCTCTTTAAAAAAGAAAACAAAAAGCCAGAATCTTC
CTTTTTTTTGTTTCATTGGGGTTTCTCTTTCTGTTTTTCTTTCTACTACCATAAAAACTATCTCAAATCACCTGA
ACATCAAGTGATATTAAGGTTGTCATCTTAAGAAAAAATATCCATTTTTTTCTTAAGTTCGGGAAACAAAGTTCG
GGGAAAATACCTGGCATGAAACTGTAGTTAGGGATACATTTCAGCATTTTACTCACTTTATCCAAGTTATTCATT
TTATTCAAGTTATATGTATGTATAATTCAACAATTTTAGATTATGGTGTAAGATACTCCAGTAACTTATCTTTCT
GTCCTTTTAAGTGTACCTGGAATTCTTTGATTTATTTTATTGCATCAATGAATTAAAACAAAAATCTTGGGGGAA
GAAATTGGCAATATCGTATAAAAATCTGCTCATATTAGAACACAGTATAATTCAGCAGTAAACACTAGAATCAAA
TGAATAGCCTTTTGTATCAGTTATTAATCTTTTCTAACTCTGCTTAGCTGCTAATAATCCTGAGGCATAGAAATT
GAAGAATTTGTAAAAATAGAATTGCCTTAAAGGATTTGAAGTAAGAACATAATTTTGGGGAGAGTTTTTTAGTGA
TTCACAGTATCCCTCTTAGCATTAATTTAAGGTAAAGAGGCAGATTGATTTTCCCTCTTTCCTGGTAATTCCTAA
GTAATTAAGAATAAATAAGTTCCAAAAGAAATTGTAGCTGGAATCTTAATAACAATTGTGAGTGGCTGTTTGAGT
TGCCCCCACCATGTCCTTAGATCTAATCTGTGCTACCTTATTAACTCACAGCAGGCTTACTGAATGGCTTCATTT
CAGATTTAGTTGATTTCTCCACCAAATGCATGTCATGTATTCTCAATAGGCTGTATTCCCAGCAGTCAATAAATG
AACACCCGTAAAAA

FIGURE 8

MVLAELYVSDREGSDATGDGTKEKPFKTGLKALMTVGKEPFPTIYVDSQKENERWNVISKSQLKNIKKMWHREQM
KSESREKKEAEDSLRREKNLEEAKKITIKNDPSLPEPKCVKIGALEGYRGQRVKVFGWVHRLRRQGKNLMFLVLR
DGTGYLQCVLADELCQCYNGVLLSTESSVAVYGMLNLTPKGKQAPGGHELSCDFWELIGLAPAGGADNLINEESD
VDVQLNNRHMMIRGENMSKILKARSMVTRCFRDHFFDRGYYEVTPPTLVQTQVEGGATLFKLDYFGEEAFLTQSS
QLYLETCLPALGDVFCIAQSYRAEQSRTRRHLAEYTHVEAECPFLTFDDLLNRLEDLVCDVVDRILKSPAGSIVH
ELNPNFQPPKRPFKRMNYSDAIVWLKEHDVKKEDGTFYEFGEDIPEAPERLMTDTINEPILLCRFPVEIKSFYMQ
RCPEDSRLTESVDVLMPNVGEIVGGSMRIFDSEEILAGYKREGIDPTPYYWYTDQRKYGTCPHGGYGLGLERFLT
WILNRYHIRDVCLYPRFVQRCTP

FIGURE 9

GGCAGTCGCGGAAGGCGCGGGAGCTTGCGTGCTGCTGGGCCTGAGCTGTCTGTCTCGTTTCTGTCCGCGCGCCCT
GCATCCCGGCCCCGGGCGCCCGCTGGAGGTCGCCGAGGAGCCACAGGGCTGACTGGTCTGCTGCCCGGGCCCAGG
AGTGCCTGGTGTAGCAGTCGCGGAGCCATCCCGGCGTCTGCTGCCATGACCGACTCTCCCCTCAGAGGAGACTCT
TCCTCAGCGGTGGCTGCAGAGACAGATGAGCGGCGGCTCCTGGCCGCGGGACCGTGAGACGGGTTCGTGGCCGGC
CATTTAGGGGGACGCTGCGACCACCGCCTGCGCCCCTCCGGACTGGTTCCTTGGGCCCCGGAAGCTCGCGGCGGG
CCCTGCGGGAGGCGGCATGCTCCCGCGGAGGCTGCTGGCCGCCTGGCTGGCGGGGACGCGGGGCGGGGGCCTGCT
GGCGCTTCTGGCCAATCAGTGCCGCTTCGTCACGGGCCTGCGCGTGCGGCGCGCGCAGCAGATCGCGCAGCTCTA
CGGCCGCCTCTACTCCGAGAGCTCACGCCGCGTTCTCCTCGGCCGCCTCTGGCGCCGGCTGCACGGCCGTCCTGG
CCATGCCTCTGCCTTGATGGCGGCGTTAGCCGGCGTCTTCGTTTGGGACGAGGAGAGGATCCAGGAGGAGGAGTT
GCAGAGATCTATTAATGAGATGAAGCGGTTGGAAGAAATGTCAAATATGTTTCAGAGCTCTGGAGTCCAGCACCA
CCCTCCAGAACCAAAAGCCCAAACAGAAGGGAATGAAGATTCAGAGGGCAAAGAGCAACGTTGGGAAATGGTGAT
GGATAAGAAACACTTTAAGCTGTGGCGGCGCCCAATTACAGGCACCCACCTTTACCAGTACCGAGTTTTTGGAAC
CTACACAGATGTGACACCTCGGCAGTTCTTCAATGTTCAGCTGGACACAGAGTATAGAAAAAAATGGGATGCCCT
GGTAATCAAGCTGGAGGTGATTGAGAGGGATGTGGTTAGTGGTTCCGAGGTTCTTCACTGGGTAACCCATTTTCC
TTATCCAATGTACTCACGGGATTATGTTTATGTTCGGCGGTATAGTGTGGATCAGGAAAACAACATGATGGTGTT
GGTGTCGCGTGCTGTGGAGCATCCGAGTGTGCCAGAGTCTCCAGAATTCGTCAGGGTCAGATCATATGAATCCCA
AATGGTTATCCGTCCCCACAAGTCATTTGATGAGAATGGCTTTGACTACTTACTAACATACAGTGACAATCCCCA
AACGGTGTTTCCTCGCTACTGTGTTAGTTGGATGGTTTCCAGTGGCATGCCAGATTTCCTGGAGAAGCTGCACAT
GGCCACTCTGAAAGCCAAGAATATGGAGATTAAAGTAAAGGACTACATCTCAGCTAAGCCTCTGGAAATGAGTAG
TGAAGCCAAGGCCACCAGCCAGTCCTCTGAGCGAAAGAACGAGGGCAGCTGTGGCCCTGCTCGGATTGAGTATGC
TTGACAGGCTTTGGGATAAGAAGGGACAAGGTGCTTCTAGCCCTGTCTCAGTCCGTTATCACTCTGCTGTAGAAG
GGGGACATGCCACATGTATTAGAAGGCATCTGCTGTAACTTCCAGTGCAAGATAATTCAATAACTGATGTCCCAT
TTCATTCAGAGCCCTTATTGCTCTTATCAAAACAGAAGAAGGCTACATTTGTGGGAGTGTTGTCATATTCTCAGG
CCAACTGTTTTGAAATTCGGTATCTCACTGAGCTAATCTGGAACAAACCTCTCACCTCAGGCCAGAAGGGGATGA
CCTCCATTTGCTTCTCTGAGTAGTTTCCTCTGCTGACATTCCAAATCCCACCATCGATTGTGCAGCGCTTTGGAT
TTCCTTCAGTTCTCCAGGTCCACCTGGAAAGTATAGTTGGCCAGTTGAGTCTCTCAAATGAGGGGCTACTGGGAG
TGCTCTTGGTAACAATCATGATGTGAATGGGTGTGAACGATACTTGGCTATGTTAAGTGCCTTGTCCGCACCTTG
CTTTTATCTCTAGAGACATGAAGTTATTATTAATTTTTTTTTTTTTTAAGTAGAGATGGAGTTTCACTCTGTTTC
CCAGGCTGGTCTTGAACTCCTGGGCCATGCCTGGCCAGGGACATGAATTTGTACAAAGAAATTTCCCTCCCTGCC
TGCACAATATCACCCATTGACTCACCTTATCCAAAGCAAGTTTCCTGTGAATCGGCCAGTTCTTCTATATTCATT
GGATCATTGCCTCCTTCCTAACCTTCCCCATTTACCAAGAACACTGGGAGACTAATCCTTTTAGATAGTAGCTTT
TTGATGCTCAAAACATCACATTTAAATTTAGTTTAAAAATTTTTTAACTTTTGTGTCAAATAGGAGTTGAGGAAT
TGAGCAGGATTCTACCCTAGTCCGATTGTATAGAAAACACCATTTTGATTCAGGTATTATTTTTCATATTTCAGG
TTTGACTTGTTCTTTTCAGAAGGCTAAAGTCAGAGGAATGGGGGCTGGGCCACTCCCTTGGAGCTCTCAGATCTA
CAGACAAGCTGTGTGAATGCATAGATGTAATCTTGTCTCAAATACTAATACAGTGGAGATTTGGTTTATGTTACC
ATTAAGTTCCTCTAAAAAGTTTTTCTTCCTCTCTTCAGAGCCAAAATAAAAGTGAACTACACTGTTCAGATAAGG
TCACAATCTGATGCTGTCAGTTTGACCGAGCTGGTTTTGCTTATGGTCATGCTGCAATTTGTTAGAATAATAGGG
ATCAAGTTTTAAATCCTCCTCCTTCCCTTTTTTCTGGAGTCTTGAGGGCCAGAGTTTTTGTTTTTGTTTTTGTTT
TTGTTTTCCTGCTTGCTACTGTTTTGTGGTGTTGAAAAGTGGTTTAAACCTGAGACTAACTTAAACACTTCCTTG
ACCTTCTTGTTGCCTGTTCATTTTTGTGCCAAGGAAGTAGCTGCCCCAGTGTATGTCTTGCCTTCTCCGCGTCAT
TGTTGGAAGAGGAGAGATGCATCGAGCAGTCCCAGCTGCTTTTCATTTATTACTTCTTCTTTCCAGGACCTGACA
GAAGTCAGGGAAGAGTCCCTGGGTTATGTCCAAACTTAGCACCTGCAATTGTTGGGATGTGGATGGATGTGTGCA
TAAGAGAGAGAGAGAATATGTGTGTGTGTGTGTGCGTCTGCGAGCGCACACACATGCACAAGTGCGAAGGAGTTG
CGGTTGCTCCATGTTCTGACTTAGGGCAATTTGATTCTGCACTTGGGGTCTGTCTGTACAGTTACTCATGTCATT
GTAATGATTTCACTCCTAACTGTGACATTTTTATCAAATGTGTGAATAAATACATAAAGATTGGTACAAAAAAAA
AAAAAAAAAA

FIGURE 10

MAALAGVFVWDEERIQEEELQRSINEMKRLEEMSNMFQSSGVQHHPPEPKAQTEGNEDSEGKEQRWEMVMDKKHF
KLWRRPITGTHLYQYRVFGTYTDVTPRQFFNVQLDTEYRKKWDALVIKLEVIERDVVSGSEVLHWVTHFPYPMYS
RDYVYVRRYSVDQENNMMVLVSRAVEHPSVPESPEFVRVRSYESQMVIRPHKSFDENGFDYLLTYSDNPQTVFPR
YCVSWMVSSGMPDFLEKLHMATLKAKNMEIKVKDYISAKPLEMSSEAKATSQSSERKNEGSCGPARIEYA

FIGURE 11

GCAACCTTTCCAAGGGAGTGGTTGTGTGATCGCCATCTTAGGGAAAAG**ATG**TTCTCGTCCGTGGCGCACCTGGCG
CGGGCGAACCCCTTCAACACGCCACATCTGCAGCTGGTGCACGATGGTCTCGGGGACCTCCGCAGCAGCTCCCCA
GGGCCCACGGGCCAGCCCCGCCGCCCTCGCAACCTGGCAGCCGCCGCCGTGGAAGAGCAGTATAGCTGTGACTAT
GGATCTGGCAGATTCTTTATCCTTTGTGGACTTGGAGGAATTATTAGCTGTGGCACAACACATACAGCATTGGTT
CCTCTAGATCTGGTTAAATGCAGAATGCAGGTGGACCCCCAAAAGTACAAGGGCATATTTAACGGATTCTCAGTT
ACACTTAAAGAGGATGGTGTTCGTGGTTTGGCTAAAGGATGGGCTCCGACTTTCCTTGGCTACTCCATGCAGGGA
CTCTGCAAGTTTGGCTTTTATGAAGTCTTTAAAGTCTTGTATAGCAATATGCTTGGAGAGGAGAATACTTATCTC
TGGCGCACATCACTATATTTGGCTGCCTCTGCCAGTGCTGAATTCTTTGCTGACATTGCCCTGGCTCCTATGGAA
GCTGCTAAGGTTCGAATTCAAACCCAGCCAGGTTATGCCAACACTTTGAGGGATGCAGCTCCCAAAATGTATAAG
GAAGAAGGCCTAAAAGCATTCTACAAGGGGGTTGCTCCTCTCTGGATGAGACAGATACCATACACCATGATGAAG
TTCGCCTGCTTTGAACGTACTGTTGAAGCACTGTACAAGTTTGTGGTTCCTAAGCCCCGCAGTGAATGTTCAAAG
CCAGAGCAGCTGGTTGTAACATTTGTAGCAGGTTACATAGCTGGAGTCTTTTGTGCAATTGTTTCTCACCCTGCT
GATTCTGTGGTATCTGTGTTGAATAAAGAAAAAGGTAGCAGTGCTTCTCTGGTCCTCAAGAGACTTGGATTTAAA
GGTGTATGGAAGGGACTGTTTGCCCGTATCATCATGATTGGTACCCTGACTGCACTACAGTGGTTTATCTATGAC
TCCGTGAAGGTCTACTTCAGACTTCCTCGCCCTCCCCCACCTGAGATGCCAGAGTCTCTGAAGAAAAAGCTTGGG
TTAACTCAG**TAG**TTAGATCAAAGCAAATGTGGACTGAATCTGCTTGTTGATCAGTGTTTGAAGAAAGTGCAAAAG
GAACTTTTATATATTTGACAGTGTAGGAAATTGTCTATTCCTGATATAATTACTGTAGTACTCTTGCTTAAGGCA
AGAGTTTCAGATTTACTGTTGAAATAAACCCAACTGTTCATGAAAAAA

FIGURE 12

MFSSVAHLARANPFNTPHLQLVHDGLGDLRSSSPGPTGQPRRPRNLAAAAVEEQYSCDYGSGRFFILCGLGGIIS
CGTTHTALVPLDLVKCRMQVDPQKYKGIFNGFSVTLKEDGVRGLAKGWAPTFLGYSMQGLCKFGFYEVFKVLYSN
MLGEENTYLWRTSLYLAASASAEFFADIALAPMEAAKVRIQTQPGYANTLRDAAPKMYKEEGLKAFYKGVAPLWM
RQIPYTMMKFACFERTVEALYKFVVPKPRSECSKPEQLVVTFVAGYIAGVFCAIVSHPADSVVSVLNKEKGSSAS
LVLKRLGFKGVWKGLFARIIMIGTLTALQWFIYDSVKVYFRLPRPPPPEMPESLKKKLGLTQ

FIGURE 13

CTGGAAGCGGGCGAGTCTCGTGCTGTGTCGGACCTGCAGCCCCTGGCCTTCCGCCACC**ATG**GAGTACCTCATCGG
TATCCAAGGCCCCGACTATGTTCTTGTCGCCTCCGACCGGGTGGCCGCCAGCAATATTGTCCAGATGAAGGACGA
TCATGACAAGATGTTTAAGATGAGTGAAAAGATATTACTCCTGTGTGTTGGAGAGGCTGGAGACACTGTACAGTT
TGCAGAATATATTCAGAAAAACGTGCAACTTTATAAGATGCGAAATGGATATGAATTGTCTCCCACGGCAGCAGC
TAACTTCACACGCCGAAACCTGGCTGACTGTCTTCGGAGTCGGACCCCATATCATGTGAACCTCCTCCTGGCTGG
CTATGATGAGCATGAAGGGCCAGCGCTGTATTACATGGACTACCTGGCAGCCTTGGCCAAGGCCCCTTTTGCAGC
CCACGGCTATGGTGCCTTCCTGACTCTCAGTATCCTCGACCGATACTACACACCGACTATCTCACGTGAGAGGGC
AGTGGAACTCCTTAGGAAATGTCTGGAGGAGCTCCAGAAACGCTTCATCCTGAATCTGCCAACCTTCAGTGTTCG
AATCATTGACAAAAATGGCATCCATGACCTGGATAACATTTCCTTCCCCAAACAGGGCTCC**TAA**CATCATGTCCT
CCCTCCCACTTGCCAGGGAACTTTTTTTTGATGGGCTCCTTTATTTTTTTCTACTCTTTTCAGGCGCACTCTTGA
TAAATGGTTAATTCAGAATAAAGGTGACTATGGATATAATTGAGCCCTCTGGTCCAGGTCTCAGTTTACCTAATA
TTACCTCAGAAAGGATATGGAGGGAAGATGATCTTTTTGCCAGGTCTGACTTTTCTTCCTGCTCCGCCCTCCATT
AACGCTCAGTACCCTTTAGCAGCTGACGGCCCCACGTTCTACTCCATGCTTGGCTTCCTTTCCAACTAGCTCTTT
CATATATTTTACTTGCTAGTATCTCCATTCTCTCTAAAGTAGTGGTTCTTTTTGCCCTTAAACTTAAATTTTTAA
ATTAATTAACCTGAATTAATAATACATGCACTTAATGTAACATGCAAACAGTACAAAAACATGTAGTGAAAAATA
TTTCTTCCAGAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACG
AGGTCAAGAGAGCGAGACCATCCTGACCAACATGGTGAAACCCCGTCTCTGCTAAAAATACAAAAATTAGCTGGG
CGTGGTGGCACGCACCCCTAGTCCCAGCTACTGGGGAGGCTGAGACGGGAGAATCGGTCGAACCCGGGAGGCGGA
GGTTGCAGTGAGCCTAGATCGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTCCGTCTCAAAAAAAAGAA
GGAAAAATGTTTCTTCCATCCCTATAATCCAGTCATCTGCTTCCTGCTTCCCTTCCTGGAGGAAACTTCAGCTAC
TAATTTCTTATGTTTTTTAAGAGATATTCTGTTACTGTGTAAAGTATACATACATACAGACACATGCCCCCTTTA
AATTTTTTAGATTTATTTATTTATTTAGAGACAGGGTCTCACTCTAGCCCAGGCTGGAGTGCTGTGGCGTAATCT
TGGCTCACTGCAACCTCCGCCTCCCGGGCCCAAGTGATCCTCCCGTCTCAGCCTCCTGAGTAGCTGGGATTACAG
GCGCACACCACCAATGCCCAGCTAGTTTTTGTGTTTTTCATAGAGACAGGGTCTCACCATGTCATTCAAGACCAG
CCTGGCCAACATGGTGAAACCCCATCTCTACTAAAAAAATATATAACAATTAGCCAGGCGTGGTGGCACACGCCT
GTAAACCCAACTACTTGGGAGGCTGAGGCAGGAGAATTGCTTGAGCCCGGGAGAGGGAGGTTGCAGTGAGCCGAG
ATCATGCCACTGCACTCCAGCCTGGCTGACAGAGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAA

FIGURE 14

MEYLIGIQGPDYVLVASDRVAASNIVQMKDDHDKMFKMSEKILLLCVGEAGDTVQFAEYIQKNVQLYKMRNGYEL
SPTAAANFTRRNLADCLRSRTPYHVNLLLAGYDEHEGPALYYMDYLAALAKAPFAAHGYGAFLTLSILDRYYTPT
ISRERAVELLRKCLEELQKRFILNLPTFSVRIIDKNGIHDLDNISFPKQGS

FIGURE 15

ACAGGCATTTTCCAAAGGCAAGCCTGGAGCGCACGGATCTGTATAACCGCGGAAGGCCCTGTTTCCGGTCCCTTG
CGCCTGCGCTCTTGCAGCCAAGAAGGCGGGAGGCTGGAGTAGAGGGAAGCCTGCAACCGGAAGTGAAGGCAGATT
TCCCTCCTTCGTCGCTGTTGCTGCCGCCATACGCGCTCTCCCTGTTTAGTTATGGCAGAGAACGATGTGGACAAT
GAGCTCTTGGACTATGAAGATGATGAGGTGGAGACAGCAGCTGGGGGAGATGGGGCTGAGGCCCCTGCCAAGAAG
GATGTCAAGGGCTCCTATGTCTCCATCCACAGCTCTGGCTTTCGTGACTTCCTGCTCAAGCCAGAGTTGCTCCGG
GCCATTGTCGACTGTGGCTTTGAGCATCCGTCAGAAGTCCAGCATGAGTGCATCCCTCAGGCCATTCTGGGAATG
GATGTCCTGTGCCAGGCCAAGTCGGGCATGGGAAAGACAGCAGTGTTTGTCTTGGCCACACTGCAACAGCTGGAG
CCAGTTACTGGGCAGGTGTCTGTGCTGGTGATGTGTCACACTCGGGAGTTGGCTTTTCAGATCAGCAAGGAATAT
GAGCGCTTCTCTAAATACATGCCCAATGTCAAGGTTGCTGTTTTTTTTGGTGGTCTGTCTATCAAGAAGGATGAA
GAGGTGCTGAAGAAGAACTGCCCGCATATCGTCGTGGGGACTCCAGGCCGTATCCTAGCCCTGGCTCGAAATAAG
AGCCTCAACCTCAAACACATTAAACACTTTATTTTGGATGAATGTGATAAGATGCTTGAACAGCTCGACATGCGT
CGGGATGTCCAGGAAATTTTTCGCATGACCCCCCACGAGAAGCAGGTCATGATGTTCAGTGCTACCTTGAGCAAA
GAGATCCGTCCAGTCTGCCGCAAGTTCATGCAAGATCCAATGGAGATCTTCGTGGATGATGAGACGAAGTTGACG
CTGCATGGGTTGCAGCAGTACTACGTGAAACTGAAGGACAACGAGAAGAACCGGAAGCTCTTTGACCTTCTGGAT
GTCCTTGAGTTCAACCAGGTGGTGATCTTTGTGAAGTCTGTGCAGCGGTGCATTGCCTTGGCCCAGCTACTAGTG
GAGCAGAACTTCCCAGCCATTGCCATCCACCGTGGGATGCCCCAGGAGGAGAGGCTTTCTCGGTATCAGCAGTTT
AAAGATTTTCAACGACGAATTCTTGTGGCTACCAACCTATTTGGCCGAGGCATGGACATCGAGCGGGTGAACATT
GCTTTTAATTATGACATGCCTGAGGATTCTGACACCTACCTGCATCGGGTGGCCAGAGCAGGCCGGTTTGGCACC
AAGGGCTTGGCTATCACATTTGTGTCCGATGAGAATGATGCCAAGATCCTCAATGATGTGCAGGATCGCTTTGAG
GTCAATATTAGTGAGCTGCCTGATGAGATAGACATCTCCTCCTACATTGAACAGACACGGTAGAAGACTCGCCCA
TTTTGGAATGTGACCGTCTGTCCTTCAGGAGAGGACACCAGGGTGGGGGTGAAGGAGACACTACTGCCCCCACCC
CTGACAGCCCCCCACCCCATGGCTTCCATCTTTTGCATCACCACCACTCCTGAACCCCCATTTCTGATTTGTCAGA
ATTTTTTTTTAACAAAACTAAAAATGAAACACATGTGTCTGTGGTATCTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

MAENDVDNELLDYEDDEVETAAGGDGAEAPAKKDVKGSYVSIHSSGFRDFLLKPELLRAIVDCGFEHPSEVQHEC
IPQAILGMDVLCQAKSGMGKTAVFVLATLQQLEPVTGQVSVLVMCHTRELAFQISKEYERFSKYMPNVKVAVFFG
GLSIKKDEEVLKKNCPHIVVGTPGRILALARNKSLNLKHIKHFILDECDKMLEQLDMRRDVQEIFRMTPHEKQVM
MFSATLSKEIRPVCRKFMQDPMEIFVDDETKLTLHGLQQYYVKLKDNEKNRKLFDLLDVLEFNQVVIFVKSVQRC
IALAQLLVEQNFPAIAIHRGMPQEERLSRYQQFKDFQRRILVATNLFGRGMDIERVNIAFNYDMPEDSDTYLHRV
ARAGRFGTKGLAITFVSDENDAKILNDVQDRFEVNISELPDEIDISSYIEQTR

FIGURE 17

GCGGCGTTGTAGTTAAGCTCGTGTAACGGCGGCGGTGTCGGCAGCTGCTGTAGCGAAGAGAGTTTGGCGCG**ATG**T
CTCACACCATTTTGCTGGTACAGCCTACCAAGAGGCCAGAAGGCAGAACTTATGCTGACTACGAATCTGTGAATG
AATGCATGGAAGGTGTTTGTAAAATGTATGAAGAACATCTGAAAAGAATGAATCCCAACAGTCCCTCTATCACAT
ATGACATCAGTCAGTTGTTTGATTTCATCGATGATCTGGCAGACCTCAGCTGCCTGGTTTACCGAGCTGATACCC
AGACATACCAGCCTTATAACAAAGACTGGATTAAAGAGAAGATCTACGTGCTCCTTCGTCGGCAGGCCCAACAGG
CTGGGAAA**TAA**TTGTGTTGGAAGCACTGGGGGGGTTGGGGTGGGCTTGGAACACAGGTGTGTACAGCGTGCTGTA
GTGGAAGTTTTGTATCATAGTAATCCTGTTTCCACTTTGTTATACTCTAGCCAAGATTGACTGTATTAGATGAAA
TGTGAGGATCTTGTTCAATCGGAAACCCCCGTTACCTCCTCTTTTTCTTTCTCTTTCTTTTTTTTTTTTTTACTT
AAACATTTTTATGATGATTTAGATGGAAGTTGTTCTTCGTCACTTAATGTTGGTTCCAGTCCTTCAACTGTTCAT
ATCTACTTTATAACATTCACATACTAACCCTTCTTCAAGATGGGGTGGGGGGTGGAAATGCAGTTTAGCCATGTC
CTCAAGATAAAGTCTTGGTAAAAATAAATAAATGTCCTTTAGTTATAAAAAAAAAAAAAAAAAAA

FIGURE 18

MSHTILLVQPTKRPEGRTYADYESVNECMEGVCKMYEEHLKRMNPNSPSITYDISQLFDFIDDLADLSCLVYRAD
TQTYQPYNKDWIKEKIYVLLRRQAQQAGK

FIGURE 19

CGGTTGGTGCGGCCTCCATTGTTCGTGTTTTAAGGCGCC**ATG**AGGGGTGACAGAGGCCGTGGTCGTGGTGGGCGC
TTTGGTTCCAGAGGAGGCCCAGGAGGAGGGTTCAGGCCCTTTGTACCACATATCCCATTTGACTTCTATTTGTGT
GAAATGGCCTTTCCCCGGGTCAAGCCAGCACCTGATGAAACTTCCTTCAGTGAGGCCTTGCTGAAGAGGAATCAG
GACCTGGCTCCCAATTCTGCTGAACAGGCATCTATCCTTTCTCTGGTGACAAAAATAAACAATGTGATTGATAAT
CTGATTGTGGCTCCAGGGACATTTGAAGTGCAAATTGAAGAAGTTCGACAGGTGGGATCCTATAAAAAGGGGACA
ATGACTACAGGACACAATGTGGCTGACCTGGTGGTGATACTCAAGATTCTGCCAACGTTGGAAGCTGTTGCTGCC
CTGGGGAACAAAGTCGTGGAAAGCCTAAGAGCACAGGATCCTTCTGAAGTTTTAACCATGCTGACCAACGAAACT
GGCTTTGAAATCAGTTCTTCTGATGCTACAGTGAAGATTCTCATTACAACAGTGCCACCCAATCTTCGAAAACTG
GATCCAGAACTCCATTTGGATATCAAAGTATTGCAGAGTGCCTTAGCAGCCATCCGACATGCCCGCTGGTTCGAG
GAAAATGCTTCTCAGTCCACAGTTAAAGTTCTCATCAGACTACTGAAGGACTTGAGGATTCGTTTTCCTGGCTTT
GAGCCCCTCACACCCTGGATCCTTGACCTACTAGGCCATTATGCTGTGATGAACAACCCCACCAGACAGCCTTTG
GCCCTAAACGTTGCATACAGGCGCTGCTTGCAGATTCTGGCTGCAGGACTGTTCCTGCCAGGTTCAGTGGGTATC
ACTGACCCCTGTGAGAGTGGCAACTTTAGAGTACACACAGTCATGACCCTAGAACAGCAGGACATGGTCTGCTAT
ACAGCTCAGACTCTCGTCCGAATCCTCTCACATGGTGGCTTTAGGAAGATCCTTGGCCAGGAGGGTGATGCCAGC
TATCTTGCTTCTGAAATATCTACCTGGGATGGAGTGATAGTAACACCTTCAGAAAAGGCTTATGAGAAGCCACCA
GAGAAGAAGGAAGGAGAGGAAGAAGAGGAGAATACAGAAAGAACCACCTCAAGGAGAGGAAGAAGAAAGCATGGA
AACTCAGGAGTGACATTCCCTTCACTCCTTTTCCTACCCAAGGGAAAGACTGGAGCC**TAA**GCTGCCTGCTACTGG
CTTTACATGGTGACAGACATTCCGTGGATAGGAAGATAGCAGGAGAAAGTAACTCCATAGAGTGTCATTCCACTG
GTTGATATTGGCTTAGCTGCCAGTCTCCCATTTGTGACCTATGCCATCCATCTATAATGGAGGATACCAACATTT
CTTCCTAATATTCTATAATCTCCAACTCCTGAAAACCCCTCTCTCAACTAATACTTTGCTGTTGAAATGTTGTGA
AATGTTAAGTGTCTGGAAATTTTTTTTTCTAAGAAAAACTATTAAAGTACTT

FIGURE 20

MRGDRGRGRGGRFGSRGGPGGGFRPFVPHIPFDFYLCEMAFPRVKPAPDETSFSEALLKRNQDLAPNSAEQASIL
SLVTKINNVIDNLIVAPGTFEVQIEEVRQVGSYKKGTMTTGHNVADLVVILKILPTLEAVAALGNKVVESLRAQD
PSEVLTMLTNETGFEISSSDATVKILITTVPPNLRKLDPELHLDIKVLQSALAAIRHARWFEENASQSTVKVLIR
LLKDLRIRFPGFEPLTPWILDLLGHYAVMNNPTRQPLALNVAYRRCLQILAAGLFLPGSVGITDPCESGNFRVHT
VMTLEQQDMVCYTAQTLVRILSHGGFRKILGQEGDASYLASEISTWDGVIVTPSEKAYEKPPEKKEGEEEEENTE
RTTSRRGRRKHGNSGVTFPSLLFLPKGKTGA

FIGURE 21

CTCCGGCGCAGTGTTGGGACTGTCTGGGTATCGGAAAGCAAGCCTACGTTGCTCACTATTACGTATAATCCTTTT
CTTTTCAAG**ATG**CCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTCAGGCAGAAATTGCC
CAACTCATGTCCCTCATCATCAATACCTTCTATTCCAACAAGGAGATTTTCCTTCGGGAGTTGATCTCTAATGCT
TCTGATGCCTTGGACAAGATTCGCTATGAGAGCCTGACAGACCCTTCGAAGTTGGACAGTGGTAAAGAGCTGAAA
ATTGACATCATCCCCAACCCTCAGGAACGTACCCTGACTTTGGTAGACACAGGCATTGGCATGACCAAAGCTGAT
CTCATAAATAATTTGGGAACCATTGCCAAGTCTGGTACTAAAGCATTCATGGAGGCTCTTCAGGCTGGTGCAGAC
ATCTCCATGATTGGGCAGTTTGGTGTTGGCTTTTATTCTGCCTACTTGGTGGCAGAGAAAGTGGTTGTGATCACA
AAGCACAACGATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTCCTTCACTGTGCGTGCTGACCATGGT
GAGCCCATTGGCAGGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTACCTAGAAGAGAGGCGG
GTCAAAGAAGTAGTGAAGAAGCATTCTCAGTTCATAGGCTATCCCATCACCCTTTATTTGGAGAAGGAACGAGAG
AAGGAAATTAGTGATGATGAGGCAGAGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAAGAAAAA
CCCAAGATCGAAGATGTGGGTTCAGATGAGGAGGATGACAGCGGTAAGGATAAGAAGAAGAAAACTAAGAAGATC
AAAGAGAAATACATTGATCAGGAAGAACTAAACAAGACCAAGCCTATTTGGACCAGAAACCCTGATGACATCACC
CAAGAGGAGTATGGAGAATTCTACAAGAGCCTCACTAATGACTGGGAAGACCACTTGGCAGTCAAGCACTTTTCT
GTAGAAGGTCAGTTGGAATTCAGGGCATTGCTATTTATTCCTCGTCGGGCTCCCTTTGACCTTTTTGAGAACAAG
AAGAAAAAGAACAACATCAAACTCTATGTCCGCCGTGTGTTCATCATGGACAGCTGTGATGAGTTGATACCAGAG
TATCTCAATTTTATCCGTGGTGTGGTTGACTCTGAGGATCTGCCCCTGAACATCTCCCGAGAAATGCTCCAGCAG
AGCAAAATCTTGAAAGTCATTCGCAAAAACATTGTTAAGAAGTGCCTTGAGCTCTTCTCTGAGCTGGCAGAAGAC
AAGGAGAATTACAAGAAATTCTATGAGGCATTCTCTAAAAATCTCAAGCTTGGAATCCACGAAGACTCCACTAAC
CGCCGCCGCCTGTCTGAGCTGCTGCGCTATCATACCTCCCAGTCTGGAGATGAGATGACATCTCTGTCAGAGTAT
GTTTCTCGCATGAAGGAGACACAGAAGTCCATCTATTACATCACTGGTGAGAGCAAAGAGCAGGTGGCCAACTCA
GCTTTTGTGGAGCGAGTGCGGAAACGGGGCTTCGAGGTGGTATATATGACCGAGCCCATTGACGAGTACTGTGTG
CAGCAGCTCAAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTACCAAGGAGGGTCTGGAGCTGCCTGAGGATGAG
GAGGAGAAGAAGAAGATGGAAGAGAGCAAGGCAAAGTTTGAGAACCTCTGCAAGCTCATGAAAGAAATCTTAGAT
AAGAAGGTTGAGAAGGTGACAATCTCCAATAGACTTGTGTCTTCACCTTGCTGCATTGTGACCAGCACCTACGGC
TGGACAGCCAATATGGAGCGGATCATGAAAGCCCAGGCACTTCGGGACAACTCCACCATGGGCTATATGATGGCC
AAAAAGCACCTGGAGATCAACCCTGACCACCCCATTGTGGAGACGCTGCGGCAGAAGGCTGAGGCCGACAAGAAT
GATAAGGCAGTTAAGGACCTGGTGGTGCTGCTGTTTGAAACCGCCCTGCTATCTTCTGGCTTTTCCCTTGAGGAT
CCCCAGACCCACTCCAACCGCATCTATCGCATGATCAAGCTAGGTCTAGGTATTGATGAAGATGAAGTGGCAGCA
GAGGAACCCAATGCTGCAGTTCCTGATGAGATCCCCCCTCTCGAGGGCGATGAGGATGCGTCTCGCATGGAAGAA
GTCGAT**TAG**GTTAGGAGTTCATAGTTGGAAAACTTGTGCCCTTGTATAGTGTCCCCATGGGCTCCCACTGCAGCC
TCGAGTGCCCCTGTCCCACCTGGCTCCCCCTGCTGGTGTCTAGTGTTTTTTTCCCTCTCCTGTCCTTGTGTTGAA
GGCAGTAAACTAAGGGTGTCAAGCCCCATTCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGTATTGTGGT
TTATTTTATTTTCTTCATTTTGTTCTGAAATTAAAGTATGCAAAATAAAGAATATGCCGTTTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 22

MPEEVHHGEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLTDPSKLDSGKELKIDI
IPNPQERTLTLVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHN
DDEQYAWESSAGGSFTVRADHGEPIGRGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREKEI
SDDEAEEEKGEKEEEDKDDEEKPKIEDVGSDEEDDSGKDKKKKTKKIKEKYIDQEELNKTKPIWTRNPDDITQEE
YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKKNNIKLYVRRVFIMDSCDELIPEYLN
FIRGVVDSEDLPLNISREMLQQSKILKVIRKNIVKKCLELFSELAEDKENYKKFYEAFSKNLKLGIHEDSTNRRR
LSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSAFVERVRKRGFEVVYMTEPIDEYCVQQL
KEFDGKSLVSVTKEGLELPEDEEEKKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTA
NMERIMKAQALRDNSTMGYMMAKKHLEINPDHPIVETLRQKAEADKNDKAVKDLVVLLFETALLSSGFSLEDPQT
HSNRIYRMIKLGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASRMEEVD

FIGURE 23

GCAAAACCAACGCCTGGCTCGGAGCAGCAGCCTCTGAGGTGTCCCTGGCCAGTGTCCTTCCACCTGTCCACAAGC
ATGGGGAACATCTTCGCCAACCTCTTCAAGGGCCTTTTTGGCAAAAAAGAAATGCGCATCCTCATGGTGGGCCTG
GATGCTGCAGGGAAGACCACGATCCTCTACAAGCTTAAGCTGGGTGAGATCGTGACCACCATTCCCACCATAGGC
TTCAACGTGGAAACCGTGGAGTACAAGAACATCAGCTTCACTGTGTGGGACGTGGGTGGCCAGGACAAGATCCGG
CCCCTGTGGCGCCACTACTTCCAGAACACACAAGGCCTGATCTTCGTGGTGGACAGCAATGACAGAGAGCGTGTG
AACGAGGCCCGTGAGGAGCTCATGAGGATGCTGGCCGAGGACGAGCTCCGGGATGCTGTCCTCCTGGTGTTCGCC
AACAAGCAGGACCTCCCCAACGCCATGAATGCGGCCGAGATCACAGACAAGCTGGGGCTGCACTCACTACGCCAC
AGGAACTGGTACATTCAGGCCACCTGCGCCACCAGCGGCGACGGGCTCTATGAAGGACTGGACTGGCTGTCCAAT
CAGCTCCGGAACCAGAAG**TGA**ACGCGACCCCCCTCCCTCTCACTCCTCTTGCCCTCTGCTTTACTCTCATGTGGC
AAACGTGCGGCTCGTGGTGTGAGTGCCAGAAGCTGCCTCCGTGGTTTGGTCACCGTGTGCATCGCACCGTGCTGT
AAATGTGGCAGACGCAGCCTGCGGCCAGGCTTTTTATTTAATGTAAATAGTTTTTGTTTCCAATGAGGCAGTTTC
TGGTACTCCTATGCAATATTACTCAGCTTTTTTTATTGTAAAAAGAAAAATCAACTCACTGTTCAGTGCTGAGAG
GGGATGTAGGCCCATGGGCACCTGGCCTCCAGGAGTCGCTGTGTTGGGAGAGCCGGCCACGCCCTTGGCTTAGAG
CTGTGTTGAAATCCATTTTGGTGGTTGGTTTTAACCCAAACTCAGTGCATTTTTTAAAATAGTTAAGAATCCAAG
TCGAGAACACTTGAACACACAGAAGGGAGACCCCGCCTAGCATAGATTTGCAGTTACGGCCTGGATGCCAGTCGC
CAGCCCAGCTGTTCCCCTCGGGAACATGAGGTGGTGGTGGCGCAGCAGACTGCGATCAATTCTGCATGGTCACAG
TAGAGATCCCCGCAACTCGCTTGTCCTTGGGTCACCCTGCATTCCATAGCCATGTGCTTGTCCCTGTGCTCCCAC
GGTTCCCAGGGGCCAGGCTGGGAGCCCACAGCCACCCCACTATGCCGCAGGCCGCCCTACCCACCTTCAGGCAGC
CTATGGGACGCAGGCCCCATCTGTCCCTCGGTCCGCGTGTGGCCAGAGTGGTCCGTCGTCCCCAACACTCGTGCT
CGCTCAGACACTTTGGCAGGATGTCTGGGGCCTCACCAGCAGGAGCGCGTGCAAGCCGGGCAGGCGGTCCACCTA
GACCCACAGCCCCTCGGGAGCACCCCACCTCTGTGTGTGATGTAGCTTTCTCTCCCTCAGCCTGCAAGGGTCCGA
TTTGCCATCGAAAAAGACAACCTCTACTTTTTTCTTTTGTATTTTGATAAACACTGAAGCTGGAGCTGTTAAATT
TATCTTGGGGAAACCTCAGAACTGGTCTATTTGGTGTCGTAGGAACCTCTTACTGCTTTCAATACACGATTAGTA
ATCAACTGTTTTGTATACTTGTTTTCAGTTTTCATTTCGACAAACAAGCACTGTAATTATAGCTATTAGAATAAA
ATCTCTTAACTATT

FIGURE 24

MGNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIR
PLWRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRH
RNWYIQATCATSGDGLYEGLDWLSNQLRNQK

FIGURE 25

CGCGCCGGGAACAGCCAGTCGGTGCCTAACGCGAGTGTATCTCGAGAGAGAAGCGATCAACAGCTGCCGGTCTGC
GCCTGCGCGGCGACGGGGCGTGGCCGCGGGCGAGTGGGGCCAAGGAGGCAGCCGGGAGCGGGGGCGCAGGTGTTA
CTGGTTGCGTCGGGTCACGTGGGCGCGCAGCAGACCGCGGTGCAGCCCGTTCGCTCACACAAAGCCCAGACGCGG
AGAAA**ATG**GCGGCAGGGGTCGAAGCGGCGGCGGAGGTGGCGGCGACGGAGATCAAAATGGAGGAAGAGAGCGGCG
CGCCCGGCGTGCCGAGCGGCAACGGGGCTCCGGGCCCTAAGGGTGAAGGAGAACGACCTGCTCAGAATGAGAAGA
GGAAGGAGAAAAACATAAAAAGAGGAGGCAATCGCTTTGAGCCATATGCCAATCCAACTAAAAGATACAGAGCCT
TCATTACAAACATACCTTTTGATGTGAAATGGCAGTCACTTAAAGACCTGGTTAAAGAAAAAGTTGGTGAGGTAA
CATACGTGGAGCTCTTAATGGACGCTGAAGGAAAGTCAAGGGGATGTGCTGTTGTTGAATTCAAGATGGAAGAGA
GCATGAAAAAAGCTGCGGAAGTCCTAAACAAGCATAGTCTGAGCGGAAGACCACTGAAAGTCAAAGAAGATCCTG
ATGGTGAACATGCCAGGAGAGCAATGCAAAAGGTGATGGCTACGACTGGTGGGATGGGTATGGGACCAGGTGGCC
CAGGAATGATTACTATCCCACCCAGTATCCTAAATAATCCCAACATCCCAAATGAGATTATCCATGCATTACAGG
CTGGAAGACTTGGAAGCACAGTATTTGTAGCAAATCTGGATTATAAAGTTGGCTGGAAGAAACTGAAGGAAGTAT
TTAGTATGGCTGGTGTGGTGGTCCGAGCAGACATTCTTGAAGATAAAGATGGAAAAAGTCGTGGAATAGGCACTG
TTACTTTTGAACAGTCCATTGAAGCTGTGCAAGCTATATCTATGTTCAATGGCCAGCTGCTATTTGATAGACCAA
TGCACGTCAAGATGGATGAGAGGGCCTTACCAAAAGGAGATTTCTTCCCTCCTGAGCGTCCACAACAACTTCCCC
ATGGCCTTGGTGGTATTGGCATGGGGTTAGGACCAGGAGGGCAACCCATTGATGCCAATCACCTGAATAAAGGCA
TCGGAATGGGAAACATAGGTCCCGCAGGAATGGGAATGGAAGGCATAGGATTTGGAATAAATAAAATGGGAGGAA
TGGAGGGGCCCTTTGGTGGTGGTATGGAAAACATGGGTCGATTTGGATCTGGGATGAACATGGGCAGGATAAATG
AAATCCTAAGTAATGCACTGAAGAGAGGAGAGATCATTGCAAAGCAGGGAGGAGGTGGAGGTGGAGGAAGCGTCC
CTGGGATCGAGAGGATGGGTCCTGGCATTGACCGCCTCGGGGGTGCCGGCATGGAGCGCATGGGCGCGGGCCTGG
GCCACGGCATGGATCGCGTGGGCTCCGAGATCGAGCGCATGGGCCTGGTCATGGACCGCATGGGCTCCGTGGAGC
GCATGGGCTCCGGCATTGAGCGCATGGGCCCGCTGGGCCTCGACCACATGGCCTCCAGCATTGAGCGCATGGGCC
AGACCATGGAGCGCATTGGCTCTGGCGTGGAGCGCATGGGTGCCGGCATGGGCTTCGGCCTTGAGCGCATGGCCG
CTCCCATCGACCGTGTGGGCCAGACCATTGAGCGCATGGGCTCTGGCGTGGAGCGCATGGGCCCTGCCATCGAGC
GCATGGGCCTGAGCATGGAGCGCATGGTGCCCGCAGGTATGGGAGCTGGCCTGGAGCGCATGGGCCCCGTGATGG
ATCGCATGGCCACCGGCCTGGAGCGCATGGGCGCCAACAATCTGGAGCGGATGGGCCTGGAGCGCATGGGCGCCA
ACAGCCTCGAGCGCATGGGCCTGGAGCGCATGGGTGCCAACAGCCTCGAGCGCATGGGCCCCGCCATGGGCCCGG
CCCTGGGCGCTGGCATTGAGCGCATGGGCCTGGCCATGGGTGGCGGTGGCGGTGCCAGCTTTGACCGTGCCATCG
AGATGGAGCGTGGCAACTTCGGAGGAAGCTTCGCAGGTTCCTTTGGTGGAGCTGGAGGCCATGCTCCTGGGGTGG
CCAGGAAGGCCTGCCAGATATTTGTGAGAAATCTGCCATTCGATTTCACATGGAAGATGCTAAAGGACAAATTCA
ACGAGTGCGGCCACGTGCTGTACGCCGACATCAAGATGGAGAATGGGAAGTCCAAGGGGTGTGGTGTGGTTAAGT
TCGAGTCGCCAGAGGTGGCCGAGAGAGCCTGCCGGATGATGAATGGCATGAAGCTGAGTGGCCGAGAGATTGACG
TTCGAATTGATAGAAACGCT**TAA**GCAGTTGCCTTTTTTAAACATCGATACGAGACCTCTGAATTTGTATTTTTTC
TTGTTAACCATTTTAATTTGTTGGCTGGATGTATAAAGATGTTTAAAAAATTCAGTTGCTTTTTGGGGTAATTTG
AATTACTTTTTTAATGACTGGGGTTCCATTTGACTGTTTGCATTGAGATTGCAATGTGCGCAATTTTTTTTGTAG
TTGTGGCATCTTGTTGACATCGAATATGACTTTGATAATAAATACCGGTTCCTGAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 26

MAAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEKRKEKNIKRGGNRFEPYANPTKRYRAFI
TNIPFDVKWQSLKDLVKEKVGEVTYVELLMDAEGKSRGCAVVEFKMEESMKKAAEVLNKHSLSGRPLKVKEDPDG
EHARRAMQKVMATTGGMGMGPGGPGMITIPPSILNNPNIPNEIIHALQAGRLGSTVFVANLDYKVGWKKLKEVFS
MAGVVVRADILEDKDGKSRGIGTVTFEQSIEAVQAISMFNGQLLFDRPMHVKMDERALPKGDFFPPERPQQLPHG
LGGIGMGLGPGGQPIDANHLNKGIGMGNIGPAGMGMEGIGFGINKMGGMEGPFGGGMENMGRFGSGMNMGRINEI
LSNALKRGEIIAKQGGGGGGGSVPGIERMGPGIDRLGGAGMERMGAGLGHGMDRVGSEIERMGLVMDRMGSVERM
GSGIERMGPLGLDHMASSIERMGQTMERIGSGVERMGAGMGFGLERMAAPIDRVGQTIERMGSGVERMGPAIERM
GLSMERMVPAGMGAGLERMGPVMDRMATGLERMGANNLERMGLERMGANSLERMGLERMGANSLERMGPAMGPAL
GAGIERMGLAMGGGGGASFDRAIEMERGNFGGSFAGSFGGAGGHAPGVARKACQIFVRNLPFDFTWKMLKDKFNE
CGHVLYADIKMENGKSKGCGVVKFESPEVAERACRMMNGMKLSGREIDVRIDRNA

FIGURE 27

CGGCGCCATTAAAGCGAGGAGGAGGCGAGAGCGGCCGCCGCTGGTGCTTATTCTTTTTTAGTGCAGCGGGAGAGA
GCGGGAGTGTGCGCCGCGCGAGAGTGGGAGGCGAAGGGGGCAGGCCAGGGAGAGGCGCAGGAGCCTTTGCAGCCA
CGCGCGCGCCTTCCCTGTCTTGTGTGCTTCGCGAGGTAGAGCGGGCGCGCGGCAGCGCGGGGATTACTTTGCTGC
TAGTTTCGGTTCGCGGCAGGCGGGTGTAGTCTCGGCGGCAGCGGCGGAGACACTAGCACT**ATG**TCGGAGGAGCAG
TTCGGCGGGGACGGGGCGGCGGCAGCGGCAACGGCGGCGGTAGGCGGCTCGGCGGGCGAGCAGGAGGGAGCCATG
GTGGCGGCGACACAGGGGGCAGCGGCGGCGGCGGGAAGCGGAGCCGGGACCGGGGGCGGAACCGCGTCTGGAGGC
ACCGAAGGGGGCAGCGCCGAGTCGGAGGGGGCGAAGATTGACGCCAGTAAGAACGAGGAGGATGAAGGCCATTCA
AACTCCTCCCCACGACACTCTGAAGCAGCGACGGCACAGCGGGAAGAATGGAAAATGTTTATAGGAGGCCTTAGC
TGGGACACTACAAAGAAAGATCTGAAGGACTACTTTTCCAAATTTGGTGAAGTTGTAGACTGCACTCTGAAGTTA
GATCCTATCACAGGGCGATCAAGGGGTTTTGGCTTTGTGCTATTTAAAGAATCGGAGAGTGTAGATAAGGTCATG
GATCAAAAAGAACATAAATTGAATGGGAAGGTGATTGATCCTAAAAGGGCCAAAGCCATGAAAACAAAAGAGCCG
GTTAAAAAAATTTTTGTTGGTGGCCTTTCTCCAGATACACCTGAAGAGAAAATAAGGGAGTACTTTGGTGGTTTT
GGTGAGGTGGAATCCATAGAGCTCCCCATGGACAACAAGACCAATAAGAGGCGTGGGTTCTGCTTTATTACCTTT
AAGGAAGAAGAACCAGTGAAGAAGATAATGGAAAAGAAATACCACAATGTTGGTCTTAGTAAATGTGAAATAAAA
GTAGCCATGTCGAAGGAACAATATCAGCAACAGCAACAGTGGGGATCTAGAGGAGGATTTGCAGGAAGAGCTCGT
GGAAGAGGTGGTGGCCCCAGTCAAAACTGGAACCAGGGATATAGTAACTATTGGAATCAAGGCTATGGCAACTAT
GGATATAACAGCCAAGGTTACGGTGGTTATGGAGGATATGACTACACTGGTTACAACAACTACTATGGATATGGT
GATTATAGCAACCAGCAGAGTGGTTATGGGAAGGTATCCAGGCGAGGTGGTCATCAAAATAGCTACAAACCATAC
TAAATTATTCCATTTGCAACTTATCCCCAACAGGTGGTGAAGCAGTATTTTCCAATTTGAAGATTCATTTGAAGG
TGGCTCCTGCCACCTGCTAATAGCAGTTCAAACTAAATTTTTTGTATCAAGTCCCTGAATGGAAGTATGACGTTG
GGTCCCTCTGAAGTTTAATTCTGAGTTCTCATTAAAAGAAATTTGCTTTCATTGTTTTATTTCTTAATTGCTATG
CTTCAGAATCAATTTGTGTGTTATGCCCTTTCCCCCAGTATTGTAGAGCAAGTCTTGTGTTAAAAGCCCAGTGTG
ACAGTGTCATGATGTAGTAGTGTCTTACTGGTTTTTTAATAAATCCTTTTGTATAAAAATGTATTGGCTCTTTTA
TCATCAGAATAGGAAAAATTGTCATGGATTCAAGTTATTAAAAGCATAAGTTTGGAAGACAGGCTTGCCGAAATT
GAGGACATGATTAAAATTGCAGTGAAGTTTGAAATGTTTTTAGCAAAATCTAATTTTTGCCATAATGTGTCCTCC
CTGTCCAAATTGGGAATGACTTAATGTCAATTTGTTTGTTGGTTGTTTTAATAATACTTCCTTATGTAGCCATTA
AGATTTATATGAATATTTTCCCAAATGCCCAGTTTTTGCTTAATATGTATTGTGCTTTTTAGAACAAATCTGGAT
AAATGTGCAAAAGTACCCCTTTGCACAGATAGTTAATGTTTTATGCTTCCATTAAATAAAAAGGACTTAAAATCT
GTTAATTATAATAGAAATGCGGCTAGTTCAGAGAGATTTTTAGAGCTGTGGTGGACTTCATAGATGAATTCAAGT
GTTGAGGGAGGATTAAAGAAAT

FIGURE 28

MSEEQFGGDGAAAAATAAVGGSAGEQEGAMVAATQGAAAAAGSGAGTGGGTASGGTEGGSAESEGAKIDASKNEE
DEGHSNSSPRHSEAATAQREEWKMFIGGLSWDTTKKDLKDYFSKFGEVVDCTLKLDPITGRSRGFGFVLFKESES
VDKVMDQKEHKLNGKVIDPKRAKAMKTKEPVKKIFVGGLSPDTPEEKIREYFGGFGEVESIELPMDNKTNKRRGF
CFITFKEEEPVKKIMEKKYHNVGLSKCEIKVAMSKEQYQQQQQWGSRGGFAGRARGRGGGPSQNWNQGYSNYWNQ
GYGNYGYNSQGYGGYGGYDYTGYNNYYGYGDYSNQQSGYGKVSRRGGHQNSYKPY

FIGURE 29

GTACTATCCTCCTTACTTTTGGGTCGGGCCCTCCGGGAAG**ATG**GCGGCCGTGCAGGCGGCCGAGGTGAAAGTGGA
TGGCAGCGAGCCGAAACTGAGCAAGAATGAGCTGAAGAGACGCCTGAAAGCTGAGAAGAAAGTAGCAGAGAAGGA
GGCCAAACAGAAAGAGCTCAGTGAGAAACAGCTAAGCCAAGCCACTGCTGCTGCCACCAACCACACCACTGATAA
TGGTGTGGGTCCTGAGGAAGAGAGCGTGGACCCAAATCAATACTACAAAATCCGCAGTCAAGCAATTCATCAGCT
GAAGGTCAATGGGGAAGACCCATACCCACACAAGTTCCATGTAGACATCTCACTCACTGACTTCATCCAAAAATA
TAGTCACCTGCAGCCTGGGGATCACCTGACTGACATCACCTTAAAGGTGGCAGGTAGGATCCATGCCAAAAGAGC
TTCTGGGGGAAAGCTCATCTTCTATGATCTTCGAGGAGAGGGGGTGAAGTTGCAAGTCATGGCCAATTCCAGAAA
TTATAAATCAGAAGAAGAATTTATTCATATTAATAACAAACTGCGTCGGGGAGACATAATTGGAGTTCAGGGGAA
TCCTGGTAAAACCAAGAAGGGTGAGCTGAGCATCATTCCGTATGAGATCACACTGCTGTCTCCCTGTTTGCATAT
GTTACCTCATCTTCACTTTGGGCTCAAAGACAAGGAAACAAGGTATCGCCAGAGATACTTGGACTTGATCCTGAA
TGACTTTGTGAGGCAGAAATTTATCATCCGCTCTAAGATCATCACATATATAAGAAGTTTCTTAGATGAGCTGGG
ATTCCTAGAGATTGAAACTCCCATGATGAACATCATCCCAGGGGGAGCCGTGGCCAAGCCTTTCATCACTTATCA
CAACGAGCTGGACATGAACTTATATATGAGAATTGCTCCAGAACTCTATCATAAGATGCTTGTGGTTGGTGGCAT
CGACCGGGTTTATGAAATTGGACGCCAGTTCCGGAATGAGGGGATTGATTTGACGCACAATCCTGAGTTCACCAC
CTGTGAGTTCTACATGGCCTATGCAGACTATCACGATCTCATGGAAATCACGGAGAAGATGGTTTCAGGGATGGT
GAAGCATATTACAGGCAGTTACAAGGTCACCTACCACCCAGATGGCCCAGAGGGCCAAGCCTACGATGTTGACTT
CACCCCACCCTTCCGGCGAATCAACATGGTAGAAGAGCTTGAGAAAGCCCTGGGGATGAAGCTGCCAGAAACGAA
CCTCTTTGAAACTGAAGAAACTCGCAAAATTCTTGATGATATCTGTGTGGCAAAAGCTGTTGAATGCCCTCCACC
TCGGACCACAGCCAGGCTCCTTGACAAGCTTGTTGGGGAGTTCCTGGAAGTGACTTGCATCAATCCTACATTCAT
CTGTGATCACCCACAGATAATGAGCCCTTTGGCTAAATGGCACCGCTCTAAAGAGGGTCTGACTGAGCGCTTTGA
GCTGTTTGTCATGAAGAAAGAGATATGCAATGCGTATACTGAGCTGAATGATCCCATGCGGCAGCGGCAGCTTTT
TGAAGAACAGGCCAAGGCCAAGGCTGCAGGTGATGATGAGGCCATGTTCATAGATGAAAACTTCTGTACTGCCCT
GGAATATGGGCTGCCCCCCACAGCTGGCTGGGGCATGGGCATTGATCGAGTCGCCATGTTTCTCACGGACTCCAA
CAACATCAAGGAAGTACTTCTGTTTCCTGCCATGAAACCCGAAGACAAGAAGGAGAATGTAGCAACCACTGATAC
ACTGGAAAGCACAACAGTTGGCACTTCTGTC**TAG**AAAATAATAATTGCAAGTTGTATAACTCAGGCGTCTTTGCA
TTTCTGCGAAAGATCAAGGTCTGCAAGGGAATTCTTGTGTGCTGCTTTCCATTTGACACCGCAGTTCTGTTCAGC
CATCAGAAGAGAGACAAGGAATTAAAAATTTCTTTTTAATCCTGTTA

FIGURE 30

MAAVQAAEVKVDGSEPKLSKNELKRRLKAEKKVAEKEAKQKELSEKQLSQATAAATNHTTDNGVGPEEESVDPNQ
YYKIRSQAIHQLKVNGEDPYPHKFHVDISLTDFIQKYSHLQPGDHLTDITLKVAGRIHAKRASGGKLIFYDLRGE
GVKLQVMANSRNYKSEEEFIHINNKLRRGDIIGVQGNPGKTKKGELSIIPYEITLLSPCLHMLPHLHFGLKDKET
RYRQRYLDLILNDFVRQKFIIRSKIITYIRSFLDELGFLEIETPMMNIIPGGAVAKPFITYHNELDMNLYMRIAP
ELYHKMLVVGGIDRVYEIGRQFRNEGIDLTHNPEFTTCEFYMAYADYHDLMEITEKMVSGMVKHITGSYKVTYHP
DGPEGQAYDVDFTPPFRRINMVEELEKALGMKLPETNLFETEETRKILDDICVAKAVECPPPRTTARLLDKLVGE
FLEVTCINPTFICDHPQIMSPLAKWHRSKEGLTERFELFVMKKEICNAYTELNDPMRQRQLFEEQAKAKAAGDDE
AMFIDENFCTALEYGLPPTAGWGMGIDRVAMFLTDSNNIKEVLLFPAMKPEDKKENVATTDTLESTTVGTSV

FIGURE 31

GGGGAGAGAAGGCCCGGAGGGGCTCTGCGTTCTGTAGTGGCGCTGCTTGGGCCCGTGGCGGATTGTAAGCTGCTG
GTTTTGCGGCTGGGAAGAGCGGCGAGAGGGTTCGGCATTTTTCGTCGGGATCCCCGCAAGG**ATG**AGTGCTGCCAG
AGAGTCTCACCCGCATGGGGTGAAGCGTTCAGCCTCCCCAGACGACGATCTGGGATCTAGCAATTGGGAGGCAGC
AGACTTGGGTAATGAAGAGAGAAAACAAAAGTTCTTGAGACTTATGGGTGCAGGAAAGAAAGAACATACTGGTCG
TCTTGTTATAGGAGATCACAAATCAACATCTCACTTCCGAACCGGGGAAGAAGACAAGAAAATTAATGAAGAACT
GGAGTCTCAATATCAGCAAAGTATGGACAGTAAATTATCAGGAAGATATCGGCGACATTGTGGACTTGGCTTCAG
TGAGGTAGAAGACCATGATGGAGAAGGTGATGTGGCTGGAGATGATGATGATGACGATGATGATTCACCTGATCC
TGAAAGTCCAGATGATTCTGAAAGCGATTCAGAGTCAGAGAAAGAAGAATCTGCTGAAGAACTCCAAGCTGCTGA
GCACCCTGATGAAGTGGAGGATCCCAAAAACAAAAAAGATGCAAAAAGCAATTATAAAATGATGTTTGTTAAATC
CAGTGGTTCA**TAA**CTCCCAAACGCTTAGTCTTTGTATTAAAAGTAAGCCTTATTGTTACAATGCACAGTGGAGGA
CTGCTTATAGAGCACAGACCTTTGTATTATAATTTTTAAAAAGGCCCTTTTAAATAATTACAAAGAGTGTTTGCT
TTCAAATGCCATGGGTTACACTTTTATGGGCATGACTATAACCATTTTTGTAAAGAGTAAGAGTTGTATAAAATA
AGAAATAAATACAGTACTCAACTTCCTTTCATATTAGCATCATCAACCCTCTAATTCACCTTATGGGGGAAATGC
TTCTTTTTGTTTGTGATAGCTATTTTATCATTTCCTTCATATTTTTCTCTTATAAAAATGTATTTGATACTGTGA
TATGTTCACGAAAAGTATTCTTTAATTATTCTTTGTTATAGTAGAGCTGTTCATTATGGATATTTCTGCTGCCAG
TCACAATCTAAATTAATTTTGGCAAAAGATTGGGTACTTAGTTGCCTGTTACTGAGTTAGCTCTACTCTTTTGGA
CCAAAGCAACATGAGAGCAAGTACTTTTCACACTTGTTAAGATGGAGTTATAACTGTCATACATTTGGAATATTA
TGATCCCAAGTAGTCTTTTTATAATTTGGATTGTATCGTATGTTAGATTTTTGATAAAATTTGGCCAATTTTTAC
AGAAGAAATTCTCTGATCATTTAGTTCTATCTATTTAGAAATATGTAAAACTGGATTTTTTTTTAAGTAATATGT
GACCAAAGTTAATTTTGTCCCAAAGGTCTAAATAAAGAGCAGTTTCCCACAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 32

MSAARESHPHGVKRSASPDDDLGSSNWEAADLGNEERKQKFLRLMGAGKKEHTGRLVIGDHKSTSHFRTGEEDKK
INEELESQYQQSMDSKLSGRYRRHCGLGFSEVEDHDGEGDVAGDDDDDDDDSPDPESPDDSESDSESEKEESAEE
LQAAEHPDEVEDPKNKKDAKSNYKMMFVKSSGS

FIGURE 33

GCGGTCAGCTATTGACACTTCCTGGTGGGATCCGAGTGAGGCGACGGGGTAGGGGTTGGCGCTCAGGCGGCGACC
ATGGCGTATCACGGCCTCACTGTGCCTCTCATTGTGATGAGCGTGTTCTGGGGCTTCGTCGGCTTCTTGGTGCCT
TGGTTCATCCCTAAGGGTCCTAACCGGGGAGTTATCATTACCATGTTGGTGACCTGTTCAGTTTGCTGCTATCTC
TTTTGGCTGATTGCAATTCTGGCCCAACTCAACCCTCTCTTTGGACCGCAATTGAAAAATGAAACCATCTGGTAT
CTGAAGTATCATTGGCCT**TGA**GGAAGAAGACATGCTCTACAGTGCTCAGTCTTTGAGGTCACGAGAAGAGAATGC
CTTCTAGATGCAAAATCACCTCCAAACCAGACCACTTTTCTTGACTTGCCTGTTTTGGCCATTAGCTGCCTTAAA
CGTTAACAGCACATTTGAATGCCTTATTCTACAATGCAGCGTGTTTTCCTTTGCCTTTTTTGCACTTTGGTGAAT
TACGTGCCTCCATAACCTGAACTGTGCCGACTCCACAAAACGATTATGTACTCTTCTGAGATAGAAGATGCTGTT
CTTCTGAGAGATACGTTACTCTCTCCTTGGAATCTGTGGATTTGAAGATGGCTCCTGCCTTCTCACGTGGGAATC
AGTGAAGTGTTTAGAAACTGCTGCAAGACAAACAAGACTCCAGTGGGGTGGTCAGTAGGAGAGCACGTTCAGAGG
GAAGAGCCATCTCAACAGAATCGCACCAAACTATACTTTCAGGATGAATTTCTTCTTTCTGCCATCTTTTGGAAT
AAATATTTTCCTCCTTTCTATGGA

FIGURE 34

MAYHGLTVPLIVMSVFWGFVGFLVPWFIPKGPNRGVIITMLVTCSVCCYLFWLIAILAQLNPLFGPQLKNETIWY
LKYHWP

FIGURE 35

AGGAGCCAGGAAGAGAGCTGTGACCAGCAGCGTCCCTTATTCGCTTGGCCTTGGTTCCTGTTTGCACTGGCTACA
GCAGGGCACTGGCCCCTACTGTCACCGCCACCTACACAAAGACCCTATCTCTGAGCGCTGCAGCCTACTGTTCAG
CCCCAGGTTTGAGG**ATG**GATGCCCTGGACGCTTCGAAGCTACTGGATGAGGAGCTGTATTCAAGACAGCTGTATG
TGCTGGGCTCACCTGCCATGCAGAGGATTCAGGGAGCCAGGGTCCTGGTGTCAGGCCTGCAGGGCCTGGGGGCCG
AGGTGGCCAAGAACTTGGTTCTGATGGGTGTGGGCAGCCTCACTCTGCATGATCCCCACCCCACCTGCTGGTCCG
ACCTGGCTGCCCAGTTTCTCCTCTCAGAGCAGGACTTGGAAAGGAGCAGAGCCGAGGCCTCTCAAGAGCTCTTGG
CTCAGCTCAACAGAGCTGTCCAGGTCGTCGTGCACACGGGTGACATCACTGAGGACCTGCTGTTGGACTTCCAGG
TGGTGGTGCTGACTGCTGCAAAGCTGGAGGAGCAGCTGAAGGTGGGCACCTTGTGTCATAAGCATGGAGTTTGCT
TTCTGGCGGCTGACACCCGGGGCCTCGTGGGGCAGTTGTTCTGTGACTTTGGTGAGGACTTCACTGTGCAGGACC
CCACAGAGGCAGAACCCCTGACAGCTGCCATCCAGCACATCTCCCAGGGCTCCCCTGGCATTCTCACTCTGAGGA
AAGGGGCCAATACCCACTACTTCCGTGATGGAGACTTGGTGACTTTCTCGGGAATTGAGGGAATGGTTGAGCTCA
ACGACTGTGATCCCCGGTCTATCCACGTGCGGGAGGATGGGTCCCTGGAGATTGGAGACACAACAACTTTCTCTC
GGTACTTGCGTGGTGGGGCTATCACTGAAGTCAAGAGACCCAAGACTGTGAGACATAAGTCCCTGGACACAGCCC
TGCTCCAGCCCCATGTGGTGGCCCAGAGCTCCCAGGAAGTTCACCATGCCCACTGCCTGCATCAGGCCTTCTGTG
CACTGCACAAGTTCCAGCACCTCCATGGCCGGCCACCCCAGCCCTGGGATCCTGTTGATGCAGAGACTGTGGTGG
GCCTGGCCCGGGACCTGGAACCACTGAAGCGGACAGAGGAAGAGCCACTGGAAGAGCCACTGGATGAGGCCCTAG
TGCGGACAGTCGCCCTAAGCAGTGCAAGGTGTCTTGAGCCTATGGTGGCATGCTGGGTCAGTAGCTGCCCAGGAA
GTGCTGAAGGCAATCTCCAGAAGTTCATGCCTCTGGACCAGTGGCTTTACTTTGATGCCCTCGATTGTCTTCCGG
AAGATGGGGAGCTCCTTCCCAGTCCTGAGGACTGTGCCCTGAGAGGCAGCCGCTATGATGGGCAAATTGCAGTGT
TTGGGGCTGGTTTTCAGGAGAAACTGAGACGCCAGCACTACCTCCTGGTGGGCGCTGGTGCCATTGGTTGTGAGC
TGCTCAAAGTCTTTGCCCTAGTGGGACTGGGGGCCGGGAACAGCGGGGGCTTGACTGTTGTTGACATGGACCACA
TAGAGCGCTCCAATCTCAGCCGTCAGTTCCTCTTCAGGTCCCAGGACGTTGGTAGACCCAAGGCAGAGGTGGCTG
CAGCAGCTGCCCGGGGCCTGAACCCAGACTTACAGGTGATCCCGCTCACCTACCCACTGGATCCCACCACAGAGC
ACATCTATGGGGATAACTTTTTCTCCCGTGTGGATGGTGTGGCTGCTGCCCTGGACAGTTTCCAGGCCCGGCGCT
ATGTGGCTGCTCGTTGCACCCACTATCTGAAGCCACTGCTGGAGGCAGGCACATCGGGCACCTGGGGCAGTGCTA
CAGTATTCATGCCACATGTGACTGAGGCCTACAGAGCCCCTGCCTCAGCTGCAGCTTCTGAGGATGCCCCCTACC
CTGTCTGTACCGTGCGGTACTTCCCTAGCACAGCCGAGCACACCCTGCAGTGGGCCCGGCATGAGTTTGAAGAAC
TCTTCCGACTGTCTGCAGAGACCATCAACCACCACCAACAGGCACACACCTCCCTGGCAGACATGGATGAGCCAC
AGACACTCACCTTACTGAAGCCAGTGCTTGGGGTCCTGAGAGTGCGTCCACAGAACTGGCAAGACTGTGTGGCGT
GGGCTCTTGGCCACTGGAAACTCTGCTTTCATTATGGCATCAAACAGCTGCTGAGGCACTTCCCACCTAATAAAG
TGCTTGAGGATGGAACTCCCTTCTGGTCAGGTCCCAAACAGTGTCCCCAGCCCTTGGAGTTTGACACCAACCAAG
ACACACACCTCCTCTACGTACTGGCAGCTGCCAACCTGTATGCCCAGATGCATGGGCTGCCTGGCTCACAGGACT
GGACTGCACTCAGGGAGCTGCTGAAGCTGCTGCCACAGCCTGACCCCCAACAGATGGCCCCCATCTTTGCTAGTA
ATCTAGAGCTGGCTTCGGCTTCTGCTGAGTTTGGCCCTGAGCAGCAGAAGGAACTGAACAAAGCCCTGGAAGTCT
GGAGTGTGGGCCCTCCCCTGAAGCCTCTGATGTTTGAGAAGGATGATGACAGCAACTTCCATGTGGACTTTGTGG
TAGCGGCAGCTAGCCTGAGATGTCAGAACTACGGGATTCCACCGGTCAACCGTGCCCAGAGCAAGCGAATTGTGG
GCCAGATTATCCCAGCCATTGCCACCACTACAGCAGCTGTGGCAGGCCTGTTGGGCCTGGAGCTGTATAAGGTGG
TGAGTGGGCCACGGCCTCGTAGTGCCTTTCGCCACAGCTACCTACATCTGGCTGAAAACTACCTCATCCGCTATA
TGCCTTTTGCCCCAGCCATCCAGACGTTCCATCACCTGAAGTGGACCTCTTGGGACCGTCTGAAGGTACCAGCTG
GGCAGCCTGAGAGGACCCTGGAGTCGCTGCTGGCTCATCTTCAGGAGCAGCACGGGTTGAGGGTGAGGATCCTGC
TGCACGGCTCAGCCCTGCTCTATGCGGCCGGATGGTCACCTGAAAAGCAGGCCCAGCACCTGCCCCTCAGGGTGA
CAGAACTGGTTCAGCAGCTGACAGGCCAGGCACCTGCTCCTGGGCAGCGGGTGTTGGTGCTAGAGCTGAGCTGTG
AGGGTGACGACGAGGACACTGCCTTCCCACCTCTGCACTATGAGCTG**TGA**CAAGGCAGCCACCCTGTCACCTAGC
TCAATGGAGCCCCGGATCCCAAGCCCTGCATTGTAAGCCCACAGTAGGCACTCAATAATTGCTTGTTAAAGGAAG
G

FIGURE 36

MDALDASKLLDEELYSRQLYVLGSPAMQRIQGARVLVSGLQGLGAEVAKNLVLMGVGSLTLHDPHPTCWSDLAAQ
FLLSEQDLERSRAEASQELLAQLNRAVQVVVHTGDITEDLLLDFQVVVLTAAKLEEQLKVGTLCHKHGVCFLAAD
TRGLVGQLFCDFGEDFTVQDPTEAEPLTAAIQHISQGSPGILTLRKGANTHYFRDGDLVTFSGIEGMVELNDCDP
RSIHVREDGSLEIGDTTTFSRYLRGGAITEVKRPKTVRHKSLDTALLQPHVVAQSSQEVHHAHCLHQAFCALHKF
QHLHGRPPQPWDPVDAETVVGLARDLEPLKRTEEEPLEEPLDEALVRTVALSSARCLEPMVACWVSSCPGSAEGN
LQKFMPLDQWLYFDALDCLPEDGELLPSPEDCALRGSRYDGQIAVFGAGFQEKLRRQHYLLVGAGAIGCELLKVF
ALVGLGAGNSGGLTVVDMDHIERSNLSRQFLFRSQDVGRPKAEVAAAAARGLNPDLQVIPLTYPLDPTTEHIYGD
NFFSRVDGVAAALDSFQARRYVAARCTHYLKPLLEAGTSGTWGSATVFMPHVTEAYRAPASAAASEDAPYPVCTV
RYFPSTAEHTLQWARHEFEELFRLSAETINHHQQAHTSLADMDEPQTLTLLKPVLGVLRVRPQNWQDCVAWALGH
WKLCFHYGIKQLLRHFPPNKVLEDGTPFWSGPKQCPQPLEFDTNQDTHLLYVLAAANLYAQMHGLPGSQDWTALR
ELLKLLPQPDPQQMAPIFASNLELASASAEFGPEQQKELNKALEVWSVGPPLKPLMFEKDDDSNFHVDFVVAAAS
LRCQNYGIPPVNRAQSKRIVGQIIPAIATTTAAVAGLLGLELYKVVSGPRPRSAFRHSYLHLAENYLIRYMPFAP
AIQTFHHLKWTSWDRLKVPAGQPERTLESLLAHLQEQHGLRVRILLHGSALLYAAGWSPEKQAQHLPLRVTELVQ
QLTGQAPAPGQRVLVLELSCEGDDEDTAFPPLHYEL

FIGURE 37

GACAGCCACGAAGATCCTACCAAA**ATG**AAGCGCTTCCTCTTCCTCCTACTCACCATCAGCCTCCTGGTTATGGTA
CAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCTCAGCATCCAGCAGCATGAGC
GGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCCACCTCTTCTGCTTCAGT**TGA**GGTGACACGTCTCAG
CCTTAGCCCTGTGCCCCCTGAAACAGCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTG
ATGCCAGACATCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGTAATGA
TGTAGGGGCCAAGCAGTGCCCAGCTGGGGGAGAATAAAGTTACCCTTGTACTGCA

FIGURE 38

MKRFLFLLLTISLLVMVQIQTGLSGQNDTSQTSSPSASSSMSGGIFLFFVANAIIHLFCFS

FIGURE 39

TATATTGGCAGTTATTGAGGGTAAAGCAATATATTGTAACAGAATGTATAAATATTTTTGATAAAACAGTCTATA
TTTTATTAAAAAATGAATTATAACCCATTTTCAGTTTTGCCTGCATCATAAGAGTGAGCACTCCATTGCTTTCTT
TCCTGGCCACACTGCTACAATCCAGCACTAACTATCCATGTCCAGGGTAAGGATCGAGATCGAGAAGCCCACACT
GCCAGTGAAAAAGCTACGTCTTTACTGCATAAATTAGAGGAAGCAATTTCGGAACAACGGAACCTTCAAACTATA
AATACTGAATTATCGAACACTTGCCAGGCACTTCAGCAGAAGACAAGGAAACTGAAGAAGCTTTTTAGATGAGGA
ATTTCCTCACTATGATTCCCTGTCCTGCGCAGATGCAATTCAACAACCTCTTCAAGAAAAATTGAAGCAGTGTTG
CCACAAACTATATGGTGGTCAAGAAGCAAGAATACATCAGACACCCCTGACCTTGAAACATACGTGCTGGTACAC
ACCTCTGCTGG**ATG**CCTTATCTCTGGATAGTTTTACAGCAGTTCCAACCCTGGAATCAACACCTTTCTCAGGTGT
AGCCAACCAAATCCACACTCTGTGTGAAAGGCCCACATATGGAGAAGTAAAGGATGGTGCTTTGGATGTAAAAAG
ACAACACAAGTGCCCAGGCCCCACAAGTGGCCCCAGCCCAGGAACGAATCTCTCAGGCTGCATCAGGATGAATGA
TGACCCAAGTATGGAAGAGAATGGTGTTGAACGCGTGTGTCCTGAGAGCCTGCTGCAGTCCAGGGGATATTCCTC
ACTACCATTACCCAGACACACTTCATCGACAGACGGTACTATAACTTCAAGTGATCCTGGATTAGAAATTCTGAA
TATGGCTTCTTGTGACCTTGACAGAAACTCGCTCTGTAAGAAAGAGGAGGATACAAGATCAGCTTCTCCCACGAT
AGAGGCCCAAGGCACAAGTCCAGCTCATGATAATATTGCATTCCAAGACTCTACGAGTAAGGATAAAACCATATT
AAATCTGGAAGCCAAAGAGGAACCAGAAACAATAGAAGAACATAAAAAAGAACATGCTTCAGGAGACTCTGTGGT
TTCCCCTCTTCCTGTAACCACTGTGAAATCGGTTAACGTTAGACAAAGTGAGAACACTTCTGCTAATGAGAAGGA
GGTGGAGGCAGAATTTCTCAGATTATCTTTGGGATTTAAGTGTGACTGGTTTACCTTGGAGAAGAGAGTGAAGCT
TGAAGAGAGGTCCCGTGACTGGGCAGAAGAAAATTTGAAGAAAGAAATCACTAACTCTTTAAAACTATTAGAGTC
TTTAACACCTCTGTGTGAAGATGACAACCAGGCACAGGAAATCATTAAGAAGCTGGAGAAGAGTATAAAGTTTCT
TAGCCAGTGTGCAGCACGAGTGGCCAGTAGGGCTGAGATGTTGGGAGCCATCAATCAGGAAAGCCGGGTTAGTAA
AGCAGTTGAAGTGATGATTCAGCACGTAGAAAACTTGAAGAGGATGTATGCCAAAGAGCACGCTGAATTAGAAGA
ACTGAAACAGGTTCTTCTGCAGAATGAAAGGTCTTTCAATCCTCTTGAAGATGATGATGACTGCCAAATTAAAAA
ACGTTCAGCTTCTCTAAACTCCAAGCCATCTTCTCTACGAAGAGTGACTATTGCCTCTTTACCCAGAAATATTGG
AAATGCAGGAATGGTGGCTGGGATGGAAAATAATGATCGATTCAGTAGAAGGTCAAGCAGTTGGCGTATTTTGGG
GTCAAAGCAGAGTGAACACCGTCCCTCATTACCTCGATTTATTAGCACCTATTCCTGGGCAGATGCTGAAGAAGA
AAAATGTGAACTAAAAACTAAAGATGACTCAGAGCCATCTGGAGAAGAAACAGTAGAAAGGACAAGGAAGCCAAG
TCTTTCTGAAAAGAAAAATAATCCATCAAAGTGGGATGTCTCTTCAGTTTATGACACAATAGCTTCCTGGGCAAC
AAATCTCAAGTCCTCCATCAGAAAGGCTAATAAGGCCCTCTGGCTCTCTATTGCATTCATTGTACTGTTTGCAGC
TTTGATGAGCTTCCTCACAGGCCAATTATTCCAGAAGTCTGTGGATGCCGCTCCCACACAGCAAGAGGACTCATG
GACGTCTCTAGAACATATCTTGTGGCCATTTACCAGACTCCGACACAATGGGCCACCACCAGTG**TGA**CAGCAGGA
CATCCTAATATATGGATCTTGATTTTTAAGTTTCAGTATCTGAACTTCGTAAATTAGTAACTTTTAGCTGGGAAA
GTATAGCATGAAACCAGAGGTTCTCAGAATGACCGTAAGATAGCTTACATTTCCTCTTTTTGCCTTTATCTCCCC
AACTAAAATACAATGGG

FIGURE 40

MESTPFSGVANQIHTLCERPTYGEVKDGALDVKRQHKCPGPTSGPSPGTNLSGCIRMNDDPSMEENGVERVCPES
LLQSRGYSSLPLPRHTSSTDGTITSSDPGLEILNMASCDLDRNSLCKKEEDTRSASPTIEAQGTSPAHDNIAFQD
STSKDKTILNLEAKEEPETIEEHKKEHASGDSVVSPLPVTTVKSVNVRQSENTSANEKEVEAEFLRLSLGFKCDW
FTLEKRVKLEERSRDWAEENLKKEITNSLKLLESLTPLCEDDNQAQEIIKKLEKSIKFLSQCAARVASRAEMLGA
INQESRVSKAVEVMIQHVENLKRMYAKEHAELEELKQVLLQNERSFNPLEDDDDCQIKKRSASLNSKPSSLRRVT
IASLPRNIGNAGMVAGMENNDRFSRRSSSWRILGSKQSEHRPSLPRFISTYSWADAEEEKCELKTKDDSEPSGEE
TVERTRKPSLSEKKNNPSKWDVSSVYDTIASWATNLKSSIRKANKALWLSIAFIVLFAALMSFLTGQLFQKSVDA
APTQQEDSWTSLEHILWPFTRLRHNGPPPV

FIGURE 41

ACGCGTCCGCTTCGGAATGAGAGACTCAACCATAATAGAAAGAATGGAGAACTATTAACCACCATTCTTCAGTGG
GCTGTGATTTTCAGAGGGGAATACTAAGAAATGGTTTTCCATACTGGAACCCAAAGGTAAAGACACTCAAGGACA
GACATTTTTGGCAGAGCATAG**ATG**AAAATGGCAAGTTCCCTGGCTTTCCTTCTGCTCAACTTTCATGTCTCCCTC
TTCTTGGTCCAGCTGCTCACTCCTTGCTCAGCTCAGTTTTCTGTGCTTGGACCCTCTGGGCCCATCCTGGCCATG
GTGGGTGAAGACGCTGATCTGCCCTGTCACCTGTTCCCGACCATGAGTGCAGAGACCATGGAGCTGAGGTGGGTG
AGTTCCAGCCTAAGGCAGGTGGTGAACGTGTATGCAGATGGAAAGGAAGTGGAAGACAGGCAGAGTGCACCATAT
CGAGGGAGAACTTCGATTCTGCGGGATGGCATCACTGCAGGGAAGGCTGCTCTCCGAATACACAACGTCACAGCC
TCTGACAGTGGAAAGTACTTGTGTTATTTCCAAGATGGTGACTTCTACGAAAAAGCCCTGGTGGAGCTGAAGGTT
GCAGCATTGGGTTCTGATCTTCACATTGAAGTGAAGGGTTATGAGGATGGAGGGATCCATCTGGAGTGCAGGTCC
ACTGGCTGGTACCCCCAACCCCAAATAAAGTGGAGCGACACCAAGGGAGAGAACATCCCGGCTGTGGAAGCACCT
GTGGTTGCAGATGGAGTGGGCCTGTATGCAGTAGCAGCATCTGTGATCATGAGAGGCAGCTCTGGTGGGGGTGTA
TCCTGCATCATCAGAAATTCCCTCCTCGGCCTGGAAAAGACAGCCAGCATATCCATCGCAGACCCCTTCTTCAGG
AGCGCCCAGCCCTGGATCGCGGCCCTGGCAGGGACCCTGCCTATCTCGTTGCTGCTTCTCGCAGGAGCCAGTTAC
TTCTTGTGGAGACAACAGAAGGAAAAAATTGCTCTGTCCAGGGAGACAGAAAGAGAGCGAGAGATGAAAGAAATG
GGATACGCTGCAACAGAGCAAGAAATAAGCCTAAGAGAGAAGCTCCAGGAGGAACTCAAGTGGAGGAAAATCCAG
TACATGGCTCGTGGAGAGAAGTCTTTGGCCTATCATGAATGGAAAATGGCCCTCTTCAAACCTGCGGATGTGATT
CTGGATCCAGACACGGCAAACGCCATCCTCCTTGTTTCTGAGGACCAGAGGAGTGTGCAGCGTGCTGAAGAGCCG
CGGGATCTGCCAGACAACCCTGAGAGATTTGAATGGCGTTACTGTGTCCTTGGCTGTGAAAACTTCACATCAGGG
AGACATTACTGGGAGGTGGAAGTGGGGGACAGAAAAGAGTGGCATATTGGGGTATGTAGTAAGAACGTGGAGAGG
AAAAAAGGTTGGGTCAAAATGACACCGGAGAACGGATACTGGACTATGGGCCTGACTGATGGGAATAAGTATCGG
GCTCTCACTGAGCCCAGAACCAACCTGAAACTTCCTGAGCCTCCTAGGAAAGTGGGGATCTTCCTGGACTATGAG
ACTGGAGAGATCTCGTTCTATAATGCCACAGATGGATCTCATATCTACACCTTTCCGCACGCCTCTTTCTCTGAG
CCTCTATATCCTGTTTTCAGAATTTTGACCTTGGAGCCCACTGCCCTGACCATTTGCCCAATACCAAAAGAAGTA
GAGAGTTCCCCCGATCCTGACCTAGTGCCTGATCATTCCCTGGAGACACCACTGACCCCGGGCTTAGCTAATGAA
AGTGGGGAGCCTCAGGCTGAAGTAACATCTCTGCTTCTCCCTGCCCACCCTGGAGCTGAGGTCTCCCCTTCTGCA
ACAACCAATCAGAACCATAAGCTACAGGCACGCACTGAAGCACTTTAC**TGA**TATTCATTCCATTATTCCATATGA
CAGTTGTTTTGAGTTTCGTACCACCTTATTGTCCCCTTATACAGATAAGGAAACTGGGGTGCAGAAAGGTGAATT
AACTTTACAAAGTAGACATGACAAGTGAACAGCAGAGCTGGGATCTAAACAGCAATAACTAACATTAACAGAGAA
TTTAAAATGTTCTTAGTGCTGTGTTATAAGCTTTGGTGGATGTCACTCCTTTAATCCTCACAACACCCTGTCGGG
TAGTCATATTTTGCAAGTATGGAAGCTGAGGCAGGGCAACATGAAGTAACTTACATAATTCATACAGTAATTTGT
GCAGTTGGGAGATGTTCAGCCTTAGTCCCTGGCTAATTGCCTGTTCTTTTCCAGCCTGATTTTTTTTCCCACAGG
AAGAGCCCACATGTAGCCCTGAGGTTTCCTTCCCAGGACAGCTGCAGGGTAGAGATCATTTTAAGTGCTTGTGGA
GTTGACATCCCTATTGACTCTTTCCCAGCTGATATCAGAGACTTAGACCCAGCACTCCTTGGATTAGCTCTGCAG
AGTGTCTTGGTTGAGAGAATAACCTCATAGTACCAACATGACATGTGACTTGGAAAGAGACTAGAGGCCACACTT
GATAAATCATGGGGCACAGATATGTTCCCACCCAACAAATGTGATAAGTGATTGTGCAGCCAGAGCCAGCCTTCC
TTCAATCAAGGTTTCCAGGCAGAGCAAATACCCTAGAGATTCTCTGTGATATAGGAAATTTGGATCAAGGAAGCT
AAAAGAATTACAGGGATGTTTTTAATCCCACTATGGACTCAGTCTCCTGGAAATAGGTCTGTCCACTCCTGGTCA
TTGGTGGATGTTAAACCCATATTCCTTTCAACTGCTGCCTGCTAGGGAAAACTGCTCCTCATTATCATCACTATT
ATTGCTCACCACTGTATCCCCTCTACTTGGCAAGTGGTTGTCAAGTTCTAGTTGTTCAATAAATGTGTTAATAAT
GAAAAAAAAAAA

FIGURE 42

MKMASSLAFLLLNFHVSLFLVQLLTPCSAQFSVLGPSGPILAMVGEDADLPCHLFPTMSAETMELRWVSSSLRQV
VNVYADGKEVEDRQSAPYRGRTSILRDGITAGKAALRIHNVTASDSGKYLCYFQDGDFYEKALVELKVAALGSDL
HIEVKGYEDGGIHLECRSTGWYPQPQIKWSDTKGENIPAVEAPVVADGVGLYAVAASVIMRGSSGGGVSCIIRNS
LLGLEKTASISIADPFFRSAQPWIAALAGTLPISLLLLAGASYFLWRQQKEKIALSRETERERREMKEMGYAATEQ
EISLREKLQEELKWRKIQYMARGEKSLAYHEWKMALFKPADVILDPDTANAILLVSEDQRSVQRAEEPRDLPDNP
ERFEWRYCVLGCENFTSGRHYWEVEVGDRKEWHIGVCSKNVERKKGWVKMTPENGYWTMGLTDGNKYRALTEPRT
NLKLPEPPRKVGIFLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRILTLEPTALTICPIPKEVESSPDPD
LVPDHSLETPLTPGLANESGEPQAEVTSLLLPAHPGAEVSPSATTNQNHKLQARTEALY

FIGURE 43A

CCGGGCTGCGCGGCGAGGCTGAGCCGGGCCCGGGCGCCGGGGCCGGGGGCGGCTGGCGCGGGCAGGAAGCGCCTC
GCGGACCCGGGCCCGCCCCCCGCCTCCCGCCGCCTCCGGGCTCCCGGCTCCCGGCCGCGCCTCGCCCCATGCACT
CGCCGCGCCGCGCAGCCCGCGCACGCCCGGATGGCTCCTCGCGCCGCGGGCGGCGCACCCCTTAGCGCCCGGGCC
GCCGCCGCCAGCCCCCCGCCGTTCCAGACGCCGCCGCGGTGCCCGGTGCCGCTGCTGTTGCTGCTGCTCCTGGGG
GCGGCGCGGGCCGGCGCCCTGGAGATCCAGCGTCGGTTCCCCTCGCCCACGCCCACCAACAACTTCGCCCTGGAC
GGCGCGGCGGGGACCGTGTACCTGGCGGCCGTCAACCGCCTCTATCAGCTGTCGGGCGCCAACCTGAGCCTGGAG
GCCGAGGCGGCCGTGGGCCCGGTGCCCGACAGCCCGCTGTGTCACGCTCCGCAGCTGCCGCAGGCCTCGTGCGAG
CACCCGCGGCGCCTCACGGACAACTACAACAAGATCCTGCAGCTGGACCCCGGCCAGGGCCTGGTAGTCGTGTGC
GGGTCCATCTACCAGGGCTTCTGCCAGCTGCGGCGCCGGGGTAACATCTCGGCCGTGGCCGTGCGCTTCCCGCCC
GCCGCGCCGCCCGCCGAGCCCGTCACGGTGTTCCCCAGCATGCTGAACGTGGCGGCCAACCACCCGAACGCGTCC
ACCGTGGGGCTAGTTCTGCCTCCCGCCGCGGGCGCGGGGGGCAGCCGCCTGCTCGTGGGCGCCACGTACACCGGT
TACGGCAGCTCCTTCTTCCCGCGCAACCGCAGCCTGGAGGACCACCGCTTCGAGAACACGCCCGAGATCGCCATC
CGCTCCCTGGACACGCGCGGCGACCTGGCCAAGCTCTTCACCTTCGACCTCAACCCCTCCGACGACAACATCCTC
AAGATCAAGCAGGGCGCCAAGGAGCAGCACAAGCTGGGCTTCGTGAGCGCCTTCCTGCACCCGTCCGACCCGCCG
CCGGGTGCACAGTCCTACGCGTACCTGGCGCTCAACAGCGAGGCGCGCGCGGGCGACAAGGAGAGCCAGGCGCGG
AGCCTGCTGGCGCGCATCTGCCTGCCCCACGGCGCCGGCGGCGACGCCAAGAAGCTCACCGAGTCCTACATCCAG
TTGGGCTTGCAGTGCGCGGGCGGCGCGGGCCGCGGCGACCTCTACAGCCGCCTGGTGTCGGTCTTCCCAGCCCGG
GAGCGGCTCTTTGCTGTCTTCGAGCGGCCCCAGGGGTCCCCCGCGGCCCGCGCTGCTCCGGCCGCACTCTGCGCC
TTCCGCTTCGCCGACGTGCGAGCCGCCATCCGAGCTGCGCGCACCGCCTGCTTCGTGGAACCGGCGCCCGACGTG
GTGGCGGTGCTCGACAGCGTGGTGCAGGGCACGGGACCGGCCTGCGAGCGCAAGCTCAACATCCAGCTCCAGCCA
GAGCAGCTGGACTGTGGAGCTGCTCACCTGCAGCACCCGCTGTCCATCCTGCAGCCCCTGAAGGCCACGCCCGTG
TTCCGCGCCCCGGGCCTCACCTCCGTGGCCGTGGCCAGCGTCAACAACTACACAGCGGTCTTCCTGGGCACGGTC
AACGGGAGGCTTCTCAAGATCAACCTGAACGAGAGCATGCAGGTGGTGAGCAGGCGGGTGGTGACTGTGGCCTAT
GGGGAGCCCGTGCACCATGTCATGCAGTTTGACCCAGCAGACTCCGTTTACCTTTACCTGATGACGTCCCACCAG
ATGGCCAGGGTGAAGGTCGCCGCCTGCAACGTGCACTCCACCTGTGGGGACTGCGTGGGTGCGGCGGACGCCTAC
TGCGGCTGGTGTGCCCTGGAGACGCGGTGCACCTTGCAGCAGGACTGCACCAATTCCAGCCAGCAGCATTTCTGG
ACCAGTGCCAGCGAGGGCCCCAGCCGCTGTCCTGCCATGACCGTCCTGCCTTCCGAGATCGATGTGCGCCAGGAG
TACCCAGGCATGATCCTGCAGATCTCGGGCAGCCTGCCCAGCCTCAGTGGCATGGAGATGGCCTGTGACTATGGG
AACAACATCCGCACTGTGGCTCGGGTCCCAGGCCCTGCCTTTGGTCACCAGATTGCCTACTGCAACCTCCTGCCG
AGGGACCAGTTTCCGCCCTTCCCCCCCAACCAGGACCACGTGACTGTTGAGATGTCTGTGAGGGTCAATGGGCGG
AACATCGTCAAGGCCAATTTCACCATCTACGACTGCAGCCGCACTGCACAAGTGTACCCCCACACAGCCTGTACC
AGCTGCCTGTCGGCACAGTGGCCCTGTTTCTGGTGCAGCCAGCAGCACTCCTGTGTTTCCAACCAGTCTCGGTGC
GAGGCCTCACCAAACCCCACGAGCCCTCAGGACTGCCCCCGGACCCTGCTCTCACCCCTGGCACCCGTGCCTACG
GGTGGCTCCCAGAACATCCTGGTGCCTCTGGCCAACACTGCCTTTTTCCAGGGTGCAGCCCTGGAGTGTAGTTTT
GGGCTGGAGGAGATCTTCGAGGCTGTGTGGGTGAATGAGTCTGTTGTACGCTGTGACCAGGTGGTGCTGCACACG
ACCCGGAAGAGCCAGGTGTTCCCGCTCAGCCTCCAACTAAAGGGGCGGCCAGCCCGATTCCTGGACAGCCCTGAG
CCCATGACAGTCATGGTCTATAACTGTGCCATGGGCAGCCCCGACTGTTCCCAGTGCCTGGGCCGCGAAGACCTG
GGTCACCTGTGCATGTGGAGTGATGGCTGCCGCCTGCGGGGGCCTCTGCAGCCCATGGCTGGCACCTGCCCCGCC
CCCGAGATCCGCGCGATTGAGCCCCTGAGTGGCCCGTTGGACGGTGGGACCCTGCTGACCATCCGAGGAAGGAAC
CTGGGCCGGCGGCTCAGTGACGTGGCCCACGGCGTGTGGATTGGTGGTGTGGCCTGTGAGCCACTGCCTGACAGA
TACACGGTGTCGGAGGAGATCGTGTGTGTCACAGGGCCAGCCCCAGGACCACTCTCAGGTGTGGTGACCGTGAAC
GCCTCTAAGGAGGGCAAGTCCCGGGACCGCTTCTCCTACGTGCTGCCCCTGGTCCACTCCCTGGAGCCTACCATG
GGCCCCAAGGCCGGGGGCACCAGGATCACCATCCATGGGAATGACCTCCATGTAGGCTCCGAGCTCCAGGTCCTG
GTGAACGACACAGACCCCTGCACGGAGCTGATGCGCACAGATACCAGCATCGCCTGCACCATGCCTGAGGGGGCC
CTGCCGGCTCCGGTGCCTGTGTGTGTGCGCTTCGAGCGTCGGGGCTGCGTGCACGGCAACCTCACCTTCTGGTAC
ATGCAGAACCCGGTCATCACGGCCATCAGTCCCCGCCGCAGCCCTGTCAGTGGCGGCAGGACCATCACAGTGGCT
GGTGAGCGTTTCCACATGGTGCAGAATGTGTCCATGGCCGTCCACCACATTGGCCGGGAGCCCACGCTCTGCAAG
GTTCTCAACTCCACCCTCATCACCTGCCCGTCCCCCGGGGCCCTGAGCAACGCATCAGCGCCAGTGGACTTCTTC

FIGURE 43B

ATCAATGGGCGGGCCTACGCAGACGAGGTGGCTGTGGCTGAGGAGCTACTGGACCCCGAGGAGGCACAGCGGGGC
AGCAGGTTCCGCCTGGACTACCTCCCCAACCCACAGTTCTCTACGGCCAAGAGGGAGAAGTGGATCAAGCACCAC
CCCGGGGAGCCTCTCACCCTCGTTATCCACAAGGAGCAGGACAGCCTGGGGCTCCAGAGTCACGAGTACCGGGTC
AAGATAGGCCAAGTAAGCTGCGACATCCAGATTGTCTCTGACAGAATCATCCACTGCTCGGTCAACGAGTCCCTG
GGCGCGGCCGTGGGGCAGCTGCCCATCACAATCCAGGTAGGGAACTTCAACCAGACCATCGCCACACTGCAGCTG
GGGGGTAGCGAGACGGCCATCATCGTGTCCATCGTCATCTGCAGCGTCCTGCTGCTGCTCTCCGTGGTGGCCCTG
TTCGTCTTCTGTACCAAGAGCCGACGTGCTGAGCGTTACTGGCAGAAGACGCTGCTGCAGATGGAGGAGATGGAA
TCTCAGATCCGAGAGGAAATCCGCAAAGGCTTCGCTGAGCTGCAGACAGACATGACAGATCTCACCAAGGAGCTG
AACCGCAGCCAGGGCATCCCCTTCCTGGAGTATAAGCACTTCGTGACCCGCACCTTCTTCCCCAAGTGTTCCTCC
CTTTATGAAGAGCGTTACGTGCTGCCCTCCCAGACCCTCAACTCCCAGGGCAGCTCCCAGGCACAGGAAACCCAC
CCACTGCTGGGAGAGTGGAAGATTCCTGAGAGCTGCCGGCCCAACATGGAAGAGGGAATTAGCTTGTTCTCCTCA
CTACTCAACAACAAGCACTTCCTCATCGTCTTTGTCCACGCGCTGGAGCAGCAGAAGGACTTTGCGGTGCGCGAC
AGGTGCAGCCTGGCCTCGCTGCTGACCATCGCGCTGCACGGCAAGCTGGAGTACTACACCAGCATCATGAAGGAG
CTGCTGGTGGACCTCATTGACGCCTCGGCCGCCAAGAACCCCAAGCTCATGCTGCGGCGCACAGAGTCTGTGGTG
GAGAAGATGCTCACCAACTGGATGTCCATCTGCATGTACAGCTGTCTGCGGGAGACGGTGGGGGAGCCATTCTTC
CTGCTGCTGTGTGCCATCAAGCAGCAAATCAACAAGGGCTCCATCGACGCCATCACAGGCAAGGCCCGCTACACA
CTCAATGAGGAGTGGCTGCTGCGGGAGAACATCGAGGCCAAGCCCCGGAACCTGAACGTGTCCTTCCAGGGCTGT
GGCATGGACTCGCTGAGCGTGCGGGCCATGGACACCGACACGCTGACACAGGTCAAGGAGAAGATCCTGGAGGCC
TTCTGCAAGAATGTGCCCTACTCCCAGTGGCCGCGTGCAGAGGACGTCGACCTTGAGTGGTTCGCCTCCAGCACA
CAGAGCTACATCCTTCGGGACCTGGACGACACCTCAGTGGTGGAAGACGGCCGCAAGAAGCTTAACACGCTGGCC
CATTACAAGATCCCTGAAGGTGCCTCCCTGGCCATGAGTCTCATAGACAAGAAGGACAACACACTGGGCCGAGTG
AAAGACTTGGACACAGAGAAGTATTTCCATTTGGTGCTGCCTACGGACGAGCTGGCGGAGCCCAAGAAGTCTCAC
CGGCAGAGCCATCGCAAGAAGGTGCTCCCGGAAATCTACCTGACCCGCCTGCTCTCCACCAAGGGCACGTTGCAG
AAGTTTCTGGATGACCTGTTCAAGGCCATTCTGAGTATCCGTGAAGACAAGCCCCCACTGGCTGTCAAGTACTTT
TTCGACTTCCTGGAGGAGCAGGCTGAGAAGAGGGGAATCTCCGACCCCGACACCCTACACATCTGGAAGACCAAC
AGCCTTCCTCTCCGGTTCTGGGTGAACATCCTGAAGAACCCCCAGTTTGTCTTTGACATCGACAAGACAGACCAC
ATCGACGCCTGCCTTTCAGTCATCGCGCAGGCCTTCATCGACGCCTGCTCCATCTCTGACCTGCAGCTGGGCAAG
GATTCGCCAACCAACAAGCTCCTCTACGCCAAGGAGATTCCTGAGTACCGGAAGATCGTGCAGCGCTACTACAAG
CAGATCCAGGACATGACGCCGCTCAGCGAGCAAGAGATGAATGCCCATCTGGCCGAGGAGTCGAGGAAATACCAG
AATGAGTTCAACACCAATGTGGCCATGGCAGAGATTTATAAGTACGCCAAGAGGTATCGGCCGCAGATCATGGCC
GCGCTGGAGGCCAACCCCACGGCCCGGAGGACACAACTGCAGCACAAGTTTGAGCAGGTGGTGGCTTTGATGGAG
GACAACATCTACGAGTGCTACAGTGAGGCC**TGA**GACACATGGAGAGTTGGTCAGGCTGCTGCTGGGAGAAATGGA
CGCCCACTGGGCCTCAACTTGATCTTCTACCCCGTGCCTGTGACTCAGACTGGGAAATACTGAGCAGAGACGGCT
GGGGCGGGGGCAGGAGGAGGGGCTGCTCTCTGAGACAGGGGCGCCCCCGCCTTGACCCCTGGGCACCTCCATCCC
CTCCCACCTGTCCCCAGATCAGTCTCTGGGATGGAGGCCAGAGAGCTGGTCAGGCTCCCCCATCTGCCCAGCACG
GCCTGCACTGTGCCCACCCACTTGCTCCACAACGTCCAGTTGGTCCTGCTGCCAAGAGCCCCGTGCATCCAGGCG
GCCAAGCACAAACTGGGGGAGAGGAGGCCGCCAGCCCGGAGGCTGCAGCCCAGAAACTCTACCTCATCCACACTG
GTGCAGGGAGCCCTCCTTGAACTGACCTTTGATTGGTTTCTGCTTCAACTACCAAAATGTTATCTCCACTTCCCC
CTCACCCGTAGAGGATCCTGGCCACAGACAGTTTCAAGTAGTGTCAGATTTTTGTTGCTTGGGCGGCTGTTGGTA
GAGTGGGCAGTGCCCGCGCCATGGGGTGCTCTGTGGGCTTCTCCAGGAGCAGGGAGGGTGGAGGGGAGGGATGGG
GGGCACAGGAGCTGGGAGCCCCGTCTCCAGGAAAAGGAGAGGGGTTAAGATGCACCGAGGCTGTAGCTGGGCTAC
TTGATCTTGCTGAAAGTGTTTCTAAAGATAGCACCACTTTTTTTTTTAAAGCTTTTATATATTAAAAAACGTATC
ATGC

FIGURE 44

PGCAARLSRARAPGPGAAGAGRKRLADPGPPPASRRLRAPGSRPRLAPCTRRAAQPAHARMAPRAAGGAPLSARA
AAASPPPFQTPPRCPVPLLLLLLLGAARAGALEIQRRFPSPTPTNNFALDGAAGTVYLAAVNRLYQLSGANLSLE
AEAAVGPVPDSPLCHAPQLPQASCEHPRRLTDNYNKILQLDPGQGLVVVCGSIYQGFCQLRRRGNISAVAVRFPP
AAPPAEPVTVFPSMLNVAANHPNASTVGLVLPPAAGAGGSRLLVGATYTGYGSSFFPRNRSLEDHRFENTPEIAI
RSLDTRGDLAKLFTFDLNPSDDNILKIKQGAKEQHKLGFVSAFLHPSDPPPGAQSYAYLALNSEARAGDKESQAR
SLLARICLPHGAGGDAKKLTESYIQLGLQCAGGAGRGDLYSRLVSVFPARERLFAVFERPQGSPAARAAPAALCA
FRFADVRAAIRAARTACFVEPAPDVVAVLDSVVQGTGPACERKLNIQLQPEQLDCGAAHLQHPLSILQPLKATPV
FRAPGLTSVAVASVNNYTAVFLGTVNGRLLKINLNESMQVVSRRVVTVAYGEPVHHVMQFDPADSVYLYLMTSHQ
MARVKVAACNVHSTCGDCVGAADAYCGWCALETRCTLQQDCTNSSQQHFWTSASEGPSRCPAMTVLPSEIDVRQE
YPGMILQISGSLPSLSGMEMACDYGNNIRTVARVPGPAFGHQIAYCNLLPRDQFPPFPPNQDHVTVEMSVRVNGR
NIVKANFTIYDCSRTAQVYPHTACTSCLSAQWPCFWCSQQHSCVSNQSRCEASPNPTSPQDCPRTLLSPLAPVPT
GGSQNILVPLANTAFFQGAALECSFGLEEIFEAVWVNESVVRCDQVVLHTTRKSQVFPLSLQLKGRPARFLDSPE
PMTVMVYNCAMGSPDCSQCLGREDLGHLCMWSDGCRLRGPLQPMAGTCPAPEIRAIEPLSGPLDGGTLLTIRGRN
LGRRLSDVAHGVWIGGVACEPLPDRYTVSEEIVCVTGPAPGPLSGVVTVNASKEGKSRDRFSYVLPLVHSLEPTM
GPKAGGTRITIHGNDLHVGSELQVLVNDTDPCTELMRTDTSIACTMPEGALPAPVPVCVRFERRGCVHGNLTFWY
MQNPVITAISPRRSPVSGGRTITVAGERFHMVQNVSMAVHHIGREPTLCKVLNSTLITCPSPGALSNASAPVDFF
INGRAYADEVAVAEELLDPEEAQRGSRFRLDYLPNPQFSTAKREKWIKHHPGEPLTLVIHKEQDSLGLQSHEYRV
KIGQVSCDIQIVSDRIIHCSVNESLGAAVGQLPITIQVGNFNQTIATLQLGGSETAIIVSIVICSVLLLLSVVAL
FVFCTKSRRAERYWQKTLLQMEEMESQIREEIRKGFAELQTDMTDLTKELNRSQGIPFLEYKHFVTRTFFPKCSS
LYEERYVLPSQTLNSQGSSQAQETHPLLGEWKIPESCRPNMEEGISLFSSLLNNKHFLIVFVHALEQQKDFAVRD
RCSLASLLTIALHGKLEYYTSIMKELLVDLIDASAAKNPKLMLRRTESVVEKMLTNWMSICMYSCLRETVGEPFF
LLLCAIKQQINKGSIDAITGKARYTLNEEWLLRENIEAKPRNLNVSFQGCGMDSLSVRAMDTDTLTQVKEKILEA
FCKNVPYSQWPRAEDVDLEWFASSTQSYILRDLDDTSVVEDGRKKLNTLAHYKIPEGASLAMSLIDKKDNTLGRV
KDLDTEKYFHLVLPTDELAEPKKSHRQSHRKKVLPEIYLTRLLSTKGTLQKFLDDLFKAILSIREDKPPLAVKYF
FDFLEEQAEKRGISDPDTLHIWKTNSLPLRFWVNILKNPQFVFDIDKTDHIDACLSVIAQAFIDACSISDLQLGK
DSPTNKLLYAKEIPEYRKIVQRYYKQIQDMTPLSEQEMNAHLAEESRKYQNEFNTNVAMAEIYKYAKRYRPQIMA
ALEANPTARRTQLQHKFEQVVALMEDNIYECYSEA

FIGURE 45

CCCCTGCCCGCCCGACAGCGCCGCCGCCTGCCCCGCC**ATG**GGTCGACAGAAGGAGCTGGTGTCCCGCTGCGGGGA
GATGCTCCACATCCGCTACCGGCTGCTCCGACAGGCGCTGGCCGAGTGCCTGGGGACCCTCATCCTGGTGATGTT
TGGCTGTGGCTCCGTGGCCCAGGTTGTGCTCAGCCGGGGCACCCACGGTGGTTTCCTCACCATCAACCTGGCCTT
TGGCTTTGCTGTCACTCTGGGCATCCTCATCGCTGGCCAGGTCTCTGGGGCCCACCTGAACCCTGCCGTGACCTT
TGCCATGTGCTTCCTGGCTCGTGAGCCCTGGATCAAGCTGCCCATCTACACCCTGGCACAGACGCTGGGAGCCTT
CTTGGGTGCTGGAATAGTTTTTGGGCTGTATTATGATGCAATCTGGCACTTCGCCGACAACCAGCTTTTTGTTTC
GGGCCCCAATGGCACAGCCGGCATCTTTGCTACCTACCCCTCTGGACACTTGGATATGATCAATGGCTTCTTTGA
CCAGTTCATAGGCACAGCCTCCCTTATCGTGTGTGTGCTGGCCATTGTTGACCCCTACAACAACCCCGTCCCCCG
AGGCCTGGAGGCCTTCACCGTGGGCCTGGTGGTCCTGGTCATTGGCACCTCCATGGGCTTCAACTCCGGCTATGC
CGTCAACCCTGCCCGGGACTTTGGCCCCCGCCTTTTTACAGCCCTTGCGGGCTGGGGCTCTGCAGTCTTCACGAC
CGGCCAGCATTGGTGGTGGGTGCCCATCGTGTCCCCACTCCTGGGCTCCATTGCGGGTGTCTTCGTGTACCAGCT
GATGATCGGCTGCCACCTGGAGCAGCCCCCACCCTCCAACGAGGAAGAGAATGTGAAGCTGGCCCATGTGAAGCA
CAAGGAGCAGATC**TGA**GTGGGCAGGGGCCATCTCCCCACTCCGCTGCCCTGGCCTTGAGCATCCACTGACTGTCC
AAGGGCCACTCCCAAGAAGCCCCCTTCACGATCCACCCTTTCAGGCTAAGGAGCTCCCTATCTACCCTCACCCCA
CGAGACAGCCCCTTCAGGATTTCCACTGGACCTTGCCCAAATAGCACCTTAGGCCACTGCCCCTAAGCTGGGGTG
GAACCGGAATTTGGGTCAATACATCCTTTTGTCTCCCAAGGGAAGAGAATGGGCAGCAGGTATGTGTGTGTGTGC
ATGTGTGTGCATGTGTGTGCATGTGTGTGCAGGGGTGTGTGTGTGTGGGGGGGGTTCCCAGATATTCAGGGCAAG
GGACCAGTCGGAAGGGATTCTGGCTATTGGGGGAGCCCAGAGACAGGGGAAGGCAGCCTGTCCATCTGTGCATAA
GGAGAGGAAAGTTCCAGGGTGTGTATGTTTCAGGGGCTTCACATGGAGGAGCTGCAGATAGATATGTGTTTCTGT
GTATGTGTATGTCTGCCTTTTTTTCTAAGTGGGGGCTTCTACAGGCTTTTGGGAAGTAGGGTGGATGTGGGTAGG
GCTGGGAGGAGGGGGCCACAGCTTAGGTTTGGAGCTCTGGATGTACATACATAAGTAGGAGCAGTGGGACGTGTT
TCTGTCATAATGCAGGCATGAAGGGTGGAGTGAAGTCAGGTCATAAGTTTCATGTTTGCTTTTGTTTTGTTTTGT
TTTTAATGTATGTAGCAGATGTTACAGTCTTAGGGATCCGGGATGGGAGACCCCACTTTAGAAAGGGTCGTCACT
CCTTTAATCCTCTACTCAACAATGTACTCTTTTACTTTTATATTAAAAAAAATAAAATAAATATGTGCCTAAAAA
AAAAAAAAAA

FIGURE 46

MGRQKELVSRCGEMLHIRYRLLRQALAECLGTLILVMFGCGSVAQVVLSRGTHGGFLTINLAFGFAVTLGILIAG
QVSGAHLNPAVTFAMCFLAREPWIKLPIYTLAQTLGAFLGAGIVFGLYYDAIWHFADNQLFVSGPNGTAGIFATY
PSGHLDMINGFFDQFIGTASLIVCVLAIVDPYNNPVPRGLEAFTVGLVVLVIGTSMGFNSGYAVNPARDFGPRLF
TALAGWGSAVFTTGQHWWWVPIVSPLLGSIAGVFVYQLMIGCHLEQPPPSNEEENVKLAHVKHKEQI

FIGURE 47

ACCAACCTCTTCGAGGCACAAGGCACAACAGGCTGCTCTGGGATTCTCTTCAGCCAATCTTCATTGCTCAAGTGT
CTGAAGCAGCC**ATG**GCAGAAGTACCTGAGCTCGCCAGTGAAATGATGGCTTATTACAGTGGCAATGAGGATGACT
TGTTCTTTGAAGCTGATGGCCCTAAACAGATGAAGTGCTCCTTCCAGGACCTGGACCTCTGCCCTCTGGATGGCG
GCATCCAGCTACGAATCTCCGACCACCACTACAGCAAGGGCTTCAGGCAGGCCGCGTCAGTTGTTGTGGCCATGG
ACAAGCTGAGGAAGATGCTGGTTCCCTGCCCACAGACCTTCCAGGAGAATGACCTGAGCACCTTCTTTCCCTTCA
TCTTTGAAGAAGAACCTATCTTCTTCGACACATGGGATAACGAGGCTTATGTGCACGATGCACCTGTACGATCAC
TGAACTGCACGCTCCGGGACTCACAGCAAAAAAGCTTGGTGATGTCTGGTCCATATGAACTGAAAGCTCTCCACC
TCCAGGGACAGGATATGGAGCAACAAGTGGTGTTCTCCATGTCCTTTGTACAAGGAGAAGAAAGTAATGACAAAA
TACCTGTGGCCTTGGGCCTCAAGGAAAAGAATCTGTACCTGTCCTGCGTGTTGAAAGATGATAAGCCCACTCTAC
AGCTGGAGAGTGTAGATCCCAAAAATTACCCAAAGAAGAAGATGGAAAAGCGATTTGTCTTCAACAAGATAGAAA
TCAATAACAAGCTGGAATTTGAGTCTGCCCAGTTCCCCAACTGGTACATCAGCACCTCTCAAGCAGAAAACATGC
CCGTCTTCCTGGGAGGGACCAAAGGCGGCCAGGATATAACTGACTTCACCATGCAATTTGTGTCTTCC**TAA**AGAG
AGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAGGGCTGGCAGAAAGGGAACAGAAAGGTTTT
TGAGTACGGCTATAGCCTGGACTTTCCTGTTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAAGA
GGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCCAATCCCCAGCCCTTTTGTTGAGCCAG
GCCTCTCTCACCTCTCCTACTCACTTAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCT
CTGTCATTCGCTCCCACATTCTGATGAGCAACCGCTTCCCTATTTATTTATTTATTTGTTTGTTTGTTTTATTCA
TTGGTCTAATTTATTCAAAGGGGGCAAGAAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAAT
CAATTCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTGAAAATATATAAGCTCAGATT
ATTTAAATGGGAATATTTATAAATGAGCAAATATCATACTGTTCAATGGTTCTGAAATAAACTTCTCTGAAG

FIGURE 48

MAEVPELASEMMAYYSGNEDDLFFEADGPKQMKCSFQDLDLCPLDGGIQLRISDHHYSKGFRQAASVVVAMDKLR
KMLVPCPQTFQENDLSTFFPFIFEEEPIFFDTWDNEAYVHDAPVRSLNCTLRDSQQKSLVMSGPYELKALHLQGQ
DMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNK
LEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS

FIGURE 49A

CCCTTTTTCCTCCCGTTTTGAAGAGACAATGCTACTTCAGTTTGGAGCACAAACATATGATCAGCACATGGAAAT
GTGGTAATTCGGATGCATTCGTGATTGCAACAGATTGAAGAAATTAGACCAGACAAAGAGTGTTTTTAGAGGAGA
GAGGAGGAGGAGGAGGCTGAGAGAGGGAGGGCGACGGGGGTGAGAAAGGGGAGGCCGCCTCTGAGCGGGACGCCG
GGACTCCCGCCGCTGCTAAATATATCCGTAGA**ATG**GAGAGGGACCGGATCTCAGCCTTGAAAAGATCTTTTGAGG
TCGAGGAGGTCGAGACACCCAACTCCACCCCACCCCGGAGGGTCCAGACTCCCCTACTCCGAGCCACTGTGGCCA
GCTCCACCCAGAAATTCCAGGACCTGGGCGTGAAGAACTCAGAACCCTCGGCCCGCCATGTGGACTCCCTAAGCC
AACGCTCCCCCAAGGCGTCCCTGCGGAGGGTGGAGCTCTCGGGCCCCAAGGCGGCCGAGCCGGTGTCCCGGCGCA
CTGAGCTGTCCATTGACATCTCGTCCAAGCAGGTGGAGAACGCCGGGGCCATCGGCCCGTCCCGGTTCGGGCTCA
AGAGGGCCGAGGTGTTGGGCCACAAGACGCCAGAACCGGCCCCTCGGAGGACGGAGATCACCATCGTCAAACCCC
AGGAGTCAGCCCACCGGAGGATGGAGCCCCCTGCCTCCAAGGTCCCCGAGGTGCCCACTGCCCCTGCCACCGACG
CAGCCCCCAAGAGGGTGGAGATCCAGATGCCCAAGCCTGCTGAGGCGCCCACCGCCCCCAGCCCAGCCCAGACCT
TGGAGAATTCAGAGCCTGCCCCTGTGTCTCAGCTGCAGAGCAGGCTGGAGCCCAAGCCCCAGCCCCCTGTGGCTG
AGGCTACACCCCGGAGCCAGGAGGCCACTGAGGCGGCTCCCAGCTGCGTTGGCGACATGGCCGACACCCCCAGAG
ATGCCGGGCTCAAGCAGGCGCCTGCATCACGGAACGAGAAGGCCCCGGTGGACTTCGGCTACGTGGGGATTGACT
CCATCCTGGAGCAGATGCGCCGGAAGGCCATGAAGCAGGGCTTCGAGTTCAACATCATGGTGGTCGGGCAGAGCG
GCTTGGGTAAATCCACCTTAATCAACACCCTCTTCAAATCCAAAATCAGCCGGAAGTCGGTGCAGCCCACCTCAG
AGGAGCGCATCCCCAAGACCATCGAGATCAAGTCCATCACGCACGATATTGAGGAGAAAGGCGTCCGGATGAAGC
TGACAGTGATTGACACACCAGGGTTCGGGGACCACATCAACAACGAGAACTGCTGGCAGCCCATCATGAAGTTCA
TCAATGACCAGTACGAGAAATACCTGCAGGAGGAGGTCAACATCAACCGCAAGAAGCGCATCCCGGACACCCGCG
TCCACTGCTGCCTCTACTTCATCCCCGCCACCGGCCACTCCCTCAGGCCCCTGGACATCGAGTTTATGAAACGCC
TGAGCAAGGTGGTCAACATCGTCCCTGTCATCGCCAAGGCGGACACACTCACCCTGGAGGAGAGGGTCCACTTCA
AACAGCGGATCACCGCAGACCTGCTGTCCAACGGCATCGACGTGTACCCCCAGAAGGAATTTGATGAGGACTCGG
AGGACCGGCTGGTGAACGAGAAGTTCCGGGAGATGATCCCATTTGCTGTGGTGGGCAGTGACCACGAGTACCAGG
TCAACGGCAAGAGGATCCTTGGGAGGAAGACCAAGTGGGGTACCATCGAAGTTGAAAACACCACACACTGTGAGT
TTGCCTACCTGCGGGACCTTCTCATCAGGACGCACATGCAGAACATCAAGGACATCACCAGCAGCATCCACTTCG
AGGCGTACCGTGTGAAGCGCCTCAACGAGGGCAGCAGCGCCATGGCCAACGGCGTGGAGGAGAAGGAGCCAGAAG
CCCCGGAGATG**TAG**ACGCCCCCTGCCCACCCCCGGGATCCTGCCCCCAAGTCATTTCCGTCCCCCCCCCAGGCCC
TCCCACCACCCCATTTTATTTTATATGATTTTCTCCATTTGTCATCGTTCCCCACCCCTTCGACATGCTGCCAGG
AAACAAGGGAAGGGGCCTCCCTCCGAGTGAGTCAGTGATGAGGCCGCGGCCTCCCCGAGGTTGTGGGGAGGCTGC
ACTGGAGCCACAGGCAGGGGTGAGAGCACCCACTGAATTGACATGACCCTCTGTCCCCAGGCCTGGCTCCCCGAG
GGCTCAGAAGAGCAGCTTCGGTGTGCAGATCATCCGTCGTGTGGGGTTCTCAGTGCCGGAGCTTGGGGTGGGGGC
CAGGCCTCGCACTTGCAGAGGAGCCCAGTGGGCTGCACGCTCCCCTCCATCCCCATCGGCCCTGTCCCCTGGAGT
GTGTCAGAGCCCAGGGGAGAATGCAGCCCACCAGGAGCACCTGGACCCCCTGCCCGCCACATGGTGTGGCCATCA
CTCAGCCCCTACCCCTGCCCTGCTCCTAAGGGTAGAAAACTCCAGGGTCCCCTGCCACCGACTGCCCAGCCACTC
CAAGCCCCCTGGCAGCTGCCCCTCCTGGAGCAGAAAGTGCCTTTATCTCAGCCATCCGCAGACTGCTGGCCAGAT
GCGGGGACAGGCTGGAATGAGGGAGGCGTCTTCATCTCCCTGCCATCCCCCTCTCACGCCACCCCCGCCCCCACC
GGGCTGCAGGTGCTGCTGATGCGCTGGGATCTGATTGAGGATAAAAAGGAAGGAGAGATGACCCCTACCCCCTCA
TCCCCCAGTTTTGAAAAGGTCTAAGCAAGTGAGTCTGGTGGAGGAGCTGAGGGAGGGAGCCATGGAAGGTGCCAG
AAGGAAGGTTGGCGGGGGCACGTGTGGGCCGTGGCTTGGGCTGGTCAGAGTGGCGTGAGCTGCCCGGCGCCTGCC
CTGCCCAAGTGACCAGGGAAGTGTGTGTGTGTCCATGTGTATGCGTGTCCGTCTGTCTGTCTAGTGTCTGGGTTT
GGCCCAAGACTGGGCTGTAGTTACATTAATGCCCAGCCAGCCACCCCTGCCACTCACCCCTCCTGGCCCAGGCCT
TGCTGACTCTCTGAGCTGGGGAGGTGGGAGGCCAGGCGAGCCTGACTCTGTTGATCTACCCGTGCCTGGGCCCCT
CCCCTCAGAGCCCATGGTAACGAACCCCTAGAAAGGAGAGAACGGGCGTCAGGGGTGCACAGTCCACAGCTGAAG
AGCAAGGTTTCGTGGCAGCACGGCCCGGCCCCTCACCCTCTGTCCCCACGAGGGGACCCATGGGGGCTGTCTTTG
CAGGGCACAGATGACCAAAGTCCCTTCCTGCTTCCTGTTACCTGTCTTGCTCCTGGGGAGAAAGAGGGGCCTGAT
GAGACTCCACTCAGGTGCACACATCACCAGGTGCATCTGCAGGCACCGGGCTGGCTGCTTGCAGCCAGGAGAAGG
TCAGCGAGAAGGAGTGTATGAGTGTGAGTGTGTGTGCATGGAAGTTGGGGCACTGGGCGTCTGACTCCCTCCCCA
CCCAAGAGAGGAAGGACCCCTCACCACCCCCACTGGCGAGACAGTTTACTTTGCCGACTTGCCATGTTTTTGCCA

FIGURE 49B

AAACCAAGATTTTGAAGGAAATGAGTGGCCAGCGCCAGGGCCCAGGCCATGTGGCCTGCCCAGCCTCAATGTCAC
TTGGCGGCGGGGTGGGGTGGGGGTGGGCAGCAGCATCCCAGCCTTGAGATGCTTCACTTTCCTTCTCTGTAACCA
GACTTTGAAAAATTGTTCGTTTCATCAGGCTCTGTTCCTCAATGGCCTTTTGCTACGTGCCTCCCGAGAAATTTG
TCTTTTTGTATAAATGACAAAGTGTTGAAAATGTATTTCCTGAAATAAATGTTTCAAATGCAGAAACCCAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

MERDRISALKRSFEVEEVETPNSTPPRRVQTPLLRATVASSTQKFQDLGVKNSEPSARHVDSLSQRSPKASLRRV
ELSGPKAAEPVSRRTELSIDISSKQVENAGAIGPSRFGLKRAEVLGHKTPEPAPRRTEITIVKPQESAHRRMEPP
ASKVPEVPTAPATDAAPKRVEIQMPKPAEAPTAPSPAQTLENSEPAPVSQLQSRLEPKPQPPVAEATPRSQEATE
AAPSCVGDMADTPRDAGLKQAPASRNEKAPVDFGYVGIDSILEQMRRKAMKQGFEFNIMVVGQSGLGKSTLINTL
FKSKISRKSVQPTSEERIPKTIEIKSITHDIEEKGVRMKLTVIDTPGFGDHINNENCWQPIMKFINDQYEKYLQE
EVNINRKKRIPDTRVHCCLYFIPATGHSLRPLDIEFMKRLSKVVNIVPVIAKADTLTLEERVHFKQRITADLLSN
GIDVYPQKEFDEDSEDRLVNEKFREMIPFAVVGSDHEYQVNGKRILGRKTKWGTIEVENTTHCEFAYLRDLLIRT
HMQNIKDITSSIHFEAYRVKRLNEGSSAMANGVEEKEPEAPEM

FIGURE 51

GGCACGAGGGGAAGTTGCCGGCGGCCGCGCGGCCTCCCGGGCGGGCCTACAGCCATGTCCCGGGACCCGGGGTCG
GGCGGCTGGGAGGAGGCCCCGCGCGCAGCTGCCGCGCTCTGCACCCTGTACCACGAGGCCGGACAGCGGCTGCGC
CGCCTGCAGGACCAGCTCGCTGCCCGCGACGCCCTCATCGCTCGCCTCCGCGCCCGCCTGGCCGCGCTGGAGGGG
GACGCCGCGCCGTCCCTAGTGGACGCGCTGCTGGAGCAGGTTGCGCGCTTCCGGGAGCAGCTGCGAAGGCAGGAG
GGCGGCGCCGCCGAGGCCCAGATGCGCCAGGAAATTGAGAGGCTGACTGAGCGACTAGAAGAAAAAGAGAGGGAG
ATGCAGCAGCTGCTGAGCCAGCCCCAACACGAGCGAGAGAAGGAAGTCGTCCTGCTACGGAGGAGCATGGCAGAA
GGGGAGCGCGCCCGGGCCGCCAGTGACGTCCTGTGCCGCTCCTTGGCCAACGAGACCCATCAGCTGCGGAGGACG
CTGACCGCCACCGCCCACATGTGTCAGCATCTGGCCAAGTGTCTGGATGAACGACAGCATGCACAAAGGAATGTG
GGGGAGAGAAGTCCTGACCAGTCGGAACACACAGATGGGCACACCTCTGTCCAGAGTGTTATTGAGAAGTTGCAG
GAAGAAAATCGACTGTTAAAACAGAAGGTGACTCACGTTGAAGACCTCAATGCCAAGTGGCAGCGCTACAACGCC
AGCAGGGACGAATACGTGAGGGGGCTCCATGCGCAGCTCAGGGGGCTGCAGATCCCCCACGAGCCCGAGCTGATG
AGGAAGGAGATCTCCCGGCTCAACAGACAGTTGGAAGAGAAAATAAATGACTGTGCCGAAGTGAAGCAGGAGCTG
GCGGCCTCCAGGACGGCCCGGGATGCTGCGTTGGAGCGGGTGCAGATGCTGGAACAGCAGATTCTCGCTTACAAG
GATGACTTCATGTCAGAAAGGGCCGATCGGGAACGGGCTCAAAGTAGGATTCAAGAACTGGAGGAAAAGGTCGCC
TCTTTGCTGCACCAGGTGTCCTGGAGACAGGATTCTCGAGAGCCAGACGCCGGCCGGATTCACGCTGGGAGCAAA
ACTGCCAAGTATTTGGCCGCCGACGCATTAGAGCTTATGGTGCCTGGTGGCTGGAGGCCTGGGACTGGGTCCCAG
CAGCCAGAACCCCCTGCAGAGGGCGGGCATCCTGGCGCGGTCCAGAGAGGCCAGGGGGACCTTCAGTGCCCTCAC
TGCCTGCAGTGCTTCAGTGACGAGCAAGGGGAAGAGCTCCTCAGGCATGTGGCCGAGTGCTGCCAG**TGA**CCGAGA
CTCACCCGTGCCCTTGCGGCCTCCTGGCCCGGTGCAGCTGCCCTCAGGGACAGGGTGGGTGCTCTCAGATGCCAT
GGGTTGAGCTCTACTGAGAGCCAAGGCCCCTAGAATAGTTGCGGGGCACTCTGATCGTTCACTTTGGTCCCTTTG
GCTATGGAACAGGCTGGGTCACAGGGAACTGCCAGTGAGGCTGGAGGCTGGAGGTGGAGATGGGGTCAGGAACAT
CTGGCAGAGGGAGGTCCCAGTCTGTGTCTCCATCAGGCTTAAGCCAGAGCTATCTGGTGCTGGTGTGCCAGCCCC
TCCCCCAGCCTGCCTAGAAAGGGGTGGCTGCCTGAGGGAGTCACTTGTATGGTCCCCAGGGTGGGAGCCCCATCC
TGTTCTATGGAATAAAGCGTCGCCTCTCTGCCTCGAACCAGTCAAATGGAGTATTGCGGCTGCACGTCACACTAG
GGTGGCCACCCCCGCCATTGCGAGCCACATGTCTGCACTGAGAAACTGCATTTCAGTAGCATTTGTCATCCAGCC
GGAAGTTAAAGCACACTTACTTTATTCACCTATTTTTATAATAAACGTTCTTGCTGCTGTGACTGCAAAAAAAAA
AAAAAAAAAA

FIGURE 52

MQQLLSQPQHEREKEVVLLRRSMAEGERARAASDVLCRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNV
GERSPDQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYNASRDEYVRGLHAQLRGLQIPHEPELM
RKEISRLNRQLEEKINDCAEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRERAQSRIQELEEKVA
SLLHQVSWRQDSREPDAGRIHAGSKTAKYLAADALELMVPGGWRPGTGSQQPEPPAEGGHPGAVQRGQGDLQCPH
CLQCFSDEQGEELLRHVAECCQ

FIGURE 53

GTTGCCGCTGCGCACCTGGCTCAGGTGAGCTGCCCCGCCCCCGCCCGGCGCGAGCCCCAGGTCCTGGCAGCAGCC
CCTGACCTGTCCAGGTGCCCTGTCCAGCTGACTGCAAGGACAGAGAGGAGTCCTGCCCAGCTCTTGGATCAGTCT
GCTGGCCGAGGAGCCCGGTGGAGCCAGGGGTGACCCTGGAGCCCAGCCTGCCCCGAGGAGGCCCCGGCTCAGAGC
C**ATG**CCAGGTGTCTGTGATAGGGCCCCTGACTTCCTCTCCCCGTCTGAAGACCAGGTGCTGAGGCCTGCCTTGGG
CAGCTCAGTGGCTCTGAACTGCACGGCTTGGGTAGTCTCTGGGCCCCACTGCTCCCTGCCTTCAGTCCAGTGGCT
GAAAGACGGGCTTCCATTGGGAATTGGGGGCCACTACAGCCTCCACGAGTACTCCTGGGTCAAGGCCAACCTGTC
AGAGGTGCTTGTGTCCAGTGTCCTGGGGGTCAACGTGACCAGCACTGAAGTCTATGGGGCCTTCACCTGCTCCAT
CCAGAACATCAGCTTCTCCTCCTTCACTCTTCAGAGAGCTGGCCCTACAAGCCACGTGGCTGCGGTGCTGGCCTC
CCTCCTGGTCCTGCTGGCCCTGCTGCTGGCCGCCCTGCTCTATGTCAAGTGCCGTCTCAACGTGCTGCTCTGGTA
CCAGGACGCGTATGGGGAGGTGGAGATAAACGACGGGAAGCTCTACGACGCCTACGTCTCCTACAGCGACTGCCC
CGAGGACCGCAAGTTCGTGAACTTCATCCTAAAGCCGCAGCTGGAGCGGCGTCGGGGCTACAAGCTCTTCCTGGA
CGACCGCGACCTCCTGCCGCGCGCTGAGCCCTCCGCCGACCTCTTGGTGAACCTGAGCCGCTGCCGACGCCTCAT
CGTGGTGCTTTCGGACGCCTTCCTGAGCCGGGCCTGGTGCAGCCACAGCTTCCGGGAGGGCCTGTGCCGGCTGCT
GGAGCTCACCCGCAGACCCATCTTCATCACCTTCGAGGGCCAGAGGCGCGACCCCGCGCACCCGGCGCTCCGCCT
GCTGCGCCAGCACCGCCACCTGGTGACCTTGCTGCTCTGGAGGCCCGGCTCCGTGACTCCTTCCTCCGATTTTTG
GAAAGAAGTGCAGCTGGCGCTGCCGCGGAAGGTGCGGTACAGGCCGGTGGAAGGAGACCCCCAGACGCAGCTGCA
GGACGACAAGGACCCCATGCTGATTCTTCGAGGCCGAGTCCCTGAGGGCCGGGCCCTGGACTCAGAGGTGGACCC
GGACCCTGAGGGCGACCTGGGTGTCCGGGGGCCTGTTTTTGGAGAGCCATCAGCTCCACCGCACACCAGTGGGGT
CTCGCTGGGAGAGAGCCGGAGCAGCGAAGTGGACGTCTCGGATCTCGGCTCGCGAAACTACAGTGCCCGCACAGA
CTTCTACTGCCTGGTGTCCAAGGATGATATG**TAG**CTCCCACCCCAGAGTGCAGGATCATAGGGACAGCGGGGGCC
AGGGCAGCGGCGTCGCTCCTCTGCTCAACAGGACCACAACCCCTGCCAGCAGCCCTGGGACCCTGCCAGCAGCCC
TGGGAAAAGGCTGTGGCCTCAGGGCGCCTCCCAGTGCCAGAAAATAAAGTCCTTTTGGATTCTGAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGGHYSLHEYSWVKANLS
EVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTSHVAAVLASLLVLLALLLAALLYVKCRLNVLLWY
QDAYGEVEINDGKLYDAYVSYSDCPEDRKFVNFILKPQLERRRGYKLFLDDRDLLPRAEPSADLLVNLSRCRRLI
VVLSDAFLSRAWCSHSFREGLCRLLELTRRPIFITFEGQRRDPAHPALRLLRQHRHLVTLLLWRPGSVTPSSDFW
KEVQLALPRKVRYRPVEGDPQTQLQDDKDPMLILRGRVPEGRALDSEVDPDPEGDLGVRGPVFGEPSAPPHTSGV
SLGESRSSEVDVSDLGSRNYSARTDFYCLVSKDDM

FIGURE 55A

GGTTGGCTCTTGCACTTCCTGGCTCTCTGGACTTGGTTATGTGATTGAGCCTCCATGGCCTCCGTGTCTTTGTCT
GTCAATGGGTTTGATTAAAGCGTTGACCTCATAGGTTCTTAGGAGGATTAATGAGAACATTTTATGTAAAGCTGC
TTACATGGAGCCTTGGTATGTGCCGGAAAGCTTTAGCCCTTTATTAAAAGTGACAGCAGACCCAGCACGGTGGCT
CATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACTTGGGGTCAGGAGTTCGAGACCAGCTAC
TCGGGAGGCAGAGGCAGGAGAATCGCTTGAACCTGGGGTGCAGAGGTTGCAGTAAGCTGAGCTCGCACCACTGCA
CTCCAGCCTGAGTGACAGAGTGAAACTCAGTCTCAAAAAAAAAAAAAAAAAAAGAGTGGCAGTAGTGGTGGGGGA
GACCCCCATCCCCCTTGCTGGGGTTTCCTAGGAAAGAAGGCTGGTGAGAGCTGTTGCTGGTGGTGGGCCCTGAGC
CGCAGGGTCTGAGGGCCTACCCTGTGCTACCCCAGAGCTGCCTGAGAACTGGACAGACACGCGGGAGACGCTGCT
GGAGGGG**ATG**CTGTTCAGCCTCAAGTACCTGGGCATGACGCTAGTGGAGCAGCCCAAGGGTGAGGAGCTGTCGGC
CGCCGCCATCAAGAGGATCGTGGCTACAGCTAAGGCCAGTGGGAAGAAGCTGCAGAAGGTGACTCTGAAGGTGTC
GCCACGGGGAATTATCCTGACAGACAACCTCACCAACCAGCTCATTGAGAACGTGTCCATATACAGGATCTCCTA
TTGCACAGCAGACAAGATGCACGACAAGGTGTTTGCATACATCGCCCAGAGCCAGCACAACCAGAGCCTCGAGTG
CCACGCCTTCCTCTGCACCAAGCGGAAGATGGCACAGGCTGTTACCCTCACCGTAGCCCAGGCCTTCAAAGTCGC
CTTTGAGTTTTGGCAGGTGTCCAAGGAAGAGAAAGAGAAGAGGGACAAAGCCAGCCAAGAGGGAGGGGACGTCCT
GGGGGCCCGCCAAGACTGCACCCCCCCCTTGAAGAGCTTGGTCGCCACTGGGAACCTGCTGGACTTAGAGGAGAC
GGCTAAGGCCCCGCTGTCCACGGTCAGCGCCAACACCACCAACATGGACGAGGTGCCGCGGCCACAAGCCTTGAG
TGGCAGCAGTGTTGTCTGGGTGAGTGGTTGTGTGGCCAGCAGATCGGTGATCCTCAGCCTGACCTCTGGG**TGA**GC
CTGGGGCTGCTCCAGGGACCAGGCTCTGGGACCCGTGACTTGTGGGCCTCTGGGAGGACCAGACCCAGCCCGGTA
GTGCCCAGGCGCAGGATAGGGGATGAACAATGTCCCTTTTGAACCTGAGGCTGCATCCCCAACAGGCTTGGCTCC
CAGCACAGCTGTCTCCTCACAATGCTTGGCCTCTTGGCCTGAGCGTCCACGGCTCTGCCCACCACAAGACCAGCC
AAAGGCGCCCTTGTTCTTGGTGTGGCAGAGCTCGCTCCTACCACCCCTCCCCCTCAGCCGCCTGAATGAGGACCC
AGAGACTTGGGCAGTCACCAGCTTGGTCCCTGACTCCCTCAGGGACTCAGGGCAAGCCCCCTGACCTCTCTGTCT
CAGCTTTTTCATCTCAGTAAGGGTGATGACCTCTGCCAACGGAATCTCCCCGAGGAACCTGAAATTTAATTTTAA
TTTTTCATTTGGAAATAATTTCAGACTGTGTTACAAAATTAGTACAGAGAATTCCTGTTCACCCGTCATCCAGAT
TCCCCAATTGTTAACATCTTGCATGACCACATTACACTGGTCAGAATCAGGAAACAAACACGATACTGTGCTGTT
ATATAATCTATAGAACTTACACATTTCTCCAGGTGCCCCTTCAGTGTCCTGTTTCTGGCCCAGGATCCATTGCAG
AATCACATGTTAACTTGTCGTCTCTTTAATTTTTAAAAATCTGGGTACTGGGGGCTCCCCTGGTGTCCCTCGAGC
CTGTTCTCTGCTGTTTGGGAACCACCCTTGCCACTTGCCCATCCTCACCAGAACGCCATGGAGGGACCTCACCTG
TCGCTTTTCTGCTGAGGCTGTGGGACTCCTGGCATCAGTTATCCCTCATGAACTTGGAATTTTGGCTTGGCTTTT
GGAAGTAAATGAAGGCAAGAAAACTCCCTTCCCCACCCTCTTCCTTTTGGAATTTGAAAGCCATAGAAGTCATCA
GGTCCAATGCCCTCCTCTTATTGAAGGAAAAGCTGAGTTTCAACGTGGAGCAGTGACTTGCCCAAGGTCTCACGG
GCAGGTAGCATGGACCAGGGCACTGAACCCACCTGGGTCTCCAGACACCCTGGGACATGGCCTTTCTCCTCTCCC
ACGTCTCCAGCTTTGGGTCCTTGGGCTGAGATGCTGGCGATGCACCCAGGCAGGAGGCCTGCCTGAGGCCGTGCC
TCCAGGCGCCCACCCTGAGCTTGTGTCCTGAGTCCCTGTAGCTTACCCAGGGCTGGGACAAGCCCCAGCTGTGAG
CATGGGCTCCCCCAAACATAGTTCTTATCTCCTGCTTTGTTTTTCCCAAGGAGCTGGATGATGGCCTGGATGAAG
CGTTTTCGAGGCTTGCCCAGTCTCGGACAAACCCTCAGGTCCTGGACACTGGCCTGACAGCCCAGGACATGCATT
ACGCCCAGTGCCTCTCGCCTGTCGACTGGGACAAGCCTGACAGCAGCGGCACAGAGCAGGATGACCTCTTCAGCT
TCTGAGGGCCCGGGGCCAGCCGGACACAAGCGGCCCTGACACGTGATGGACCAAAGCCACCTGCTGCGGGGGAGC
CAGTTCTGGGGCCCGCCTGCCACCTCTCCCAGCCCTCAGCATTGTCAGCCTGAAGATCAGAGCTGCAGCCAGTCA
GGCAGGGGAGAGATTTTTCTTTTAAGCCCTGCTCTTTCTCTGAGAACCAAAAGATGCCTTGAATATTTATTCAGT
GACTTCTGGCTTATGCTCAGAAGCCAGTCTGCGTCAGGCACGTCTCCTGCTGCGTGACATGTGCAGTGCTGTAAT
CGGCTCCCGCTTGCTCTCCTGGAGCAAGCTCTGCCCTGGCTGTGGGTATCAGGACTGTGACCAAAGCATTTCTAG
TCCCTTCTCTCTTTCTAAGGACCCAAATTTCCCTGGGGGCATCCTGCTTCCTGAAAGCTGTTGGATTTCAGTGAT
TTTTCCCCCCACCCCCCAGCACAGGAGAGCACCCACAGCCGCAGAAGGGGAATGTGTCCTCCTGCTCTGCTTCCT
CAGGGCCCAGCAGGCGGGGGTTTGAGCCCTGGACCCCAGGCTCTTAGAGACTAAGGGGCAGCTCCTGACCAAAGA
CGATACAGCTTGGCACTTTAAAGCATTAACAGCAGGTGTGACCCTGAGGGCTCCTCCATGGTGCTGCATTGAGTC
CAGCTTTCCTTCTGCCCTTCCTCCAGGAGAAGGGGCCCAAGGTCCCCGTGGATGGTCTCCACCTGTGCTTGGAAC
CAGTGTAACTGGCTGCTCCCTGCTCCCAGGGACTGACACGGGGATCATCTCTGTGACCGCCCTCCGTCGGGCCCC

FIGURE 55B

TGCCTGCCTTCTCCCCTCCACGCAAGGCTGTGCTCTTCCTCTGGTTTCTGTGTGTCCGTTTGAGTGTCTGCGCCC
CGCCTCCCCATACTTCCTGGGATGATGTGTGAAACCTGACACCTAGATTTATTTGGAAATATTCTATGACCACTT
TACAGATGAGGAAACTGAGGCCTCAAGCGTGGAGGGGTAGAGTGAAGAGTAGAACCCAGGTCTGATGCCAAAGCT
GCTTTCTTCTCTGCCTCCTCCTCACGCAACTCACACCTCCTTTTCTTCTAGCTTTGTTGTCCTCCCAGGAACCAA
AAAACCCCAGCTATTTTCTGACCAAAATGTGTTTCATAACAAACCATCTGGTGCCTTTCCACACAGAACTGGCAG
GAGCCTCGTGTCCTGCTAGCTGTCTCTCTTGTTGATTTCCGTGAAAATGCAAGTGTTTGAAGTCTGCTCATTCCG
AGGGTGAAACAAAATCCAACCCTGTCAGAATCATGCTGTTCTCTTTGCTGACACTGTGACCCTGGGTCGGGACAG
ACCAGCAGCAATCTGTCTTTAGAATCGCTTTCCTTCCTCCCCTTTTGCCCCCGTGGGGCTCCCGGCATCCTGAAA
GCCAGCAAAGCCTCCAGCATCTTTTCCATCCTGAGGTGCCTCCCAGTGGCCTGGCTTGTCGGAGCAAGTTTCATC
AGCCCTAGGGAAAACACGGCCCTCCTGGGAACCTCCTTACCTGGAGTAACCGGACACCTTAGACGGAGGTGCCTG
AGGGTGGGGTGGGATTTGCAGGGTCATTATCAGAACATGAGGATAACTTCCTTGCCCCTGCTCTGTAGCCACCTC
CTTGGCACCGGCCTCTATTTGTCATAAGGCGGCGTGGGCGAGGCCTGACACAGGCCAGCCTTGGCACGAGGGGGG
CCAGGGGTTCTGAGAAGCGCTGCCCTGTGAGAGCCACGCTGGCCTTCGTCTCCATCTCTGGTTGACGGGCTGTCC
GTTTGCCTCCTGTGTGTCTGCAGACAAGTCTTGCTGTGCTTTATTTGTGAAACTTTAATGAGGAAAAAACAAATA
ATAAATGTTCTCGTTTTGAAACTC

FIGURE 56

MLFSLKYLGMTLVEQPKGEELSAAAIKRIVATAKASGKKLQKVTLKVSPRGIILTDNLTNQLIENVSIYRISYCT
ADKMHDKVFAYIAQSQHNQSLECHAFLCTKRKMAQAVTLTVAQAFKVAFEFWQVSKEEKEKRDKASQEGGDVLGA
RQDCTPPLKSLVATGNLLDLEETAKAPLSTVSANTTNMDEVPRPQALSGSSVVWVSGCVASRSVILSLTSG

FIGURE 57

GGCACGAGGGTTAGATTAGTCTGAAGCCGCCACCAGCCCCAGGCCCCCGTGCAGAAGAAAAGCGGGAGGGAACGG
CGGAGGCCGCCGCTGCCCTGCACCGCCCTCCTGGAGGCCACTTGGAGAGTCCGGCCCCGAGGAGGCCATGGCCAC
AAGTGCCCACAGCTGGCCCCAGGTTGCCAGCGTCGCTACAGCCCAGACCAAGGCAGAATAATCTCCGGATGAGCT
GGTGGCACCGCTGAGCCTTTGGTCTCACCAGGGCTTCCTGTTGCTGGCAGGCGGGGTGGAGCGGAGCTGCTGGGA
GGCTGCTGGATAGGAGAGGGGTCACGGCTGCGGAAGAGGAGGTTCTTCGGGACACCCGTGGATGGACACGGCAAG
GAAACACCAGGCCAACCACAGCTGGGGATAAAATAGCACAACCACACCCTGCCGTCCAGCGCCTCCCAGCCTGTG
CCCCTTCCTAGTACCACCAGCAACCATCAATCCCGTCTCCTCCTGCCTCCTCTCCTGCAATCCACCCCGCCACGA
CTATCGCC**ATG**GCAGCCCTGATCGCAGAGAACTTCCGCTTCCTGTCACTTTTCTTCAAGAGCAAGGATGTGATGA
TTTTCAACGGCCTGGTGGCACTGGGCACGGTGGGCAGCCAGGAGCTGTTCTCTGTGGTGGCCTTCCACTGCCCCT
GCTCGCCGGCCCGGAACTACCTGTACGGGCTGGCGGCCATCGGCGTGCCCGCCCTGGTGCTCTTCATCATTGGCA
TCATCCTCAACAACCACACCTGGAACCTCGTGGCCGAGTGCCAGCACCGGAGGACCAAGAACTGCTCCGCCGCCC
CCACCTTCCTCCTTCTAAGCTCCATCCTGGGACGTGCGGCTGTGGCCCCTGTCACCTGGTCTGTCATCTCCCTGC
TGCGTGGTGAGGCTTATGTCTGTGCTCTCAGTGAGTTCGTGGACCCTTCCTCACTCACGGCCAGGGAAGAGCACT
TCCCATCAGCCCACGCCACTGAAATCCTGGCCAGGTTCCCCTGCAAGGAGAACCCTGACAACCTGTCAGACTTCC
GGGAGGAGGTCAGCCGCAGGCTCAGGTATGAGTCCCAGCTCTTTGGATGGCTGCTCATCGGCGTGGTGGCCATCC
TGGTGTTCCTGACCAAGTGCCTCAAGCATTACTGCTCACCACTCAGCTACCGCCAGGAGGCCTACTGGGCGCAGT
ACCGCGCCAATGAGGACCAGCTGTTCCAGCGCACGGCCGAGGTGCACTCTCGGGTGCTCGCTGCCAACAATGTGC
GCCGCTTCTTTGGCTTTGTGGCGCTCAACAAGGATGATGAGGAACTGATTGCCAACTTCCCAGTGGAAGGCACGC
AGCCACGGCCACAGTGGAATGCCATCACCGGCGTCTACTTGTACCGTGAGAACCAGGGCCTCCCACTCTACAGCC
GCCTGCACAAGTGGGCCCAGGGTCTGGCAGGCAACGGCGCGGCCCCTGACAACGTGGAGATGGCCCTGCTCCCCT
CC**TAA**GGAGGTGCTTCCCATGCTCTTTGTAAATGGCACTACTTGGTCCCAAACTGAACCCCACTGCTTGCTCACA
TCCATATCAGAAGGGGATTTTTAAAAAACTGTTATCTTCTTGGCCAGGGGAAAGGACCACAAGGCAATCTGGGGT
GTGGACAGACCCAGTAGACAATGGAAGCCCAGCCAGCAGGGCCAGGTGACAGTGAAGCTCACCAGTGGGCTCCTT
TATGGTACTCTATGCAGTTAACATGTATCTAGCTGCATAGGGACACCCAGCGCAGCAGTGCACCACTGGGAAGTG
GCCTCCAGTGCAGCCTCTGGCCTTATTTTATATATTTAAATTTTTGATAAAGTTTTTCTTACTAAAAAAAAAAAA
AAAAAA

FIGURE 58

MAALIAENFRFLSLFFKSKDVMIFNGLVALGTVGSQELFSVVAFHCPCSPARNYLYGLAAIGVPALVLFIIGIIL
NNHTWNLVAECQHRRTKNCSAAPTFLLLSSILGRAAVAPVTWSVISLLRGEAYVCALSEFVDPSSLTAREEHFPS
AHATEILARFPCKENPDNLSDFREEVSRRLRYESQLFGWLLIGVVAILVFLTKCLKHYCSPLSYRQEAYWAQYRA
NEDQLFQRTAEVHSRVLAANNVRRFFGFVALNKDDEELIANFPVEGTQPRPQWNAITGVYLYRENQGLPLYSRLH
KWAQGLAGNGAAPDNVEMALLPS

FIGURE 59

ACGAGGGACGCAGCC**ATG**GCGGAGGCGGCTTTGGAAGCCGTGCGGAGCGAGTTACGAGAATTCCCGGCCGCTGCA
AGGGAGCTCTGCGTGCCTCTTGCTGTGCCCTACCTGGACAAACCCCCAACTCCGCTCCACTTCTACCGGGACTGG
GTCTGCCCCAACAGGCCGTGCATTATCCGCAACGCTCTGCAGCACTGGCCGGCCCTCCAGAAGTGGTCCCTCCCC
TATTTCAGAGCCACAGTGGGCTCCACAGAGGTGAGTGTGGCCGTGACCCCAGATGGTTACGCGGATGCCGTGAGA
GGGGATCGCTTCATGATGCCAGCTGAGCGCCGCCTGCCCCTGAGCTTCGTGCTGGATGTGCTGGAGGGCCGGGCC
CAGCACCCTGGAGTCCTCTATGTGCAGAAGCAGTGCTCCAACCTGCCCAGCGAGCTGCCCCAGCTGCTGCCTGAT
CTGGAATCCCATGTGCCCTGGGCCTCCGAAGCCCTGGGAAAGATGCCCGATGCTGTGAACTTCTGGCTGGGGGAG
GCGGCTGCAGTGACTTCTTTGCACAAGGACCACTATGAGAACCTCTACTGCGTGGTCTCAGGAGAGAAGCATTTC
CTGTTCCATCCGCCCAGCGACCGGCCCTTCATCCCCTATGAGCTGTACACGCCGGCAACCTACCAGCTAACTGAA
GAGGGCACCTTTAAGGTGGTGGATGAAGAGGCCATGGAGAAGGCAGAGGTGTCCAGGACCTGCCTGCTCACGGTT
CGTGTCCTGCAGGCCCATCGCCTACCCTCTAAGGACCTAGTGACCCCCTCTGACTGCTACGTGACTCTCTGGCTG
CCCACGGCCTGCAGCCACAGGCTCCAGACACGCACGGTCAAGAACAGCAGTAGCCCTGTCTGGAACCAGAGCTTT
CACTTCAGGATCCACAGGCAGCTCAAGAATGTCATGGAACTGAAAGTCTTTGACCAGGACCTGGTGACCGGAGAT
GACCCTGTGTTGTCAGTACTGTTTGATGCGGGGACTCTGCGGGCTGGGGAGTTCCGGCGCGAGAGCTTCTCACTG
AGCCCTCAGGGTGAGGGGCGCCTGGAAGTTGAATTTCGCCTGCAGAGTCTGGCTGACCGTGGCGAGTGGCTCGTC
AGCAATGGCGTTCTGGTGGCCCGGGAGCTCTCCTGCTTGCACGTTCAACTGGAGGAGACAGGAGACCAGAAGTCC
TCAGAGCACAGAGTTCAGCTTGTGGTTCCTGGGTCCTGTGAGGGTCCGCAGGAGGCCTCTGTGGGCACTGGCACC
TTCCGCTTCCACTGCCCAGCCTGCTGGGAGCAGGAGCTGAGTATTCGCCTGCAGGATGCCCCCGAGGAGCAACTA
AAGGCGCCACTGAGTGCCCTGCCCTCTGGTCAAGTGGTGAGGCTTGTCTTCCCCACGTCCCAGGAGCCCCTGATG
AGAGTGGAGCTGAAAAAAGAAGCAGGACTGAGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTGCAGAGGAG
CAGGCCTTCCTGAGCAGGAGGAAGCAGGTGGTGGCCGCGGCCTTGAGGCAGGCCCTGCAGCTGGATGGAGACCTG
CAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGGCAATGACTTCCCTGTATGGG
CAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCGTCTCCTACATCACCGGGGCCTCGGGCTCCACCTGG
GCCTTGGCCAACCTTTATGAGGACCCAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACC
CAGGTGACCAAGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCGAGCGT
GCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGCGCTGCTGCATGATGAGCCC
CATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTC
AACACCAAAGGGCAGAGCCTGACCACTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTC
CCCAAGTACGGGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCTT
CCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCTCCAGGACAGCTTATAC
TGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCC
CTTCTGAAGATAGAAGAACCACCCTCAACAGCCGGCAGRATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGT
CCACTGGCCCAGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTTC
TCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCGGAGCCCCACCTGTGCCTGCTG
GATGTTGGCTACCTCATCAATACCAGCTGCCTGCCCCTCCTGCAGCCCACTCGGGACGTGGACCTCATCCTGTCA
TTGGACTACAACCTCCACGGAGCCTTCCAGCAGTTGCAGCTCCTGGGCCGGTTCTGCCAGGAGCAGGGGATCCCG
TTCCCACCCATCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCACCTGC
CCCGGAGCCCCTGCGGTGCTGCACTTTCCTCTGGTCAGCGACTCCTTCCGGGAGTACTCGGCCCCTGGGGTCCGG
CGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGTCTTCATCGGACTCTCCCTACCACTACACGAAGGTG
ACCTACAGCCAGGAGGACGTGGACAAGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTG
CTGGAGGCTCTGCGCCAGGCAGTGCAGCGGAGGCGGCAGCGCAGGCCCCAC**TGA**TGGCCGGGGCCCCTGCCACCC
CTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTGCTTCAGAGCCTCGGGC
TCAGGTGGCACKGTCCCAGGGTCCAGGCTGAGGGCTGGGAGCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAA
GGAGGCCAAGCCCATTTGTGTAATCACCCAAAACCCCCCGGCCTGTGCCTGTTTTCCCTTCTGCGCTACCTTGAG
TAGTTGGAGCACTTGATACATCACAGACTCATACAAAAAAAAAAAAAAAAAA

FIGURE 60

MAEAALEAVRSELREFPAAARELCVPLAVPYLDKPPTPLHFYRDWVCPNRPCIIRNALQHWPALQKWSLPYFRAT
VGSTEVSVAVTPDGYADAVRGDRFMMPAERRLPLSFVLDVLEGRAQHPGVLYVQKQCSNLPSELPQLLPDLESHV
PWASEALGKMPDAVNFWLGEAAAVTSLHKDHYENLYCVVSGEKHFLFHPPSDRPFIPYELYTPATYQLTEEGTFK
VVDEEAMEKAEVSRTCLLTVRVLQAHRLPSKDLVTPSDCYVTLWLPTACSHRLQTRTVKNSSSPVWNQSFHFRIH
RQLKNVMELKVFDQDLVTGDDPVLSVLFDAGTLRAGEFRRESFSLSPQGEGRLEVEFRLQSLADRGEWLVSNGVL
VARELSCLHVQLEETGDQKSSEHRVQLVVPGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLS
ALPSGQVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEI
PVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKN
KLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQ
SLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEP
SQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKA
TTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPIS
PSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQE
DVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH

FIGURE 61

CTTCGGGTGTACGTGCTCCGGGATCTTCAGCACCCGCGGCCGCCATCGCCGTCGCTTGGCTTCTTCTGGACTCAT
CTGCGCCACTTGTCCGCTTCACACTCCGCCGCCATC**ATG**GTGAAGCTCGCGAAGGCAGGTAAAAATCAAGGTGAC
CCCAAGAAAATGGCTCCTCCTCCAAAGGAGGTAGAAGAAGATAGTGAAGATGAGGAAATGTCAGAAGATGAAGAA
GATGATAGCAGTGGAGAAGAGGTCGTCATACCTCAGAAGAAAGGCAAGAAGGCTGCTGCAACCTCAGCAAAGAAG
GTGGTCGTTTCCCCAACAAAAAAGGTTGCAGTTGCCACACCAGCCAAGAAAGCAGCTGTCACTCCAGGCAAAAAG
GCAGCAGCAACACCTGCCAAGAAGACAGTTACACCAGCCAAAGCAGTTACCACACCTGGCAAGAAGGGAGCCACA
CCAGGCAAAGCATTGGTAGCAACTCCTGGTAAGAAGGGTGCTGCCATCCCAGCCAAGGGGGCAAAGAATGGCAAG
AATGCCAAGAAGGAAGACAGTGATGAAGAGGAGGATGATGACAGTGAGGAGGATGAGGAGGATGACGAGGACGAG
GATGAGGATGAAGATGAAATTGAACCAGCAGCGATGAAAGCAGCAGCTGCTGCCCCTGCCTCAGAGGATGAGGAC
GATGAGGATGACGAAGATGATGAGGATGACGATGACGATGAGGAAGATGACTCTGAAGAAGAAGCTATGGAGACT
ACACCAGCCAAAGGAAAGAAAGCTGCAAAAGTTGTTCCTGTGAAAGCCAAGAACGTGGCTGAGGATGAAGATGAA
GAAGAGGATGATGAGGACGAGGATGACGACGACGACGAAGATGATGAAGATGATGATGATGAAGATGATGAGGAG
GAGGAAGAAGAGGAGGAGGAAGAGCCTGTCAAAGAAGCACCTGGAAAACGAAAGAAGGAAATGGCCAAACAGAAA
GCAGCTCCTGAAGCCAAGAAACAGAAAGTGGAAGGCACAGAACCGACTACGGCTTTCAATCTCTTTGTTGGAAAC
CTAAACTTTAACAAATCTGCTCCTGAATTAAAAACTGGTATCAGCGATGTTTTTGCTAAAAATGATCTTGCTGTT
GTGGATGTCAGAATTGGTATGACTAGGAAATTTGGTTATGTGGATTTTGAATCTGCTGAAGACCTGGAGAAAGCG
TTGGAACTCACTGGTTTGAAAGTCTTTGGCAATGAAATTAAACTAGAGAAACCAAAAGGAAAAGACAGTAAGAAA
GAGCGAGATGCGAGAACACTTTTGGCTAAAAATCTCCCTTACAAAGTCACTCAGGATGAATTGAAAGAAGTGTTT
GAAGATGCTGCGGAGATCAGATTAGTCAGCAAGGATGGGAAAAGTAAAGGGATTGCTTATATTGAATTTAAGACA
GAAGCTGATGCAGAGAAAACCTTTGAAGAAAAGCAGGGAACAGAGATCGATGGGCGATCTATTTCCCTGTACTAT
ACTGGAGAGAAAGGTCAAAATCAAGACTATAGAGGTGGAAAGAATAGCACTTGGAGTGGTGAATCAAAAACTCTG
GTTTTAAGCAACCTCTCCTACAGTGCAACAGAAGAAACTCTTCAGGAAGTATTTGAGAAAGCAACTTTTATCAAA
GTACCCCAGAACCAAAATGGCAAATCTAAAGGGTATGCATTTATAGAGTTTGCTTCATTCGAAGACGCTAAAGAA
GCTTTAAATTCCTGTAATAAAAGGGAAATTGAGGGCAGAGCAATCAGGCTGGAGTTGCAAGGACCCAGGGGATCA
CCTAATGCCAGAAGCCAGCCATCCAAAACTCTGTTTGTCAAAGGCCTGTCTGAGGATACCACTGAAGAGACATTA
AAGGAGTCATTTGACGGCTCCGTTCGGGCAAGGATAGTTACTGACCGGGAAACTGGGTCCTCCAAAGGGTTTGGT
TTTGTAGACTTCAACAGTGAGGAGGATGCCAAGGAGGCCATGGAAGACGGTGAAATTGATGGAAATAAAGTTACC
TTGGACTGGGCCAAACCTAAGGGTGAAGGTGGCTTCGGGGGTCGTGGTGGAGGCAGAGGCGGCTTTGGAGGACGA
GGTGGTGGTAGAGGAGGCCGAGGAGGATTTGGTGGCAGAGGCCGGGGAGGCTTTGGAGGGCGAGGAGGCTTCCGA
GGAGGCAGAGGAGGAGGAGGTGACCACAAGCCACAAGGAAAGAAGACGAAGTTTGAA**TAG**CTTCTGTCCCTCTGC
TTTCCCTTTTCCATTTGAAAGAAAGGACTCTGGGGTTTTTACTGTTACCTGATCAATGACAGAGCCTTCTGAGGA
CATTCCAAGACAGTATACAGTCCTGTGGTCTCCTTGGAAATCCGTCTAGTTAACATTTCAAGGGCAATACCGTGT
TGGTTTTGACTGGATATTCATATAAACTTTTTAAAGAGTTGAGTGATAGAGCTAACCCTTATCTGTAAGTTTTGA
ATTTATATTGTTTCATCCCATGTACAAAACCATTTTTTCCTAC

FIGURE 62

MVKLAKAGKNQGDPKKMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGKKAAATSAKKVVVSPTKKVAVA
TPAKKAAVTPGKKAAATPAKKTVTPAKAVTTPGKKGATPGKALVATPGKKGAAIPAKGAKNGKNAKKEDSDEEED
DDSEEDEEDDEDEDEDEDEIEPAAMKAAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAKGKKAAKVV
PVKAKNVAEDEDEEEDDEDEDDDDDEDDEDDDDEDDEEEEEEEEEEPVKEAPGKRKKEMAKQKAAPEAKKQKVEG
TEPTTAFNLFVGNLNFNKSAPELKTGISDVFAKNDLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNE
IKLEKPKGKDSKKERDARTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADAEKTFEEKQ
GTEIDGRSISLYYTGEKGQNQDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEKATFIKVPQNQNGKSKGY
AFIEFASFEDAKEALNSCNKREIEGRAIRLELQGPRGSPNARSQPSKTLFVKGLSEDTTEETLKESFDGSVRARI
VTDRETGSSKGFGFVDFNSEEDAKEAMEDGEIDGNKVTLDWAKPKGEGGFGGRGGGRGGFGGRGGGRGGRGGFGG
RGRGGFGGRGGFRGGRGGGGDHKPQGKKTKFE

FIGURE 63

CTCCCAAAGCAGAATTGCAGCTGCCGCCGCCGCCACCTCCAGGCCACT**ATG**GCGCCTGGGGCTGCCCAGGAGCTT
CAGGCCAAGTTGGCAGAGATCGGAGCTCCGATCCAGGGTAATCGCGAGGAGCTGGTGGAGCGGCTGCAGAGCTAC
ACCCGCCAGACTGGCATCGTGCTGAATCGGCCGGTTTTGAGAGGGGAAGATGGGGACAAAGCCGCTCCACCTCCC
ATGTCGGCACAGCTCCCTGGAATTCCCATGCCACCACCACCTTTGGGACTCCCCCCTCTGCAGCCTCCTCCGCCA
CCCCCACCACCTCCACCAGGCCTTGGCCTTGGCTTTCCTATGGCCCACCCACCAAATTTGGGGCCCCCGCCTCCT
CTCCGTGTGGGTGAGCCAGTGGCACTGTCAGAGGAGGAGCGGCTGAAGTTGGCTCAGCAGCAGGCGGCATTGCTG
ATGCAGCAGGAGGAGCGTGCCAAGCAGCAGGGAGATCATTCGCTGAAGGAACATGAGCTCTTGGAGCAGCAGAAG
CGGGCAGCTGTGTTACTGGAGCAGGAACGACAGCAGGAGATTGCCAAGATGGGCACCCCAGTCCCTCGGCCCCCA
CAAGACATGGGCCAGATTGGTGTGCGCACTCCTCTGGGTCCTCGAGTAGCTGCTCCAGTGGGCCCAGTGGGCCCC
ACTCCTACAGTTTTGCCCATGGGAGCCCCTGTTCCCCGGCCTCGTGGTCCCCCACCGCCCCCTGGAGATGAGAAC
AGAGAGATGGATGACCCCTCTGTGGGCCCCAAGATCCCCCAGGCTTTGGAGAAGATCCTGCAGCTGAAGGAGAGC
CGCCAGGAAGAGATGAATTCTCAGCAGGAGGAAGAGGAAATGGAAACAGATGCTCGCTCGTCCCTGGGCCAGTCA
GCGTCAGAGACTGAGGAGGACACAGTGTCCGTATCTAAAAAGGAGAAAAACCGGAAGCGTAGGAACCGAAAGAAG
AAGAAAAAGCCCCAGCGGGTGCGAGGGGTGTCCTCTGAGAGCTCTGGGGACCGGGAGAAAGACTCAACCCGGTCC
CGTGGCTCTGATTCCCCAGCAGCTGATGTTGAGATTGAGTATGTGACTGAAGAACCTGAAATTTACGAGCCCAAC
TTTATCTTCTTTAAGAGGATCTTTGAGGCTTTTAAGCTCACTGATGATGTGAAGAAGGAGAAAGAGAAAGAGCCA
GAGAAACTTGACAAACTGGAGAACTCTGCAGCCCCCAAGAAGAAGGGATTTGAAGAGGAGCACAAGGACAGTGAT
GATGACAGCAGTGATGACGAGCAGGAAAAGAAGCCAGAAGCCCCCAAGCTGTCCAAGAAGAAGTTGCGCCGAATG
AACCGCTTCACTGTGGCTGAACTCAAGCAGCTGGTGGCTCGGCCCGATGTCGTGGAGATGCACGATGTGACAGCG
CAGGACCCTAAGCTCTTGGTTCACCTCAAGGCCACTCGGAACTCTGTGCCTGTGCCACGCCACTGGTGTTTTAAG
CGCAAATACCTGCAGGGCAAACGGGGCATTGAGAAGCCCCCCTTCGAGCTGCCAGACTTCATCAAACGCACAGGC
ATCCAGGAGATGCGAGAGGCCCTGCAGGAGAAGGAAGAACAGAAGACCATGAAGTCAAAAATGCGAGAGAAAGTT
CGGCCTAAGATGGGCAAAATTGACATCGACTACCAGAAACTGCATGATGCCTTCTTCAAGTGGCAGACCAAGCCA
AAGCTGACCATCCATGGGGACCTGTACTATGAGGGGAAGGAGTTCGAGACACGACTGAAGGAGAAGAAGCCAGGA
GATCTGTCTGATGAGCTAAGGATTTCCTTGGGGATGCCAGTAGGACCAAATGCCCACAAGGTCCCTCCCCCATGG
CTGATTGCCATGCAGCGATATGGACCACCCCCATCGTATCCCAACCTGAAAATCCCTGGGCTGAACTCGCCCATC
CCTGAGAGCTGTTCCTTTGGGTACCATGCTGGTGGCTGGGGCAAACCTCCAGTGGATGAGACTGGGAAACCGCTC
TATGGGGACGTGTTTGGAACCAATGCTGCTGAATTTCAGACCAAGACTGAGGAAGAAGAGATTGATCGGACCCCT
TGGGGGGAACTGGAACCATCTGATGAAGAATCCTCAGAAGAAGAGGAAGAGGAAGAAAGTGATGAAGACAAACCA
GATGAGACAGGCTTTATTACCCCTGCAGACAGTGGCCTTATCACTCCTGGAGGCTTTTCATCAGTGCCTGCTGGA
ATGGAGACCCCTGAACTCATTGAGCTGAGGAAGAAGAAGATTGAGGAGGCGATGGACGGAAGTGAGACACCTCAG
CTCTTCACTGTGTTGCCAGAGAAGAGAACAGCCACTGTTGGAGGGGCCATGATGGGATCAACCCACATTTATGAC
ATGTCCACGGTTATGAGCCGGAAGGGCCCGGCTCCTGAGCTGCAAGGTGTGGAAGTGGCGCTGGCGCCTGAAGAG
TTGGAGCTGGATCCTATGGCCATGACCCAGAAGTATGAGGAGCATGTGCGGGAGCAGCAGGCTCAAGTAGAGAAG
GAGGACTTCAGTGACATGGTGGCTGAGCACGCTGCCAAACAGAAGCAAAAAAAAACGGAAAGCTCAGCCCCAGGAC
AGCCGTGGGGGCAGCAAGAAATATAAGGAGTTCAAGTTT**TAG**GTCCCCTCACACTAGCCCTTTTTTTGGCCCTAC
GTCTGGATGCCTGGGCTTCACACAAGAACCACCTCTCCCGCAGTTCCCAAGGACTTGTCATTTCATGTTCTTATT
TTAGACCTGTTTTGTAAATAAAGCTGTTTCCCAAGGAAAGAGATGAAAAAAAAAAAAAAAAAAA

FIGURE 64

MAPGAAQELQAKLAEIGAPIQGNREELVERLQSYTRQTGIVLNRPVLRGEDGDKAAPPPMSAQLPGIPMPPPPLG
LPPLQPPPPPPPPPPGLGLGFPMAHPPNLGPPPPLRVGEPVALSEEERLKLAQQQAALLMQQEERAKQQGDHSLK
EHELLEQQKRAAVLLEQERQQEIAKMGTPVPRPPQDMGQIGVRTPLGPRVAAPVGPVGPTPTVLPMGAPVPRPRG
PPPPPGDENREMDDPSVGPKIPQALEKILQLKESRQEEMNSQQEEEEMETDARSSLGQSASETEEDTVSVSKKEK
NRKRRNRKKKKKPQRVRGVSSESSGDREKDSTRSRGSDSPAADVEIEYVTEEPEIYEPNFIFFKRIFEAFKLTDD
VKKEKEKEPEKLDKLENSAAPKKKGFEEEHKDSDDDSSDDEQEKKPEAPKLSKKKLRRMNRFTVAELKQLVARPD
VVEMHDVTAQDPKLLVHLKATRNSVPVPRHWCFKRKYLQGKRGIEKPPFELPDFIKRTGIQEMREALQEKEEQKT
MKSKMREKVRPKMGKIDIDYQKLHDAFFKWQTKPKLTIHGDLYYEGKEFETRLKEKKPGDLSDELRISLGMPVGP
NAHKVPPPWLIAMQRYGPPPSYPNLKIPGLNSPIPESCSFGYHAGGWGKPPVDETGKPLYGDVFGTNAAEFQTKT
EEEEIDRTPWGELEPSDEESSEEEEEEESDEDKPDETGFITPADSGLITPGGFSSVPAGMETPELIELRKKKIEE
AMDGSETPQLFTVLPEKRTATVGGAMMGSTHIYDMSTVMSRKGPAPELQGVEVALAPEELELDPMAMTQKYEEHV
REQQAQVEKEDFSDMVAEHAAKQKQKKRKAQPQDSRGGSKKYKEFKF

FIGURE 65

CGAAAAAAGAGGGGAAGAGTATTAAAGACCATTTCTGGCTGGGCAGGGCACTCTCAGCAGCTCAACTGCCCAGCG
TGACCAGTGGCCACCTCTGCAGTGTCTTCCACAACCTGGTCTTGACTCGTCTGCTGAACAAATCCTCTGACCTCA
GGCCGGCTGTGAACGTAGTTCCTGAGAGATAGCAAAC**ATG**CCCAACAGTGAGCCCGCATCTCTGCTGGAGCTGTT
CAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCCTCAAAGCGGGAAATGCGTCAAAGGATGAAATTGATTC
TGCAGTAAAGATGTTGGTGTCATTAAAAATGAGCTACAAAGCTGCCGCGGGGGAGGATTACAAGGCTGACTGTCC
TCCAGGGAACCCAGCACCTACCAGTAATCATGGCCCAGATGCCACAGAAGCTGAAGAGGATTTTGTGGACCCATG
GACAGTACAGACAAGCAGTGCAAAAGGCATAGACTACGATAAGCTCATTGTTCGGTTTGGAAGTAGTAAAATTGA
CAAAGAGCTAATAAACCGAATAGAGAGAGCCACCGGCCAAAGACCACACCACTTCCTGCGCAGAGGCATCTTCTT
CTCACACAGAGATATGAATCAGGTTCTTGATGCCTATGAAAATAAGAAGCCATTTTATCTGTACACGGGCCGGGG
CCCCTCTTCTGAAGCAATGCATGTAGGTCACCTCATTCCATTTATTTTCACAAAGTGGCTCCAGGATGTATTTAA
CGTGCCCTTGGTCATCCAGATGACGGATGACGAGAAGTATCTGTGGAAGGACCTGACCCTGGACCAGGCCTATGG
CGATGCTGTTGAGAATGCCAAGGACATCATCGCCTGTGGCTTTGACATCAACAAGACTTTCATATTCTCTGACCT
GGACTACATGGGGATGAGCTCAGGTTTCTACAAAAATGTGGTGAAGATTCAAAAGCATGTTACCTTCAACCAAGT
GAAAGGCATTTTCGGCTTCACTGACAGCGACTGCATTGGGAAGATCAGTTTTCCTGCCATCCAGGCTGCTCCCTC
CTTCAGCAACTCATTCCCACAGATCTTCCGAGACAGGACGGATATCCAGTGCCTTATCCCATGTGCCATTGACCA
GGATCCTTACTTTAGAATGACAAGGGACGTCGCCCCCAGGATCGGCTATCCTAAACCAGCCCTGTTGCACTCCAC
CTTCTTCCCAGCCCTGCAGGGCGCCCAGACCAAAATGAGTGCCAGCGACCCAAACTCCTCCATCTTCCTCACCGA
CACGGCCAAGCAGATCAAAACCAAGGTCAATAAGCATGCGTTTTCTGGAGGGAGAGACACCATCGAGGAGCACAG
GCAGTTTGGGGGCAACTGTGATGTGGACGTGTCTTTCATGTACCTGACCTTCTTCCTCGAGGACGACGACAAGCT
CGAGCAGATCAGGAAGGATTACACCAGCGGAGCCATGCTCACCGGTGAGCTCAAGAAGGCACTCATAGAGGTTCT
GCAGCCCTTGATCGCAGAGCACCAGGCCCGGCGCAAGGAGGTCACGGATGAGATAGTGAAAGAGTTCATGACTCC
CCGGAAGCTGTCCTTCGACTTTCAG**TAG**CACTCGTTTTACATATGCTTATAAAAGAAGTGATGTATCAGTAATGT
ATCAATAATCCCAGCCCAGTCAAAGCACCGCCACCTGTAGGCTTCTGTCTCATGGTAATTACTGGGCCTGGCCTC
TGTAAGCCTGTGTATGTTATCAATACTGTTTCTTCCTGTGAGTTCCATTATTTCTATCTCTTATGGGCAAAGCAT
TGTGGGTAATTGGTGCTGGCTAACATTGCATGGTCGGATAGAGAAGTCCAGCTGTGAGTCTCTCCCCAAAGCAGC
CCCACAGTGGAGCCTTCGGCTGGAAGTCCATGGGCCACCCTGTTCTTGTCCATGGAGGACTTCCGAGGGTTCCAA
GTATACTCTTAAGACCCACTCTGTTTAAAAATATATATTCTATGTATGCGTATATGGAATTGAAATGTCATTATT
GTAACCTAGAAAGTGCTTTGAAATATTGATGTGGGGAGGTTTATTGAGCACAAGATGTATTTCAGCCCATGCCCC
CTCCCAAAAAGAAATTGATAAGTAAAAGCTTCGTTATACATTTGACTAAGAAATCACCCAGCTTTAAAGCTGCTT
TTAACAATGAAGATTGAACAGAGTTCAGCAATTTTGATTAAATTAAGACTTGGGGGTGAAACTTTCCAGTTTACT
GAACTCCAGACCATGCATGTAGTCCACTCCAGAAATCATGCTCGCTTCCCTTGGCACACCAGTGTTCTCCTGCCA
AATGACCCTAGACCCTCTGTCCTGCAGAGTCAGGGTGGCTTTTCCCCTGACTGTGTCCGATGCCAAGGAGTCCTG
GCCTCCGCAGATGCTTCATTTTGACCCTTGGCTGCAGTGGAAGTCAGCACAGAGCAGTGCCCTGGCTGTGTCCTG
GACGGGTGGACTTAGCTAGGGAGAAAGTCGAGGCAGCAGCCCTCGAGGCCCTCACAGATGTCTAGGCAGGCCTCA
TTTCATCACGCAGCATGTGCAGGCCTGGAAGAGCAAAGCCAAATCTCAGGGAAGTCCTTGGTTGATGTATCTGGG
TCTCCTCTGGAGCACTCTGCCCTCCTGTCACCCAGTAGAGTAAATAAACTTCCTTGGCTCCTAAAAAA

FIGURE 66

MPNSEPASLLELFNSIATQGELVRSLKAGNASKDEIDSAVKMLVSLKMSYKAAAGEDYKADCPPGNPAPTSNHGP
DATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAY
ENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIAC
GFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDR
TDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH
AFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQARRK
EVTDEIVKEFMTPRKLSFDFQ

FIGURE 67

GCGGAGCGTGTGAGCAGTACTGCGGCCTCCTCTCCTCTCCTAACCTCGCTCTCGCGGCCTACCTTTACCCGCCCG
CCTGCTCGGCGACCAGCGGGGATCCTCCCCCAGCCGCAAGTCCACGAAGAAAGCAACGAATGAAAATTATGAAGA
CAACGAGAAGTCAGACTCCTCCGGGTCGCGCTCCAGCTGCTTCGGCTTCGTCGCCTACTCTGTGAACTCCGGGGA
GAGATCTCGAGTCAAGATTAAGACCTTAACCCACCAACCTGCCTGTTCGGACACCCCCCGGGCCGGCCGCTGTCT
GTCCCCTTCTCCATCGCCCTCTCCCAGAAAGCTCCGGTGCTTGGACCAGCTAGAGTCTGAGAAAGAGGAGAGGCG
CGAACGCCACTCCAAAAAGAGAAGGGTTAAAGAGGGCAACCCTAACGATACGCTTGACTTTCTGTGGCTGGGAAC
ACCTTCCACC**ATG**ACCACCTCAGCAAGTTCCCACTTAAATAAAGGCATCAAGCAGGTGTACATGTCCCTGCCTCA
GGGTGAGAAAGTCCAGGCCATGTATATCTGGATCGATGGTACTGGAGAAGGACTGCGCTGCAAGACCCGGACCCT
GGACAGTGAGCCCAAGTGTGTGGAAGAGTTGCCTGAGTGGAATTTCGATGGCTCCAGTACTTTACAGTCTGAGGG
TTCCAACAGTGACATGTATCTCGTGCCTGCTGCCATGTTTCGGGACCCCTTCCGTAAGGACCCTAACAAGCTGGT
GTTATGTGAAGTTTTCAAGTACAATCGAAGGCCTGCAGAGACCAATTTGAGGCACACCTGTAAACGGATAATGGA
CATGGTGAGCAACCAGCACCCCTGGTTTGGCATGGAGCAGGAGTATACCCTCATGGGGACAGATGGGCACCCCTT
TGGTTGGCCTTCCAACGGCTTCCCAGGGCCCCAGGGTCCATATTACTGTGGTGTGGGAGCAGACAGAGCCTATGG
CAGGGACATCGTGGAGGCCCATTACCGGGCCTGCTTGTATGCTGGAGTCAAGATTGCGGGGACTAATGCCGAGGT
CATGCCTGCCCAGTGGGAATTTCAGATTGGACCTTGTGAAGGAATCAGCATGGGAGATCATCTCTGGGTGGCCCG
TTTCATCTTGCATCGTGTGTGTGAAGACTTTGGAGTGATAGCAACCTTTGATCCTAAGCCCATTCCTGGGAACTG
GAATGGTGCAGGCTGCCATACCAACTTCAGCACCAAGGCCATGCGGGAGGAGAATGGTCTGAAGTACATCGAGGA
GGCCATTGAGAAACTAAGCAAGCGGCACCAGTACCACATCCGTGCCTATGATCCCAAGGGAGGCCTGGACAATGC
CCGACGTCTAACTGGATTCCATGAAACCTCCAACATCAACGACTTTTCTGCTGGTGTAGCCAATCGTAGCGCCAG
CATACGCATTCCCCGGACTGTTGGCCAGGAGAAGAAGGGTTACTTTGAAGATCGTCGCCCCTCTGCCAACTGCGA
CCCCTTTTCGGTGACAGAAGCCCTCATCCGCACGTGTCTTCTCAATGAAACCGGCGATGAGCCCTTCCAGTACAA
AAAT**TAA**GTGGACTAGACCTCCAGCTGTTGAGCCCCTCCTAGTTCTTCATCCCACTCCAACTCTTCCCCCTCTCC
CAGTTGTCCCGATTGTAACTCAAAGGGTGGAATATCAAGGTCGTTTTTTTCATTCCATGTGCCCAGTTAATCTTG
CTTTCTTTGTTTGGCTGGGATAGAGGGGTCAAGTTATTAATTTCTTCACACCTACCCTCCTTTTTTTCCCTATCA
CTGAAGCTTTTTAGTGCATTAGTGGGGAGGAGGGTGGGGAGACATAACCACTGCTTCCATTTAATGGGGTGCACC
TGTCCAATAGGCGTAGCTATCCGGACAGAGCACGTTTGCAGAAGGGGGACTCTTCTTCCAGGTAGCTGAAAGGGG
AAGACCTGACGTACTCTGGTTAGGTTAGGACTTGCCCTCGTGGTGGAAACTTTTCTTAAAAAGTTATAACCAACT
TTTCTATTAAAAGTGGGAATTAGGAGAGAAGGTAGGGGTTGGGAATCAGAGAGAATGGCTTTGGTCTCTTGCTTG
TGGGACTAGCCTGGCTTGGGACTAAATGCCCTGCTCTGAACACGAAGCTTAGTATAAACTGATGGATATCCCTAC
CTTGAAAGAAGAAAAGGTTCTTACTGCTTGGTCCTTGATTTATCACACAAAGCAGAATAGTATTTTTATATTTAA
ATGTAAAGACAAAAAACTATATGTATGGTTTTGTGGATTATGTGTGTTTTGCTAAAGGAAAAAACCATCCAGGTC
ACGGGGCACCAAATTTGAGACAAATAGTCGGATTAGAAATAAAGCATCTCATTTTGAGTAGAGAGCAAGGGAAGT
GGTTCTTAGATGGTGATCTGGGATTAGGCCCTCAAGACCCTTTTGGGTTTCTGCCCTGCCCACCCTCTGGAGAAG
GTGGGCACTGGATTAGTTAACAGACGACACGTTACTAGCAGTCACTTGATCTCCGTGGCTTTGGTTTAAAAGACA
CACTTGTCCACATAGGTTTAGAGATAAGAGTTGGCTGTTCAACTTGAGCATGTTACTGACAGAGGGGGTATTGGG
GTTATTTTCTGGTAGGAATAGCATGTCACTAAAGCAGGCCTTTTGATATTAAATTTTTTAAAAAGCAAAATTATA
GAAGTTTAGATTTTAATCAAATTTGTAGGGTTTCTAGGTAATTTTTACAGAATTGCTTGTTTGCTTCAACTGTCT
CCTACCTCTGCTCTTGGAGGAGATGGGGACAGGGCTGGAGTCAAAACACTTGTAATTTTGTATCTTGATGTCTTT
GTTAAGACTGCTGAAGAATTATTTTTTTTCTTTTATAATAAGGAATAAACCCCACCTTTATTCCTTCATTTCATC
TACCATTTTCTGGTTCTTGTGTTGGCTGTGGCAGGCCAGCTGTGGTTTTCTTTTGCCATGACAACTTCTAATTGC
CATGTACAGTATGTTCAAAGTCAAATAACTCCTCATTGTAAACAAACTGTGTAACTGCCCAAAGCAGCACTTATA
AATCAGCCTAACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MTTSASSHLNKGIKQVYMSLPQGEKVQAMYIWIDGTGEGLRCKTRTLDSEPKCVEELPEWNFDGSSTLQSEGSNS
DMYLVPAAMFRDPFRKDPNKLVLCEVFKYNRRPAETNLRHTCKRIMDMVSNQHPWFGMEQEYTLMGTDGHPFGWP
SNGFPGPQGPYYCGVGADRAYGRDIVEAHYRACLYAGVKIAGTNAEVMPAQWEFQIGPCEGISMGDHLWVARFIL
HRVCEDFGVIATFDPKPIPGNWNGAGCHTNFSTKAMREENGLKYIEEAIEKLSKRHQYHIRAYDPKGGLDNARRL
TGFHETSNINDFSAGVANRSASIRIPRTVGQEKKGYFEDRRPSANCDPFSVTEALIRTCLLNETGDEPFQYKN

FIGURE 69

TGCTGCAGCCGCTGCCGCCGATTCCGGATCTCATTGCCACGCGCCCCCGACGACCGCCCGACGTGCATTCCCGAT
TCCTTTTGGTTCCAAGTCCAAT**ATG**GCAACTCTAAAGGATCAGCTGATTTATAATCTTCTAAAGGAAGAACAGAC
CCCCCAGAATAAGATTACAGTTGTTGGGGTTGGTGCTGTTGGCATGGCCTGTGCCATCAGTATCTTAATGAAGGA
CTTGGCAGATGAACTTGCTCTTGTTGATGTCATCGAAGACAAATTGAAGGGAGAGATGATGGATCTCCAACATGG
CAGCCTTTTCCTTAGAACACCAAAGATTGTCTCTGGCAAAGACTATAATGTAACTGCAAACTCCAAGCTGGTCAT
TATCACGGCTGGGGCACGTCAGCAAGAGGGAGAAAGCCGTCTTAATTTGGTCCAGCGTAACGTGAACATATTTAA
ATTCATCATTCCTAATGTTGTAAAATACAGCCCGAACTGCAAGTTGCTTATTGTTTCAAATCCAGTGGATATCTT
GACCTACGTGGCTTGGAAGATAAGTGGTTTTCCCAAAAACCGTGTTATTGGAAGTGGTTGCAATCTGGATTCAGC
CCGATTCCGTTACCTGATGGGGGAAAGGCTGGGAGTTCACCCATTAAGCTGTCATGGGTGGGTCCTTGGGGAACA
TGGAGATTCCAGTGTGCCTGTATGGAGTGGAATGAATGTTGCTGGTGTCTCTCTGAAGACTCTGCACCCAGATTT
AGGGACTGATAAAGATAAGGAACAGTGGAAAGAGGTTCACAAGCAGGTGGTTGAGAGTGCTTATGAGGTGATCAA
ACTCAAAGGCTACACATCCTGGGCTATTGGACTCTCTGTAGCAGATTTGGCAGAGAGTATAATGAAGAATCTTAG
GCGGGTGCACCCAGTTTCCACCATGATTAAGGGTCTTTACGGAATAAAGGATGATGTCTTCCTTAGTGTTCCTTG
CATTTTGGGACAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAGGAAGAGGCCCGTTTGAAGAA
GAGTGCAGATACACTTTGGGGGATCCAAAAGGAGCTGCAATTT**TAA**AGTCTTCTGATGTCATATCATTTCACTGT
CTAGGCTACAACAGGATTCTAGGTGGAGGTTGTGCATGTTGTCCTTTTTATCTGATCTGTGATTAAAGCAGTAAT
ATTTTAAGATGGACTGGGAAAAACATCAACTCCTGAAGTTAGAAATAAGAATGGTTTGTAAAATCCACAGCTATA
TCCTGATGCTGGATGGTATTAATCTTGTGTAGTCTTCAACTGGTTAGTGTGAAATAGTTCTGCCACCTCTGACGC
ACCACTGCCAATGCTGTACGTACTGCATTTGCCCCTTGAGCCAGGTGGATGTTTACCGTGTGTTATATAACTTCC
TGGCTCCTTCACTGAACATGCCTAGTCCAACATTTTTTCCCAGTGAGTCACATCCTGGGATCCAGTGTATAAATC
CAATATCATGTCTTGTGCATAATTCTTCCAAAGGATCTTATTTTGTGAACTATATCAGTAGTGTACATTACCATA
TAATGTAAAAAGATCTACATACAAACAATGCAACCAACTATCCAAGTGTTATACCAACTAAAACCCCCAATAAAC
CTTGAACAGTG

FIGURE 70

MATLKDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLRTP
KIVSGKDYNVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKI
SGFPKNRVIGSGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDKE
QWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKGLYGIKDDVFLSVPCILGQNGI
SDLVKVTLTSEEEARLKKSADTLWGIQKELQF

FIGURE 71

CCGCAGCGCCGGAGTCAAACGGTTCCCGGCCCAGTCCCGTCCTGCAGCAGTCTGCCTCCTCTTTCAAC**ATG**ACAG
ATGCCGCTGTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGCAGCCATCTCCAAGACGGCGGTAGCGC
CCATCGAGCGGGTCAAGCTGCTGCTGCAGGTGCAGCATGCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAG
GCATTATAGACTGCGTGGTCCGTATTCCCAAGGAGCAGGGAGTTCTGTCCTTCTGGCGCGGTAACCTGGCCAATG
TCATCAGATACTTCCCCACCCAGGCTCTTAACTTCGCCTTCAAAGATAAATACAAGCAGATCTTCCTGGGTGGTG
TGGACAAGAGAACCCAGTTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGGTGGTGCCGCAGGGGCCACATCCC
TGTGTTTTGTGTACCCTCTTGATTTTGCCCGTACCCGTCTAGCAGCTGATGTGGGTAAAGCTGGAGCTGAAAGGG
AATTCCGAGGCCTCGGTGACTGCCTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTA
ACGTGTCTGTGCAGGGTATTATCATCTACCGAGCCGCCTACTTCGGTATCTATGACACTGCAAAGGGAATGCTTC
CGGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATCGCACAGACTGTCACTGCTGTTGCCGGGTTGACTT
CCTATCCATTTGACACCGTTCGCCGCCGCATGATGATGCAGTCAGGGCGCAAAGGAACTGACATCATGTACACAG
GCACGCTTGACTGCTGGCGGAAGATTGCTCGTGATGAAGGAGGCAAAGCTTTTTTCAAGGGTGCATGGTCCAATG
TTCTCAGAGGCATGGGTGGTGCTTTTGTGCTTGTCTTGTATGATGAAATCAAGAAGTACACA**TAA**GTTATTTCCT
AGGATTTTTCCCCCTGTGAACAGGCATGTTGTATTCTATAACACAATCTTGAGCATTCTTGACAGACTCCTGGCT
GTCAGTTTCTCAGTGGCAACTACTTTACTGGTTGAAAATGGGAAGCAATAATATTCATCTGACCAGTTTTCCTCT
AAAGCCATTTCCATGATGATGATGATGGGACTCAATTGTATTTTTTATTTCAGTCACTCCTGATAAATAACAAAT
TTGGAGAAATAAAAATATCTAAAAT

FIGURE 72

MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVRIPKEQGVLSFWRGNL
ANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKAGA
EREFRGLGDCLVKIYKSDGIKGLYQGFNVSVQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAG
LTSYPFDTVRRRMMMQSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYT

FIGURE 73

AGTATGTGTGGTTGGGGAATTCATGTGGAGGTCAGAGTGGAAGCAGGTGTGAGAGGGTCCAGCAGAAGGAAAC**AT**
GGCTGCCAAAGTGTTTGAGTCCATTGGCAAGTTTGGCCTGGCCTTAGCTGTTGCAGGAGGCGTGGTGAACTCTGC
CTTATATAATGTGGATGCTGGGCACAGAGCTGTCATCTTTGACCGATTCCGTGGAGTGCAGGACATTGTGGTAGG
GGAAGGGACTCATTTTCTCATCCCGTGGGTACAGAAACCAATTATCTTTGACTGCCGTTCTCGACCACGTAATGT
GCCAGTCATCACTGGTAGCAAAGATTTACAGAATGTCAACATCACACTGCGCATCCTCTTCCGGCCTGTCGCCAG
CCAGCTTCCTCGCATCTTCACCAGCATCGGAGAGGACTATGATGAGCGTGTGCTGCCGTCCATCACAACTGAGAT
CCTCAAGTCAGTGGTGGCTCGCTTTGATGCTGGAGAACTAATCACCCAGAGAGAGCTGGTCTCCAGGCAGGTGAG
CGACGACCTTACAGAGCGAGCCGCCACCTTTGGGCTCATCCTGGATGACGTGTCCTTGACACATCTGACCTTCGG
GAAGGAGTTCACAGAAGCGGTGGAAGCCAAACAGGTGGCTCAGCAGGAAGCAGAGAGGGCCAGATTTGTGGTGGA
AAAGGCTGAGCAACAGAAAAAGGCGGCCATCATCTCTGCTGAGGGCGACTCCAAGGCAGCTGAGCTGATTGCCAA
CTCACTGGCCACTGCAGGGGATGGCCTGATCGAGCTGCGCAAGCTGGAAGCTGCAGAGGACATCGCGTACCAGCT
CTCACGCTCTCGGAACATCACCTACCTGCCAGCGGGGCAGTCCGTGCTCCTCCAGCTGCCCCAG**TGA**GGGCCCAC
CCTGCCTGCACCTCCGCGGGCTGACTGGGCCACAGCCCCGATGATTCTTAACACAGCCTTCCTTCTGCTCCCACC
CCAGAAATCACTGTGAAATTTCATGATTGGCTTAAAGTGAAGGAAATAAAGGTAAAATCACTTCAGATCTCTAAT
TAGTCTATCAAATGAAACTCTTTCATTCTTCTCACATCCATCTACTTTTTTATCCACCTCCCTACCAAAAATTGC
CAAGTGCCTATGCAAACCAGCTTTAGGTCCCAATTCGGGGCCTGCTGGAGTTCCGGCCTGGGCACCAGCATTTGG
CAGCACGCAGGCGGGGCAGTATGTGATGGACTGGGGAGCACAGGTGTCTGCCTAGATCCACGTGTGGCCTCCGTC
CTGTCACTGATGGAAGGTTTGCGGATGAGGGCATGTGCGGCTGAACTGAGAAGGCAGGCCTCCGTCTTCCCAGCG
GTTCCTGTGCAGATGCTGCTGAAGAGAGGTGCCGGGGAGGGGCAGAGAGGAAGTGGTCTGTCTGTTACCATAAGT
CTGATTCTCTTTAACTGTGTGACCAGCGGAAACAGGTGTGTGTGAACTGGGCACAGATTGAAGAATCTGCCCCTG
TTGAGGTGGGTGGGCCTGACTGTTGCCCCCCAGGGTCCTAAAACTTGGATGGACTTGTATAGTGAGAGAGGAGGC
CTGGACCGAGATGTGAGTCCTGTTGAAGACTTCCTCTCTACCCCCCACCTTGGTCCCTCTCAGATACCCAGTGGA
ATTCCAACTTGAAGGATTGCATCCTGCTGGGGCTGAACATGCCTGCCAAAGACGTGTCCGACCTACGTTCCTGGC
CCCCTCGTTCAGAGACTGCCCTTCTCACGGGCTCTATGCCTGCACTGGGAAGGAAACAAATGTGTATAAACTGCT
GTCAATAAATGACACCCAGACCTTCC

FIGURE 74

MAAKVFESIGKFGLALAVAGGVVNSALYNVDAGHRAVIFDRFRGVQDIVVGEGTHFLIPWVQKPIIFDCRSRPRN
VPVITGSKDLQNVNITLRILFRPVASQLPRIFTSIGEDYDERVLPSITTEILKSVVARFDAGELITQRELVSRQV
SDDLTERAATFGLILDDVSLTHLTFGKEFTEAVEAKQVAQQEAERARFVVEKAEQQKKAAIISAEGDSKAAELIA
NSLATAGDGLIELRKLEAAEDIAYQLSRSRNITYLPAGQSVLLQLPQ

FIGURE 75

GGCACGAGGGGAGCGCTTGTTTGCTGCCTCGTACTCCTCCATTTATCCGCC**ATG**ATAAGTGCCAGCCGAGCTGCA
GCAGCCCGTCTCGTGGGCGCCGCAGCCTCCCGGGGCCCTACGGCCGCCCGCCACCAGGATAGCTGGAATGGCCTT
AGTCATGAGGCTTTTAGACTTGTTTCAAGGCGGGATTATGCATCAGAAGCAATCAAGGGAGCAGTTGTTGGTATT
GATTTGGGTACTACCAACTCCTGCGTGGCAGTTATGGAAGGTAAACGAGCAAAGGTGCTGGAGAATGCCGAAGGT
GCCAGAACCACCCCTTCAGTTGTGGCCTTTACAGCAGATGGTGAGCGACTTGTTGGAATGCCGGCCAAGCGACAG
GCTGTCACCAACCCAAACAATACATTTTATGCTACCAAGCGTCTCATTGGCCGGCGATATGATGATCCTGAAGTA
CAGAAAGACATTAAAAATGTTCCCTTTAAAATTGTCCGTGCCTCCAATGGTGATGCCTGGGTTGAGGCTCATGGG
AAATTGTATTCTCCGAGTCAGATTGGAGCATTTGTGTTGATGAAGATGAAAGAGACTGCAGAAAATTACTTGGGG
CGCACAGCAAAAAATGCTGTGATCACAGTCCCAGCTTATTTCAATGACTCGCAGAGACAGGCCACTAAAGATGCT
GGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAGCCCACAGCTGCTGCTCTTGCCTATGGTCTAGAC
AAATCAGAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGGAACTTTTGATATTTCTATCCTGGAAATTCAG
AAAGGAGTATTTGAGGTGAAATCCACAAATGGGGATACCTTCTTAGGTGGGGAAGACTTTGACCAGGCCTTGCTA
CGGCACATTGTGAAGGAGTTCAAGAGAGAGACAGGGGTTGATTTGACTAAAGACAACATGGCACTTCAGAGGGTA
CGGGAAGCTGCTGAAAAGGCTAAGTGTGAACTCTCCTCATCTGTGCAGACTGACATCAATTTGCCCTATCTTACA
ATGGATTCTTCTGGACCCAAGCATTTGAATATGAAGTTGACCCGTGCTCAATTTGAAGGGATTGTCACTGATCTA
ATCAGAAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAGTCAGCAAGAGTGACATAGGAGAAGTG
ATTCTTGTGGGTGGCATGACTAGGATGCCCAAGGTTCAGCAGACTGTACAGGATCTTTTTGGCAGAGCCCCAAGT
AAAGCTGTCAATCCTGATGAGGCTGTGGCCATTGGAGCTGCCATTCAGGGAGGTGTGTTGGCCGGCGATGTCACG
GATGTGCTGCTCCTTGATGTCACTCCCCTGTCTCTGGGTATTGAAACTCTAGGAGGTGTCTTTACCAAACTTATT
AATAGGAATACCACTATTCCAACCAAGAAGAGCCAGGTATTCTCTACTGCCGCTGATGGTCAAACGCAAGTGGAA
ATTAAAGTGTGTCAGGGTGAAAGAGAGATGGCTGGAGACAACAAACTCCTTGGACAGTTTACTTTGATTGGAATT
CCACCAGCCCCTCGTGGAGTTCCTCAGATTGAAGTTACATTTGACATTGATGCCAATGGGATAGTACATGTTTCT
GCTAAAGATAAAGGCACAGGACGTGAGCAGCAGATTGTAATCCAGTCTTCTGGTGGATTAAGCAAAGATGATATT
GAAAATATGGTTAAAAATGCAGAGAAATATGCTGAAGAAGACCGGCGAAAGAAGGAACGAGTTGAAGCAGTTAAT
ATGGCTGAAGGAATCATTCACGACACAGAAACCAAGATGGAAGAATTCAAGGACCAATTACCTGCTGATGAGTGC
AACAAGCTGAAAGAAGAGATTTCCAAAATGAGGGAGCTCCTGGCTAGAAAAGACAGCGAAACAGGAGAAAATATT
AGACAGGCAGCATCCTCTCTTCAGCAGGCATCATTGAAGCTGTTCGAAATGGCATACAAAAAGATGGCATCTGAG
CGAGAAGGCTCTGGAAGTTCTGGCACTGGGGAACAAAAGGAAGATCAAAAGGAGGAAAAACAG**TAA**TAATAGCAG
AAATTTTGAAGCCAGAAGGACAACATATGAAGCTTAGGAGTGAAGAGACTTCCTGAGCAGAAATGGGCGAACTTC
AGTCTTTTTACTGTGTTTTTGCAGTATTCTATATATAATTTCCTTAATTTGTAAATTTAGTGACCATTAGCTAGT
GATCATTTAATGGACAGTGATTCTAACAGTATAAAGTTCACAATATTCTATGTCCCTAGCCTGTCATTTTTCAGC
TGCATGTAAAAGGAGGTAGGATGAATTGATCATTATAAAGATTTAACTATTTTATGCTGAAGTGACCATATTTTC
AAGGGGTGAAACCATCTCGCACACAGCAATGAAGGTAGTCATCCATAGACTTGAAATGAGACCACATATGGGGAT
GAGATCCTTCTAGTTAGCCTAGTACTGCTGTACTGGCCTGTATGTACATGGGGTCCTTCAACTGAGGCCTTGCAA
GTCAAGCTGGCTGTGCCATGTTTGTAGATGGGGCAGAGGAATCTAGAACAATGGGAAACTTAGCTATTTATATTA
GGTACAGCTATTAAAACAAGGTAGGAATGAGGCTAGACCTTTAACTTCCCTAAGGCATACTTTTCTAGCTACCTT
CTGCCCTGTGTCTGGCACCTACATCCTTGATGATTGTTCTCTTACCCATTCTGGAATTTTTTTTTTTTTTAAATA
AATACAGAAAGCATCTTGAAAAAAAAAAAAAAAAAA

FIGURE 76

MISASRAAAARLVGAAASRGPTAARHQDSWNGLSHEAFRLVSRRDYASEAIKGAVVGIDLGTTNSCVAVMEGKRA
KVLENAEGARTTPSVVAFTADGERLVGMPAKRQAVTNPNNTFYATKRLIGRRYDDPEVQKDIKNVPFKIVRASNG
DAWVEAHGKLYSPSQIGAFVLMKMKETAENYLGRTAKNAVITVPAYFNDSQRQATKDAGQISGLNVLRVINEPTA
AALAYGLDKSEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGGEDFDQALLRHIVKEFKRETGVDLTK
DNMALQRVREAAEKAKCELSSSVQTDINLPYLTMDSSGPKHLNMKLTRAQFEGIVTDLIRRTIAPCQKAMQDAEV
SKSDIGEVILVGGMTRMPKVQQTVQDLFGRAPSKAVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIETL
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIGIPPAPRGVPQIEVTFDID
ANGIVHVSAKDKGTGREQQIVIQSSGGLSKDDIENMVKNAEKYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFK
DQLPADECNKLKEEISKMRELLARKDSETGENIRQAASSLQQASLKLFEMAYKKMASEREGSGSSGTGEQKEDQK
EEKQ

FIGURE 77

GGCACGAGGGGAGCGCTTGTTTGCTGCCTCGTACTCCTCCATTTATCCGCC**ATG**ATAAGTGCCAGCCGAGCTGCA
GCAGCCCGTCTCGTGGGCGCCGCAGCCTCCCGGGGCCCTACGGCCGCCCGCCACCAGGATAGCTGGAATGGCCTT
AGTCATGAGGCTTTTAGACTTGTTTCAAGGCGGGATTATGCATCAGAAGCAATCAAGGGAGCAGTTGTTGGTATT
GATTTGGGTACTACCAACTCCTGCGTGGCAGTTATGGAAGGTAAACGAGCAAAGGTGCTGGAGAATGCCGAAGGT
GCCAGAACCACCCCTTCAGTTGTGGCCTTTACAGCAGATGGTGAGCGACTTGTTGGAATGCCGGCCAAGCGACAG
GCTGTCACCAACCCAAACAATACATTTTATGCTACCAAGCGTCTCATTGGCCGGCGATATGATGATCCTGAAGTA
CAGAAAGACATTAAAAATGTTCCCTTTAAAATTGTCCGTGCCTCCAATGGTGATGCCTGGGTTGAGGCTCATGGG
AAATTGTATTCTCCGAGTCAGATTGGAGCATTTGTGTTGATGAAGATGAAAGAGACTGCAGAAAATTACTTGGGG
CGCACAGCAAAAAATGCTGTGATCACAGTCCCAGCTTATTTCAATGACTCGCAGAGACAGGCCACTAAAGATGCT
GGCCAGATATCTGGACTGAATGTGCTTCGGGTGATTAATGAGCCCACAGCTGCTGCTCTTGCCTATGGTCTAGAC
AAATCAGAAGACAAAGTCATTGCTGTATATGATTTAGGTGGTGGAACTTTTGATATTTCTATCCTGGAAATTCAG
AAAGGAGTATTTGAGGTGAAATCCACAAATGGGGATACCTTCTTAGGTGGGGAAGACTTTGACCAGGCCTTGCTA
CGGCACATTGTGAAGGAGTTCAAGAGAGAGACAGGGGTTGATTTGACTAAAGACAACATGGCACTTCAGAGGGTA
CGGGAAGCTGCTGAAAAGGCTAAGTGTGAACTCTCCTCATCTGTGCAGACTGACATCAATTTGCCCTATCTTACA
ATGGATTCTTCTGGACCCAAGCATTTGAATATGAAGTTGACCCGTGCTCAATTTGAAGGGATTGTCACTGATCTA
ATCAGAAGGACTATCGCTCCATGCCAAAAAGCTATGCAAGATGCAGAAGTCAGCAAGAGTGACATAGGAGAAGTG
ATTCTTGTGGGTGGCATGACTAGGATGCCCAAGGTTCAGCAGACTGTACAGGATCTTTTTGGCAGAGCCCCAAGT
AAAGCTGTCAATCCTGATGAGGCTGTGGCCATTGGAGCTGCCATTCAGGGAGGTGTGTTGGCCGGCGATGTCACG
GATGTGCTGCTCCTTGATGTCACTCCCCTGTCTCTGGGTATTGAAACTCTAGGAGGTGTCTTTACCAAACTTATT
AATAGGAATACCACTATTCCAACCAAGAAGAGCCAGGTATTCTCTACTGCCGCTGATGGTCAAACGCAAGTGGAA
ATTAAAGTGTGTCAGGGTGAAAGAGAGATGGCTGGAGACAACAAACTCCTTGGACAGTTTACTTTGATTGGAATT
CCACCAGCCCCTCGTGGAGTTCCTCAGATTGAAGTTACATTTGACATTGATGCCAATGGGATAGTACATGTTTCT
GCTAAAGATAAAGGCACAGGACGTGAGCAGCAGATTGTAATCCAGTCTTCTGGTGGATTAAGCAAAGATGATATT
GAAAATATGGTTAAAAATGCAGAGAAATATGCTGAAGAAGACCGGCGAAAGAAGGAACGAGTTGAAGCAGTTAAT
ATGGCTGAAGGAATCATTCACGACACAGAAACCAAGATGGAAGAATTCAAGGACCAATTACCTGCTGATGAGTGC
AACAAGCTGAAAGAAGAGATTTCCAAAATGAGGGAGCTCCTGGCTAGAAAAGACAGCGAAACAGGAGAAAATATT
AGACAGGCAGCATCCTCTCTTCAGCAGGCATCATTGAAGCTGTTCGAAATGGCATACAAAAAGATGGCATCTGAG
CGAGAAGGCTCTGGAAGTTCTGGCACTGGGGAACAAAAGGAAGATCAAAAGGAGGAAAAACAG**TAA**TAATAGCAG
AAATTTTGAAGCCAGAAGGACAACATATGAAGCTTAGGAGTGAAGAGACTTCCTGAGCAGAAATGGGCGAACTTC
AGTCTTTTTACTGTGTTTTTGCAGTATTCTATATATAATTTCCTTAATTTGTAAATTTAGTGACCATTAGCTAGT
GATCATTTAATGGACAGTGATTCTAACAGTATAAAGTTCACAATATTCTATGTCCCTAGCCTGTCATTTTTCAGC
TGCATGTAAAAGGAGGTAGGATGAATTGATCATTATAAAGATTTAACTATTTTATGCTGAAGTGACCATATTTTC
AAGGGGTGAAACCATCTCGCACACAGCAATGAAGGTAGTCATCCATAGACTTGAAATGAGACCACATATGGGGAT
GAGATCCTTCTAGTTAGCCTAGTACTGCTGTACTGGCCTGTATGTACATGGGGTCCTTCAACTGAGGCCTTGCAA
GTCAAGCTGGCTGTGCCATGTTTGTAGATGGGGCAGAGGAATCTAGAACAATGGGAAACTTAGCTATTTATATTA
GGTACAGCTATTAAAACAAGGTAGGAATGAGGCTAGACCTTTAACTTCCCTAAGGCATACTTTTCTAGCTACCTT
CTGCCCTGTGTCTGGCACCTACATCCTTGATGATTGTTCTCTTACCCATTCTGGAATTTTTTTTTTTTTTAAATA
AATACAGAAAGCATCTTGAAAAAAAAAAAAAAAAAA

FIGURE 78

MISASRAAAARLVGAAASRGPTAARHQDSWNGLSHEAFRLVSRRDYASEAIKGAVVGIDLGTTNSCVAVMEGKRA
KVLENAEGARTTPSVVAFTADGERLVGMPAKRQAVTNPNNTFYATKRLIGRRYDDPEVQKDIKNVPFKIVRASNG
DAWVEAHGKLYSPSQIGAFVLMKMKETAENYLGRTAKNAVITVPAYFNDSQRQATKDAGQISGLNVLRVINEPTA
AALAYGLDKSEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGGEDFDQALLRHIVKEFKRETGVDLTK
DNMALQRVREAAEKAKCELSSSVQTDINLPYLTMDSSGPKHLNMKLTRAQFEGIVTDLIRRTIAPCQKAMQDAEV
SKSDIGEVILVGGMTRMPKVQQTVQDLFGRAPSKAVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIETL
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIGIPPAPRGVPQIEVTFDID
ANGIVHVSAKDKGTGREQQIVIQSSGGLSKDDIENMVKNAEKYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFK
DQLPADECNKLKEEISKMRELLARKDSETGENIRQAASSLQQASLKLFEMAYKKMASEREGSGSSGTGEQKEDQK
EEKQ

FIGURE 79

GTGGTGGGACTCGCGTCGCGGCCGCGGAGACGTGAAGCTCTCGAGGCTCCTCCCGCTGCGGGTCGGCGCTCGCCC
TCGCTCTCCTCGCCCTCCGCCCCGGCCCCGGCCCCGCGCCCGCC**ATG**GAGAAGACTGAGCTGATCCAGAAGGCCA
AGCTGGCCGAGCAGGCCGAGCGCTACGACGACATGGCCACCTGCATGAAGGCAGTGACCGAGCAGGGCGCCGAGC
TGTCCAACGAGGAGCGCAACCTGCTCTCCGTGGCCTACAAGAACGTGGTCGGGGGCCGCAGGTCCGCCTGGAGGG
TCATCTCTAGCATCGAGCAGAAGACCGACACCTCCGACAAGAAGTTGCAGCTGATTAAGGACTATCGGGAGAAAG
TGGAGTCCGAGCTGAGATCCATCTGCACCACGGTGCTGGAATTGTTGGATAAATATTTAATAGCCAATGCAACTA
ATCCAGAGAGTAAGGTCTTCTATCTGAAAATGAAGGGTGATTACTTCCGGTACCTTGCTGAAGTTGCGTGTGGTG
ATGATCGAAAACAAACGATAGATAATTCCCAAGGAGCTTACCAAGAGGCATTTGATATAAGCAAGAAAGAGATGC
AACCCACACACCCAATCCGCCTGGGGCTTGCTCTTAACTTTTCTGTATTTTACTATGAGATTCTTAATAACCCAG
AGCTTGCCTGCACGCTGGCTAAAACGGCTTTTGATGAGGCCATTGCTGAACTTGATACACTGAATGAAGACTCAT
ACAAAGACAGCACCCTCATCATGCAGTTGCTTAGAGACAACCTAACACTTTGGACATCAGACAGTGCAGGAGAAG
AATGTGATGCGGCAGAAGGGGCTGAAAAC**TAA**ATCCATACAGGGTGTCATCCTTCTTTCCTTCAAGAAACCTTTT
TACACATCTCCATTCCTTATTCCACTTGGATTTCCTATAGCAAAGAAACCCATTCATGTGTATGGAATCAACTGT
TTATAGTCTTTTCACACTGCAGCTTTGGGAAAACTTCATTCCTTGATTTGTGTTTGTCTTGGCCTTCCTGGTGTG
CAGTACTGCTGTAGAAAAGTATTAATAGCTTCATTTCATATAAACATAAGTAACTCCCAAACACTTATGTAGAGG
ACTAAAAATGTATCTGGTATTTAAGTAATCTGAACCAGTTCTGCAAGTGACTGTGTTTTGTATTACTGTGAAAAT
AAGAAAATGTAGTTAATTACAATTTAAAGAGTATTCCACATAACTTCTTAATTTCTACATTCCCTCCCTTACTCT
TCGGGGGTTTCCTTTCAGTAAGCAACTTTTCCATGCTCTTAATGTATTCCTTTTTAGTAGGAATCCGGAAGTATT
AGATTGAATGGAAAAGCACTTGCCATCTCTGTCTAGGGGTCACAAATTGAAATGGCTCCTGTATCACATACGGAG
GTCTTGTGTATCTGTGGCAACAGGGAGTTTCCTTATTCACTCTTTATTTGCTGCTGTTTAAGTTGCCAACCTCCC
CTCCCAATAAAAATTCACTTACACCTCCTGCCTTTGTAGTTCTGGTATTCACTTTACTATGTGATAGAAGTAGCA
TGTTGCTGCCAGAATACAAGCATTGCTTTTGGCAAATTAAAGTGCATGTCATTTCTTAATACACTAGAAAGGGGA
AATAAATTAAAGTACACAAGTCCAAGTCTAAAACTTTAGTACTTTTCCATGCAGATTTGTGCACATGTGAGAGGG
TGTCCAGTTTGTCTAGTGATTGTTATTTAGAGAGTTGGACCACTATTGTGTGTTGCTAATCATTGACTGTAGTCC
CAAAAAAGCCTTGTGAAAATGTTATGCCCTATGTAACAGCAGAGTAACATAAAATAAAAGTACATTTTATAAACC
ATTTACTATGGCTTTGTAACAATTGCATACCCATATTTTAAGGGACAGGTGAATTTACTACTTTCTAAAGTTTAT
TGATACTTCCCTTTTATGTAAAATGTAGTAGTGATACCTATATTTCCACATTGTGCATTGTGACACACTTGTCTA
GGGATGCCTGGAAGTGTATAAAATTGGACTGCATTTCTTAGAGTGTTTTACTATAGATCAGTCTCATGGGCCATC
TCTTCCTCAGATGTAAATGATATCTGGTTAAGTGTTATATGGAATAAAGTGGACATTTTAAAACTA

FIGURE 80

MEKTELIQKAKLAEQAERYDDMATCMKAVTEQGAELSNEERNLLSVAYKNVVGGRRSAWRVISSIEQKTDTSDKK
LQLIKDYREKVESELRSICTTVLELLDKYLIANATNPESKVFYLKMKGDYFRYLAEVACGDDRKQTIDNSQGAYQ
EAFDISKKEMQPTHPIRLGLALNFSVFYYEILNNPELACTLAKTAFDEAIAELDTLNEDSYKDSTLIMQLLRDNL
TLWTSDSAGEECDAAEGAEN

FIGURE 81

AGCGCACGTCGGCAGTCGGCTCCCTCGTTGACCGAATCACCGACCTCTCTCCCCAGCTGTATTTCCAAA**ATG**TCG
CTTTCTAACAAGCTGACGCTGGACAAGCTGGACGTTAAAGGGAAGCGGGTCGTTATGAGAGTCGACTTCAATGTT
CCTATGAAGAACAACCAGATAACAAACAACCAGAGGATTAAGGCTGCTGTCCCAAGCATCAAATTCTGCTTGGAC
AATGGAGCCAAGTCGGTAGTCCTTATGAGCCACCTAGGCCGGCCTGATGGTGTGCCCATGCCTGACAAGTACTCC
TTAGAGCCAGTTGCTGTAGAACTCAAATCTCTGCTGGGCAAGGATGTTCTGTTCTTGAAGGACTGTGTAGGCCCA
GAAGTGGAGAAAGCCTGTGCCAACCCAGCTGCTGGGTCTGTCATCCTGCTGGAGAACCTCCGCTTTCATGTGGAG
GAAGAAGGGAAGGGAAAAGATGCTTCTGGGAACAAGGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCCGAGCT
TCACTTTCCAAGCTAGGGGATGTCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCCACAGCTCCATGGTA
GGAGTCAATCTGCCACAGAAGGCTGGTGGGTTTTTGATGAAGAAGGAGCTGAACTACTTTGCAAAGGCCTTGGAG
AGCCCAGAGCGACCCTTCCTGGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATG
CTGGACAAAGTCAATGAGATGATTATTGGTGGTGGAATGGCTTTTACCTTCCTTAAGGTGCTCAACAACATGGAG
ATTGGCACTTCTCTGTTTGATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGAATGGT
GTGAAGATTACCTTGCCTGTTGACTTTGTCACTGCTGACAAGTTTGATGAGAATGCCAAGACTGGCCAAGCCACT
GTGGCTTCTGGCATACCTGCTGGCTGGATGGGCTTGGACTGTGGTCCTGAAAGCAGCAAGAAGTATGCTGAGGCT
GTCACTCGGGCTAAGCAGATTGTGTGGAATGGTCCTGTGGGGGTATTTGAATGGGAAGCTTTTGCCCGGGGAACC
AAAGCTCTCATGGATGAGGTGGTGAAAGCCACTTCTAGGGGCTGCATCACCATCATAGGTGGTGGAGACACTGCC
ACTTGCTGTGCCAAATGGAACACGGAGGATAAAGTCAGCCATGTGAGCACTGGGGGTGGTGCCAGTTTGGAGCTC
CTGGAAGGTAAAGTCCTTCCTGGGGTGGATGCTCTCAGCAATATT**TAG**TACTTTCCTGCCTTTTAGTTCCTGTGC
ACAGCCCCTAAGTCAACTTAGCATTTTCTGCATCTCCACTTGGCATTAGCTAAAACCTTCCATGTCAAGATTCAG
CTAGTGGCCAAGAGATGCAGTGCCAGGAACCCTTAAACAGTTGCACAGCATCTCAGCTCATCTTCACTGCACCCT
GGATTTGCATACATTCTTCAAGATCCCATTTGAATTTTTTAGTGACTAAACCATTGTGCATTCTAGAGTGCATAT
ATTTATATTTTGCCTGTTAAAAAGAAAGTGAGCAGTGTTAGCTTAGTTCTCTTTTGATGTAGGTTATTATGATTA
GCTTTGTCACTGTTTCACTACTCAGCATGGAAACAAGATGAAATTCCATTTGTAGGTAGTGAGACAAAATTGATG
ATCCATTAAGTAAACAATAAAAGTGTCCATTGAAACCGTGATTTTTTTTTTTTTCCTGTCATACTTTGTTAGGAA
GGGTGAGAATAGAATCTTGAGGAACGGATCAGATGTCTATATTGCTGAATGCAAGAAGTGGGGCAGCAGCAGTGG
AGAGATGGGACAATTAGATAAATGTCCATTCTTTATCAAGGGCCTACTTTATGGCAGACATTGTGCTAGTGCTTT
TATTCTAACTTTTATTTTTATCAGTTACACATGATCATAATTTAAAAAGTCAAGGCTTATAACAAAAAAGCCCCA
GCCCATTCCTCCCATTCAAGATTCCCACTCCCCAGAGGTGACCACTTTCAACTCTTGAGTTTTTCAGGTATATAC
CTCCATGTTTCTAAGTAATATGCTTATATTGTTCACTTCCTTTTTTTTTATTTTTTAAAGAAATCTATTTCATAC
CATGGAGGAAGGCTCTGTTCCACATATATTTCCACTTCTTCATTCTCTCGGTATAGTTTTGTCACAATTATAGAT
TAGATCAAAAGTCTACATAACTAATACAGCTGAGCTATGTAGTATGCTATGATTAAATTTACTTATGTAAAAAAA
AAAAAAAAAAAAA

FIGURE 82

MSLSNKLTLDKLDVKGKRVVMRVDFNVPMKNNQITNNQRIKAAVPSIKFCLDNGAKSVVLMSHLGRPDGVPMPDK
YSLEPVAVELKSLLGKDVLFLKDCVGPEVEKACANPAAGSVILLENLRFHVEEEGKGKDASGNKVKAEPAKIEAF
RASLSKLGDVYVNDAFGTAHRAHSSMVGVNLPQKAGGFLMKKELNYFAKALESPERPFLAILGGAKVADKIQLIN
NMLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEEGAKIVKDLMSKAEKNGVKITLPVDFVTADKFDENAKTGQ
ATVASGIPAGWMGLDCGPESSKKYAEAVTRAKQIVWNGPVGVFEWEAFARGTKALMDEVVKATSRGCITIIGGGD
TATCCAKWNTEDKVSHVSTGGGASLELLEGKVLPGVDALSNI

FIGURE 83

CGCCCCTGCTCTCGCGCCGGCGTCGGCTGCGTCTCCGGCGTTTGAATTGCGCTTCCGCCATCTTTCCAGCCTCAG
TCGGACGGGCGCGGAGGCGCTTCTGGAAGGAACGCCGCG**ATG**GCTGCGCAGGGAGAGCCCCAGGTCCAGTTCAAA
CTTGTATTGGTTGGTGATGGTGGTACTGGAAAAACGACCTTCGTGAAACGTCATTTGACTGGTGAATTTGAGAAG
AAGTATGTAGCCACCTTGGGTGTTGAGGTTCATCCCCTAGTGTTCCACACCAACAGAGGACCTATTAAGTTCAAT
GTATGGGACACAGCCGGCCAGGAGAAATTCGGTGGACTGAGAGATGGCTATTATATCCAAGCCCAGTGTGCCATC
ATAATGTTTGATGTAACATCGAGAGTTACTTACAAGAATGTGCCTAACTGGCATAGAGATCTGGTACGAGTGTGT
GAAAACATCCCCATTGTGTTGTGTGGCAACAAAGTGGATATTAAGGACAGGAAAGTGAAGGCGAAATCCATTGTC
TTCCACCGAAAGAAGAATCTTCAGTACTACGACATTTCTGCCAAAAGTAACTACAACTTTGAAAAGCCCTTCCTC
TGGCTTGCTAGGAAGCTCATTGGAGACCCTAACTTGGAATTTGTTGCCATGCCTGCTCTCGCCCCACCAGAAGTT
GTCATGGACCCAGCTTTGGCAGCACAGTATGAGCACGACTTAGAGGTTGCTCAGACAACTGCTCTCCCGGATGAG
GATGATGACCTG**TGA**GAATGAAGCTGGAGCCCAGCGTCAGAAGTCTAGTTTTATAGGCAGCTGTCCTGTGATGTC
AGCGGTGCAGCGTGTGTGCCACCTCATTATTATCTAGCTAAGCGGAACATGTGCTTTATCTGTGGGATGCTGAAG
GAGATGAGTGGGCTTCGGAGTGAATGTGGCAGTTTAAAAAATAACTTCATTGTTTGGACCTGCATATTTAGCTGT
TTGGACGCAGTTGATTCCTTGAGTTTCATATATAAGACTGCTGCAGTCACATCACAATATTCAGTGGTGAAATCT
TGTTTGTTACTGTCATTCCCATTCCTTTTCTTTAGAATCAGAATAAAGTTGTATTTCAAATATCTAAGCAAGTGA
ACTCATCCCTTGTTTATAAATAGCATTTGGAAACCACTAAAGTAGGGAAGTTTTATGCCATGTTAATATTTGAAT
TGCCTTGCTTTTATCACTTAATTTGAAATCTATTGGGTTAATTTCTCCCTATGTTTATTTTTGTACATTTGAGCC
ATGTCACACAAACTGATGATGACAGGTCAGCAGTATTCTATTTGGTTAGAAGGGTTACATGGTGTAAATATTAGT
GCAGTTAAGCTAAAGCAGTGTTTGCTCCACCTTCATATTGGCTAGGTAGGGTCACCTAGGGAAGCACTTGCTCAA
AATCTGTGACCTGTCAGAATAAAAATGTGGTTTGTACATATCAAATAGATATTTTAAGGGTAATATTTTCTTTTA
TGGCAAAAGTAATCATGTTTTAATGTAGAACCTCAAACAGGATGGAACATCAGTGGATGGCAGGAGGTTGGGAAT
TCTTGCTGTTAAAAATAATTACAAATTTTGCACTTTTTGTTTGAATGTTAGATGCTTAGTGTGAAGTTGATACGC
AAGCCG

FIGURE 84

MAAQGEPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGL
RDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDIS
AKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTTALPDEDDDL

FIGURE 85

CGCTAGCCTGCGGAGCCCGTCCGTGCTGTTCTGCGGCAAGGCCTTTCCCAGTGTCCCCACGCGGAAGGCAACTGC
CTGAAAGGCGCGGCGTCGCACCGCCCAGAGCTGAGGAAGCCGGCGCCAGTTCGCGGGGCTCCGGGCCGCCACTCA
GAGCT**ATG**AGCTACGGCCGCCCCCCTCCCGATGTGGAGGGTATGACCTCCCTCAAGGTGGACAACCTGACCTACC
GCACCTCGCCCGACACGCTGAGGCGCGTCTTCGAGAAGTACAGGCGCGTCGGCGACGTGTACATCCCGCGGGATC
GCTACACCAAGGAGTCCCGCGGCTTCGCCTTCGTTCGCTTTCACGACAAGCGCGACGCTGAGGACGCTATGGATG
CCATGGACGGGGCCGTGCTGGACGGCCGCGAGCTGCGGGTGCAAATGGCGCGCTACGGCCGCCCCCCGGACTCAC
ACCACAGCCGCCGGGGACCGCCACCCCGCAGGTACGGGGGCGGTGGCTACGGACGCCGGAGCCGCAGCCCTAGGC
GGCGTCGCCGCAGCCGATCCCGGAGTCGGAGCCGTTCCAGGTCTCGCAGCCGATCTCGCTACAGCCGCTCGAAGT
CTCGGTCCCGCACTCGTTCTCGATCTCGGTCGACCTCCAAGTCCAGATCCGCACGAAGGTCCAAGTCCAAGTCCT
CGTCGGTCTCCAGATCTCGTTCGCGGTCCAGGTCCCGGTCTCGGTCCAGGAGTCCTCCCCCAGTGTCCAAGAGGG
AATCCAAATCCAGGTCGCGATCGAAGAGTCCCCCCAAGTCTCCTGAAGAGGAAGGAGCGGTGTCCTCT**TAA**GAAA
ATGATGTATCGGCAAGCAGTGTAAACGGAGGACTTGGGGAAAAAGGACCACATAGTCCATCGAAGAAGAGTCCTT
GGAACAAGCAACTGGCTATTGAAAAGGTTATTTTGTAACATTTGTCTAACTTTTTACTTGTTTAAGCTTTGCCTC
AGTTGGCAAACTTCATTTTATGTGCCATTTTGTTGCTGTTATTCAAATTTCTTGTAATTTAGTGAGGTGAACGAC
TTCAGATTTCATTATTGGATTTGGATATTTGAGGTAAAATTTCATTTTGTTATATAGTGCTGACTTTTTTTTTTT
GAAATTAAACAGATTGGTAACCTAATTTGTGGCCTCCTGACTTTTAAGGAAAACGTGTGCAGCCATTACACACAG
CCTAAAGCTGTCAAGAGATTGACTCGGCATTCGTTCATTCCTTAAAATTAAAAACCTACAAAAGTTGGTGTAAAT
TTGTATATGTTATTTACCTTCAGATCTAAATGGTAATCTGAACCCAAATTTGTATAAAGACTTTTCAGGTGAAAA
GACTTGATTTTTTGAAAGGATTGTTTATCAAACACAATTCTAATCTCTTCTCTTATGTATTTTTGTGCACTAGGC
GCAGTTGTGTAGCAGTTGAGTAATGCTGGTTAGCTGTTAAGGTGGCGTGTTGCAGTGCAGAGTGCTTGGCTGTTT
CCTGTTTTCTCCCGATTGCTCCTGTGTAAAGATGCCTTGTCGTGCAGAAACAAATGGCTGTCCAGTTTATTAAAA
TGCCTGACAACTGCACTTCCAGACACCCGGGCCTTGCATATAAATAACGGAGCATACAGTGAGCACATCTAGCTG
ATGATAAATACACCTTTTTTTCCCTCTTCCCCCTAAAAATGGTAAATCTGATCATATCTACATGTATGAACTTAA
CATGGAAAATGTTAAGGAAGCAAATGGTTGTAACTTTGTAAGTACTTATAACATGGTGTATCTTTTTGCTTATGA
ATATCTGTATTATAACCATTGTTTCTGTAGTTTAATTAAAACATTTTCTTGGTGTTAGCTTTAAAAAAAAAAAAA
AAAA

FIGURE 86

MSYGRPPPDVEGMTSLKVDNLTYRTSPDTLRRVFEKYRRVGDVYIPRDRYTKESRGFAFVRFHDKRDAEDAMDAM
DGAVLDGRELRVQMARYGRPPDSHHSRRGPPPRRYGGGGYGRRSRSPRRRRRSRSRSRSRSRSRSRSRYSRSKSR
SRTRSRSRSTSKSRSARRSKSKSSSVSRSRSRSRSRSRSRSPPPVSKRESKSRSRSKSPPKSPEEEGAVSS

FIGURE 87

GAGAGGAGACACCGCCGCAGTTGCCGGTACATCGGGGATTTCTGGCTCTTTCCTCTTCGCCTTAAATTCGGGTGT
CTTTT**ATG**AATAATCAAAAGCAGCAAAAGCCAACGCTATCAGGCCAGCGTTTTAAAACTAGAAAAAGAGATGAAA
AAGAGAGGTTTGACCCTACTCAGTTTCAAGACTGTATTATTCAAGGCTTAACTGAAACCGGTACTGATTTGGAAG
CAGTAGCTAAGTTTCTTGATGCTTCTGGAGCAAAACTTGATTACCGTCGATATGCAGAAACACTCTTTGACATTC
TGGTGGCTGGTGGAATGCTGGCCCCAGGTGGTACACTGGCAGATGACATGATGCGTACAGATGTCTGCGTGTTTG
CAGCCCAAGAAGATCTAGAGACCATGCAAGCATTTGCTCAGGTTTTTAACAAGTTAATCAGGCGCTACAAATACC
TGGAGAAAGGTTTTGAAGATGAAGTAAAAAAGCTGCTGCTGTTCTTGAAGGGTTTTTCAGAGTCGGAGAGGAACA
AGCTAGCTATGTTGACTGGTGTTCTTCTGGCTAATGGAACACTTAATGCATCCATTCTTAATAGCCTTTATAATG
AAAATTTGGTTAAAGAAGGAGTTTCAGCAGCTTTTGCTGTGAAGCTCTTTAAATCATGGATAAATGAAAAAGATA
TCAATGCAGTAGCTGCAAGTCTTCGGAAAGTCAGCATGGATAACAGACTGATGGAACTCTTTCCTGCCAATAAGC
AAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAAGAGCTTTCAGAATATGTTCGGAATCAGC
AAACCATCGGAGCTCGTAAGGAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATA
TAATTTTATATGTCAAGGAGGAGATGAAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAA
GTGTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAAT
ACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTCAGGAGTATT
GCTATGACAACATTCATTTCATGAAAGCCTTCCAGAAAATAGTGGTGCTTTTTTATAAAGCTGAAGTCCTGAGCG
AGGAGCCCATTTTGAAGTGGTATAAAGATGCACATGTTGCAAAGGGGAAGAGTGTTTTCCTTGAGCAAATGAAAA
AGTTTGTAGAATGGCTCAAAAATGCTGAAGAAGAATCTGAATCTGAAGCTGAAGAAGGTGAC**TGA**ATTTTGAAAC
TACACCCTCAGTAAAGCAAACAGGAGTTGTAGATAAAATGTCATGTCTCATGTGTCCTGGTTCTTACATCTTCCT
ACCTCCCTGTATCAAGCATGATATAAGGGCTTTCATGGCAAATTTTATTTTAACTGTTTCTATGGTTGCTGGAAA
TGTTGGGTTTAGTTTCTAAAACCATGTTTTAAGTAGCTACAGGAGCTATAGATTTGAATCTAATGTTGCATTAGT
CTTTTCAGTTATCTTCTACCTCCTGTATTTTCTACTGTAATAATGTAATTTAAGGCCTTCCACAATGAACAGTTC
ACTTTATTCCCTGGGTTTTCTATAAACAGTTTTAAGGATATGATTTGGTTAAAAAATAATTTGTTATAAAAATTC
TGTTTGCAAATTAAACTGGAAAAGTATCCAGAGTCTCAAAAGGCAATGATTTGTGAGATAATATGGCATGCCCGG
AGCCCTGCTCATCAATGAAAAACCCATATGTAATAATCGAATTCATTTAACATGAATCTTGAGTACGTGGACCAT
TGCTTGCATGTTAACTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGCATTTTTAACTCCAGATATCCTAAAGCTC
AATTGTTTGGTCTCTGGTTTTCATCCTTAGAGAAGCCATGGAGAACAGACTTGAAAAGTTTAGGAAATCATAATG
TGGCAGAGGTGGTGGGAAGAAGAAAGTTGAGCTTTTTCCCCTTGAGAAACTTCTGCATTTAGTTTCTATCTTTCC
AGGCAAAACAAATGGGTATTCTTTTCATACAACCATTTTCAAATGAACCTTAGAAAAGTCTTAACATTTAAGGTA
TTTTATGCACAGAATACACTTAGATTGATAGGAAAGAACTCGTAATGGAGTTTGAGTAAAGAAAATGACTGATGT
ACTAAACCCAGTAAAAATTGTTGAAAATGTTAAAGGTCAGCATGTTCTAATTGGGAATCTAGATATAGCTTAGAT
TTCCTATTGGCTTAGAGTATTTGCTATAACAAATGAAGTGCAATGACAATTATATATTCCTACTCGGTCATACTG
GACTGGCTTCGTTCTCTTAATATACTCAGTAATGACTCAAGCCTCTGGCTATTAACATACCCTAGTTGCCGTTTT
TTAATTGCCATGAGCCAAATACTTCTTGGTATACAATTGATCCATTTATTTTAATGGCTGCCTTTTCATTTTCAT
CTTTTCTTGCTGCTACCCATCTATGTATGTAGTCATTGGGGGGAAAATGTAGCCACATTTTTTATGGGAAGACTT
TGTGTTAAAAGTGAACATTTTGAAGGTTTTTAACTGGTGAAACTAGCCTGGAATAATGCCACCAGAGACTGAGTG
GAAATCGCCCCTTTTGAAGGTGCCATTCTTATGAGCCAAAAGTTTGTCATTTAAAAGTTCATTTTGAGGGAATAA
CATGTAATATAATTTGAAATAAAGGTATAGTAACCTTAAAAAGAACATTATAACTGATTGTTGTGAATGGGGTGA
ATTTGTTAAAATGAGTAACTTTGATAAAGTTTTTCATGCACAGGCAAAATGTATTCACTAGATTTCTACGTAGTG
ATCTGCTTTTACTTTGTAATTTGTAGTTCTCAAAAGACTTTTTTTTAAAAAAATAAAGTCCATACTTACACTT

FIGURE 88

MNNQKQQKPTLSGQRFKTRKRDEKERFDPTQFQDCIIQGLTETGTDLEAVAKFLDASGAKLDYRRYAETLFDILV
AGGMLAPGGTLADDMMRTDVCVFAAQEDLETMQAFAQVFNKLIRRYKYLEKGFEDEVKKLLLFLKGFSESERNKL
AMLTGVLLANGTLNASILNSLYNENLVKEGVSAAFAVKLFKSWINEKDINAVAASLRKVSMDNRLMELFPANKQS
VEHFTKYFTEAGLKELSEYVRNQQTIGARKELQKELQEQMSRGDPFKDIILYVKEEMKKNNIPEPVVIGIVWSSV
MSTVEWNKKEELVAEQAIKHLKQYSPLLAAFTTQGQSELTLLLKIQEYCYDNIHFMKAFQKIVVLFYKAEVLSEE
PILKWYKDAHVAKGKSVFLEQMKKFVEWLKNAEEESESEAEEGD

FIGURE 89

GTCAGTCCCTCCTGTAGCCGCCGCCGCCGCCGCCCGCCGCCCCTCTGCCAGCAGCTCCGGCGCCACCTCGGGCCG
GCGTCTCCGGCGGGCGGGAGCCAGGCGCTGACGGGCGCGGCGGGGGCGGCCGAGCGCTCCTGCGGCTGCGACTCA
GGCTCCGGCGTCTGCGCTTCCCCATGGGGCTGGCCTGCGGCGCCTGGGCGCTCTGAGATTGTCACTGCTGTTCCA
AGGGCACACGCAGAGGGATTTGGAATTCCTGGAGAGTTGCCTTTGTGAGAAGCTGGAAATATTTCTTTCAATTCC
ATCTCTTAGTTTTCCATAGGAACATCAAGAAATC**ATG**AACAACTTTGGTAATGAAGAGTTTGACTGCCACTTCCT
CGATGAAGGTTTTACTGCCAAGGACATTCTGGACCAGAAAATTAATGAAGTTTCTTCTTCTGATGATAAGGATGC
CTTCTATGTGGCAGACCTGGGAGACATTCTAAAGAAACATCTGAGGTGGTTAAAAGCTCTCCCTCGTGTCACCCC
CTTTTATGCAGTCAAATGTAATGATAGCAAAGCCATCGTGAAGACCCTTGCTGCTACCGGGACAGGATTTGACTG
TGCTAGCAAGACTGAAATACAGTTGGTGCAGAGTCTGGGGGTGCCTCCAGAGAGGATTATCTATGCAAATCCTTG
TAAACAAGTATCTCAAATTAAGTATGCTGCTAATAATGGAGTCCAGATGATGACTTTTGATAGTGAAGTTGAGTT
GATGAAAGTTGCCAGAGCACATCCCAAAGCAAAGTTGGTTTTGCGGATTGCCACTGATGATTCCAAAGCAGTCTG
TCGTCTCAGTGTGAAATTCGGTGCCACGCTCAGAACCAGCAGGCTCCTTTTGGAACGGGCGAAAGAGCTAAATAT
CGATGTTGTTGGTGTCAGCTTCCATGTAGGAAGCGGCTGTACCGATCCTGAGACCTTCGTGCAGGCAATCTCTGA
TGCCCGCTGTGTTTTTGACATGGGGGCTGAGGTTGGTTTCAGCATGTATCTGCTTGATATTGGCGGTGGCTTTCC
TGGATCTGAGGATGTGAAACTTAAATTTGAAGAGATCACCGGCGTAATCAACCCAGCGTTGGACAAATACTTTCC
GTCAGACTCTGGAGTGAGAATCATAGCTGAGCCCGGCAGATACTATGTTGCATCAGCTTTCACGCTTGCAGTTAA
TATCATTGCCAAGAAAATTGTATTAAAGGAACAGACGGGCTCTGATGACGAAGATGAGTCGAGTGAGCAGACCTT
TATGTATTATGTGAATGATGGCGTCTATGGATCATTTAATTGCATACTCTATGACCACGCACATGTAAAGCCCCT
TCTGCAAAAGAGACCTAAACCAGATGAGAAGTATTATTCATCCAGCATATGGGGACCAACATGTGATGGCCTCGA
TCGGATTGTTGAGCGCTGTGACCTGCCTGAAATGCATGTGGGTGATTGGATGCTCTTTGAAAACATGGGCGCTTA
CACTGTTGCTGCTGCCTCTACGTTCAATGGCTTCCAGAGGCCGACGATCTACTATGTGATGTCAGGGCCTGCGTG
GCAACTCATGCAGCAATTCCAGAACCCCGACTTCCCACCCGAAGTAGAGGAACAGGATGCCAGCACCCTGCCTGT
GTCTTGTGCCTGGGAGAGTGGGATGAAACGCCACAGAGCAGCCTGTGCTTCGGCTAGTATTAATGTG**TAG**ATAGC
ACTCTGGTAGCTGTTAACTGCAAGTTTAGCTTGAATTAAGGGATTTGGGGGGACCATGTAACTTAATTACTGCTA
GTTTTGAAATGTCTTTGTAAGAGTAGGGTCGCCATGATGCAGCCATATGGAAGACTAGGATATGGGTCACACTTA
TCTGTGTTCCTATGGAAACTATTTGAATATTTGTTTTATATGGATTTTTATTCACTCTTCAGACACGCTACTCAA
GAGTGCCCCTCAGCTGCTGAACAAGCATTTGTAGCTTGTACAATGGCAGAATGGGCCAAAAGCTTAGTGTTGTGA
CCTGTTTTTAAAATAAAGTATCTTGAAATAATTAGGC

FIGURE 90

MNNFGNEEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVADLGDILKKHLRWLKALPRVTPFYAVKCNDSKA
IVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAK
LVLRIATDDSKAVCRLSVKFGATLRTSRLLLERAKELNIDVVGVSFHVGSGCTDPETFVQAISDARCVFDMGAEV
GFSMYLLDIGGGFPGSEDVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASAFTLAVNIIAKKIVLKEQ
TGSDDEDESSEQTFMYYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDEKYYSSSIWGPTCDGLDRIVERCDLPEM
HVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPPEVEEQDASTLPVSCAWESGMKRH
RAACASASINV

FIGURE 91

CACGCTTGCCGCCGCCCCGCAGAA**ATG**CTTCGGTTACCCACAGTCTTTCGCCAGATGAGACCGGTGTCCAGGGTA
CTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAAATTTGGTGCAGATGCCCGAGCCTTAATGCTTCAA
GGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGGAAGAACAGTGATTATTGAGCAGGGT
TGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATTGACTTAAAAGATAAATACAAGAAC
ATTGGAGCTAAACTTGTTCAAGATGTTGCCAATAACACAAATGAAGAAGCTGGGGATGGCACTACCACTGCTACT
GTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGTGCTAATCCAGTGGAAATCAGGAGA
GGTGTGATGTTAGCTGTTGATGCTGTAATTGCTGAACTTAAAAAGCAGTCTAAACCTGTGACCACCCCTGAAGAA
ATTGCACAGGTTGCTACGATTTCTGCAAACGGAGACAAAGAAATTGGCAATATCATCTCTGATGCAATGAAAAAA
GTTGGAAGAAAGGGTGTCATCACAGTAAAGGATGGAAAAACACTGAATGATGAATTAGAAATTATTGAAGGCATG
AAGTTTGATCGAGGCTATATTTCTCCATACTTTATTAATACATCAAAAGGTCAGAAATGTGAATTCCAGGATGCC
TATGTTCTGTTGAGTGAAAAGAAAATTTCTAGTATCCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGCTCAC
CGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACTCGTCTTGAATAGGCTAAAG
GTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGGTGACAATAGAAAGAACCAGCTTAAAGATATGGCT
ATTGCTACTGGTGGTGCAGTGTTTGGAGAAGAGGGATTGACCCTGAATCTTGAAGACGTTCAGCCTCATGACTTA
GGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTTAAAAGGAAAAGGTGACAAGGCTCAAATT
GAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAGTGAATATGAAAAGGAAAAACTGAATGAA
CGGCTTGCAAAACTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGGGACAAGTGATGTTGAAGTGAATGAAAAG
AAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGAAGAAGGCATTGTTTTGGGAGGGGGTTGT
GCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAATGAAGATCAAAAAATTGGTATAGAAATT
ATTAAAAGAACACTCAAAATTCCAGCAATGACCATTGCTAAGAATGCAGGTGTTGAAGGATCTTTGATAGTTGAG
AAAATTATGCAAAGTTCCTCAGAAGTTGGTTATGATGCTATGGCTGGAGATTTTGTGAATATGGTGGAAAAAGGA
ATCATTGACCCAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGCTGGTGTGGCCTCTCTGTTAACTACAGCA
GAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCCTGGAATGGGTGCAATGGGTGGAATGGGAGGTGGT
ATGGGAGGTGGCATGTTC**TAA**CTCCTAGACTAGTGCTTTACCTTTATTAATGAACTGTGACAGGAAGCCCAAGGC
AGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAA
CCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCATTGTCCATGCCTACAGATAATTT
ATTTTGTATTTTTGAATAAAAAACATTTGTACATTCCTGATACTGGGTACAAGAGCCATGTACCAGTGTACTGCT
TTCAACTTAAATCACTGAGGCATTTTTACTACTATTCTGTTAAAATCAGGATTTTAGTGCTTGCCACCACCAGAT
GAGAAGTTAAGCAGCCTTTCTGTGGAGAGTGAGAATAATTGTGTACAAAGTAGAGAAGTATCCAATTATGTGACA
ACCTTTGTGTAATAAAAATTTGTTTAA

FIGURE 92

MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQGWGSPKVTK
DGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEIRRGVMLAVDA
VIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDELEIIEGMKFDRGYIS
PYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDGEALSTLVLNRLKVGLQVVAV
KAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIVTKDDAMLLKGKGDKAQIEKRIQEII
EQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLRCIPA
LDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLIVEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVV
RTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGGMGGGMF

FIGURE 93

GTTCCAAGGTTTGCGGCCCGGTCTCGGAGAAGAGGGGAGAGTGGAGGGCCGCTGAATAAGCTTCCAAA**ATG**ATGC
CCACACCAGTTATCCTATTGAAAGAGGGGACTGATAGCTCCCAAGGCATCCCCCAGCTTGTGAGTAACATCAGTG
CCTGCCAGGTGATTGCTGAGGCTGTAAGAACTACCCTGGGTCCCCGTGGCATGGACAAGCTTATTGTAGATGGCA
GAGGCAAAGCAACAATTTCTAATGATGGGGCCACAATTCTGAAACTTCTTGATGTTGTCCATCCTGCAGCAAAGA
CTTTGGTAGACATTGCCAAATCCCAAGATGCTGAGGTGGGTGATGGCACCACCTCAGTGACCTTGCTGGCTGCAG
AGTTTCTGAAGCAGGTGAAACCCTATGTGGAGGAAGGTTTACACCCCCAGATCATCATTCGAGCTTTCCGCACAG
CCACCCAGCTGGCAGTTAACAAGATCAAAGAGATTGCTGTGACCGTGAAGAAGGCAGATAAAGTGGAGCAGAGGA
AGCTGCTGGAAAAGTGTGCCATGACCGCTCTGAGCTCCAAGCTGATCTCCCAGCAGAAAGCTTTCTTTGCTAAGA
TGGTGGTGGATGCAGTGATGATGCTCGATGATTTGCTGCAGCTTAAAATGATTGGAATCAAGAAGGTACAGGGTG
GAGCCCTCGAGGATTCTCAGCTGGTAGCTGGTGTTGCATTCAAGAAGACTTTCTCTTACGCTGGGTTTGAAATGC
AACCCAAAAAGTACCACAATCCCAAGATTGCCCTTTTGAATGTCGAGCTCGAGTTGAAAGCTGAGAAAGACAATG
CTGAGATAAGAGTCCACACAGTTGAGGATTATCAGGCAATTGTTGATGCTGAGTGGAACATTCTCTATGACAAGT
TAGAGAAGATCCATCATTCTGGAGCCAAAGTTGTCTTGTCCAAACTCCCCATTGGGGATGTGGCCACCCAGTACT
TTGCTGACAGGGACATGTTCTGTGCTGGCCGAGTACCTGAGGAGGATCTGAAGAGGACAATGATGGCCTGTGGAG
GCTCAATCCAGACCAGTGTGAATGCTCTGTCAGCAGATGTGCTGGGTCGATGCCAGGTGTTTGAAGAGACCCAGA
TTGGAGGCGAGAGGTACAATTTTTTTACTGGCTGCCCCAAGGCCAAGACATGCACCTTCATTCTCCGTGGCGGCG
CCGAGCAGTTTATGGAGGAGACAGAGCGGTCCCTGCATGATGCCATCATGATCGTCAGGAGGGCCATCAAGAATG
ATTCAGTGGTGGCTGGTGGCGGGGCCATTGAGATGGAACTCTCCAAGTACCTGCGGGATTACTCAAGGACTATTC
CAGGAAAACAGCAGCTGTTGATTGGGGCTTATGCCAAGGCCTTGGAGATTATCCCACGCCAGCTGTGTGACAATG
CTGGCTTTGATGCCACAAACATTCTCAACAAGCTGCGGGCTCGGCATGCCCAGGGGGGTACATGGTATGGAGTAG
ACATCAACAACGAGGACATTGCTGACAACTTTGAAGCTTTCGTGTGGGAGCCAGCTATGGTGCGGATCAATGCGC
TGACAGCAGCCTCTGAGGCTGCGTGCCTGATCGTGTCTGTAGATGAAACCATCAAGAACCCCCGCTCGACTGTGG
ATGCTCCCACAGCAGCAGGCCGGGGCCGTGGTCGTGGCCGCCCCCAC**TGA**GAGGCACCCCACCCATCACATGGCT
GGCTGGCTGCTGGGTGCACTTACCCTCCTTGGCTTGGTTACTTCATTTTACAAGGAAGGGGTAGTAATTGGCCCA
CTCTCTTCTTACTGGAGGCTATTTAAATAAAATGTAAGACTTCAAAAAAAAAAAAAAAAAAAA

FIGURE 94

MMPTPVILLKEGTDSSQGIPQLVSNISACQVIAEAVRTTLGPRGMDKLIVDGRGKATISNDGATILKLLDVVHPA
AKTLVDIAKSQDAEVGDGTTSVTLLAAEFLKQVKPYVEEGLHPQIIIRAFRTATQLAVNKIKEIAVTVKKADKVE
QRKLLEKCAMTALSSKLISQQKAFFAKMVVDAVMMLDDLLQLKMIGIKKVQGGALEDSQLVAGVAFKKTFSYAGF
EMQPKKYHNPKIALLNVELELKAEKDNAEIRVHTVEDYQAIVDAEWNILYDKLEKIHHSGAKVVLSKLPIGDVAT
QYFADRDMFCAGRVPEEDLKRTMMACGGSIQTSVNALSADVLGRCQVFEETQIGGERYNFFTGCPKAKTCTFILR
GGAEQFMEETERSLHDAIMIVRRAIKNDSVVAGGGAIEMELSKYLRDYSRTIPGKQQLLIGAYAKALEIIPRQLC
DNAGFDATNILNKLRARHAQGGTWYGVDINNEDIADNFEAFVWEPAMVRINALTAASEAACLIVSVDETIKNPRS
TVDAPTAAGRGRGRGRPH

FIGURE 95

CGGGGCGGCAGGCTTCTCGAGCTCCGGGCCCGCGGCAACCTCGGGCGCTGTTCTGCAGGCCGCGACCGGC**ATG**TA
CGAGCAACTCAAGGGCGAGTGGAACCGTAAAAGCCCCAATCTTAGCAAGTGCGGGGAAGAGCTGGGTCGACTCAA
GCTAGTTCTTCTGGAGCTCAACTTCTTGCCAACCACAGGGACCAAGCTGACCAAACAGCAGCTAATTCTGGCCCG
TGACATACTGGAGATCGGGGCCCAATGGAGCATCCTACGCAAGGACATCCCCTCCTTCGAGCGCTACATGGCCCA
GCTCAAATGCTACTACTTTGATTACAAGGAGCAGCTCCCCGAGTCAGCCTATATGCACCAGCTCTTGGGCCTCAA
CCTCCTCTTCCTGCTGTCCCAGAACCGGGTGGCTGAGTTCCACACGGAGTTGGAGCGGCTGCCTGCCAAGGACAT
ACAGACCAATGTCTACATCAAGCACCCAGTGTCCCTGGAGCAATACCTGATGGAGGGCAGCTACAACAAAGTGTT
CCTGGCCAAGGGTAACATCCCCGCCGAGAGCTACACCTTCTTCATTGACATCCTGCTCGACACTATCAGGGATGA
GATCGCTGGGTGCATCGAGAAGGCCTACGAGAAAATCCTTTTCACTGAGGCCACCCGGATCCTCTTCTTCAACAC
ACCCAAAAAGATGACAGACTACGCCAAGAAGCGAGGGTGGGTCCTGGGCCCCAACAACTACTACAGTTTTGCCAG
CCAGCAGCAGAAGCCGGAAGACACCACCATTCCCTCCACAGAACTGGCCAAACAGGTCATCGAGTATGCCCGGCA
GCTGGAGATGATCGTC**TGA**GCCCCCCGGGCACTGGGTGGGGCAGGGCACGAGTTATTTAAAACAGTTACACTGCA
GGGTTTCGCCCAATAAAGGTGGACTGAC

FIGURE 96

MYEQLKGEWNRKSPNLSKCGEELGRLKLVLLELNFLPTTGTKLTKQQLILARDILEIGAQWSILRKDIPSFERYM
AQLKCYYFDYKEQLPESAYMHQLLGLNLLFLLSQNRVAEFHTELERLPAKDIQTNVYIKHPVSLEQYLMEGSYNK
VFLAKGNIPAESYTFFIDILLDTIRDEIAGCIEKAYEKILFTEATRILFFNTPKKMTDYAKKRGWVLGPNNYYSF
ASQQQKPEDTTIPSTELAKQVIEYARQLEMIV

FIGURE 97

GGCACGAGG**ATG**GAGGAGGGAGGCCGGGACAAGGCGCCGGTGCAGCCCCAGCAGTCTCCAGCGGCGGCCCCCGGC
GGCACGGACGAGAAGCCGAGCGGCAAGGAGCGGCGGGATGCCGGGGACAAGGACAAAGAACAGGAGCTGTCTGAA
GAGGATAAACAGCTTCAAGATGAACTGGAGATGCTCGTGGAACGACTAGGGGAGAAGGATACATCCCTGTATCGA
CCAGCGCTGGAGGAATTGCGAAGGCAGATTCGTTCTTCTACAACTTCCATGACTTCAGTGCCCAAGCCTCTCAAA
TTTCTGCGTCCACACTATGGCAAACTGAAGGAAATCTATGAGAACATGGCCCCTGGGGAGAATAAGCGTTTTGCT
GCTGACATCATCTCCGTTTTGGCCATGACCATGAGTGGGGAGCGTGAGTGCCTCAAGTATCGGCTAGTGGGCTCC
CAGGAGGAATTGGCATCATGGGGTCATGAGTATGTCAGGCATCTGGCAGGAGAAGTGGCTAAGGAGTGGCAGGAG
CTGGATGACGCAGAGAAGGTCCAGCGGGAGCCTCTGCTCACTCTGGTGAAGGAAATCGTCCCCTATAACATGGCC
CACAATGCAGAGCATGAGGCTTGCGACCTGCTTATGGAAATTGAGCAGGTGGACATGCTGGAGAAGGACATTGAT
GAAAATGCATATGCAAAGGTCTGCCTTTATCTCACCAGTTGTGTGAATTACGTGCCTGAGCCTGAGAACTCAGCC
CTACTGCGTTGTGCCCTGGGTGTGTTCCGAAAGTTTAGCCGCTTCCCTGAAGCTCTGAGATTGGCATTGATGCTC
AATGACATGGAGTTGGTAGAAGACATCTTCACCTCCTGCAAGGATGTGGTAGTACAGAAACAGATGGCATTCATG
CTAGGCCGGCATGGGGTGTTCCTGGAGCTGAGTGAAGATGTCGAGGAGTATGAGGACCTGACAGAGATCATGTCC
AATGTACAGCTCAACAGCAACTTCTTGGCCTTAGCTCGGGAGCTGGACATCATGGAGCCCAAGGTGCCTGATGAC
ATCTACAAAACCCACCTAGAGAACAACAGGTTTGGGGGCAGTGGCTCTCAGGTGGACTCTGCCCGCATGAACCTG
GCCTCCTCTTTTGTGAATGGCTTTGTGAATGCAGCTTTTGGCCAAGACAAGCTGCTAACAGATGATGGCAACAAA
TGGCTTTACAAGAACAAGGACCACGGAATGTTGAGTGCAGCTGCATCTCTTGGGATGATTCTGCTGTGGGATGTG
GATGGTGGCCTCACCCAGATTGACAAGTACCTGTACTCCTCTGAGGACTACATTAAGTCAGGAGCTCTTCTTGCC
TGTGGCATAGTGAACTCTGGGGTCCGGAATGAGTGTGACCCTGCTCTGGCACTGCTCTCAGACTATGTTCTCCAC
AACAGCAACACCATGAGACTTGGTTCCATCTTTGGGCTAGGCTTGGCTTATGCTGGCTCAAATCGTGAAGATGTC
CTAACACTGCTGCTGCCTGTGATGGGAGATTCAAAGTCCAGCATGGAGGTGGCAGGTGTCACAGCTTTAGCCTGT
GGAATGATAGCAGTAGGGTCCTGCAATGGAGATGTAACTTCCACTATCCTTCAGACCATCATGGAGAAGTCAGAG
ACTGAGCTCAAGGATACTTATGCTCGTTGGCTTCCTCTTGGACTGGGTCTCAACCACCTGGGGAAGGGTGAGGCC
ATCGAGGCAATCCTGGCTGCACTGGAGGTTGTGTCAGAGCCATTCCGCAGTTTTGCCAACACACTGGTGGATGTG
TGTGCATATGCAGGCTCTGGGAATGTGCTGAAGGTGCAGCAGCTGCTCCACATTTGTAGCGAACACTTTGACTCC
AAAGAGAAGGAGGAAGACAAAGACAAGAAGGAAAAGAAAGACAAGGACAAGAAGGAAGCCCCTGCTGACATGGGA
GCACATCAGGGAGTGGCTGTTCTGGGGATTGCCCTTATTGCTATGGGGGAGGAGATTGGTGCAGAGATGGCATTA
CGAACCTTTGGCCACTTGCTGAGATATGGGGAGCCTACACTCCGGAGGGCTGTACCTTTAGCACTGGCCCTCATC
TCTGTTTCAAATCCACGACTCAACATCCTGGATACCCTAAGCAAATTCTCTCATGATGCTGATCCAGAAGTTTCC
TATTACTCCATTTTTGCCATGGGCATGGTGGGCAGTGGTACCAATAATGCCCGTCTGGCTGCAATGCTGCGCCAG
TTAGCTCAATATCATGCCAAGGACCCAAACAACCTCTTCATGGTGCGCTTGGCACAGGGCCTGACACATTTAGGG
AAGGGCACCCTTACCCTCTGCCCCTACCACAGCGACCGGCAGCTTATGAGCCAGGTGGCCGTGGCTGGACTGCTC
ACTGTGCTTGTCTCTTTCCTGGATGTTCGAAACATTATTCTAGGCAAATCACACTATGTATTGTATGGGCTGGTG
GCTGCCATGCAGCCCCGAATGCTGGTTACGTTTGATGAGGAGCTGCGGCCATTGCCAGTGTCTGTCCGTGTGGGC
CAGGCAGTGGATGTGGTGGGCCAGGCTGGCAAGCCGAAGACTATCACAGGGTTCCAGACGCATACAACCCCAGTG
TTGTTGGCCCACGGGGAACGGGCAGAATTGGCCACTGAGGAGTTTCTTCCTGTTACCCCCATTCTGGAAGGTTTT
GTTATCCTTCGGAAGAACCCCAATTATGATCTC**TAA**GTGACCACCAGGGGCTCTGAACTGCAGCTGATGTTATCA
GCAGGCCATGCATCCTGCTGCCAAGGGTGGACACGGCTGCAGACTTCTGGGGGAATTGTCGCCTCCTGCTCTTTT
GTTACTGAGTGAGATAAGGTTGTTCAATAAAGACTTTTATCCCCAAGGTCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 98

MEEGGRDKAPVQPQQSPAAAPGGTDEKPSGKERRDAGDKDKEQELSEEDKQLQDELEMLVERLGEKDTSLYRPAL
EELRRQIRSSTTSMTSVPKPLKFLRPHYGKLKEIYENMAPGENKRFAADIISVLAMTMSGERECLKYRLVGSQEE
LASWGHEYVRHLAGEVAKEWQELDDAEKVQREPLLTLVKEIVPYNMAHNAEHEACDLLMEIEQVDMLEKDIDENA
YAKVCLYLTSCVNYVPEPENSALLRCALGVFRKFSRFPEALRLALMLNDMELVEDIFTSCKDVVVQKQMAFMLGR
HGVFLELSEDVEEYEDLTEIMSNVQLNSNFLALARELDIMEPKVPDDIYKTHLENNRFGGSGSQVDSARMNLASS
FVNGFVNAAFGQDKLLTDDGNKWLYKNKDHGMLSAAASLGMILLWDVDGGLTQIDKYLYSSEDYIKSGALLACGI
VNSGVRNECDPALALLSDYVLHNSNTMRLGSIFGLGLAYAGSNREDVLTLLLPVMGDSKSSMEVAGVTALACGMI
AVGSCNGDVTSTILQTIMEKSETELKDTYARWLPLGLGLNHLGKGEAIEAILAALEVVSEPFRSFANTLVDVCAY
AGSGNVLKVQQLLHICSEHFDSKEKEEDKDKKEKKDKDKKEAPADMGAHQGVAVLGIALIAMGEEIGAEMALRTF
GHLLRYGEPTLRRAVPLALALISVSNPRLNILDTLSKFSHDADPEVSYYSIFAMGMVGSGTNNARLAAMLRQLAQ
YHAKDPNNLFMVRLAQGLTHLGKGTLTLCPYHSDRQLMSQVAVAGLLTVLVSFLDVRNIILGKSHYVLYGLVAAM
QPRMLVTFDEELRPLPVSVRVGQAVDVVGQAGKPKTITGFQTHTTPVLLAHGERAELATEEFLPVTPILEGFVIL
RKNPNYDL

FIGURE 99A

TATACTTCGCTACTTGGCTAGAGTTGCAACTACAGCTGGGTTATATGGCTCTAATCTG**ATG**GAACATACTGAGAT
TGATCACTGGTTGGAGTTCAGTGCTACAAAATTATCTTCATGTGATTCCTTTACTTCTACAATTAATGAACTCAA
TCATTGCCTGTCTCTGAGAACATACTTAGTTGGAAACTCCTTGAGTTTAGCAGATTTATGTGTTTGGGCCACCCT
AAAAGGAAATGCTGCCTGGCAAGAACAGTTGAAACAGAAGAAAGCTCCAGTTCATGTAAAACGTTGGTTTGGCTT
TCTTGAAGCCCAGCAGGCCTTCCAGTCAGTAGGTACCAAGTGGGATGTTTCAACAACCAAAGCTCGAGTGGCACC
TGAGAAAAAGCAAGATGTTGGGAAATTTGTTGAGCTTCCAGGTGCGGAGATGGGAAAGGTTACCGTCAGATTTCC
TCCAGAGGCCAGTGGTTACTTACACATTGGGCATGCAAAAGCTGCTCTTCTGAACCAGCACTACCAGGTTAACTT
TAAAGGGAAACTGATCATGAGATTTGATGACACAAATCCTGAAAAAGAAAAGGAAGATTTTGAGAAGGTTATCTT
GGAAGATGTTGCAATGTTGCATATCAAACCAGATCAATTTACTTATACTTCGGATCATTTTGAAACTATAATGAA
GTATGCAGAGAAGCTAATTCAAGAAGGGAAGGCTTATGTGGATGATACTCCTGCTGAACAGATGAAAGCAGAACG
TGAGCAGAGGATAGAATCTAAACATAGAAAAAACCCTATTGAGAAGAATCTACAAATGTGGGAAGAAATGAAAAA
AGGGAGCCAGTTTGGTCACTCCTGTTGTTTGCGAGCAAAAATTGACATGAGTAGTAACAATGGATGCATGAGAGA
TCCAACCCTTTATCGCTGCAAAATTCAACCACATCCAAGAACTGGAAATAAATACAATGTTTATCCAACATATGA
TTTTGCCTGCCCCATAGTTGACAGCATCGAAGGTGTTACACATGCCCTGAGAACAACAGAATACCATGACAGAGA
TGAGCAGTTTTACTGGATTATTGAAGCTTTAGGCATAAGAAAACCATATATTTGGGAATATAGTCGGCTAAATCT
CAACAACACAGTGCTATCCAAAAGAAAACTCACATGGTTTGTCAATGAAGGACTAGTAGATGGATGGGATGACCC
AAGATTTCCTACGGTTCGTGGTGTACTGAGAAGAGGGATGACAGTTGAAGGACTGAAACAGTTTATTGCTGCTCA
GGGCTCCTCACGTTCAGTCGTGAACATGGAGTGGGACAAAATCTGGGCGTTTAACAAAAAGGTTATTGACCCAGT
GGCTCCACGATATGTTGCATTACTGAAGAAAGAAGTGATCCCAGTGAATGTACCTGAAGCTCAGGAGGAGATGAA
AGAAGTAGCCAAACACCCAAAGAATCCTGAGGTTGGCTTGAAGCCTGTGTGGTATAGTCCCAAAGTTTTCATTGA
AGGTGCTGATGCAGAGACTTTTTCGGAGGGTGAGATGGTTACATTTATAAATTGGGGCAACCTCAACATTACAAA
AATACACAAAAATGCAGATGGAAAAATCATATCTCTTGATGCAAAGTTTAATTTGGAAAACAAAGACTACAAGAA
AACCACTAAGGTCACTTGGCTTGCAGAGACTACACATGCTCTTCCTATTCCAGTAATCTGTGTCACTTATGAGCA
CTTGATCACAAAGCCAGTGCTAGGAAAAGACGAGGACTTTAAGCAGTATGTCAACAAGAACAGTAAGCATGAAGA
GCTAATGCTAGGGGATCCCTGCCTTAAGGATTTGAAAAAAGGAGATATTATACAACTCCAGAGAAGAGGATTCTT
CATATGTGATCAACCTTATGAACCTGTTAGCCCATATAGTTGCAAGGAAGCCCCGTGTGTTTTGATATACATTCC
TGATGGGCACACAAAGGAAATGCCAACATCAGGGTCAAAGGAAAAGACCAAAGTAGAAGCCACAAAAAATGAGAC
CTCTGCTCCTTTTAAGGAAAGACCAACACCTTCTCTGAATAATAATTGTACTACATCTGAGGATTCCTTGGTCCT
TTACAATAGAGTGGCTGTTCAAGGAGATGTGGTTCGTGAATTAAAAGCCAAGAAAGCACCAAAGGAAGATGTAGA
TGCAGCTGTAAAACAGCTTTTGTCTTTGAAAGCTGAATATAAGGAGAAAACTGGCCAGGAATATAAACCTGGAAA
CCCTCCTGCTGAAATAGGACAGAATATTTCTTCTAATTCCTCAGCAAGTATTCTGGAAAGTAAATCTCTGTATGA
TGAAGTTGCTGCACAAGGGGAGGTGGTTCGTAAGCTAAAAGCTGAAAAATCCCCTAAGGCTAAAATAAATGAAGC
TGTAGAATGCTTACTGTCCCTGAAGGCTCAGTATAAAGAAAAAACTGGGAAGGAGTACATACCTGGTCAGCCCCC
ATTATCTCAAAGTTCGGATTCAAGCCCAACCAGAAATTCTGAACCTGCTGGTTTAGAAACACCAGAAGCGAAAGT
ACTTTTTGACAAAGTAGCTTCTCAAGGGGAAGTAGTTCGGAAACTTAAAACTGAAAAAGCCCCTAAGGATCAAGT
AGATATAGCTGTTCAAGAACTCCTTCAGCTAAAGGCACAGTACAAGTCTTTGATAGGAGTAGAGTATAAGCCTGT
GTCGGCCACTGGAGCTGAGGACAAAGATAAGAAGAAGAAAGAAAAAGAAAATAAATCTGAAAAGCAGAATAAGCC
TCAGAAACAAAATGATGGCCAAAGGAAAGACCCTTCTAAAAACCAAGGAGGTGGGCTCTCATCAAGTGGAGCAGG
AGAAGGGCAGGGGCCTAAGAAACAGACCAGGTTGGGTCTTGAGGCAAAAAAAGAAGAAAATCTTGCTGATTGGTA
TTCTCAGGTCATCACAAAGTCAGAAATGATTGAATACCATGACATAAGTGGCTGTTATATTCTTCGTCCCTGGGC
CTATGCCATTTGGGAAGCCATCAAGGACTTTTTTGATGCTGAGATCAAGAAACTTGGTGTTGAAAACTGCTACTT
CCCCATGTTTGTGTCTCAAAGTGCATTAGAGAAAGAGAAGACTCATGTTGCTGACTTTGCCCCAGAGGTTGCTTG
GGTTACAAGATCTGGCAAAACCGAGCTGGCAGAACCAATTGCCATTCGTCCTACTAGTGAAACAGTAATGTATCC
TGCATATGCAAAATGGGTACAATCACACAGAGACCTGCCCATCAAGCTCAATCAGTGGTGCAATGTGGTGCGTTG
GGAATTCAAGCATCCTCAGCCTTTCCTACGTACTCGTGAATTTCTTTGGCAGGAAGGGCACAGTGCTTTTGCTAC
CATGGAAGAGGCAGCGGAAGAGGTCTTGCAGATACTTGACTTATATGCTCAGGTATATGAAGAACTCCTGGCAAT
TCCTGTTGTTAAAGGAAGAAAGACGGAAAAGGAAAAATTTGCAGGAGGAGACTATACAACTACAATAGAAGCATT
TATATCTGCTAGTGGAAGAGCTATCCAGGGAGGAACATCACATCATTTAGGGCAGAATTTTTCCAAAATGTTTGA

FIGURE 99B

AATCGTTTTTGAAGATCCAAAGATACCAGGAGAGAAGCAATTTGCCTATCAAAACTCCTGGGGCCTGACAACTCG
AACTATTGGTGTTATGACCATGGTTCATGGGGACAACATGGGTTTAGTATTACCACCCCGTGTAGCATGTGTTCA
GGTGGTGATTATTCCTTGTGGCATTACCAATGCACTTTCTGAAGAAGACAAAGAAGCGCTGATTGCAAAATGCAA
TGATTATCGAAGGCGATTACTCAGTGTTAACATCCGCGTTAGAGCTGATTTACGAGATAATTATTCTCCAGGTTG
GAAATTCAATCACTGGGAGCTCAAGGGAGTTCCCATTAGACTTGAAGTTGGGCCACGTGATATGAAGAGCTGTCA
GTTTGTAGCCGTCAGACGAGATACTGGAGAAAAGCTGACAGTTGCTGAAAATGAGGCAGAGACTAAACTTCAAGC
TATTTTGGAAGACATCCAGGTCACCCTTTTCACAAGGGCTTCTGAAGACCTTAAGACTCATATGGTTGTGGCTAA
TACAATGGAAGACTTTCAGAAGATACTAGATTCTGGAAAGATTGTTCAGATTCCATTCTGTGGGGAAATTGACTG
TGAGGACTGGATCAAAAAGACCACTGCCAGGGATCAAGATCTTGAACCTGGTGCTCCATCCATGGGAGCTAAAAG
CCTTTGCATCCCCTTCAAACCACTCTGTGAACTGCAGCCTGGAGCCAAATGTGTCTGTGGCAAGAACCCTGCCAA
GTACTACACCTTATTTGGTCGCAGCTAC**TGA**GGGATGAACGAAAGCCCCCTCTTCAACTCCTCTCACTTTTTAAA
GCATTGATATTAGTATCTTCTCAGATACAGACCGTTTTATGATTTTTTAAAAAGTAAAAGTTCTAAAATGAAGTC
ACACAGGACAATTATTCTTATGCCTAAGTTAACAGTGGATAAAAGACTTTTCTGTAAACAACTCCAGTAATAAAT
ATCATGAACTA

FIGURE 100

MEHTEIDHWLEFSATKLSSCDSFTSTINELNHCLSLRTYLVGNSLSLADLCVWATLKGNAAWQEQLKQKKAPVHV
KRWFGFLEAQQAFQSVGTKWDVSTTKARVAPEKKQDVGKFVELPGAEMGKVTVRFPPEASGYLHIGHAKAALLNQ
HYQVNFKGKLIMRFDDTNPEKEKEDFEKVILEDVAMLHIKPDQFTYTSDHFETIMKYAEKLIQEGKAYVDDTPAE
QMKAEREQRIESKHRKNPIEKNLQMWEEMKKGSQFGHSCCLRAKIDMSSNNGCMRDPTLYRCKIQPHPRTGNKYN
VYPTYDFACPIVDSIEGVTHALRTTEYHDRDEQFYWIIEALGIRKPYIWEYSRLNLNNTVLSKRKLTWFVNEGLV
DGWDDPRFPTVRGVLRRGMTVEGLKQFIAAQGSSRSVVNMEWDKIWAFNKKVIDPVAPRYVALLKKEVIPVNVPE
AQEEMKEVAKHPKNPEVGLKPVWYSPKVFIEGADAETFSEGEMVTFINWGNLNITKIHKNADGKIISLDAKFNLE
NKDYKKTTKVTWLAETTHALPIPVICVTYEHLITKPVLGKDEDFKQYVNKNSKHEELMLGDPCLKDLKKGDIIQL
QRRGFFICDQPYEPVSPYSCKEAPCVLIYIPDGHTKEMPTSGSKEKTKVEATKNETSAPFKERPTPSLNNNCTTS
EDSLVLYNRVAVQGDVVRELKAKKAPKEDVDAAVKQLLSLKAEYKEKTGQEYKPGNPPAEIGQNISSNSSASILE
SKSLYDEVAAQGEVVRKLKAEKSPKAKINEAVECLLSLKAQYKEKTGKEYIPGQPPLSQSSDSSPTRNSEPAGLE
TPEAKVLFDKVASQGEVVRKLKTEKAPKDQVDIAVQELLQLKAQYKSLIGVEYKPVSATGAEDKDKKKKEKENKS
EKQNKPQKQNDGQRKDPSKNQGGGLSSSGAGEGQGPKKQTRLGLEAKKEENLADWYSQVITKSEMIEYHDISGCY
ILRPWAYAIWEAIKDFFDAEIKKLGVENCYFPMFVSQSALEKEKTHVADFAPEVAWVTRSGKTELAEPIAIRPTS
ETVMYPAYAKWVQSHRDLPIKLNQWCNVVRWEFKHPQPFLRTREFLWQEGHSAFATMEEAAEEVLQILDLYAQVY
EELLAIPVVKGRKTEKEKFAGGDYTTTIEAFISASGRAIQGGTSHHLGQNFSKMFEIVFEDPKIPGEKQFAYQNS
WGLTTRTIGVMTMVHGDNMGLVLPPRVACVQVVIIPCGITNALSEEDKEALIAKCNDYRRRLLSVNIRVRADLRD
NYSPGWKFNHWELKGVPIRLEVGPRDMKSCQFVAVRRDTGEKLTVAENEAETKLQAILEDIQVTLFTRASEDLKT
HMVVANTMEDFQKILDSGKIVQIPFCGEIDCEDWIKKTTARDQDLEPGAPSMGAKSLCIPFKPLCELQPGAKCVC
GKNPAKYYTLFGRSY

FIGURE 101

AGAATACACTCACAAGCCACTCCGCTGCTCGCCTCTCCGCCCCGCGTCCAGCTCGCCCAGCTCGCCCAGCGTCCG
CCGCGCCTCGCCAAGGCTTCAACGGACCACACCAAA**ATG**CCATCTCAAATGGAACACGCCATGGAAACCATGATG
TTTACATTTCACAAATTCGCTGGGGATAAAGGCTACTTAACAAAGGAGGACCTGAGAGTACTCATGGAAAAGGAG
TTCCCTGGATTTTTGGAAAATCAAAAAGACCCTCTGGCTGTGGACAAAATAATGAAGGACCTGGACCAGTGTAGA
GATGGCAAAGTGGGCTTCCAGAGCTTCTTTTCCCTAATTGCGGGCCTCACCATTGCATGCAATGACTATTTTGTA
GTACACATGAAGCAGAAGGGAAAGAAG**TAG**GCAGAAATGAGCAGTTCGCTCCTCCCTGATAAGAGTTGTCCAAAG
GGTCGCTTAAGGAATCTGCCCCACAGCTTCCCCCATAGAAGGATTTCATGAGCAGATCAGGACACTTAGCAAATG
TAAAAATAAAATCTAACTCTCATTTGACAAGCAGAGAAAGAAAAGTTAAATACCAGATAAGCTTTTGATTTTTGT
ATTGTTTGCATCCCCTTGCCCTCAATAAATAAAGTTCTTTTTTAGTTCC

FIGURE 102

MPSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFQSFFSL
IAGLTIACNDYFVVHMKQKGKK

FIGURE 103

CGCGTGAACTGCTTCCTGCAGGCTGGCC**ATG**GCGCTTCACGTTCCCAAGGCTCCGGGCTTTGCCCAGATGCTCAA
GGAGGGAGCGAAACACTTTTCAGGATTAGAAGAGGCTGTGTATAGAAACATACAAGCTTGCAAGGAGCTTGCCCA
AACCACTCGTACAGCATATGGACCAAAAGGAATGAACAAAATGGTTATCAACCACTTGGAGAAGTTGTTTGTGAC
AAACGATGCAGCAACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAAAATGATTGTAATGGCTTCTCA
TATGCAAGAGCAAGAAGTTGGAGATGGCACAAACTTTGTTCTGGTATTTGCTGGAGCTCTCCTGGAATTAGCTGA
AGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAATAGCCTGCAGAAAAGCTCATGA
GATTCTTCCTAATTTGGTATGTTGTTCTGCAAAAAACCTTCGAGATATTGATGAAGTCTCATCTCTACTTCGTAC
CTCCATAATGAGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGCTCAGGCATGCGTATCTATTTT
TCCTGATTCCGGCCATTTCAATGTTGATAACATCAGAGTTTGTAAAATTCTGGGCTCTGGTATCAGTTCCTCTTC
AGTATTGCATGGCATGGTTTTTAAGAAGGAAACCGAAGGTGATGTAACATCTGTCAAAGATGCAAAAATAGCAGT
GTACTCTTGTCCTTTTGATGGCATGATAACAGAAACTAAGGGAACAGTGTTGATAAAGACTGCTGAAGAATTGAT
GAATTTTAGTAAGGGAGAAGAAAACCTCATGGATGCACAAGTCAAAGCTATTGCTGATACTGGTGCAAATGTCGT
AGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAATAAATATAATATCATGTTAGTGAGGCTAAA
CTCAAAATGGGATCTCCGAAGACTTTGTAAAACTGTTGGTGCTACAGCTCTTCCTAGATTGACACCTCCTGTCCT
TGAAGAAATGGGACACTGTGACAGTGTTTACCTCTCAGAAGTTGGAGATACTCAGGTGGTGGTTTTTAAGCATGA
AAAGGAAGATGGCGCCATTTCTACCATAGTACTTCGAGGCTCTACAGACAATCTGATGGATGACATAGAAAGGGT
AGTAGACGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTACCCGGAGGTGGAGCAACAGA
AATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCCTGGACTTGAACAGTATGCTATTAAGAAGTT
TGCTGAGGCATTTGAAGCTATTCCCCGCGCACTGGCAGAAAACTCTGGAGTTAAGGCCAATGAAGTAATCTCTAA
ACTTTATGCAGTACATCAAGAAGGAAATAAAAACGTTGGATTAGATATTGAGGCTGAAGTCCCTGCTGTAAAGGA
CATGCTGGAAGCTGGTATTCTAGATACTTACCTGGGAAAATATTGGGCTATCAAACTCGCTACTAATGCTGCAGT
CACTGTACTTAGAGTGGATCAGATCATCATGGCAAAACCAGCTGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGA
CTGGGATGATGACCAAAATGAT**TGA**AATTGGCTTAATTTTTACTGTAGGTGAAGGCTGTATTTGTAGTAGTACTC
AAGAATCACCTGATGTTTTCTTATTCTCCTTAAATTAAGAGTTATTTTGTGTTTGTATTCTTGGCTGGATGTTAT
AATAAACATATTGTTACTGTC

FIGURE 104

MALHVPKAPGFAQMLKEGAKHFSGLEEAVYRNIQACKELAQTTRTAYGPKGMNKMVINHLEKLFVTNDAATILRE
LEVQHPAAKMIVMASHMQEQEVGDGTNFVLVFAGALLELAEELLRIGLSVSEVIEGYEIACRKAHEILPNLVCCS
AKNLRDIDEVSSLLRTSIMSKQYGNEVFLAKLIAQACVSIFPDSGHFNVDNIRVCKILGSGISSSSVLHGMVFKK
ETEGDVTSVKDAKIAVYSCPFDGMITETKGTVLIKTAEELMNFSKGEENLMDAQVKAIADTGANVVVTGGKVADM
ALHYANKYNIMLVRLNSKWDLRRLCKTVGATALPRLTPPVLEEMGHCDSVYLSEVGDTQVVVFKHEKEDGAISTI
VLRGSTDNLMDDIERVVDDGVNTFKVLTRDKRLVPGGGATEIELAKQITSYGETCPGLEQYAIKKFAEAFEAIPR
ALAENSGVKANEVISKLYAVHQEGNKNVGLDIEAEVPAVKDMLEAGILDTYLGKYWAIKLATNAAVTVLRVDQII
MAKPAGGPKPPSGKKDWDDDQND

FIGURE 105

GGATCCGGCAACGAAGGTACC**ATG**GCGGGACGTGGCGCCATGGTGCTGTTGCACGTGCTGTTTGAGCACGCGGTC
GGCTACGCGCTCGTGGCGCTGAAGGAAGTGGAGGAGATCAGTCTGCTGCAGCCGCAGGTGGAGGAGTCCGTGCTC
AACCTGGGCAAATTCCACAGCATCGTTCGTCTGGTGGCCTTTTGTCCCTTTGCCTCATCCCAGGTTGCCTTGGAA
AATGCCAACGCCGTGTCTGAAGGGGTTGTTCATGAGGACCTCCGCCTGCTCTTGGAGACCCACCTGCCGTCCAAA
AAGAAGAAAGTACTCTTGGGAGTTGGGGATCCCAAGATTGGTGCCGCAATACAGGAGGAGTTAGGGTACAACTGC
CAGACTGGAGGAGTCATAGCTGAGATCCTGCGAGGAGTTCGTCTGCACTTCCACAATCTGGTGAAGGGTCTGACC
GATCTGTCAGCTTGTAAAGCACAGCTGGGGCTGGGACACAGCTATTCCCGTGCCAAAGTTAAGTTTAATGTGAAC
CGGGTGGACAATATGATCATCCAGTCCATTAGCCTCCTGGACCAGCTGGATAAGGACATCAATACCTTCTCTATG
CGTGTCAGGGAGTGGTACGGGTATCACTTTCCGGAGCTGGTGAAGATCATCAACGACAATGCCACATACTGCCGT
CTTGCCCAGTTTATTGGAAACCGAAGGGAACTGAATGAGGACAAGCTGGAGAAGCTGGAGGAGCTGACAATGGAT
GGGGCCAAGGCTAAGGCTATTCTGGATGCCTCACGGTCCTCCATGGGCATGGACATATCTGCCATTGACTTGATA
AACATCGAGAGCTTCTCCAGTCGTGTGGTGTCTTTATCTGAATACCGCCAGAGCCTACACACTTACCTGCGCTCC
AAGATGAGCCAAGTAGCCCCCAGCCTGTCAGCCCTAATTGGGGAAGCGGTAGGTGCACGTCTCATCGCACATGCT
GGCAGCCTCACCAACCTGGCCAAGTATCCAGCATCCACAGTGCAGATCCTTGGGGCTGAAAAGGCCCTGTTCAGA
GCCCTGAAGACAAGGGGTAACACTCCAAAATATGGACTCATTTTCCACTCCACCTTCATTGGCCGAGCAGCTGCC
AAGAACAAAGGCCGCATCTCCCGATACCTGGCAAACAAATGCAGTATTGCCTCACGAATCGATTGCTTCTCTGAG
GTGCCCACGAGTGTATTCGGGGAGAAGCTTCGAGAACAAGTTGAAGAGCGACTGTCCTTCTATGAGACTGGAGAG
ATACCACGAAAGAATCTGGATGTCATGAAGGAAGCAATGGTTCAGGCAGAGGCAGAGGAAGCGGCTGCTGAGATT
ACTAGGAAGCTGGAGAAACAGGAGAAGAAACGCTTAAAGAAGGAAAAGAAACGGCTGGCTGCACTTGCCCTCGCG
TCTTCAGAAAACAGCAGTAGTACTCCAGAGGAGTGTGAGGAGACGAGTGAAAAACCCAAAAAGAAGAAAAAGCAA
AAGCCCCAGGAGGTTCCTCAGGAGAATGGAATGGAAGACCCATCTATCTCTTTCTCCAAACCCAAGAAAAAGAAA
TCTTTTTCCAAGGAGGAGTTGATGAGTAGCGATCTTGAAGAGACCGCTGGCAGCACCAGTATTCCCAAGAGGAAG
AAGTCTACACCCAAGGAGGAAACAGTTAATGACCCTGAGGAGGCAGGCCACAGAAGTCGGTCCAAGAAAAAGAGG
AAATTCTCCAAAGAGGAGCCGGTCAGCAGTGGGCCTGAAGAGGCGGTTGGCAAGAGCAGCTCCAAGAAGAAGAAA
AAGTTCCATAAAGCATCCCAGGAAGAT**TAG**AATGCAAATGGACATTCTCTGGGAGGTGGGGCATACCATAGCCCA
AGGTGACATTTCCCACCCTGTGCCCGTGTTCCCAATAAAAACAAATTCACAAGAAAAAAAAAAAAAAAAAAAAAA
TTCCTGAGGCCGCAAGGGAATTC

FIGURE 106

MAGRGAMVLLHVLFEHAVGYALVALKEVEEISLLQPQVEESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSE
GVVHEDLRLLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEILRGVRLHFHNLVKGLTDLSACKA
QLGLGHSYSRAKVKFNVNRVDNMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNATYCRLAQFIGN
RRELNEDKLEKLEELTMDGAKAKAILDASRSSMGMDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAP
SLSALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKTRGNTPKYGLIFHSTFIGRAAAKNKGRIS
RYLANKCSIASRIDCFSEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAEAEEAAAEITRKLEKQ
EKKRLKKEKKRLAALALASSENSSSTPEECEETSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSRSKKKRKFSKEEPVSSGPEEAVGKSSSKKKKKFHKASQ
ED

FIGURE 107

CGCAGCCGTGCG**ATG**TTGTCCTCTACAGCCATGTATTCGGCTCCTGGCAGAGACTTGGGGATGGAACCGCACAGA
GCCGCGGGCCCTTTGCAGCTGCGATTTTCGCCCTACGTTTTCAACGGAGGTACTATACTGGCAATTGCTGGAGAA
GATTTTGCAATTGTTGCTTCTGATACTCGATTGAGTGAAGGGTTTTCAATTCATACGCGGGATAGCCCCAAATGT
TACAAATTAACAGACAAAACAGTCATTGGATGCAGCGGTTTTCATGGAGACTGTCTTACGCTGACAAAGATTATT
GAAGCAAGACTAAAGATGTATAAGCATTCCAATAATAAGGCCATGACTACGGGGGCAATTGCTGCAATGCTGTCT
ACAATCCTGTATTCAAGGCGCTTCTTTCCATACTATGTTTACAACATCATCGGTGGACTTGATGAAGAAGGAAAG
GGGGCTGTATACAGCTTTGATCCAGTAGGGTCTTACCAGAGAGACTCCTTCAAGGCTGGAGGCTCAGCAAGTGCC
ATGCTACAGCCCCTGCTTGACAACCAGGTTGGTTTTAAGAACATGCAGAATGTGGAGCATGTTCCGCTGTCCTTG
GACAGAGCCATGCGGCTGGTGAAAGATGTCTTCATTTCTGCGGCTGAGAGAGATGTGTACACTGGGGACGCACTC
CGGATCTGCATAGTGACCAAAGAGGGCATCAGGGAGGAAACTGTTTCCTTAAGGAAGGAC**TGA**TCTGTGTGCTCT
TATCACCAATCAGTTCAGACCTGGTTGATTTTGTACTTTGGAACTGTACCTTGGATGGTTTTGTTTATTAAAA

FIGURE 108

MLSSTAMYSAPGRDLGMEPHRAAGPLQLRFSPYVFNGGTILAIAGEDFAIVASDTRLSEGFSIHTRDSPKCYKLT
DKTVIGCSGFHGDCLTLTKIIEARLKMYKHSNNKAMTTGAIAAMLSTILYSRRFFPYYVYNIIGGLDEEGKGAVY
SFDPVGSYQRDSFKAGGSASAMLQPLLDNQVGFKNMQNVEHVPLSLDRAMRLVKDVFISAAERDVYTGDALRICI
VTKEGIREETVSLRKD

FIGURE 109

ATGCCCGAGAATGTGGCACCCCGGAGCGGGGCGACTGCCGGGGCTGCCGGCGGCCGCGGGAAAGGCGCCTATCAG
GACCGCGACAAGCCAGCCCAGATCCGCTTCAGCAACATTTCCGCCGCCAAAGCGGTTGCTGATGCTATTAGAACA
AGCCTTGGACCAAAAGGAATGGATAAAATGATTCAAGATGGAAAAGGTGATGTAACCATTACAAATGATGGTGCT
ACCATTCTGAAACAAATGCAAGTATTACATCCAGCAGCCAGAATGCTGGTGGAGCTGTCTAAGGCTCAAGATATA
GAAGCAGGAGATGGCACCACATCAGTAGTCATCATTGCTGGCTCCCTCTTAGATTCTTGTACCAAGCTTCTTCAG
AAAGGGATTCATCCAACCATCATTTCTGAGTCATTCCAGAAGGCCCTGGAAAAGGGCATTGAAATCTTGACTGAC
ATGTCTCGACCTGTGGAACTGAGTGACAGAGAAACTTTGTTAAATAGTGCAACCACTTCACTGAACTCAAAGGTG
GTTTCTCAGTATTCAAGTCTGCTTTCTCCAATGAGTGTAAATGCAGTGATGAAAGTGATTGACCCAGCCACAGCC
ACCAGTGTAGATCTTAGAGATATTAAAATAGTTAAGAAGCTTGGTGGGACAATTGATGACTGTGAGTTGGTGGAA
GGGCTGGTTCTCACCCAAAAAGTGTCAAATTCTGGCATAACCAGAGTTGAAAAGGCCAAGATTGGGCTTATTCAG
TTTTGCTTATCTGCTCCCAAAACAGACATGGATAATCAAATAGTGGTTTCTGACTATGCCCAGATGGACCGAGTG
CTGCGAGAAGAGAGAGCCTATATTTTAAATTTAGTGAAGCAAATTAAAAAAACAGGATGTAATGTCCTTCTCATA
CAGAAATCTATTCTAAGAGATGCTCTTAGTGATCTTGCATTACACTTTCTGAATAAAATGAAGATCATGGTGATT
AAGGATATTGAAAGAGAAGACATTGAATTCATTTGTAAGACAATTGGAACCAAGCCAGTTGCTCATATTGACCAA
TTTACTGCTGACATGCTGGGTTCTGCTGAGTTAGCTGAGGAGGTCAATTTAAATGGTTCTGGCAAACTGCTCAAG
ATTACAGGCTGTGCCAGCCCTGGAAAAACAGTTACAATTGTTGTTCGTGGTTCTAACAAACTGGTGATTGAAGAA
GCTGAGCGCTCCATTCATGATGCCCTATGTGTTATTCGTTGTTTAGTGAAGAAGAGGGCTCTTATTGCAGGAGGT
GGTGCTCCAGAAATAGAGTTGGCCCTAGCATTAACTGAATATTCACGAACACTGAGTGGTATGGAATCCTACTGC
GTTCGTGCTTTTGCAGATGCTATGGAGGTCATTCCATCTACACTAGCTGAAAATGCCGGCCTGAATCCCATTTCT
ACAGTAACAGAACTAAGAAACCGGCATGCCCAGGGAGAAAAAACTGCAGGCATTAATGTCCGAAAGGGTGGTATT
TCCAACATTTTGGAGGAACTGGTTGTCCAGCCTCTGTTGGTATCAGTCAGTGCTCTGACTCTTGCAACTGAAACT
GTTCGGAGCATTCTGAAAATAGATGATGTGGTAAACACTCGA**TAA**TCTGGATAACTGACTAGCACCATTATGATC
ACCAGTATTGTGGCTGGAATGGAAGAAGATCACCTTGGTGTTCCTTGTTTGGAAGATTATTTCCTCTGAATTTCT
GGGCTTGGTCTTCCAGTTGGCATTTGCCTGAAGTTGTATTGAAACAATTTAATGAAAATATTAAATATTTGGTTT
CAAAAGGCAGATTTATCTTCTCCCAACATTCTGTTATTTCTGATACTTTTGAAAAACTAATAAAAACTAATAAAA
GAAGCGTA

FIGURE 110

MPENVAPRSGATAGAAGGRGKGAYQDRDKPAQIRFSNISAAKAVADAIRTSLGPKGMDKMIQDGKGDVTITNDGA
TILKQMQVLHPAARMLVELSKAQDIEAGDGTTSVVIIAGSLLDSCTKLLQKGIHPTIISESFQKALEKGIEILTD
MSRPVELSDRETLLNSATTSLNSKVVSQYSSLLSPMSVNAVMKVIDPATATSVDLRDIKIVKKLGGTIDDCELVE
GLVLTQKVSNSGITRVEKAKIGLIQFCLSAPKTDMDNQIVVSDYAQMDRVLREERAYILNLVKQIKKTGCNVLLI
QKSILRDALSDLALHFLNKMKIMVIKDIEREDIEFICKTIGTKPVAHIDQFTADMLGSAELAEEVNLNGSGKLLK
ITGCASPGKTVTIVVRGSNKLVIEEAERSIHDALCVIRCLVKKRALIAGGGAPEIELALALTEYSRTLSGMESYC
VRAFADAMEVIPSTLAENAGLNPISTVTELRNRHAQGEKTAGINVRKGGISNILEELVVQPLLVSVSALTLATET
VRSILKIDDVVNTR

FIGURE 111

CTGCGGCGCGCCGGGCGGAACTTTCTAGAACGCTCGGTGAGAGGCGGAGGAGCGGTAACTACCCCGGCTGCGCAC
AGCTCGGCGCTCCTTCCCGCTCCCTCACACACCGGCCTCAGCCCGCACCGGCAGTAGAAG**ATG**GTGAAAGAAACA
ACTTACTACGATGTTTTGGGGGTCAAACCCAATGCTACTCAGGAAGAATTGAAAAAGGCTTATAGGAAACTGGCT
TTGAAGTACCATCCTGATAAGAACCCAAATGAAGGAGAGAAGTTTAAACAGATTTCTCAAGCTTACGAAGTTCTC
TCTGATGCAAAGAAAAGGGAATTATATGACAAAGGAGGAGAACAGGCAATTAAAGAGGGTGGAGCAGGTGGCGGT
TTTGGCTCCCCCATGGACATCTTTGATATGTTTTTTGGAGGAGGAGGAAGGATGCAGAGAGAAAGGAGAGGTAAA
AATGTTGTACATCAGCTCTCAGTAACCCTAGAAGACTTATATAATGGTGCAACAAGAAAACTGGCTCTGCAAAAG
AATGTGATTTGTGACAAATGTGAAGGTAGAGGAGGTAAGAAAGGAGCAGTAGAGTGCTGTCCCAATTGCCGAGGT
ACTGGAATGCAAATAAGAATTCATCAGATAGGACCTGGAATGGTTCAGCAAATTCAGTCTGTGTGCATGGAGTGC
CAGGGCCATGGGGAGCGGATCAGTCCTAAAGATAGATGTAAAAGCTGCAACGGAAGGAAGATAGTTCGAGAGAAG
AAAATTTTAGAAGTTCATATTGACAAAGGCATGAAAGATGGCCAGAAGATAACATTCCATGGTGAAGGAGACCAA
GAACCAGGACTGGAGCCAGGCGATATTATCATTGTGTTAGATCAGAAGGACCATGCTGTTTTTACTCGACGAGGA
GAAGACCTTTTCATGTGTATGGACATACAGCTCGTTGAAGCACTGTGTGGCTTCCAGAAGCCAATATCTACTCTT
GACAACCGAACCATCGTCATCACCTCTCATCCAGGTCAGATTGTCAAGCATGGAGATATCAAGTGTGTACTAAAT
GAAGGCATGCCAATTTATCGTAGACCATATGAAAAGGGTCGCCTAATCATCGAATTTAAGGTAAACTTTCCTGAG
AATGGCTTTCTCTCTCCTGATAAACTGTCTTTGCTGGAAAAACTCCTACCCGAGAGGAAGGAAGTGGAAGAGACT
GATGAGATGGACCAAGTAGAACTGGTGGACTTTGATCCAAATCAGGAAAGACGGCGCCACTACAATGGAGAAGCA
TATGAGGATGATGAACATCATCCCAGAGGTGGTGTTCAGTGTCAGACCTCT**TAA**TGGGCCAGTGAATAACACTCA
CTGCTGGCATTTAATGTGCAGTAGTGAATGAGTGAAGGACTGTAATCATAATATGCTCACTACTTGCTCTTGTTT
TTGTTTTAATAAACTATAGTAGTGTTTTAAAAAGTTAAATGAAGAATAAACGCAAATATAAAAGCTCTGATTTTG
CCCTGTATGTATGATGACTTCAGTGTGCAAGATGAAGTTTAATACCTGTAAAAACTACAAAGAAGTTCCCCTAGC
ATTTCTAGGCCAAACCTTGTAATTGACTTCAGCTATGTACGTGGACAAGCTTAGACTGAAATGCTAGGTATATGT
ATTGGCTTCAGTGTATGACCCTTCATTGTTAAGCTATGAAAGTAAAACTCTGTATTTAACTGGCAATGAGGAAAA
AAAAATTTTGTAGAGAAGTGTTGGTCTGTATAGTTCTTTATATTAAGTGGGATTCATTGTAATGCCTCTGCATTT
ATTCTGTTGCCTCAGCTGTTACTTGAAGATGGCGTAATATATAATTTATCCTGTGGTATCAGTGATAAAAATGAT
ACCTTTCTGTAGGAGGGGTTTATCATAATATGCTGCTTCTTGAAGGCTTGCACTTCCAGAATTGTGTTTCCTTCT
GCTGTGCCATTCATATATATATACATATATATATATAATCTTGACCAGTCCTGGTCATTTGCTCCCCTCCTTGTC
TGTGGACCATGATAAGCCCAAGTAGTGACTTCAGAGCTGGGTAACAGAAATTAAAGTGAAAAGACCTTTACGTGG
AGAATTTGCATGCGTAATATAGGAAGGTGTTCTTTAGGTATGTTACAGGATTACTTTAAACCATTTGACTTTCGC
TCCAAAGTTATGTTGGTAGTATAGCAAATTATGATGAATAGCTTTAATTGTATGTTTAAAAGTCTCATATGTTCA
CATGCTTAAATCTGGGTATCAGAATTTAAGCAATTCTTGAAATGTATTGTCTCCTTAATATACTAATTACAAAGC
ATCTCCAATGTGTGTCACTACAGGCTTTTTTTTCCCAGATCATCAAATTTTGGCTTTTAACTAAGATACATAGCT
TTATTTTAGCTAGTCTGAATGAGTGATACAAAAATACTATTGAACTATAGTTAAATAATATTAAATAGGATGGAG
AGTAAAAGTGGAGGACTGGGTAATGAGCCAAGAAGAAGGGGTG

FIGURE 112

MVKETTYYDVLGVKPNATQEELKKAYRKLALKYHPDKNPNEGEKFKQISQAYEVLSDAKKRELYDKGGEQAIKEG
GAGGGFGSPMDIFDMFFGGGGRMQRERRGKNVVHQLSVTLEDLYNGATRKLALQKNVICDKCEGRGGKKGAVECC
PNCRGTGMQIRIHQIGPGMVQQIQSVCMECQGHGERISPKDRCKSCNGRKIVREKKILEVHIDKGMKDGQKITFH
GEGDQEPGLEPGDIIIVLDQKDHAVFTRRGEDLFMCMDIQLVEALCGFQKPISTLDNRTIVITSHPGQIVKHGDI
KCVLNEGMPIYRRPYEKGRLIIEFKVNFPENGFLSPDKLSLLEKLLPERKEVEETDEMDQVELVDFDPNQERRRH
YNGEAYEDDEHHPRGGVQCQTS

FIGURE 113

CGGTAACTACCCCGGCTGCGCACAGCTCGGCGCTCCTTCCCGCTCCCTCACACACCGCCTCAGCCCGCACCGGCA
GTAGAAG**ATG**GTGAAAGAAACAACTTACTACGATGTTTTGGGGGTCAAACCCAATGCTACTCAGGAAGAATTGAA
AAAGGCTTATAGGAAACTGGCCTTGAAGTACCATCCTGATAAGAACCCAAATGAAGGAGAGAAGTTTAAACAGAT
TTCTCAAGCTTACGAAGTTCTCTCTGATGCAAAGAAAAGGGAATTATATGACAAAGGAGGAGAACAGGCAATTAA
AGAGGGTGGAGCAGGTGGCGGTTTTGGCTCCCCCATGGACATCTTTGATATGTTTTTTGGAGGAGGAGGAAGGAT
GCAGAGAGAAAGGAGAGGTAAAAATGTTGTACATCAGCTCTCAGTAACCCTAGAAGACTTATATAATGGTGCAAC
AAGAAAACTGGCTCTGCAAAAGAATGTGATTTGTGACAAATGTGAAGGTAGAGGAGGTAAGAAAGGAGCAGTAGA
GTGCTGTCCCAATTGCCGAGGTACTGGAATGCAAATAAGAATTCATCAGATAGGACCTGGAATGGTTCAGCAAAT
TCAGTCTGTGTGCATGGAGTGCCAGGGCCATGGGGAGCGGATCAGTCCTAAAGATAGATGTAAAAGCTGCAACGG
AAGGAAGATAGTTCGAGAGAAGAAAATTTTAGAAGTTCATATTGACAAAGGCATGAAAGATGGCCAGAAGATAAC
ATTCCATGGTGAAGGAGACCAAGAACCAGGACTGGAGCCAGGCGATATTATCATTGTGTTAGATCAGAAGGACCA
TGCTGTTTTTACTCGACGAGGAGAAGACCTTTTCATGTGTATGGACATACAGCTCGTTGAAGCACTGTGTGGCTT
CCAGAAGCCAATATCTACTCTTGACAACCGAACCATCGTCATCACCTCTCATCCAGGTCAGATTGTCAAGCATGG
AGATATCAAGTGTGTACTAAATGAAGGCATGCCAATTTATCGTAGACCATATGAAAAGGGTCGCCTAATCATCGA
ATTTAAGGTAAACTTTCCTGAGAATGGCTTTCTCTCTCCTGATAAACTGTCTTTGCTGGAAAAACTCCTACCCGA
GAGGAAGGAAGTGGAAGAGACTGATGAGATGGACCAAGTAGAACTGGTGGACTTTGATCCAAATCAGGAAAGACG
GCGCCACTACAATGGAGAAGCATATGAGGATGATGAACATCATCCCAGAGGTGGTGTTCAGTGTCAGACCTCT**TA**
ATGGCCAGTGAATAACACTCACTGCTGGCATTTAATGTGCAGTAGTGAATGAGTGAAGGACTGTAATCATAATAT
GCTCACTACTTGCTCTTGTTTTTGTTTTAATAAACTATAGTAGTGTTATAAAAAGTTAAATGAAGAATAAACGCA
AATATAAAAGCTC

FIGURE 114

MVKETTYYDVLGVKPNATQEELKKAYRKLALKYHPDKNPNEGEKFKQISQAYEVLSDAKKRELYDKGGEQAIKEG
GAGGGFGSPMDIFDMFFGGGGRMQRERRGKNVVHQLSVTLEDLYNGATRKLALQKNVICDKCEGRGGKKGAVECC
PNCRGTGMQIRIHQIGPGMVQQIQSVCMECQGHGERISPKDRCKSCNGRKIVREKKILEVHIDKGMKDGQKITFH
GEGDQEPGLEPGDIIIVLDQKDHAVFTRRGEDLFMCMDIQLVEALCGFQKPISTLDNRTIVITSHPGQIVKHGDI
KCVLNEGMPIYRRPYEKGRLIIEFKVNFPENGFLSPDKLSLLEKLLPERKEVEETDEMDQVELVDFDPNQERRRH
YNGEAYEDDEHHPRGGVQCQTS

FIGURE 115

GGGCGGGGTGCCGCATCCCCAGCCCGCCGCC**ATG**GCCGCCTACAAACTGGTGCTGATCCGGCACGGCGAGAGCGC
ATGGAACCTGGAGAACCGCTTCAGCGGCTGGTACGACGCCGACCTGAGCCCGGCGGGCCACGAGGAGGCGAAGCG
CGGCGGGCAGGCGCTACGAGATGCTGGCTATGAGTTTGACATCTGCTTCACCTCAGTGCAGAAGAGAGCGATCCG
GACCCTCTGGACAGTGCTAGATGCCATTGATCAGATGTGGCTGCCAGTGGTGAGGACTTGGCGCCTCAATGAGCG
GCACTATGGGGGTCTAACCGGTCTCAATAAAGCAGAAACTGCTGCAAAGCATGGTGAGGCCCAGGTGAAGATCTG
GAGGCGCTCCTATGATGTCCCACCACCTCCGATGGAGCCCGACCATCCTTTCTACAGCAACATCAGTAAGGATCG
CAGGTATGCAGACCTCACAGAAGATCAGCTACCCTCCTGTGAGAGTCTGAAGGATACTATTGCCAGAGCTCTGCC
CTTCTGGAATGAAGAAATAGTTCCCCAGATCAAGGAGGGGAAACGTGTACTGATTGCAGCCCATGGCAACAGCCT
CCGGGGCATTGTCAAGCATCTGGAGGGTCTCTCTGAAGAGGCTATCATGGAGCTGAACCTGCCGACTGGTATTCC
CATTGTCTATGAATTGGACAAGAACTTGAAGCCTATCAAGCCCATGCAGTTTCTGGGGGGATGAAGAGACGGTGCG
CAAAGCCATGGAAGCTGTGGCTGCCCAGGGCAAGGCCAAGAAG**TGA**AGGCCGGCGGGGAGGATACTGTCCCCAGG
AGCACCCTCCCTGCCCGTCTTGTCCCTCTGCCCCTCCCACCTGCACATGTCACACTGACCACATCTGTAGACATC
TTGAGTTGTAGCTGCAGACGGGGACCAGTGGCTCCCATTTTCATTTTAGCCATTTTGTCGCCTGCACCCACTCCC
TTCATACAATCTAGTCAGAATAGCAGTTCTAGAGCACAGGTTCTCAGTCTAAGCTATGGAAAAGCTCCCCTTATC
CAACAGAGTTTAAAAGTAGTGACTTGGGTTTTTGCGAGTGCTTTGTTTACTAAGGACTTTGGGGAGGAACCATGC
TAAGCCATGACCAGTGAGGAGAAGCAACAGAGCCTGTCTGTCCCCATGAGCGGAGTCTGTCCTCTGCTCTTCTGC
AGTCAGGTCACTGCCTACTGCCTGGGGGCTCTAGTCATTCCAGTGGAAGACGAATGTAACCTGCGTGGTGATGTG
ACAACTGTTTCCTCCCTGACCCCAGAGGATCTGGCTCTAGGTTGGGATCAATCCTGAATTTCGTTATGTGTTAAT
TTACTTTTATTAAAAAAGTATAGTATATATAATACAAAACAATAACCCTTCTGGGGTTTCTTGTGGCGGTTGAAA
TAGTCCCACATGTGGTCATCAGAAATAGCATTCCTCATACCAATATAGGATCAGCTCCTTGACCTCTGAGGGGTC
AGGAGTGCTTCCTGGTGTGTGTATTAGAATCCCTTCCTGCCTTGTTTCATGGCAGTGAAATGCCTCTTGGTCCTG
TCCAGTGTATCTTTCACTGATTTCTGAATCATGTTCTAGTTGCTTGACCCTGCCACATGGGTCCAGTGTTCATCT
GAGCATAACTGTACTAAATCCTTTTTCCATATCAGTATAATAAAGGAGTGATGTGCAAT

FIGURE 116

MAAYKLVLIRHGESAWNLENRFSGWYDADLSPAGHEEAKRGGQALRDAGYEFDICFTSVQKRAIRTLWTVLDAID
QMWLPVVRTWRLNERHYGGLTGLNKAETAAKHGEAQVKIWRRSYDVPPPPMEPDHPFYSNISKDRRYADLTEDQL
PSCESLKDTIARALPFWNEEIVPQIKEGKRVLIAAHGNSLRGIVKHLEGLSEEAIMELNLPTGIPIVYELDKNLK
PIKPMQFLGDEETVRKAMEAVAAQGKAKK

FIGURE 117

GAATTCGGCACGAGGGCGACCGGCGCGTCGTGCGGGGCTGCGGCGGAGCCTCCTTAAGGAAGGTGCAAGAGGTTG
GCAGCTTCGATTGAAGCACATCGACCGGCGACAGCAGCCAGGAGTC**ATG**AGCGACAGCGGCGAGCAGAACTACGG
CGAGCGGGAATCCCGTTCTGCTTCCAGAAGTGGAAGTGCTCACGGATCGGGGAAATCTGCAAGGCATACCCCTGC
AAGGTCTCGCTCCAAGGAAGATTCCAGGCGTTCCAGATCAAAGTCCAGGTCCCGATCTGAATCTAGGTCTAGATC
CAGAAGAAGCTCCCGAAGGCATTATACCCGGTCACGGTCTCGCTCCCGCTCCCATAGACGATCACGTAGCAGGTC
TTACAGTCGAGATTATCGTAGACGGCACAGCCACAGCCATTCTCCCATGTCTACTCGCAGGCGTCATGTTGGGAA
TCGGGCAAATCCTGATCCTAACTGTTGTCTTGGAGTATTTGGGCTGAGCTTGTACACCACAGAAAGAGATCTAAG
AGAAGTGTTCTCTAAATATGGTCCCATTGCCGATGTGTCTATTGTATATGACCAGCAGTCTAGGCGTTCAAGAGG
ATTTGCCTTTGTATATTTTGAAAATGTAGATGATGCCAAGGAAGCTAAAGAACGTGCCAATGGAATGGAGCTTGA
TGGGCGTAGGATCAGAGTTGATTTCTCTATAACAAAAAGACCACATACGCCAACACCAGGAATTTACATGGGGAG
ACCTACCTATGGCAGCTCTCGCCGTCGGGATTACTATGACAGAGGATATGATCGGGGCTATGATGATCGGGACTA
CTATAGCAGATCATACAGAGGAGGAGGTGGAGGAGGAGGAGGATGGAGAGCTGCCCAAGACAGGGATCAGATTTA
TAGAAGGCGGTCACCTTCTCCTTACTATAGTCGTGGAGGATACAGATCACGTTCCAGATCTCGATCATACTCACC
TCGTCGCTAT**TAA**AGCATGAAGACTTTCTGAAACCTGCCCTAGAGCTGGGATATTGTTTGTGGGCAATATTTTTT
ATTGTCTCTTGTTTAAAAAGTGAACAGTGCCTAGTGAAGTTAGGTGACTTTTACACCTTTTACGATGACTACTTT
TGGTGGAGTTGAAATGCTGTTTTCATTCTGCATTTGTGTAGTTTGGTGCTTTGTTCCAAGTTAAGTGTTTTCAGA
AAAGTATGTTTTGCATGTATTTTTTTACAGTCTAAATTTTGACTGCTGAGAAGTTTCTATTGTACAAAACTTCAT
TTAAAAGGTTTTTCTACTGAATCCAGGGTATTCTGAAGATCGAAGCCTGTGTAAAATGCTACCAAATGGCAAAAA
GCAACAATAAACAGTTTGATTTTTACTTTTCTTTCTAACATATCAATGCTTAGCAGAACTATTCAGATTGTCAGT
AGTAAATTTAAAGACAAATGCCCGTTTTCCTCCAGTCCATGAAACATACCATACTTATATACCTGCAACTAAGTG
TTTAAAATTATGCTCTGTAACTCTGTACTGCTAGTATTAGAACTAAAAATCTTAAAATACAGCCAGTGCTTAATG
CTTATATCAATGTGGATTTGTCGGCTTTTATGTAATCTGTAATATGTATAGCAGGAAATACGAAGAGTTACACAG
TGTATGCCTTAAAAGGCTGTTTCTTAAAGGTGTTACAAGGGGATAATGGTATTTCAACTAGTTATCAGCAAGTGA
CAATACATTCCACCACAAATACACTCTTGTTCTTCTAGCTTTTAGACTATATGAAAAAACCGGGTGCTTCAAAGT
ACATGATAAGGGAACACTATACCTGTCATGGATGAACTGAAGACTTTGCCTGTTCATTTTTTAAATATTATTTTC
AGGTCCTTTGCTTACCAAAGGAGGCCCAATTTCACTCAAATGTTTTGAGAACTGTGTTTAAATAAACGCAAATGA
AAAGAAAAAAAAAAAAAAAAAA

FIGURE 118

MSDSGEQNYGERESRSASRSGSAHGSGKSARHTPARSRSKEDSRRSRSKSRSRSESRSRSRRSSRRHYTRSRSRS
RSHRRSRSRSYSRDYRRRHSHSHSPMSTRRRHVGNRANPDPNCCLGVFGLSLYTTERDLREVFSKYGPIADVSIV
YDQQSRRSRGFAFVYFENVDDAKEAKERANGMELDGRRIRVDFSITKRPHTPTPGIYMGRPTYGSSRRRDYYDRG
YDRGYDDRDYYSRSYRGGGGGGGGWRAAQDRDQIYRRRSPSPYYSRGGYRSRSRSRSYSPRRY

FIGURE 119

ATACACGTGCCATGTGCAGCATGAGGGGCTACCCGAGCCCGTCACCCTGAGATGGAAGCCGGCTTCCCAGCCCAC
CATCCCCATCGTGGGCATCATTGCTGGCCTGGTTCTCCTTGGATCTGTGGTCTCTGGAGCTGTGGTTGCTGCTGT
GATATGGAGGAAGAAGAGCTCAGGTGGAAAAGGAGGGAGCTACTCTAAGGCTGAGTGGAGCGACAGTGCCCAGGG
GTCTGAGTCTCACAGCTTGTAAAGCCTGAGACAGCTGCCTTGTGTGCGACTGAGATGCACAGCTGCCTTGTGTGC
GACTGAGATGCAGGATTTCCTCACGCCTCCCCTATGTGTCTTAGGGGACTCTGGCTTCTCTTTTTGCAAGGGCCT
CTGAATCTGTCTGTGTCCCTGTTAGCACAATGTGAGGAGGTAGAGAAACAGTCCACCTCTGTGTCTACCATGACC
CCCTTCCTCACACTGACCTGTGTTCCTTCCCTGTTCTCTTTTCTATTAAAAATAAGAACCTGGGCAGAGTGCGGC
AGCTCATGCCTGTAATCCCAGCACTTAGGGAGGCCGAGGAGGGCAGATCACGAGGTCAGGAGATCGAAACCATCC
TGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAATTAGCTGGGCGCAGAGGCACGGGCCTGTAG
TCCCAGCTACTCAGGAGGCGGAGGCAGGAGAATGGCGTCAACCCGGGAGGCGGAGGTTGCAGTGAGCCAGGATTG
TGCGACTGCACTCCAGCCTGGGTGACAGGGTGAAACGCCATCTCAAAAAATAAAAATTAAAAAATAAAAAAAGAA
CCTGGATCTCAATTTAATTTTTCATATTCTTGCAATGAAATGGACTTGAGGAAGCTAAGATCATAGCTAGAAATA
CAGATAATTCCACAGCACATCTCTAGCAAATTTAGCCTATTCCTATTCTCTAGCCTATTCCTTACCACCTGTAAT
CTTGACCATATACCTTGGAGTTGAATATTGTTTTCATACTGCTGTGGTTTGAATGTTCCCTCCAACACTCATGTT
GAGACTTAATCCCTAATGTGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGCCTT
CATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATAAGAAGAGGAAAAGAGAAC
TGAGCTAGCATGCCCAACCCACAGAGAGCCTCCACTAGAGTGATGCTAAGTGGAAATGTGAGGTGCAGCTGCCAC
AGAGGGCCCCCACCAGGGAAATGTCTAGTGTCTAGTGGATCCAGGCCACAGGAGAGAGTGCCTTGTGGAGCGCTG
GGAGCAGGACCTGACCACCACCAGGACCCCAGAACTGTGGAGTCAGTGGCAGCATGCAGCGCCCCCTTGGGAAAG
CTTTAGGCACCAGCCTGCAACCCATTCGAGCAGCCACGTAGGCTCGACCCAGCAAAGCCACAGGCACGGGGCTAC
CTGAGGCCTTGGGGGCCAATCCCTGCTCCAGTGTGTCCGTGAGGCAGCACACGAAGTCAAAAGAGATTATCTCTT
CCCACAGATACCTTTTCTCTCCCATGACCCTTTAACAGCATCTGCTTCATTCCCCTCACCTTCCCAGGCTGATCT
GAGGTAAACTTTGAAGTAAAATAAAAGCTGTGTTTGAGCATC

FIGURE 120

ATGGGGCATCGGCCGGTGCTCGTGCTCAGCCAGAACACAAAGCGTGAATCCGGAAGAAAAGTTCAATCTGGAAAC
ATCAATGCTGCCAAGACTATTGCAGATATCATCCGAACATGTTTGGGACCCAAGTCCATGATGAAGATGCTTTTG
GACCCAATGGGAGGCATTGTGATGACCAATGATGGCAATGCCATTCTTCGAGAGATTCAAGTCCAGCATCCAGCG
GCCAAGTCCATGATCGAAATTAGCCGGACCCAGGATGAAGAAGTTGGAGATGGGACCACATCAGTAATTATTCTT
GCAGGGGAAATGCTGTCTGTAGCTGAGCACTTCCTGGAGCAGCAGATGCACCCAACAGTGGTGATCAGTGCTTAC
CGCAAGGCATTGGATGATATGATCAGCACCCTAAAGAAAATAAGTATCCCAGTCGACATCAGTGACAGTGATATG
ATGCTGAACATCATCAACAGCTCTATTACTACCAAAGCCATCAGCCGGTGGTCATCTTTGGCTTGCAACATTGCC
CTGGATGCTGTCAAGATGGTACAGTTTGAGGAGAATGGTCGGAAAGAGATTGACATAAAAAAATATGCAAGAGTG
GAAAAGATACCTGGAGGCATCATTGAAGACTCCTGTGTCTTGCGTGGAGTCATGATTAACAAGGATGTGACCCAT
CCACGTATGCGGCGCTATATCAAGAACCCTCGCATTGTGCTGCTGGATTCTTCTCTGGAATACAAGAAAGGAGGA
AGCCAGACTGACATTGAGATTACACGAGAGGAGGACTTCACCCGAATTCTCCAGATGGAGGAAGAGTACATCCAG
CAGCTCTGTGAGGACATTATCCAACTGAAGCCCGATGTGGTCATCACTGAAAAGGGCATCTCAGATTTAGCTCAG
CACTACCTTATGCGGGCCAATATCACAGCCATCCGCAGAGTCCGGAAGACAGACAATAATCGCATTGCTAGAGCC
TGTGGGGCCCGGATAGTCAGCCGACCAGAGGAACTGAGAGAAGATGATGTTGGAACAGGAGCAGGCCTGTTGGAA
ATCAAGAAAATTGGAGATGAATACTTTACTTTCATCACTGACTGCAAAGACCCCAAGGCCTGCACCATTCTCCTC
CGGGGGGCTAGCAAAGAGATTCTCTCGGAAGTAGAACGCAACCTCCAGGATGCCATGCAAGTGTGTCGCAATGTT
CTCCTGGACCCTCAGCTGGTGCCAGGGGGTGGGGCCTCCGAGATGGCTGTCGCCCATGCCTTGACAGAAAAATCC
AAGGCCATGACTGGTGTGGAACAATGGCCATACAGGGCTGTTGCCCAGGCCCTAGAGGTCATTCCTCGTACCCTG
ATCCAGAACTGTGGGGCCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAACTGTGAG
ACCTGGGGTGTAAATGGTGAGACGGGTACTTTGGTGGACATGAAGGAACTGGGCATATGGGAGCCATTGGCTGTG
AAGCTGCAGACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGACATCGTTTCAGGCCAC
AAAAAGAAAGGCGATGACCAGAGCCGGCAAGGCGGGGCTCCTGATGCTGGCCAGGAG**TGA**GTGCTAGGCAAGGCT
ACTTCAATGCACAGAACCAGCAGAGTCTCCCCTTTTCCTGAGCCAGAGTGCCAGGAACACTGTGGACGTCTTTGT
TCAGAAGGGATCAGGTTGGGGGGCAGCCCCCAGTCCCTTTCTGTCCCAGCTCAGTTTTCCAAAAGACACTGACAT
GTAATTCTTCTCTATTGTAAGGTTTCCATTTAGTTTGCTTCCGATGATTAAATCTAAGTCATTTGAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 121

MGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMKMLLDPMGGIVMTNDGNAILREIQVQHPA
AKSMIEISRTQDEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTVVISAYRKALDDMISTLKKISIPVDISDSDM
MLNIINSSITTKAISRWSSLACNIALDAVKMVQFEENGRKEIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH
PRMRRYIKNPRIVLLDSSLEYKKGGSQTDIEITREEDFTRILQMEEEYIQQLCEDIIQLKPDVVITEKGISDLAQ
HYLMRANITAIRRVRKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDCKDPKACTILL
RGASKEILSEVERNLQDAMQVCRNVLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTL
IQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTLVDMKELGIWEPLAVKLQTYKTAVETAVLLLRIDDIVSGH
KKKGDDQSRQGGAPDAGQE

FIGURE 122

GGCACGAGGACCGACCGCATTGCGGCTTGGTTTTCTCACCCAGTGCATGTGGCAGGAGCGGTGAGATCACTGCCT
CACGGCGATCCTGGACTGACGGTCACGACTGCCTACCCTCTAACCCTGTTCTGAGCTGCCCCTTGCCCACACACC
CCAAACCTGTGTGCAGGATCCGCCTCCATGGAGCTACAGCCTCCTGAAGCCTCGATCGCCGTCGTGTCGATTCCG
CGCCAGTTGCCTGGCTCACATTCGGAGGCTGGTGTCCAGGGTCTCAGCGCGGGGGACGACTCAGAGTTGGGGTCT
CACTGTGTTGCCCAGACTGGTCTCGAACTCTTGGCCTCAGGTGATCCTCTTCCCTCAGCTTCCCAGAATGCCGAG
ATGATAGAGACGGGGTCTGACTGTGTTACCCAGGCTGGTCTTCAACTCTTGGCCTCAAGTGATCCTCCTGCCTTA
GCTTCCAAGAATGCTGAGGTTACAGGCACC**ATG**AGCCAGGACACCGAGGTGGATATGAAGGAGGTGGAGCTGAAT
GAGTTAGAGCCCGAGAAGCAGCCGATGAACGCGGCGTCTGGGGCGGCCATGTCCCTGGCGGGAGCCGAGAAGAAT
GGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCGGCAGCCGCGGCTAAGTTCACGGGCCTGTCCAAG
GAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGCACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTC
GGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTCATAATCGTGCGAGCGCCGCGTTGTCGCGAGCTACCGGCGCAG
AAGTGGTGGCACACGGGCGCCCTCTACCGCATCGGCGACCTTCAGGCCTTCCAGGGCCACGGCGCGGGCAACCTG
GCGGGTCTGAAGGGGCGTCTCGATTACCTGAGCTCTCTGAAGGTGAAGGGCCTTGTGCTGGGTCCAATTCACAAG
AACCAGAAGGATGATGTCGCTCAGACTGACTTGCTGCAGATCGACCCCAATTTTGGCTCCAAGGAAGATTTTGAC
AGTCTCTTGCAATCGGCTAAAAAAAAGAGCATCCGTGTCATTCTGGACCTTACTCCCAACTACCGGGGTGAGAAC
TCGTGGTTCTCCACTCAGGTTGACACTGTGGCCACCAAGGTGAAGGATGCTCTGGAGTTTTGGCTGCAAGCTGGC
GTGGATGGGTTCCAGGTTCGGGACATAGAGAATCTGAAGGATGCATCCTCATTCTTGGCTGAGTGGCAAAATATC
ACCAAGGGCTTCAGTGAAGACAGGCTCTTGATTGCGGGGACTAACTCCTCCGACCTTCAGCAGATCCTGAGCCTA
CTCGAATCCAACAAAGACTTGCTGTTGACTAGCTCATACCTGTCTGATTCTGGTTCTACTGGGGAGCATACAAAA
TCCCTAGTCACACAGTATTTGAATGCCACTGGCAATCGCTGGTGCAGCTGGAGTTTGTCTCAGGCAAGGCTCCTG
ACTTCCTTCTTGCCGGCTCAACTTCTCCGACTCTACCAGCTGATGCTCTTCACCCTGCCAGGGACCCCTGTTTTC
AGCTACGGGGATGAGATTGGCCTGGATGCAGCTGCCCTTCCTGGACAGCCTATGGAGGCTCCAGTCATGCTGTGG
GATGAGTCCAGCTTCCCTGACATCCCAGGGGCTGTAAGTGCCAACATGACTGTGAAGGGCCAGAGTGAAGACCCT
GGCTCCCTCCTTTCCTTGTTCCGGCGGCTGAGTGACCAGCGGAGTAAGGAGCGCTCCCTACTGCATGGGGACTTC
CACGCGTTCTCCGCTGGGCCTGGACTCTTCTCCTATATCCGCCACTGGGACCAGAATGAGCGTTTTCTGGTAGTG
CTTAACTTTGGGGATGTGGGCCTCTCGGCTGGACTGCAGGCCTCCGACCTGCCTGCCAGCGCCAGCCTGCCAGCC
AAGGCTGACCTCCTGCTCAGCACCCAGCCAGGCCGTGAGGAGGGCTCCCCTCTTGAGCTGGAACGCCTGAAACTG
GAGCCTCACGAAGGGCTGCTGCTCCGCTTCCCCTACGCGGCC**TGA**CTTCAGCCTGACATGGACCCACTACCCTTC
TCCTTTCCTTCCCAGGCCCTTTGGCTTCTGATTTTTCTCTTTTTTTAAAAACAAACAAACAAACTGTTGCAAAAAA
AAAAAAAAAAAAA

FIGURE 123

MSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAGAEKNGLVKIKVAEDEAEAAAAAKFTGLSKEELLKVAGSP
GWVRTRWALLLLFWLGWLGMLAGAVVIIVRAPRCRELPAQKWWHTGALYRIGDLQAFQGHGAGNLAGLKGRLDYL
SSLKVKGLVLGPIHKNQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAKKKSIRVILDLTPNYRGENSWFSTQVDTV
ATKVKDALEFWLQAGVDGFQVRDIENLKDASSFLAEWQNITKGFSEDRLLIAGTNSSDLQQILSLLESNKDLLLT
SSYLSDSGSTGEHTKSLVTQYLNATGNRWCSWSLSQARLLTSFLPAQLLRLYQLMLFTLPGTPVFSYGDEIGLDA
AALPGQPMEAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLLSLFRRLSDQRSKERSLLHGDFHAFSAGPGLF
SYIRHWDQNERFLVVLNFGDVGLSAGLQASDLPASASLPAKADLLLSTQPGREEGSPLELERLKLEPHEGLLLRF
PYAA

FIGURE 124

GGCACGAGGCCCCGGTTCCGGCGCGGTTGAGGCCTTCGGTGGTGAACGAGTCTCCAGCACC**ATG**TCTGGTTTGTC
TGGCCCACCAGCCCGGCGCGGCCCTTTTCCGTTAGCGTTGCTGCTTTTGTTCCTGCTCGGCCCCAGATTGGTCCT
TGCCATCTCCTTCCATCTGCCCATTAACTCTCGCAAGTGCCTCCGTGAGGAGATTCACAAGGACCTGCTAGTGAC
TGGCGCGTACGAGATCTCCGACCAGTCTGGGGGCGCTGGCGGCCTGCGCAGCCACCTCAAGATCACAGATTCTGC
TGGCCATATTCTCTACTCCAAAGAGGATGCAACCAAGGGGAAATTTGCCTTTACCACTGAAGATTATGACATGTT
TGAAGTGTGTTTTGAGAGCAAGGGAACAGGGCGGATACCTGACCAACTCGTGATCCTAGACATGAAGCATGGAGT
GGAGGCGAAAAATTACGAAGAGATTGCAAAAGTTGAGAAGCTCAAACCATTAGAGGTAGAGCTGCGACGCCTAGA
AGACCTTTCAGAATCTATTGTTAATGATTTTGCCTACATGAAGAAGAGAGAAGAGGAGATGCGTGATACCAACGA
GTCAACAAACACTCGGGTCCTATACTTCAGCATCTTTTCAATGTTCTGTCTCATTGGACTAGCTACCTGGCAGGT
CTTCTACCTGCGACGCTTCTTCAAGGCCAAGAAATTGATTGAG**TAA**TGAATGAGGCATATTCTCCTCCCACCTTG
TACCTCAGCCAGCAGAACATCGCTGGGACGTGCCTGGCCTAAGGCATCCTACCAACAGCACCATCAAGGCACGTT
GGAGCTTTCTTGCCAGAACTGATCTCTTTTGGTGTGGGAGGACATGGGGTACCACCTACACCCAACAAGTCAATG
AGGGACTTCTTTTTAATTTGGTAGGATTTTGACTGGTTTTGCAACAATAGGTCTATTATTAGAGTCACCTATGAC
AAAAAATAGGGGTTACCTAGATAATGCCAAAGTCAGCATTTGTCCTGGGTTCCCTTGTGTGATCTGTTTGGACTA
TGTTTTCTTTTCTTCTCCCACTTGCTCAGCAGCTTGGGCTTCCATTCTAGTTCTTTTACCAAGATTTTTGTGTGA
CCATGTTGACTTCATTTGGATTGCCCTCTTTCAATTTCCTTGTGAAAACACCCTTAACTTTCTCTTTACCCTTAG
CTGAAATGTTTACATAGCTTCTGGTGATATCTTTTCATGATTTTATATCTCTTAAAATGGTGATGGATGTGACAC
CTCATAAAAGTGAGCTTTGAACTGTAGATAACTCTTAAAGAAAATGTCATTTTAGACAATTAAAATATTTGTGCT
CAACTGCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

MSGLSGPPARRGPFPLALLLLFLLGPRLVLAISFHLPINSRKCLREEIHKDLLVTGAYEISDQSGGAGGLRSHLK
ITDSAGHILYSKEDATKGKFAFTTEDYDMFEVCFESKGTGRIPDQLVILDMKHGVEAKNYEEIAKVEKLKPLEVE
LRRLEDLSESIVNDFAYMKKREEEMRDTNESTNTRVLYFSIFSMFCLIGLATWQVFYLRRFFKAKKLIE

FIGURE 126A

AGAGCGAGCAGGGGAGAGCGAGACCAGTTTTAAGGGGAGGACCGGTGCGAGTGAGGCAGCCCCGAGGCTCTGCTC
GCCCACCACCCAATCCTCGCCTCCCTTCTGCTCCACCTTCTCTCTCTGCCCTCACCTCTCCCCCGAAAACCCCCT
ATTTAGCCAAAGGAAGGAGGTCAGGGGAACGCTCTCCCCTCCCCTTCCAAAAAACAAAAACAGAAAAACCCTTTT
CCAGGCCGGGGAAAGCAGGAGGGAGAGGGGCCGCCGGGCTGGCC**ATG**GAGCTGCTGTGCCACGAGGTGGACCCGG
TCCGCAGGGCCGTGCGGGACCGCAACCTGCTCCGAGACGACCGCGTCCTGCAGAACCTGCTCACCATCGAGGAGC
GCTACCTTCCGCAGTGCTCCTACTTCAAGTGCGTGCAGAAGGACATCCAACCCTACATGCGCAGAATGGTGGCCA
CCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCGAAGAAGAGGTCTTCCCTCTGGCCATGAATTACCTGGACC
GTTTCTTGGCTGGGGTCCCGACTCCGAAGTCCCATCTGCAACTCCTGGGTGCTGTCTGCATGTTCCTGGCCTCCA
AACTCAAAGAGACCAGCCCGCTGACCGCGGAGAAGCTGTGCATTTACACCGACAACTCCATCAAGCCTCAGGAGC
TGCTGGAGTGGGAACTGGTGGTGCTGGGGAAGTTGAAGTGGAACCTGGCAGCTGTCACTCCTCATGACTTCATTG
AGCACATCTTGCGCAAGCTGCCCCAGCAGCGGGAGAAGCTGTCTCTGATCCGCAAGCATGCTCAGACCTTCATTG
CTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACCCACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCA
TCTGTGGGCTCCAGCAGGATGAGGAAGTGAGCTCGCTCACTTGTGATGCCCTGACTGAGCTGCTGGCTAAGATCA
CCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGGAGCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAGT
ACCGTCAGGACCAACGTGACGGATCCAAGTCGGAGGATGAACTGGACCAAGCCAGCACCCCTACAGACGTGCGGG
ATATCGACCTG**TGA**GGATGCCAGTTGGGCCGAAAGAGAGAGACGCGTCCATAATCTGGTCTCTTCTTCTTTCTGG
TTGTTTTTGTTCTTTGTGTTTTAGGGTGAAACTTAAAAAAAAAATTCTGCCCCCACCTAGATCATATTTAAAGAT
CTTTTAGAAGTGAGAGAAAAAGGTCCTACGAAAACGGAATAATAAAAAGCATTTGGTGCCTATTTGAAGTACAGC
ATAAGGGAATCCCTTGTATATGCGAACAGTTATTGTTTGATTATGTAAAAGTAATAGTAAAATGCTTACAGGAAA
ACCTGCAGAGTAGTTAGAGAATATGTATGCCTGCAATATGGGAACAAATTAGAGGAGACTTTTTTTTTTCATGTT
ATGAGCTAGCACATACACCCCTTGTAGTATAATTTCAAGGAACTGTGTACGCCATTTATGGCATGATTAGATTG
CAAAGCAATGAACTCAAGAAGGAATTGAAATAAGGAGGGACATGATGGGGAAGGAGTACAAAACAATCTCTCAAC
ATGATTGAACCATTTGGGATGGAGAAGCACCTTTGCTCTCAGCCACCTGTTACTAAGTCAGGAGTGTAGTTGGAT
CTCTACATTAATGTCCTCTTGCTGTCTACAGTAGCTGCTACCTAAAAAAAGATGTTTTATTTTGCCAGTTGGACA
CAGGTGATTGGCTCCTGGGTTTCATGTTCTGTGACATCCTGCTTCTTCTTCCAAATGCAGTTCATTGCAGACACC
ACCATATTGCTATCTAATGGGGAAATGTAGCTATGGGCCATAACCAAAACTCACATGAAACGGAGGCAGATGGAG
ACCAAGGGTGGGATCCAGAATGGAGTCTTTTCTGTTATTGTATTTAAAAGGGTAATGTGGCCTTGGCATTTCTTC
TTAGAAAAAAACTAATTTTTGGTGCTGATTGGCATGTCTGGTTCACAGTTTAGCATTGTTATAAACCATTCCATT
CGAAAAGCACTTTGAAAAATTGTTCCCGAGCGATAGATGGGATGGTTTATGCAAGTCATGCTGAATACTCCTCCC
CTCTTCTCTTTTGCCCCCTCCCTTCCTGCCCCCAGTCTGGGTTACTCTTCGCTTCTGGTATCTGGCGTTCTTTGG
TACACAGTTCTGGTGTTCCTACCAGGACTCAAGAGACACCCCTTCCTGCTGACATTCCCATCACAACATTCCTCA
GACAAGCCTGTAAACTAAAATCTGTTACCATTCTGATGGCACAGAAGGATCTTAATTCCCATCTCTATACTTCTC
CTTTGGACATGGAAAGAAAAGTTATTGCTGGTGCAAAGATAGATGGCTGAACATCAGGGTGTGGCATTTTGTTCC
CTTTTCCGTTTTTTTTTTTTTTATTGTTGTTGTTAATTTTATTGCAAAGTTGTATTCAGCGTACTTGAATTTTTC
TTCCTCTCCACTTCTTAGAGGCATTCAGTTAGCAAAGAGGTTGGAGCAACAACTTTTTTTTTTTTTTTTGCACAA
TTGTAATTGACAGGTAATGAAGCTATTTGTTAAAATATTTGCCTTTTTAAGTAAAAAAGAAAAATCAGAACAGGG
CTATTTGAAGAATTATTTTATACACAGATTCTGCCTTGTTTCATAGTATGAGGGTTGAAGACGGAAAACAATCTA
AGGGTCTCTCATTTTTTTAATTTTGTTTTGTTCAGTTTGGTTTTTTTTTTTTTTTGCGCTGCTAAGAAGCTAAAG
TCATCCATCCTTATTCACGTTGACAGTACCTAGCTGTAATGTTTCACAGAGTGTGCTGCTATTTTATAAACATTT
TTATAATATATTATTTTACTGCTTAAATTCCAAGTCCTGAAGTAGATGGTTGAGATATGAGTTCTTCGTACTGGA
AAAGCCCTTCCGTAGTTTGTTTTCTTCTGGTAGCATATTCATGGTTGTTTTTTTTTTTCTTTTTTGGTTTTTTGG
TTTTTTTTTTTTCCTCTGATCACATTCTTCAAAGACGGAGTATTCTTTACCTCAGGTTTACTGGACAAAATCAAT
AACTACAAAAGGCAATGATTCACGCTTTTGTTTTCATAATACCTCACAACCGTACAGTTTCTGCTTGGGAGCCCA
TTCGCATGAGGAATACAGAAGCAGTGTGAGCAGGGCTGACTCCCTCTCAGGTGGAAGGCAGGGCGGTCTCACTCC
CAGGGACCTTTTTGGTCATGGAGGCCATCGGGCTCCCAGTTAGACCCTGGTATCCTCATCATGATGGAAAAAATA
CATTGAACCAAGGGATCCTCCCTCCCCTTCAAGGCAGACGTTCAGTACAAACATTTATGCGGTAGGCTCAGATGT
CGTAATTTGCACTTAGGTACCAGGTGTCAGGAAACAGACTAAAAAGAATTCCACCAGGCTGTTTGGAGATCCTCA
TCTTGGAGCTTTTTCAAAAGCGGGGCTTCATCTGCAAAGGGCCCTTTCATCTTGAAGTTTTTCCCCTCCGTCTTT

FIGURE 126B

CCCCTCCCCTGGCATGGACACCTTGTGTTTAGGATCATCTCTGCAGGTTTCCTAGGTCTGAATCTGCGAGTAGAT
GAACCTGCAGCAAGCAGCGTTTATGGTGCTTCCTTCTCCCTCCTCTGTCTCAAACTGCGCAGGCAAGCACTATGC
AAGCCCAGGCCCTCTGCTGAGCGGTACTAAACGGTCGGGTTTTCAATCACACTGAATTGGCAGGATAAGAAAAAT
AGGTCAGATAAGTATGGGATGATAGTTGAAGGGAGGTGAAGAGGCTGCTTCTCTACAGAGGTGAAATTCCAGATG
AGTCAGTCTCTTGGGAAGTGTGTTTAGAAGGGTTCAGGACTTTGTGAGTTAGCATGACCCTAAAATTCTAGGGGA
TTTCTGGTGGGACAATGGGTGGTGAATTTTGAAGTTTTGGAGAGGGAAGTGGAGCAGCCAGCAAGTAAGCTAGCC
AGAGTTTTCTCAAGAGCCAGCTTTGCTCAGCACACTCTCCTGGGCCCCAAGGAGTCCCACGGAATGGGGAAAGTG
GGAACCCTGGAGTTCTTGGGAATCTTGGAGCCTAAAGAGAAACCGAGGTGCAAATTCATTTCATGGTGACTGACC
CTTGAGCTTAAACAGAAGCAGCAAATGAAAGAACCGGACAAATAAGGAAGGGCACAAGCCTACCCGACTCTATTT
ACAGTCTGTAACTTTCCACTCTTCCTGTAGTCCCGAGGCCCCTGGGTCCTTCTAGCTTTTCTCTTTCCCATCCTT
GGGGCCTTGTGTGATGATGGGTGTGGGGCTGCCGATGGGAAAGTCGGGGGTTGTTAGGCTTTTCTGCCTGCTCCT
GCTTAAACACAAGAAGGAATCCTGGATTTTGCCCTCTCCTTAGCTCTTAGTCTCTTTGGTAGGAGTTTTGTTCCA
GAGGAGCTCTCCCCCTTGGATTTGAACTTGCTCTTTTTGTTGTTGTTGTTCTTTCTCTTCTTTTTCTTACCTCCC
ACTAAAGGGGTTCCAAATTATCCTGGTCTTTTTCTACCTTGTTGTGTTTCTATCTCGTCTTTACTTCCATCTGTT
TGTTTTTTTCTCCATCAGTGGGGGCCGAGTTGTTCCCCCAGCCTGCCAAATTTTGATCCTTCCCCTCTTTTGGCC
AAATCCTAGGGGGAAGAAATCCTAGTATGCCAAAAATATATGCTAAGCATAATTAAACTCCATGCGGGTCCATAA
CAGCCAAGAAGCCTGCAGGAGAAAGCCAAGGGCAGTTCCCTCCGCAGAACACCCCATGCGTGCTGAGAGGCGAGC
TCCTTGAAGAAGGGGCTGTTCTTCCAGGAGGCCTTATTTTGAACTGCCTCAGGACCCCACTGGAGAGCACAGCAT
GCCTTACTACTGGGTCATCCTTGGTCTATGTGCTCTGTACTGGAGGCTCTGTTCTGCCTCTTATCAGCCAGGTCA
GGGGCACACATGGCTTAAGTGACAAAGCCAGAGGAGAAGACAACCCTGACAGCATCACGCTGCATCCCATTGCTA
GCAGGATTGGCAACTCTTCAGACGGAGCTGCGCTTCCCTGCAGTCTAGCACCTCTAGGGCCTCTCCAGACTGTGC
CCTGGGAGCTCTGGGACTGAAAGGTTAAGAACATAAGGCAGGATCAGATGACTCTCTCCAAGAGGGCAGGGGAAT
TTTCTCTCCATGGGCCACAGGGGACAGGGCTGGGAGAAGAAATAGACTTGCACCTTATGTCATGTAAATAATTGA
TTTTCTAGTTCAAGAAGATAATATTGGTAGTGTGGGAATTGGAGGTAGGAAGGGGAGGAAGTCTGAGTAAGCCAG
TTGGCTTCTAAGCCAAAAGGATTCCTCTTTGTTTATCTCTGAGACAGTCCAACCTTGAGAATAGCTTTAAAAGGG
AAATTAATGCTGAGATGATAAAGTCCCCTTAAGCCAACAAACCCTCTGTAGCTATAGAATGAGTGCAGGTTTCTA
TTGGTGTGGACTCAGAGCAATTTACAAGAGCTGTTCATGCAGCCATCCATTTGTGCAAAATAGGGTAAGAAGATT
CAAGAGGATATTTATTACTTCCTCATACCACATGGCTTTTGATGATTCTGGATTCTAAACAACCCAGAATGGTCA
TTTCAGGCACAACGATACTACATTCGTGTGTGTCTGCTTTTAAACTTGGCTGGGCTATCAGACCCTATTCTCGGC
TCAGGTTTTGAGAAGCCATCAGCAAATGTGTACGTGCATGCTGTAGCTGCAGCCTGCATCCCTTCGCCTGCAGCC
TACTTTGGGGAAATAAAGTGCCTTACTGACTGTAGCCATTACAGTATCCAATGTCTTTTGACAGGTGCCTGTCCT
TGAAAAACAAAGTTTCTATTTTTATTTTTAATTGGTTTAGTTCTTAACTGCTGGCCAACTCTTACATCCCCAGCA
AATCATCGGGCCATTGGATTTTTTCCATTATGTTCATCACCCTTATATCATGTACCTCAGATCTCTCTCTCTCTC
CTCTCTCTCAGTTATATAGTTTCTTGTCTTGGACTTTTTTTTTCTTTTCTTTTTCTTTTTTTTTTTTGCTTTAAAA
CAAGTGTGATGCCATATCAAGTCCATGTTATTCTCTCACAGTGTACTCTATAAGAGGTGTGGGTGTCTGTTTGGT
CAGGATGTTAGAAAGTGCTGATAAGTAGCATGATCAGTGTATGCGAAAAGGTTTTTAGGAAGTATGGCAAAAATG
TTGTATTGGCTATGATGGTGACATGATATAGTCAGCTGCCTTTTAAGAGGTCTTATCTGTTCAGTGTTAAGTGAT
TTAAAAAAATAATAACCTGTTTTCTGACTAGTTTAAAGATGGATTTGAAAATGGTTTTGAATGCAATTAGGTTAT
GCTATTTGGACAATAAACTCACCTTGACCT

FIGURE 127

MELLCHEVDPVRRAVRDRNLLRDDRVLQNLLTIEERYLPQCSYFKCVQKDIQPYMRRMVATWMLEVCEEQKCEEE
VFPLAMNYLDRFLAGVPTPKSHLQLLGAVCMFLASKLKETSPLTAEKLCIYTDNSIKPQELLEWELVVLGKLKWN
LAAVTPHDFIEHILRKLPQQREKLSLIRKHAQTFIALCATDFKFAMYPPSMIATGSVGAAICGLQQDEEVSSLTC
DALTELLAKITNTDVDCLKACQEQIEAVLLNSLQQYRQDQRDGSKSEDELDQASTPTDVRDIDL

FIGURE 128A

TGTGGCTGTGACCTGGCACAAGGGGGCTTCTTCATAAAGAACGGAGAGTATCTCTGCACCCTGGACTACCAGCGG
ATGTACGGGACACGCTGCCATGGCTGTGGGGAGTTCGTGGAGGGCGAAGTGGTGACTGCTCTGGGCAAGACCTAC
CATCCCAATTGCTTTGCTTGTACTATCTGCAAGCGCCCGTTTCCACCCGGAGACCGAGTCACATTCAATGGGAGA
GACTGCCTTTGTCAACTCTGTGCACAGCCGATGTCGTCCAGTCCGAAAGAAACCACCTTCTCCAGCAATTGTGCC
GGCTGCGGAAGAGATATCAAGAACGGGCAGGCGCTGCTGGCGCTGGATAAGCAGTGGCACTTGGGGTGCTTTAAA
TGCAAGTCCTGCGGGAAGGTCCTCACCGGGGAGTACATCAGCAAGGATGGTGCTCCGTACTGTGAAAAGGACTAC
CAGGGACTCTTTGGGGTGAAATGTGAGGCGTGTCACCAGTTTATCACAGGGAAAGTCCTGGAGGCAGGTGACAAA
CATTACCACCCCAGCTGTGCACGATGCAGCAGATGCAACCAGATGTTCACAGAAGGAGAGGAAATGTATCTTCAA
GGCTCCACCGTTTGGCATCCCGACTGTAAGCAATCTACGAAGACCGAGGAAAAGCTGCGGCCTACCAGGACATCC
TCGGAAAGTATTTATTCTAGGCCAGGCTCCAGTATTCCTGGCTCACCAGGTCATACTATCTATGCAAAAGTAGAC
AATGAGATCCTGGATTACAAGGATTTAGCAGCCATTCCGAAGGTCAAGGCAATTTATGACATTGAACGTCCAGAT
CTTATTACCTATGAGCCTTTCTACACTTCGGGCTATGATGACAAACAGGAGAGACAGAGCCTTGGAGAGTCTCCG
AGGACTTTGTCTCCTACTCCATCAGCAGAAGGGTACCAGGATGTTCGGGATCGGATGATCCATCGGTCCACGAGC
CAGGGCTCCATCAACTCCCCTGTGTACAGCCGCCACAGCTACACTCCAACCACGTCCCGCTCTCCCCAGCATTTC
CACAGACCTGGCAATGAGCCGTCCAGCGGCCGGAACTCCCCTCTCCCTTACCGGCCAGACAGCCGCCCTCTAACT
CCAACTTACGCTCAGGCCCCTAAACATTTCCATGTTCCAGATCAAGGAATCAACATTTACCGAAAGCCACCCATC
TACAAACAGCATGCTGCCTTGGCAGCCCAGAGCAAGTCCTCAGAAGATATCATCAAGTTTTCCAAGTTCCCAGCA
GCCCAGGCACCAGACCCCAGCGAGACACCAGAGATTGAGACGGACCACTGGCCTGGTCCCCCCTCATTTGCTGTC
ATAGGACCTGACATGAAACGCAGATCTAGTGGCAGAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGCTT
CAAGAAGAGCAATTAATGAAGCTTAACTCAGGCCTGGGACAGTTGATCTTGAAAGAAGAGATGGAGAAAGAGAGC
CGGGAAAGGTCATCTCTGTTAGCCAGTCGCTACGATTCTCCCATCAACTCAGCTTCACATATTCCATCATCTAAA
ACTGCATCTCTCCCTGGCTATGGAAGAAATGGGCTTCACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGC
TATGGGGATGTCAGCGGGGGAGTGCGAGATTACCAGACACTCCCAGATGGCCACATGCCTGCAATGAGAATGGAC
CGAGGAGTGTCTATGCCCAACATGTTGGAACCAAAGATATTTCCATATGAAATGCTCATGGTGACCAACAGAGGG
CGAAACAAAATCCTCAGAGAGGTGGACAGAACCAGGCTGGAGCGCCACTTAGCCCCTGAAGTGTTTCGGGAAATC
TTTGGAATGTCCATACAGGAGTTTGACAGGTTACCTCTTTGGAGACGCAACGACATGAAGAAAAAAGCAAAACTC
TTC**TAA**GTCCCACTCGTGAATGGCAATTAGAGAAAGGACTGACAGTGGCGGTGCCCCATAGGATGTCATATTGAG
GCCCAAACTTGATTGGAGAATTTGCAAACTACCGTCGCTCAGCAACACCAAAAAGAGAAAGTCTGGTTAAAACAC
CATGAGTCAAATGTCGGGCCAGCCAACAGTAACACTTGCCAAGAAGCATGGCGTAGAAATTTCTATGTTCCGAAA
CACAGAGTAGTGTCCACATGTGACCTTTTCACATTACCTTATGTATACAACAGGAGCTGCGTTGTTTTCTTCTTT
TTCTTTTCCTTTATCTGTTGTCCAACAACAGTGCTGACTGTCCGGATAAGAGCTGGCAAGTGCCCTTAGGATGCC
GCATGGGAAAAATCGGTTATCATAATTTCAAAGTATAAATATATTTATTATGTAGCGCTGCGGCTAAGAAGGAAG
AGTGAGGGGTCTGTCCATGGGGTGGCAGTGATTTCACACCCGCCTTTCTTGAATGGCTTCGTGTTACTCAGCCGT
GCCCTGGCAGGAATGGAACTCCATCAGGGAACAGGGCAGCTCTGTTTGAATGGGGTGAAAAACAGCAAAATTAAT
TCTTAGCAAGCTCCTTGTTCTCTACTGTTCACCGGGACCTGGCTGGCAAATGACTTAGCTATTAGTATATTTAAA
AACTGTTCAAAAGCAAAAGAGAAGGAACAGGAATGAAAGGAAACCTTCCCTTAACTCTTTCTGCTTCCCATAGCA
GGTCTGGTTCCTGCTCCCCGCCTAGGACAGGAGCTGTCTGGAGCTCCACCTTTGCAAAGAAAGGAAAAACACAAA
TTGCCCCCAGATTGGCCCAGTGGCATGCCATTAGGTGATTTTGCGTAGGGGCCATATCATTCATGGCCAAAAAAA
ACCAAAAAGCAAAAAACAAAAACAAGTCCCATGTCCTACTGACTCTAGTTCTTCCAGTCGTTATCCTCTGCTGTC
TCTCTGGCATCCTATGAATCAGATCAAGCCCATGCTGTTGTTGGTTTTTAAGGTTTCTTTCAATAATAGGCTAAG
GAAAGACATGTTTTTCTCTTTTAAATCTCTGCAACTCCAAAGTAGACTCCTTCGAACGTATTTAATTTGGCCTTT
TCAGCTTTCTTCTTGCCCAGCTCTGTCGAATTCATGGGTGTGTGTGCACATGTTGGTTTCACTCACCCAGAGTAA
TTTTGTGAGCATGCATGTGCTTTTTAATTTCTGCTTGAATGTTTGTCCTGCTGTGTTGCAGCTTCTAAAGACATT
GTCACCGAGTGTGTGTGACTCAAAGATCAAGAGTGAGGCTAAACTGCGACCCCAACATCACTTCCTTCATGGAAA
GGTGTTGGCGCTGATGTAGCTCATGGAAGGATCAGACTGGGAACCACAGAGGAAGGATGAGGTGGGATGTGGAGG
TCAGAGCATCTCACGAGAGTCCCTCAGGCTCTGCAACACTAGATTCGAATATGAGCCTAGGGTTTCCCCAACACG
TGCGTGCATATGAAACCACATCATGATTCCCGACGTGAGTTAGATGAGGGAGAGTTTGTGTAACTCCACACCCAG
GAGGGTAAGCCACTTTATTATCATGCTTTGGGGCTGTGCTTAAGAATTTAAGCTCTGTTTTAAAGCCGAAGAAGA

FIGURE 128B

AAACATTTGAATTTACCTTCATATGCCACTAAGAACAAAAGCTCTGAAGTTCTTCCTGCTGGCACCAAATATTAG
GATTACAAGCTGTCTCTCTGACACCAGTGGTAAAAAAGCAAGTAGAATAGTTTCTGAGTCTGTGTTGCAGCCTCT
GACACGTGGCTCACTGCTGTCATTTGGGGGGTGGAATGAACAGTCACTGTTCTATAGCATCCTCCTGTGCTCTTA
CCTAAGGAATCTAAATTGTCCTAGCCTTCCATTGCTATGCACTGAATGAGGACTACTCTCGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGGATCTACTAACATGTTTAGCAAATGGCTCTGACAGGGTGG
CCATGAGCAGATGAGACCAGCTCTTGCTTGGTTGGAAGCCACACTGCAGTTTGCAGTTTAGCCTTTGGTGTCTCA
GTGGCCTCTTGCTTATTCCATGCTTTTTCTATCCCATCCTCTCTCTGTGCCCTCCTGCAATGGCAGCCTTGGCAC
AATGCCTGGGTGTCCTCATCCTTGCTTTACTCTGGAAAGTGTGGGGATGGAGAGGATGGTGCATTTCCAGTGCTT
CCTTACCTGTCAATAACAATGGTGGCCACCTGGGTCCCAGCACTTGGCTGGTGGAGAGATTTTTTTCATTATGGA
GCTAATAAAGGGTCCCTACGTTTTACATTGATTAATGAATTATCACCCAGACATGTGCAGATGAAATGTCAATAT
AAGAAAAATCAAGGTATTTGGGAAACATGGGCATAATCAGGTAGTTTTGCTAAAATTCCTCTTCCTTGGTCTACA
TAAAGAAGACATGGGTCTGTCATAGAATGGGGACATTAGACTGAAAACTGGGACAACCCCCTTCCTTATTTTATA
GAGACTAGGAGTTAAGGGGCCTGCCTAAGATTGCAGTGATAAAGAACTGAACCCTAAATCAGCTCCCACTAATGA
AACCCTGCTTTCCTTGTATCTTTTAAACTCAGTTCTGCATCCAACTTGAGAAGAAAAAAAGCTTCTTTCCATATC
AAGTACCATATGAGTTCATTTAAACTGCACCTTGCAGAAATGCATTGCCAGAAAGCACCAGTAGCCTCCTATCTG
CAAGCAGAGTAGTGCTCTGCTCTGGGGAGGGGTCATTGGAAACCATAATGCAGAGTGGGCCCCCTACTCCATTTC
CCAGCAAAAGGCTCCAGCTGGAGGGATGGGTTGTGGGGCAACCTGGTTCCTGCTAACTGCCAGATTGAATGTGTG
GGCTAGAATGCCTGCGCATTTAGTTAAACTGGGCTCAGCATGCTTGTCCTCAAAATGTCCATCCTGGTCACAGCA
CACAAGATGGCTATTGGTCTGCTTTTACCCTACCCTGTACTATACATGAAAATTCCAGTTATTAACACACTCAAA
CTGGTGGAGCTTGTTCACCCTAGGAAGGGGATTGTATATATGGCAGGCTTCCCTGGTGCCGATGTAAAGGGCTAC
ATTTGGGAACATTTGACTTCCTTGGGACTCTTAAGTGCATACTGATGGCATGAAGTAAAAGGGGCCTCAATGATG
ATAGGAAAATCAGTTCTTTTAAAATTTCTTCAAGAAAATCCAGGCTATCACATAGTCTTTCTGTGTGACTTATTA
GGAGATAGGAAGAGCATTGGGAAACTTGCACAGCTAGCTATGCATCTACATTTTGGTTTGGGGTTAGTTATGAAA
TGTTCTTAATATGACGTGTTCAATAACTTCACATAAACTTCCTGTTCTCCAAAACCTCAAAGAGATAGAGTTAAT
GAGTTGTTGTTTTTTTTTAAATGGGGGTAGTTTTCTATCTGTCATGGGCTCTAGCATCTACTCCGCTACCCAATT
CTGTCATCTCCAAGCTGAGTTTCCTCTTCTGAGGCAGAGGCTGGAGCAGTTCTTTTTCAGTTCTCATCCTCTCCA
TCCCAATCCAGTATATCAATCAACTCTAACTCGGAGACGTCTAGCTGGCAATGTTTCTAAAACTTTCACTGGATT
TCTTTAGACATTGAAGCAAACATTTTTTTCTAAGAATTGCTTCTCAGATGATGATATCAAATGTATATGCTTTTG
CAAGTTTGAAAAGTTCAAATTAACCACTTTTGACTAGGTAAGTCTTTCTAAAAACCATTTAAAGCTAACTGGGTC
TTAGCATCCTCCTGTGTATGGAAGAGACAGGTGACCGCTCCAGGTTGGGTGCTCACAGAACCCTTTTCCTGACTC
TCATGGAAGATGGTGGAAGGAAAATAGACTGTCTCATCAACCCTCCTGTGTCCTCTGAAGCAATCTCAGTTTTTA
TTAACCACCTCTTCTGTGTTTCTGGTAGCTATTTAACCTGTATTTAATCTGTACTTCCTATGCCAGCCTCAATTT
TATTTGATTTTTAAAATTATTCTCTTCTAACCAATGAAGTGTTTGTCAGTATGCCCCAAAGCTTGCTCTTTTGTG
CTCCCTTTTGAATAACTTTCTATCCAGAAAAAGAGATTATTTGGGACTTGAGATTTGCAGTGATACCAACTTATA
GCAATGATGTACTTTAAGGGAACTACCCAACTATGTTGTGATAGAAGAAAGAGAAACCTTCACTTTGGCATTTTT
TTTAATCACTGTTTATTTTTCTGTTTGCGGCCCAGGAAGCAGTGGGAGGTGGTGGCAGATATGCTTTGCATATGG
ATTGTTATGTTTTTATTTGGGCAAGTTTAATCATGGAAAACTCAAAAAGAAGGGGGGAAATGGTCAGTTTAAGCC
AAAAGAAACTTTCTAAACAATGTATAGGTACACAGCAAAATTAAACAAATCCAACAATTTCTGAAGCTTAGTGTA
ATTGAGTGGTGGTTGTTATTCAATAAAATTATTCCCAAAAGTGTTTCTCCTAAGAGTGCAGTTCCCATGAGTCAC
TTCCTGAACCCATTGACCAAAGGTGGACAGAGACAATCCTGTAGACCTTGACATTCAGAAAGATGTGAGCTGCTT
ACTGATCATATATGCATACGTTTCTTTACAGCAGAGGAAACCATTGTCCACAAAACTGATGTTCTTTTGGGGTTT
TATGTACAGACTTGTCCAATCATGTGTGTGGTTCCTGCGAGTTGCTGATGACTCCGCATTGAAGCTCTCTGAGTT
CTTTGATTTTAAGTTGGGTTTATGGAATTTTTTCAAATGTTGGAAGGCGTGTGGTTCTTCCTGCCCTCCCTCCCC
TTTTGGAAATATGAAAGCAAATGTTTAGAAGAATTCCTTTTGAAAAGCTGTGTCGTGTTCCCTGTGAAACTGAGC
AGGTGTGTGTTGGCGCGCTAAGTGCCACATGCTTGTGTGTAGAGGAGGAGGTGGCCCTGCCGGCTCCGCGCTGCT
GTGCCTGTGATCCCTACCTGCTCCCCGCTCCTGTTGCCAGCAGCACTCACTGCACTCCTTTGTCATATACTCTGC
ATCACTGTCATACTCACAACTTCGTGAATAAAGTTGTGTGCTTTATTCGTC

FIGURE 129

MYGTRCHGCGEFVEGEVVTALGKTYHPNCFACTICKRPFPPGDRVTFNGRDCLCQLCAQPMSSSPKETTFSSNCA
GCGRDIKNGQALLALDKQWHLGCFKCKSCGKVLTGEYISKDGAPYCEKDYQGLFGVKCEACHQFITGKVLEAGDK
HYHPSCARCSRCNQMFTEGEEMYLQGSTVWHPDCKQSTKTEEKLRPTRTSSESIYSRPGSSIPGSPGHTIYAKVD
NEILDYKDLAAIPKVKAIYDIERPDLITYEPFYTSGYDDKQERQSLGESPRTLSPTPSAEGYQDVRDRMIHRSTS
QGSINSPVYSRHSYTPTTSRSPQHFHRPGNEPSSGRNSPLPYRPDSLPLTPTYAQAPKHFHVPDQGINIYRKPPI
YKQHRALAAQSKSSEDIIKFSKFPAAQAPDPSETPKIETDHWPGPPSFAVVGPDMKRRSSGREEDDEELLRRRQL
QEEQLMKLNSGLGQLILKEEMEKESRERSSLLASRYDSPINSASHIPSSKTASLPGYGRNGLHRPVSTDFAQYNS
YGDVSGGVRDYQTLPDGHMPAMRMDRGVSMPNMLEPKIFPYEMLMVTNRGRNKILREVDRTRLERHLAPEVFREI
FGMSIQEFDRLPLWRRNDMKKKAKLF

FIGURE 130A

CACGAGGCAGCACTCTCTTCGTCGCTTCGGCCAGTGTGTCGGGCTGGGCCCTGACAAGCCACCTGAGGAGAGGCT
CGGAGCCGGGCCCGGACCCCGGCGATTGCCGCCCGCTTCTCTCTAGTCTCACGAGGGGTTTCCCGCCTCGCACCC
CCACCTCTGGACTTGCCTTTCCTTCTCTTCTCCGCGTGTGGAGGGAGCCAGCGCTTAGGCCGGAGCGAGCCTGGG
GGCCGCCCGCCGTGAAGACATCGCGGGGACCGATTCACC**ATG**GAGGGCGCCGGCGGCGCGAACGACAAGAAAAAG
ATAAGTTCTGAACGTCGAAAAGAAAAGTCTCGAGATGCAGCCAGATCTCGGCGAAGTAAAGAATCTGAAGTTTTT
TATGAGCTTGCTCATCAGTTGCCACTTCCACATAATGTGAGTTCGCATCTTGATAAGGCCTCTGTGATGAGGCTT
ACCATCAGCTATTTGCGTGTGAGGAAACTTCTGGATGCTGGTGATTTGGATATTGAAGATGACATGAAAGCACAG
ATGAATTGCTTTTATTTGAAAGCCTTGGATGGTTTTGTTATGGTTCTCACAGATGATGGTGACATGATTTACATT
TCTGATAATGTGAACAAATACATGGGATTAACTCAGTTTGAACTAACTGGACACAGTGTGTTTGATTTTACTCAT
CCATGTGACCATGAGGAAATGAGAGAAATGCTTACACACAGAAATGGCCTTGTGAAAAAGGGTAAAGAACAAAAC
ACACAGCGAAGCTTTTTTCTCAGAATGAAGTGTACCCTAACTAGCCGAGGAAGAACTATGAACATAAAGTCTGCA
ACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATACCAACAGTAACCAACCTCAGTGTGGGTAT
AAGAAACCACCTATGACCTGCTTGGTGCTGATTTGTGAACCCATTCCTCACCCATCAAATATTGAAATTCCTTTA
GATAGCAAGACTTTCCTCAGTCGACACAGCCTGGATATGAAATTTTCTTATTGTGATGAAAGAATTACCGAATTG
ATGGGATATGAGCCAGAAGAACTTTTAGGCCGCTCAATTTATGAATATTATCATGCTTTGGACTCTGATCATCTG
ACCAAAACTCATCATGATATGTTTACTAAAGGACAAGTCACCACAGGACAGTACAGGATGCTTGCCAAAAGAGGT
GGATATGTCTGGGTTGAAACTCAAGCAACTGTCATATATAACACCAAGAATTCTCAACCACAGTGCATTGTATGT
GTGAATTACGTTGTGAGTGGTATTATTCAGCACGACTTGATTTTCTCCCTTCAACAAACAGAATGTGTCCTTAAA
CCGGTTGAATCTTCAGATATGAAAATGACTCAGCTATTCACCAAAGTTGAATCAGAAGATACAAGTAGCCTCTTT
GACAAACTTAAGAAGGAACCTGATGCTTTAACTTTGCTGGCCCCAGCCGCTGGAGACACAATCATATCTTTAGAT
TTTGGCAGCAACGACACAGAAACTGATGACCAGCAACTTGAGGAAGTACCATTATATAATGATGTAATGCTCCCC
TCACCCAACGAAAAATTACAGAATATAAATTTGGCAATGTCTCCATTACCCACCGCTGAAACGCCAAAGCCACTT
CGAAGTAGTGCTGACCCTGCACTCAATCAAGAAGTTGCATTAAAATTAGAACCAAATCCAGAGTCACTGGAACTT
TCTTTTACCATGCCCCAGATTCAGGATCAGACACCTAGTCCTTCCGATGGAAGCACTAGACAAAGTTCACCTGAG
CCTAATAGTCCCAGTGAATATTGTTTTTATGTGGATAGTGATATGGTCAATGAATTCAAGTTGGAATTGGTAGAA
AAACTTTTTGCTGAAGACACAGAAGCAAAGAACCCATTTTCTACTCAGGACACAGATTTAGACTTGGAGATGTTA
GCTCCCTATATCCCAATGGATGATGACTTCCAGTTACGTTCCTTCGATCAGTTGTCACCATTAGAAAGCAGTTCC
GCAAGCCCTGAAAGCGCAAGTCCTCAAAGCACAGTTACAGTATTCCAGCAGACTCAAATACAAGAACCTACTGCT
AATGCCACCACTACCACTGCCACCACTGATGAATTAAAAACAGTGACAAAAGACCGTATGGAAGACATTAAAATA
TTGATTGCATCTCCATCTCCTACCCACATACATAAAGAAACTACTAGTGCCACATCATCACCATATAGAGATACT
CAAAGTCGGACAGCCTCACCAAACAGAGCAGGAAAAGGAGTCATAGAACAGACAGAAAAATCTCATCCAAGAAGC
CCTAACGTGTTATCTGTCGCTTTGAGTCAAAGAACTACAGTTCCTGAGGAAGAACTAAATCCAAAGATACTAGCT
TTGCAGAATGCTCAGAGAAAGCGAAAAATGGAACATGATGGTTCACTTTTTCAAGCAGTAGGAATTGGAACATTA
TTACAGCAGCCAGACGATCATGCAGCTACTACATCACTTTCTTGGAAACGTGTAAAAGGATGCAAATCTAGTGAA
CAGAATGGAATGGAGCAAAAGACAATTATTTTAATACCCTCTGATTTAGCATGTAGACTGCTGGGGCAATCAATG
GATGAAAGTGGATTACCACAGCTGACCAGTTATGATTGTGAAGTTAATGCTCCTATACAAGGCAGCAGAAACCTA
CTGCAGGGTGAAGAATTACTCAGAGCTTTGGATCAAGTTAAC**TGA**GCTTTTTCTTAATTTCATTCCTTTTTTTGG
ACACTGGTGGCTCACTACCTAAAGCAGTCTATTTATATTTTCTACATCTAATTTTAGAAGCCTGGCTACAATACT
GCACAAACTTGGTTAGTTCAATTTTTGATCCCCTTTCTACTTAATTTACATTAATGCTCTTTTTTTAGTATGTTCT
TTAATGCTGGATCACAGACAGCTCATTTTCTCAGTTTTTTGGTATTTAAACCATTGCATTGCAGTAGCATCATTT
TAAAAAATGCACCTTTTTATTTATTTATTTTTGGCTAGGGAGTTTATCCCTTTTTCGAATTATTTTTAAGAAGAT
GCCAATATAATTTTTGTAAGAAGGCAGTAACCTTTCATCATGATCATAGGCAGTTGAAAAATTTTTACACCTTTT
TTTTCACATTTTACATAAATAATAATGCTTTGCCAGCAGTACGTGGTAGCCACAATTGCACAATATATTTTCTTA
AAAAATACCAGCAGTTACTCATGGAATATATTCTGCGTTTATAAAACTAGTTTTTAAGAAGAAATTTTTTTTGGC
CTATGAAATTGTTAAACCTGGAACATGACATTGTTAATCATATAATAATGATTCTTAAATGCTGTATGGTTTATT
ATTTAAATGGGTAAAGCCATTTACATAATATAGAAAGATATGCATATATCTAGAAGGTATGTGGCATTTATTTGG
ATAAAATTCTCAATTCAGAGAAATCATCTGATGTTTCTATAGTCACTTTGCCAGCTCAAAAGAAAACAATACCCT
ATGTAGTTGTGGAAGTTTATGCTAATATTGTGTAACTGATATTAAACCTAAATGTTCTGCCTACCCTGTTGGTAT

FIGURE 130B

AAAGATATTTTGAGCAGACTGTAAACAAGAAAAAAAAAATCATGCATTCTTAGCAAAATTGCCTAGTATGTTAAT
TTGCTCAAAATACAATGTTTGATTTTATGCACTTTGTCGCTATTAACATCCTTTTTTTCATGTAGATTTCAATAA
TTGAGTAATTTTAGAAGCATTATTTTAGGAATATATAGTTGTCACAGTAAATATCTTGTTTTTTCTATGTACATT
GTACAAATTTTTCATTCCTTTTGCTCTTTGTGGTTGGATCTAACACTAACTGTATTGTTTTGTTACATCAAATAA
ACATCTTCTGTGGAAAAAAAAAAAAAAAAAAA

FIGURE 131

MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDA
GDLDIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYMGLTQFELTGHSVFDFTHPCDHEEMREMLTH
RNGLVKKGKEQNTQRSFFLRMKCTLTSRGRTMNIKSATWKVLHCTGHIHVYDTNSNQPQCGYKKPPMTCLVLICE
PIPHPSNIEIPLDSKTFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHLTKTHHDMFTKGQV
TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSGIIQHDLIFSLQQTECVLKPVESSDMKMTQLF
TKVESEDTSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTETDDQQLEEVPLYNDVMLPSPNEKLQNINLAM
SPLPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDS
DMVNEFKLELVEKLFAEDTEAKNPFSTQDTDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT
VFQQTQIQEPTANATTTTATTDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYRDTQSRTASPNRAGKG
VIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKRKMEHDGSLFQAVGIGTLLQQPDDHAATTSL
SWKRVKGCKSSEQNGMEQKTIILIPSDLACRLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQV
N

FIGURE 132

GCTTAGTGTAACCAGCGGCGTATATTTTTTAGGCGCCTTTTCGAAAACCTAGTAGTTAATATTCATTTGTTTAAA
TCTTATTTTATTTTTAAGCTCAAACTGCTTAAGAATACCTTAATTCCTTAAAGTGAAATAATTTTTTGCAAAGGG
GTTTCCTCGATTTGGAGCTTTTTTTTTCTTCCACCGTCATTTCTAACTCTTAAAACCAACTCAGTTCCATC**ATG**G
TGATGTTCAAGAAGATCAAGTCTTTTGAGGTGGTCTTTAACGACCCTGAAAAGGTGTACGGCAGTGGCGAGAGGG
TGGCTGGCCGGGTGATAGTGGAGGTGTGTGAAGTTACTCGTGTCAAAGCCGTTAGGATCCTGGCTTGCGGAGTGG
CTAAAGTGCTTTGGATGCAGGGATCCCAGCAGTGCAAACAGACTTCGGAGTACCTGCGCTATGAAGACACGCTTC
TTCTGGAAGACCAGCCAACAGGTGAGAATGAGATGGTGATCATGAGACCTGGAAACAAATATGAGTACAAGTTCG
GCTTTGAGCTTCCTCAGGGGCCTCTGGGAACATCCTTCAAAGGAAAATATGGGTGTGTAGACTACTGGGTGAAGG
CTTTTCTTGACCGCCCGAGCCAGCCAACTCAAGAGACAAAGAAAAACTTTGAAGTAGTGGATCTGGTGGATGTCA
ATACCCCTGATTTAATGGCACCTGTGTCTGCTAAAAAAGAAAAGAAAGTTTCCTGCATGTTCATTCCTGATGGGC
GGGTGTCTGTCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGGTGATGAGATTTCCATCCATGCTGACTTTG
AGAATACATGTTCCCGAATTGTGGTCCCCAAAGCTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGA
CCAAGGTGCTGACTCAGAAGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTG
GCAAGAGCCTTCGGGTTCAGAAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTGAATATTCCTTAC
TGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGCCCCTGGTAATTGGCAGCAGATCAGGTC
TAAGCAGCAGAACATCCAGCATGGCCAGCCGAACCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATA
CCCCAGAAGCTCCTCCCTGCTATATGGATGTCATTCCTGAAGATCACCGATTGGAGAGCCCAACAACTCCTCTGC
TAGATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCATGCCACCACCGA
CTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAG**TGA**GCATGTGGAAGAAAAGAAGCAGCTTTAC
CTACTTGTTTCTTTTTGTCTCTCTTCCTGGACACTCACTTTTTCAGAGACTCAACAGTCTCGTCAATGGAGTGTG
GGTCCACCTTAGCCTCTGACTTCCTAATGTAGGAGGTGGTCAGCAGGCAATCTCCTGGGCCTTAAAGGATGCGGA
CTCATCCTCAGCCAGCGCCCATGTTGTGATACAGGGGTGTTTGTTGGATGGGTTTAAAAATAACTAGAAAAACTC
AGGCCCATCCATTTTCTCAGATCTCCTTGAAAATTGAGGCCTTTTCGATAGTTTCGGGTCAGGTAAAAATGGCCT
CCTGGCGTAAGCTTTTCAAGGTTTTTTGGAGGCTTTTTGTAAATTGTGATAGGAACTTTGGACCTTGAACTTACG
TATCATGTGGAGAAGAGCCAATTTAACAAACTAGGAAGATGAAAAGGGAAATTGTGGCCAAAACTTTGGGAAAAG
GAGGTTCTTAAAATCAGTGTTTCCCCTTTGTGCACTTGTAGAAAAAAAAGAAAAACCTTCTAGAGCTGATTTGAT
GGACAATGGAGAGAGCTTTCCCTGTGATTATAAAAAAGGAAGCTAGCTGCTCTACGGTCATCTTTGCTTAGAGTA
TACTTTAACCTGGCTTTTAAAGCAGTAGTAACTGCCCCACCAAAGGTCTTAAAAGCCATTTTTGGAGCCTATTGC
ACTGTGTTCTCCTACTGCAAATATTTTCATATGGGAGGATGGTTTTCTCTTCATGTAAGTCCTTGGAATTGATTC
TAAGGTGATGTTCTTAGCACTTTAATTCCTGTCAAATTTTTTGTTCTCCCCTTCTGCCATCTTAAATGTAAGCTG
AAACTGGTCTACTGTGTCTCTAGGGTTAAGCCAAAAGACAAAAAAAATTTTACTACTTTTGAGATTGCCCCAATG
TACAGAATTATATAATTCTAACGCTTAAATCATGTGAAAGGGTTGCTGCTGTCAGCCTTGCCCACTGTGACTTCA
AACCCAAGGAGGAACTCTTGATCAAGATGCCCAACCCTGTGATCAGAACCTCCAAATACTGCCATGAGAAACTAG
AGGGCAGGTGTTCATAAAAGCCCTTTGAACCCCCTTCCTGCCCTGTGTTAGGAGATAGGGATATTGGCCCCTCAC
TGCAGCTGCCAGCACTTGGTCAGTCACTCTCAGCCATAGCACTTTGTTCACTGTCCTGTGTCAGAGCACTGAGCT
CCACCCTTTTCTGAGAGTTATTACAGCCAGAAAGTGTGGGCTGAAGATGGTTGGTTTCATGTGGGGGTATTATGT
ACCC

FIGURE 133

MVMFKKIKSFEVVFNDPEKVYGSGERVAGRVIVEVCEVTRVKAVRILACGVAKVLWMQGSQQCKQTSEYLRYEDT
LLLEDQPTGENEMVIMRPGNKYEYKFGFELPQGPLGTSFKGKYGCVDYWVKAFLDRPSQPTQETKKNFEVVDLVD
VNTPDLMAPVSAKKEKKVSCMFIPDGRVSVSARIDRKGFCEGDEISIHADFENTCSRIVVPKAAIVARHTYLANG
QTKVLTQKLSSVRGNHIISGTCASWRGKSLRVQKIRPSILGCNILRVEYSLLIYVSVPGSKKVILDLPLVIGSRS
GLSSRTSSMASRTSSEMSWVDLNIPDTPEAPPCYMDVIPEDHRLESPTTPLLDDMDGSQDSPIFMYAPEFKFMPP
PTYTEVDPCILNNNVQ

FIGURE 134

AGTGTGAAATCTTCAGAGAAGAATTTCTCTTTAGTTCTTTGCAAGAAGGTAGAGATAAAGACACTTTTTCAAAA**A**
TGGCAATGGTATCAGAATTCCTCAAGCAGGCCTGGTTTATTGAAAATGAAGAGCAGGAATATGTTCAAACTGTGA
AGTCATCCAAAGGTGGTCCCGGATCAGCGGTGAGCCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCT
TGCATAAGGCCATAATGGTTAAAGGTGTGGATGAAGCAACCATCATTGACATTCTAACTAAGCGAAACAATGCAC
AGCGTCAACAGATCAAAGCAGCATATCTCCAGGAAACAGGAAAGCCCCTGGATGAAACACTTAAGAAAGCCCTTA
CAGGTCACCTTGAGGAGGTTGTTTTAGCTCTGCTAAAAACTCCAGCGCAATTTGATGCTGATGAACTTCGTGCTG
CCATGAAGGGCCTTGGAACTGATGAAGATACTCTAATTGAGATTTTGGCATCAAGAACTAACAAAGAAATCAGAG
ACATTAACAGGGTCTACAGAGAGGAACTGAAGAGAGATCTGGCCAAAGACATAACCTCAGACACATCTGGAGATT
TTCGGAACGCTTTGCTTTCTCTTGCTAAGGGTGACCGATCTGAGGACTTTGGTGTGAATGAAGACTTGGCTGATT
CAGATGCCAGGGCCTTGTATGAAGCAGGAGAAAGGAGAAAGGGGACAGACGTAAACGTGTTCAATACCATCCTTA
CCACCAGAAGCTATCCACAACTTCGCAGAGTGTTTCAGAAATACACCAAGTACAGTAAGCATGACATGAACAAAG
TTCTGGACCTGGAGTTGAAAGGTGACATTGAGAAATGCCTCACAGCTATCGTGAAGTGCGCCACAAGCAAACCAG
CTTTCTTTGCAGAGAAGCTTCATCAAGCCATGAAAGGTGTTGGAACTCGCCATAAGGCATTGATCAGGATTATGG
TTTCCCGTTCTGAAATTGACATGAATGATATCAAAGCATTCTATCAGAAGATGTATGGTATCTCCCTTTGCCAAG
CCATCCTGGATGAAACCAAAGGAGATTATGAGAAAATCCTGGTGGCTCTTTGTGGAGGAAAC**TAA**ACATTCCCTT
GATGGTCTCAAGCTATGATCAGAAGACTTTAATTATATATTTTCATCCTATAAGCTTAAATAGGAAAGTTTCTTC
AACAGGATTACAGTGTAGCTACCTACATGCTGAAAAATATAGCCTTTAAATCATTTTTATATTATAACTCTGTAT
AATAGAGATAAGTCCATTTTTTAAAAATGTTTTCCCCAAACCATAAAACCCTATACAAGTTGTTCTAGTAACAAT
ACATGAGAAAGATGTCTATGTAGCTGAAAATAAAATGACGTCACAAGAC

FIGURE 135

MAMVSEFLKQAWFIENEEQEYVQTVKSSKGGPGSAVSPYPTFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNA
QRQQIKAAYLQETGKPLDETLKKALTGHLEEVVLALLKTPAQFDADELRAAMKGLGTDEDTLIEILASRTNKEIR
DINRVYREELKRDLAKDITSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTIL
TTRSYPQLRRVFQKYTKYSKHDMNKVLDLELKGDIEKCLTAIVKCATSKPAFFAEKLHQAMKGVGTRHKALIRIM
VSRSEIDMNDIKAFYQKMYGISLCQAILDETKGDYEKILVALCGGN

FIGURE 136

GAAAGCTGTATTTGCTGCACGTGGAAATCTCCGTTATTTTCCAGCACCCAACAGTAGCGTAATGGGAGTAACGGA
CTTAACCTCATTTCTCTTTCAGAGCATTTAGCCTTCATATGCCCTTCCCTGCATGCTTCCCCCAGGCCGTCAAGA
CTTGAGTTCTGCCTCGCTTCCCGGCGCGGTCGCAGCCCTCAGCCCACTTAGGATA**ATG**GCGACAGCTGAGGTACT
GAACATTGGTAAAAAATTATATGAGGGTAAAACAAAAGAAGTCTACGAATTGTTAGACAGTCCAGGAAAAGTCCT
CCTGCAGTCCAAGGACCAGATTACAGCAGGAAATGCAGCTAGAAAAAACCACCTGGAAGGAAAAGCTGCAATCTC
AAATAAAATCACCAGTTGTATTTTTCAGTTATTACAGGAAGCAGGTATTAAAACTGCCTTCACCAGAAAATGTGG
GGAGACAGCTTTCATTGCACCGCAGTGTGAAATGATTCCAATTGAATGGGTTTGCAGAAGAATAGCAACTGGTTC
TTTTCTCAAAAGAAATCCTGGTGTCAAGGAAGGATATAAGTTTTACCCACCTAAAGTGGAGTTGTTTTTCAAGGA
TGATGCCAATAATGACCCACAGTGGTCTGAGGAACAGCTGATTGCTGCAAAATTTTGCTTTGCTGGACTTCTTAT
AGGCCAGACTGAAGTGGATATCATGAGTCATGCTACACAGGCTATATTTGAAATACTGGAGAAATCCTGGTTGCC
CCAGAATTGTACACTGGTTGATATGAAGATTGAATTTGGTGTTGATGTAACCACCAAAGAAATTGTTCTTGCTGA
TGTTATTGACAATGATTCCTGGAGACTCTGGCCATCAGGAGATCGAAGCCAACAGAAAGACAAACAGTCTTATCG
GGACCTCAAAGAAGTAACTCCTGAAGGGCTCCAAATGGTAAAGAAAAACTTTGAGTGGGTTGCAGAGAGAGTAGA
GTTGCTTTTGAAATCAGAAAGTCAGTGCAGGGTTGTAGTGTTGATGGGCTCTACTTCTGATCTTGGTCACTGTGA
AAAAATCAAGAAGGCCTGTGGAAATTTTGGCATTCCATGTGAACTTCGAGTAACATCTGCGCATAAAGGACCAGA
TGAAACTCTGAGGATTAAAGCTGAGTATGAAGGGGATGGCATTCCTACTGTATTTGTGGCAGTGGCAGGCAGAAG
TAATGGTTTGGGACCAGTGATGTCTGGGAACACTGCATATCCAGTTATCAGCTGTCCTCCCCTCACACCAGACTG
GGGAGTTCAGGATGTGTGGTCTTCTCTTCGACTACCCAGTGGTCTTGGCTGTTCAACCGTACTTTCTCCAGAAGG
ATCAGCTCAATTTGCTGCTCAGATATTTGGGTTAAGCAACCATTTGGTATGGAGCAAACTGCGAGCAAGCATTTT
GAACACATGGATTTCCTTGAAGCAGGCTGACAAGAAAATCAGAGAATGTAATTTA**TAA**GAAAGAATGCCATTGAA
TTTTTTAGGGGAAAAACTACAAATTTCTAATTTAGCTGAAGGAAAATCAAGCAAGATGAAAAGGTAATTTTAAAT
TAGAGAACACAAATAAAATGTATTAGTGAATAAATGCTTCTCTAGATCCATATTAATAAACATGAGCATCTAACC
CCTCCTTTCTTAGGCTAGACACCAAGATATTTCAGCCAGCCTTTATCATTCCTCTTACTTTATCCTTTTTCCTTA
AGTATTGGTGGTCACTACTATTGAGTTTCTTCCTTAACACTGATTAAATGATCTTAACTCCCTCAGCTAAAACTG
GCATTACTGACTCCCAGCTATATTTCTCCAGACTTGCATTTTTTTTTTTTTTTTTGAGACAGGGTCTCACTGTCG
CCCAGGCTGGAGTGCAGTGGCGTGATCTCAGTTCACTGCTGCTTTCCCTCCTGGGCTCAAGCAGTTCTCCCACCT
CAGCCTCTCGACTAACAGGGACTATAATCTTGCAGCACCATGCCGAGCTAATTTTATTTTTTGTAGAGATGAGCT
CTCACTATGTCACCCAGGTTCGTCTCAAACTCCTGAACCCTAGTAATTCTCCTATCTCAGCCTCCCAAAGTGCTA
GGGTTACAGACATGAGCCACTGTGCCTGTCTAGACTTGTACTTTCAACTGTCCATTTCTCCCTGTCTGTCCCATG
GGCACTCATGAAAAAACAGAATGCTCCCAACTTTATTCATCTTCCAAGCCTGTAGCTCTTGGTATACTCACTGTT
GCAAGTCAGAAGCTTGATTTCATCATTGATGTTTTTCTCACGTTTCACATCTCACTCATCACCAAGTCATGTTGG
TGTTAATTTCTGATTAACCCTTGAATTTACCGTCTTCTCATCCTCTGTACAAAAGCCTCAAGTGAGGGTCAAATT
CAACATTATCCTGATCTAGACAGCCCCCATTCTCAATCCACCCTTTTCCAAGTTGATTGCCCAAGGACTTCTAAC
AATAAACTCTCTTTTGCACCACAGACTTCTTTGAAAATATACATGCTGTTGACCCTCTCTGTAGAAAACCGCACA
CATAAAACTTACCAACAGATTTCATTGGTTCTTGGGTTCTCCCGAAGCCTATCCATGGTTTATAGATTAAGAATT
GATGAGGTAGCTGGGCACAGTGGCTCACACCTACGATCACAGCACTTCGGGAGGCTGAAGCAAGCAGATCACTTG
AGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAGTAGCCAGC
CGTGATGACAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCATGAGAATTGCTTGAACCCGGGAGGCGGA
GGTTGCAGTGAGCCTGGATCATGCCACTGCACTCCAACCTGGGCAGCAGAGCAAGACTCTGTCTCAAAAGGGGAA
AAAAAAAATTGCTGATGTGACCCATGAAGGGAACTCATTTTCCTCGTAATTTTGGACTGCCACACATTGGTACCT
TTAGTTCTCTGAAGGCCCACGTTTTTATCATTAAGACCTATTTGTTAGCTAGTAGAGCTTTATGTTCGCTGTCCA
TGAAACCTTCTGTAACCACAGTGACTACAAGTAGTTCTTTCTCTATTGAATTATTAGGTCCAGAATAGAAGATGT
CATTGTACACTTTATTTCCCTCACACTGTGTTATGCTCTGATGTGCTATGCTTAGCTATCTGTCAGAGATTAGTA
AATTATAAAACTCATGTGTACTACTTAAGTTTATATCTTATGCTAGTTTATAAGAACAATTAAAAGGACTTAGAA
GATTAAAAAAAAAAAAAAAAAA

FIGURE 137

MATAEVLNIGKKLYEGKTKEVYELLDSPGKVLLQSKDQITAGNAARKNHLEGKAAISNKITSCIFQLLQEAGIKT
AFTRKCGETAFIAPQCEMIPIEWVCRRIATGSFLKRNPGVKEGYKFYPPKVELFFKDDANNDPQWSEEQLIAAKF
CFAGLLIGQTEVDIMSHATQAIFEILEKSWLPQNCTLVDMKIEFGVDVTTKEIVLADVIDNDSWRLWPSGDRSQQ
KDKQSYRDLKEVTPEGLQMVKKNFEWVAERVELLLKSESQCRVVVLMGSTSDLGHCEKIKKACGNFGIPCELRVT
SAHKGPDETLRIKAEYEGDGIPTVFVAVAGRSNGLGPVMSGNTAYPVISCPPLTPDWGVQDVWSSLRLPSGLGCS
TVLSPEGSAQFAAQIFGLSNHLVWSKLRASILNTWISLKQADKKIRECNL

FIGURE 138

AAGAAAAAAATAGGCCTGGTTGCCAXATTAAGGTCCCCTGGGCTATTTTAAACCGGATTTGGATACCXAGGTCTT
TCCAXAGGCCGTATTTTGCCCCCCGTAACCCXTAAAAAAAAAAAAAAGATTTCCAAAATGCCGTTTTCAGAACCTG
GGTTTTAATAGCAGTATTGAATTTGTAAGCTTAGTAGTTGCAGAAATTGAACACTAGGTGGCACTCAGTTATCTT
AACAGGGGAAGTACTGATACAATTGTTGACTTTTCTTTTACTATGTGTAAGAAATACCCCAAACATGAAAAGATT
GTTTTGATCATATGCATGTATGTAGAATATTTTTGCAGAGCAGAAAGATTATGTTAGAAGTGTGATTTTTATTTT
CAGAAGTCATATACATGTAAGCTACAATTTTGAGTGCTTTATAAACACTTAAGATATATATATAAATTTTAATTT
CATAGCAACTTGTAAAAAATAAAATACTTGTTGAAAAGCCTTTTTCAACATATCCCTAAGCTAAGGGAAGAGGAA
GGAATAACAACTCAGTGAAAAGATGGTCTCCAGTTTCTGAATGAAAAAGCTACAGCTGAGAAATAAAATAAAATG
TCATGCTGCAGAATATGTTATACCCTTATTTTGTGTTAAGGATATATTTTATTATGTGA**ATG**GTTTTGTTTTTGT
TTTTTGTTTTTGTTTTTTGCTTGTATTGGGAATTAGCTTTACTGGTAACTTCCTTATTTAGTTTT**TAG**TGGTCAA
CTCTAATAAAATGAAACTAGGGCTGAGCTAGTTAGCCCTCACTAGCCAAACTGAAACTCTATGCAACATTAAAAG
AAGAGATCCATCATGTAGCTTGTGACACTTTTATTTTATTAGTCACCGGGGAACTTTTCAGTGATGAAAATACAC
AGGGTAATAAACCTTCACATGGCTTCAAAAGGAAAACAAGCAAATCTTCTCTAATCTACTCTTACTATAATTTCC
TAAGTGTACACCAAACTCTGGATTTAAAAATCTGAAGTACTATAGAACATTAAGTTGAAGAATGGAAATTAAGAG
TACGTATTCATGGTTTATATTTCTTATTCTATGGAGTTCGTGAACACATCTAGGTGGAATGCATCTGAGACTAAG
GGCTGGTTTTTAATCCTCATAAGAAACCAGCCTTGAAGAATTAACAATTCTCTTCATTGGTATTCTAAACCTCCT
AAGATATTTAGGCTTCTGTACATAAAAGTGTTTTTGCTAAATTTACAGTATATATAGATCCTTTCATATTATTTT
ACTAAGAATGTTTGAACTTTGCATATTTGATATAGTTCCTGGTAGGAATAGCACAGCTCAAACATTAGTTTTTCT
ACTTACCTCCTCTAACACGTGGTTTGTCTGGAGAGTTTCTAAAAATTCAGCTATAACCCCAGTTCATGTATTTAC
TGGTGATTGTTCTTGCTGAGGTAGTAACAGCCCAATCTTGGGCTGTTAAATCCTAGGAAATCTCGAATCATAGTG
ATTAAAATAGTTGGGGTAAAGTTGTAGCTTATATGCAATACTACTTGGAGGAATTCTTCTACTAATTTGTATTTA
ATGTGGAAATTGTATAGTTTCATTGATTTAATCATAAATAATGGAAATGGTCTCCAAGAAGTTTTATTTTTCATT
TTTTTGCTTATACACTCTGATTCCTATAATACAGTGCTATAAGCTATGCACAGAAAATAAAATGTTTGAAATCCA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAXGGGGG

FIGURE 139

MVLFLFFVFVFCLYWELALLVTSLFSF

FIGURE 140A

CGCGGGTCTGTGGAGAGCCGGGTGCGAGCGGCGGCAGCACGAGGGGAAAAGAGCTGAGCGGAGACCAAAGTCAGC
CGGGAGACAGTGGGTCTGTGAGAGACCGAATAGAGGGGCTGGGGCCACGAGCGCCATTGACAAGCA**ATG**GGGAAG
AAACAGAAAAACAAGAGCGAAGACAGCACCAAGGATGACATTGATCTTGATGCCTTGGCTGCAGAAATAGAAGGA
GCTGGTGCTGCCAAAGAACAGGAGCCTCAAAAGTCAAAAGGGAAAAAGAAAAAAGAGAAAAAAAAAGCAGGACTTT
GATGAAGATGATATCCTGAAAGAACTGGAAGAATTGTCTTTGGAAGCTCAAGGCATCAAAGCTGACAGAGAAACT
GTTGCAGTGAAGCCAACAGAAAACAATGAAGAGGAATTCACCTCAAAAGATAAAAAAAAGAAAGGACAGAAGGGC
AAAAAACAGAGTTTTGATGATAATGATAGCGAAGAATTGGAAGATAAAGATTCAAAATCAAAAAAGACTGCAAAA
CCGAAAGTGGAAATGTACTCTGGGAGTGATGATGATGATGATTTTAACAAACTTCCTAAAAAAAGCTAAAGGGAAA
GCTCAAAAATCAAATAAGAAGTGGGATGGGTCAGAGGAGGATGAGGATAACAGTAAAAAAATTAAAGAGCGTTCA
AGAATAAATTCTTCTGGTGAAAGTGGTGATGAATCAGATGAATTTTTGCAATCTAGAAAAGGACAGAAAAAAAAT
CAGAAAAACAAGCCAGGTCCTAACATAGAAAGTGGGAATGAAGATGATGACGCCTCCTTCAAAATTAAGACAGTG
GCCCAAAAGAAGGCAGAAAAGAAGGAGCGCGAGAGAAAAAAGCGAGATGAAGAAAAAGCGAAACTGCGGAAGCTG
AAAGAAAAAGAAGAGTTAGAAACAGGTAAAAAGGATCAGAGTAAACAAAAGGAATCTCAAAGGAAATTTGAAGAA
GAAACTGTAAAATCCAAAGTGACTGTTGATACTGGAGTAATTCCTGCCTCTGAAGAGAAAGCAGAGACTCCCACA
GCTGCAGAAGATGACAATGAAGGAGACAAAAAGAAGAAAGATAAGAAGAAAAAGAAAGGAGAAAAGGAAGAAAAA
GAGAAAGAGAAGAAAAAAGGACCTAGCAAAGCCACTGTTAAAGCTATGCAAGAAGCTCTGGCTAAGCTTAAAGAG
GAAGAAGAAAGACAGAAGAGAGAAGAGGAAGAACGTATAAAACGGCTTGAAGAATTAGAAGCCAAGCGTAAAGAA
GAGGAACGATTGGAACAAGAAAAAAGAGAAAGGAAAAAGCAAAAAGAAAAAGAAAGAAAAGAACGCTTGAAAAAA
GAAGGGAAACTTTTAACTAAATCCCAGAGAGAAGCCAGAGCCAGAGCCGAAGCTACTCTTAAACTGCTACAAGCT
CAGGGTGTTGAAGTGCCATCAAAAGACTCTTTGCCAAAGAAGAGGCCAATTTATGAAGATAAAAAGAGGAAAAAA
ATACCACAGCAGCTAGAAAGTAAAGAAGTGTCTGAATCAATGGAATTATGTGCTGCTGTAGAAGTTATGGAACAA
GGAGTACCAGAAAAGGAAGAGACACCACCTCCTGTTGAACCAGAAGAAGAAGAAGATACTGAGGATGCTGGATTG
GATGATTGGGAAGCTATGGCCAGTGATGAGGAGACAGAAAAAGTAGAAGGAAACACAGTTCATATAGAAGTAAAA
GAAAACCCTGAAGAGGAGGAGGAGGAGGAAGAAGAGGAAGAAGAAGATGAAGAAAGTGAAGAAGAGGAGGAAGAG
GAGGGAGAAAGTGAAGGCAGTGAAGGTGATGAGGAAGATGAAAAGGTGTCAGATGAGAAGGATTCAGGGAAGACA
TTAGATAAAAAGCCAAGTAAAGAAATGAGCTCAGATTCTGAATATGACTCTGATGATGATCGGACTAAAGAAGAA
AGGGCTTATGACAAAGCAAAACGGAGGATTGAGAAACGGCGACTTGAACATAGTAAAAATGTAAACACCGAAAAG
CTAAGAGCCCCTATTATCTGCGTACTTGGGCATGTGGACACAGGGAAGACAAAAATTCTAGATAAGCTCCGTCAC
ACACATGTACAAGACGGTGAAGCAGGTGGTATCACACAACAAATTTGGGCCACCAATGTTCCTCTTGAAGCTATT
AATGAACAGACTAAGATGATTAAAAATTTTGATAGAGAGAATGTACGGATTCCAGGAATGCTAATTATTGATACT
CCTGGGCATGAATCTTTCAGTAATCTGAGAAATAGAGGAAGCTCTCTTTGTGACATTGCCATTTTAGTTGTTGAT
ATTATGCATGGTTTGGAGCCCCAGACAATTGAGTCTATCAACCTTCTCAAATCTAAAAAATGTCCCTTCATTGTT
GCACTCAATAAGATTGATAGGTTATATGATTGGAAAAAGAGTCCTGACTCTGATGTGGCTGCTACTTTAAAGAAG
CAGAAAAAGAATACAAAAGATGAATTTGAGGAGCGAGCAAAGGCTATTATTGTAGAATTTGCACAGCAGGGTTTG
AATGCTGCTTTGTTTTATGAGAATAAAGATCCCCGCACTTTTGTGTCTTTGGTACCTACCTCTGCACATACTGGT
GATGGCATGGGAAGTCTGATCTACCTTCTTGTAGAGTTAACTCAGACCATGTTGAGCAAGAGACTTGCACACTGT
GAAGAGCTGAGAGCACAGGTGATGGAGGTTAAAGCTCTCCCGGGGATGGGCACCACTATAGATGTCATTTTGATC
AATGGGCGTTTGAAGGAAGGAGATACAATCATTGTTCCTGGAGTAGAAGGGCCCATTGTAACTCAGATTCGAGGC
CTCCTGTTACCTCCTCCTATGAAGGAATTACGAGTGAAGAACCAGTATGAAAAGCATAAAGAAGTAGAAGCAGCT
CAGGGGGTAAAGATTCTTGGAAAAGACCTGGAGAAAACATTGGCTGGTTTACCCCTCCTTGTGGCTTATAAAGAA
GATGAAATCCCTGTTCTTAAAGATGAATTGATCCATGAGTTAAAGCAGACACTAAATGCTATCAAATTAGAAGAA
AAAGGAGTCTATGTCCAGGCATCTACACTGGGTTCTTTGGAAGCTCTACTGGAATTTCTGAAAACATCAGAAGTG
CCCTATGCAGGAATTAACATTGGCCCAGTGCATAAAAAAGATGTTATGAAGGCTTCAGTGATGTTGGAACATGAC
CCTCAGTATGCAGTAATTTTGGCCTTCGATGTGAGAATTGAACGAGATGCACAAGAAATGGCTGATAGTTTAGGA
GTTAGAATTTTTAGTGCAGAAATTATTTATCATTTATTTGATGCCTTTACAAAATATAGACAAGACTACAAGAAA
CAGAAACAAGAAGAATTTAAGCACATAGCAGTATTTCCCTGCAAGATAAAAATCCTCCCTCAGTACATTTTTAAT
TCTCGAGATCCGATAGTGATGGGGGTGACGGTGGAAGCAGGTCAGGTGAAACAGGGGACACCCATGTGTGTCCCA
AGCAAAAATTTTGTTGACATCGGAATAGTAACAAGTATTGAAATAAACCATAAACAAGTGGATGTTGCAAAAAAA

FIGURE 140B

GGACAAGAAGTTTGTGTAAAAATAGAACCTATCCCTGGTGAGTCACCCAAAATGTTTGGAAGACATTTTGAAGCT
ACAGATATTCTTGTTAGTAAGATCAGCCGGCAGTCCATTGATGCACTCAAAGACTGGTTCAGAGATGAAATGCAG
AAGAGTGACTGGCAGCTTATTGTGGAGCTGAAGAAAGTATTTGAAATCATC**TAA**TTTTTTCACATGGAGCAGGAA
CTGGAGTAAATGCAATACTGTGTTGTAATATCCCAACAAAAATCAGACAAAAAATGGAACAGACGTATTTGGACA
CTGATGGACTTAAGTATGGAAGGAAGAAAAATAGGTGTATAAAATGTTTTCCATGAGAAACCAAGAAACTTACAC
TGGTTTGACAGTGGTCAGTTACATGTCCCCACAGTTCCAATGTGCCTGTTCACTCACCTCTCCCTTCCCCAACCC
TTCTCTACTTGGCTGCTGTTTTAAAGTTTGCCCTTCCCCAAATTTGGATTTTTATTACAGAGTCTAAAGCTCTTT
CGATTTTATACTGATTAAATCAGTACTGCAGTATTTGATTAACCA

FIGURE 141

MGKKQKNKSEDSTKDDIDLDALAAEIEGAGAAKEQEPQKSKGKKKKEKKKQDFDEDDILKELEELSLEAQGIKAD
RETVAVKPTENNEEEFTSKDKKKKGQKGKKQSFDDNDSEELEDKDSKSKKTAKPKVEMYSGSDDDDDFNKLPKKA
KGKAQKSNKKWDGSEEDEDNSKKIKERSRINSSGESGDESDEFLQSRKGQKKNQKNKPGPNIESGNEDDDASFKI
KTVAQKKAEKKERERKKRDEEKAKLRKLKEKEELETGKKDQSKQKESQRKFEEETVKSKVTVDTGVIPASEEKAE
TPTAAEDDNEGDKKKKDKKKKKGEKEEKEKEKKKGPSKATVKAMQEALAKLKEEEERQKREEEERIKRLEELEAK
RKEEERLEQEKRERKKQKEKERKERLKKEGKLLTKSQREARARAEATLKLLQAQGVEVPSKDSLPKKRPIYEDKK
RKKIPQQLESKEVSESMELCAAVEVMEQGVPEKEETPPPVEPEEEEDTEDAGLDDWEAMASDEETEKVEGNTVHI
EVKENPEEEEEEEEEEEDEESEEEEEEEGESEGSEGDEEDEKVSDEKDSGKTLDKKPSKEMSSDSEYDSDDDRT
KEERAYDKAKRRIEKRRLEHSKNVNTEKLRAPIICVLGHVDTGKTKILDKLRHTHVQDGEAGGITQQIWATNVPL
EAINEQTKMIKNFDRENVRIPGMLIIDTPGHESFSNLRNRGSSLCDIAILVVDIMHGLEPQTIESINLLKSKKCP
FIVALNKIDRLYDWKKSPDSDVAATLKKQKKNTKDEFEERAKAIIVEFAQQGLNAALFYENKDPRTFVSLVPTSA
HTGDGMGSLIYLLVELTQTMLSKRLAHCEELRAQVMEVKALPGMGTTIDVILINGRLKEGDTIIVPGVEGPIVTQ
IRGLLLPPPMKELRVKNQYEKHKEVEAAQGVKILGKDLEKTLAGLPLLVAYKEDEIPVLKDELIHELKQTLNAIK
LEEKGVYVQASTLGSLEALLEFLKTSEVPYAGINIGPVHKKDVMKASVMLEHDPQYAVILAFDVRIERDAQEMAD
SLGVRIFSAEIIYHLFDAFTKYRQDYKKQKQEEFKHIAVFPCKIKILPQYIFNSRDPIVMGVTVEAGQVKQGTPM
CVPSKNFVDIGIVTSIEINHKQVDVAKKGQEVCVKIEPIPGESPKMFGRHFEATDILVSKISRQSIDALKDWFRD
EMQKSDWQLIVELKKVFEII

FIGURE 142

CCCGGACGTGCGGCTCCCCTCGGCCTCCTCGCC**ATG**GACGCGGACGACTCCCGGGCCCCCAAGGGCTCCTTGCGG
AAGTTCCTGGAGCACCTCTCCGGGGCCGGCAAGGCCATCGGCGTGCTGACCAGCGGCGGGGATGCTCAAGGTATG
AACGCTGCCGTCCGTGCCGTGGTGCGCATGGGTATCTACGTGGGGGCCAAGGTGTACTTCATCTACGAGGGCTAC
CAGGGCATGGTGGACGGAGGCTCAAACATCGCAGAGGCCGACTGGGAGAGTGTCTCCAGCATCCTGCAAGTGGGC
GGGACGATCATTGGCAGTGCGCGGTGCCAGGCCTTCCGCACGCGGGAAGGCCGCCTGAAGGCTGCTTGCAACCTG
CTGCAGCGCGGCATCACCAACCTGTGTGTGATCGGCGGGGACGGGAGCCTCACCGGGGCCAACCTCTTCCGGAAG
GAGTGGAGTGGGCTGCTGGAGGAGCTGGCCAGGAACGGCCAGATCGATAAGGAGGCCGTGCAGAAGTACGCCTAC
CTCAACGTGGTGGGCATGGTGGGCTCCATCGACAATGATTTCTGCGGCACCGACATGACCATCGGCACGGACTCC
GCCCTGCACAGGATCATCGAGGTCGTCGACGCCATCATGACCACGGCCCAGAGCCACCAGAGGACCTTCGTTCTG
GAGGTGATGGGACGACACTGTGGGTACCTGGCCCTGGTGAGTGCCTTGGCCTGCGGTGCGGACTGGGTGTTCCTT
CCAGAATCTCCACCAGAGGAAGGCTGGGAGGAGCAGATGTGTGTCAAACTCTCGGAGAACCGTGCCCGGAAAAAA
AGGCTGAATATTATTATTGTGGCTGAAGGAGCAATTGATACCCAAAATAAACCCATCACCTCTGAGAAAATCAAA
GAGCTTGTCGTCACGCAGCTGGGCTATGACACACGTGTGACCATCCTCGGGCACGTGCAGAGAGGAGGGACCCCT
TCGGCATTCGACAGGATCTTGGCCAGCCGCATGGGAGTGGAGGCAGTCATCGCCTTGCTAGAGGCCACCCCGGAC
ACCCCAGCTTGCGTCGTGTCACTGAACGGGAACCACGCCGTGCGCCTGCCGCTGATGGAGTGCGTGCAGATGACT
CAGGATGTGCAGAAGGCGATGGACGAGAGGAGATTTCAAGATGCGGTTCGACTCCGAGGGAGGAGCTTTGCGGGC
AACCTGAACACCTACAAGCGACTTGCCATCAAGCTGCCGGATGATCAGATCCCAAAGACCAATTGCAACGTAGCT
GTCATCAACGTGGGGGCACCCGCGGCTGGGATGAACGCGGCCGTACGCTCAGCTGTGCGCGTGGGCATTGCCGAC
GGCCACAGGATGCTCGCCATCTATGATGGCTTTGACGGCTTCGCCAAGGGCCAGATCAAAGAAATCGGCTGGACA
GATGTCGGGGGCTGGACCGGCCAAGGAGGCTCCATTCTTGGGACAAAACGCGTTCTCCCGGGGAAGTACTTGGAA
GAGATCGCCACACAGATGCGCACGCACAGCATCAACGCGCTGCTGATCATCGGTGGATTCGAGGCCTACCTGGGA
CTCCTGGAGCTGTCAGCCGCCCGGGAGAAGCACGAGGAGTTCTGTGTCCCCATGGTCATGGTTCCCGCTACTGTG
TCCAACAATGTGCCGGGTTCCGATTTCAGCATCGGGGCAGACACCGCCCTGAACACTATCACCGACACCTGCGAC
CGCATCAAGCAGTCCGCCAGCGGAACCAAGCGGCGCGTGTTCATCATCGAGACCATGGGCGGCTACTGTGGCTAC
CTGGCCAACATGGGGGGGCTCGCGGCCGGAGCTGATGCCGCATACATTTTCGAAGAGCCCTTCGACATCAGGGAT
CTGCAGTCCAACGTGGAGCACCTGACGGAGAAAATGAAGACCACCATCCAGAGAGGCCTTGTGCTCAGAAATGAG
AGCTGCAGTGAAAACTACACCACCGACTTCATTTACCAGCTGTATTCAGAAGAGGGCAAAGGCGTGTTTGACTGC
AGGAAGAACGTGCTGGGTCACATGCAGCAGGGTGGGGCACCCTCTCCATTTGATAGAAACTTTGGAACCAAAATC
TCTGCCAGAGCTATGGAGTGGATCACTGCAAAACTCAAGGAGGCCCGGGGCAGAGGAAAAAAATTTACCACCGAT
GATTCCATTTGTGTGCTGGGAATAAGCAAAAGAAACGTTATTTTTCAACCTGTGGCAGAGCTGAAGAAGCAAACG
GATTTTGAGCACAGGATTCCCAAAGAACAGTGGTGGCTCAAGCTACGGCCCCTCATGAAAATCCTGGCCAAGTAC
AAGGCCAGCTATGACGTGTCGGACTCAGGCCAGCTGGAACATGTGCAGCCCTGGAGTGTC**TGA**CCCAGTCCCGCC
TGCATGTGCCTGCAGCCACCGTGGACTGTCTGTTTTTGTAACACTTAAGTTATTTTATCAGCACTTTATGCACGT
ATTATTGACATTAATACCTAATCGGCGAGTGCCCATCTGCCCCACCAGCTCCAGTGCGTGCTGTCTGTGGAGTGT
GTCTCATGCTTTCAGATGTGCATATGAGCAGAATTAATTAA

FIGURE 143

MDADDSRAPKGSLRKFLEHLSGAGKAIGVLTSGGDAQGMNAAVRAVVRMGIYVGAKVYFIYEGYQGMVDGGSNIA
EADWESVSSILQVGGTIIGSARCQAFRTREGRLKAACNLLQRGITNLCVIGGDGSLTGANLFRKEWSGLLEELAR
NGQIDKEAVQKYAYLNVVGMVGSIDNDFCGTDMTIGTDSALHRIIEVVDAIMTTAQSHQRTFVLEVMGRHCGYLA
LVSALACGADWVFLPESPPEEGWEEQMCVKLSENRARKKRLNIIIVAEGAIDTQNKPITSEKIKELVVTQLGYDT
RVTILGHVQRGGTPSAFDRILASRMGVEAVIALLEATPDTPACVVSLNGNHAVRLPLMECVQMTQDVQKAMDERR
FQDAVRLRGRSFAGNLNTYKRLAIKLPDDQIPKTNCNVAVINVGAPAAGMNAAVRSAVRVGIADGHRMLAIYDGF
DGFAKGQIKEIGWTDVGGWTGQGGSILGTKRVLPGKYLEEIATQMRTHSINALLIIGGFEAYLGLLELSAAREKH
EEFCVPMVMVPATVSNNVPGSDFSIGADTALNTITDTCDRIKQSASGTKRRVFIIETMGGYCGYLANMGGLAAGA
DAAYIFEEPFDIRDLQSNVEHLTEKMKTTIQRGLVLRNESCSENYTTDFIYQLYSEEGKGVFDCRKNVLGHMQQG
GAPSPFDRNFGTKISARAMEWITAKLKEARGRGKKFTTDDSICVLGISKRNVIFQPVAELKKQTDFEHRIPKEQW
WLKLRPLMKILAKYKASYDVSDSGQLEHVQPWSV

FIGURE 144

CCATTGTGCTCTAAAGGGAAGGTGCTGTGTAATCATTAAGGAGCGGAGGCTTTTGGAGCTGCTAAA**ATG**CCGGAT
TACCTCGGTGCCGATCAGCGGAAGACCAAAGAGGATGAGAAGGACGACAAGCCCATCCGAGCTCTGGATGAGGGG
GATATTGCCTTGTTGAAAACTTATGGTCAGAGCACTTACTCTAGGCAGATCAAGCAAGTTGAAGATGACATTCAG
CAACTTCTCAAGAAAATTAATGAGCTCACTGGTATTAAAGAATCTGACACTGGCCTGGCCCCACCAGCACTCTGG
GATTTGGCTGCAGATAAGCAGACACTCCAGAGTGAACAGCCTTTACAGGTTGCCAGGTGTACAAAGATAATCAAT
GCTGATTCGGAGGACCCAAAATACATTATCAACGTAAAGCAGTTTGCCAAGTTTGTGGTGGACCTTAGTGATCAG
GTGGCACCTACTGACATTGAAGAAGGGATGAGAGTGGGCGTGGATAGAAATAAATATCAAATTCACATTCCATTG
CCTCCTAAGATTGACCCAACAGTTACCATGATGCAGGTGGAAGAGAAACCTGATGTCACATACAGTGATGTTGGT
GGCTGTAAGGAACAGATTGAGAAACTGCGAGAAGTAGTTGAAACCCCATTACTTCATCCAGAGAGGTTTGTGAAC
CTTGGCATTGAGCCTCCCAAGGGCGTGCTGCTCTTTGGTCCACCCGGTACAGGCAAGACACTCTGTGCGCGGGCA
GTTGCTAATCGGACTGATGCGTGCTTCATTCGAGTTATTGGATCTGAGCTTGTACAGAAATACGTCGGTGAGGGG
GCTCGAATGGTTCGTGAACTCTTTGAAATGGCCAGAACAAAAAAAGCCTGCCTTATCTTCTTTGATGAAATTGAT
GCTATTGGAGGGGCTCGTTTTGATGATGGTGCTGGAGGTGACAATGAAGTGCAGAGAACAATGTTGGAACTGATC
AATCAGCTTGATGGTTTTGATCCTCGAGGCAATATTAAAGTGCTGATGGCCACTAACAGACCTGATACTTTGGAT
CCAGCACTGATGAGGCCAGGGAGATTGGATAGAAAAATTGAATTTAGCTTGCCCGATCTAGAGGGTCGGACCCAC
ATATTTAAGATTCACGCTCGTTCAATGAGTGTTGAAAGAGATATCAGATTTGAACTGTTAGCACGACTGTGTCCA
AATAGCACTGGTGCTGAGATTAGAAGCGTCTGCACAGAGGCTGGTATGTTTGCCATCAGAGCACGGCGAAAAATT
GCTACCGAGAAGGATTTCTTGGAAGCTGTAAATAAGGTCATTAAGTCTTATGCCAAATTCAGTGCTACTCCTCGT
TACATGACATACAAC**TGA**ACCCTGAAGGCTTTCAAGTGAAAACTTTAAATTGGAATCCTAACCTTATATAGACTT
GTTAATAACCAATTCATAAACAAATAAATGGCTTCAACTTTAGAGCACAATGG

FIGURE 145

MPDYLGADQRKTKEDEKDDKPIRALDEGDIALLKTYGQSTYSRQIKQVEDDIQQLLKKINELTGIKESDTGLAPP
ALWDLAADKQTLQSEQPLQVARCTKIINADSEDPKYIINVKQFAKFVVDLSDQVAPTDIEEGMRVGVDRNKYQIH
IPLPPKIDPTVTMMQVEEKPDVTYSDVGGCKEQIEKLREVVETPLLHPERFVNLGIEPPKGVLLFGPPGTGKTLC
ARAVANRTDACFIRVIGSELVQKYVGEGARMVRELFEMARTKKACLIFFDEIDAIGGARFDDGAGGDNEVQRTML
ELINQLDGFDPRGNIKVLMATNRPDTLDPALMRPGRLDRKIEFSLPDLEGRTHIFKIHARSMSVERDIRFELLAR
LCPNSTGAEIRSVCTEAGMFAIRARRKIATEKDFLEAVNKVIKSYAKFSATPRYMTYN

FIGURE 146

ATCCGTGTCCTTGCGGTGCTGGGCAGCAGACCGTCCAAACCGACACGCGTGGTATCCTCGCGGTGTCCGGCAAGA
GACTACCAAGACAGACGCT**ATG**ACTGAGGCTGATGTGAATCCAAAGGCCTATCCCCTTGCCGATGCCCACCTCAC
CAAGAAGCTACTGGACCTCGTTCAGCAGTCATGTAACTATAAGCAGCTTCGGAAAGGAGCCAATGAGGCCACCAA
AACCCTCAACAGGGGCATCTCTGAGTTCATCGTGATGGCTGCAGACGCCGAGCCACTGGAGATCATTCTGCACCT
GCCGCTGCTGTGTGAAGACAAGAATGTGCCCTACGTGTTTGTGCGCTCCAAGCAGGCCCTGGGGAGAGCCTGTGG
GGTCTCCAGGCCTGTCATCGCCTGTTCTGTCACCATCAAAGAAGGCTCGCAGCTGAAACAGCAGATCCAATCCAT
TCAGCAGTCCATTGAAAGGCTCTTAGTC**TAA**ACCTGTGGCCTCTGCCACGTGCTCCCTGCCAGCTTCCCCCCTGA
GGTTGTGTATCATATTATCTGTGTTAGCATGTAGTATTTTCAGCTACTCTCTATTGTTATAAAATGTAGTACTAA
ATCTGGTTTCTGGATTTTTGTGTTGTTTTTGTTCTGTTTTACAGGGTTGCTATCCCCCTTCCTTTCCTCCCTCCC
TCTGCCATCCTTCATCCTTTTATCCTCCCTTTTTGGAACAAGTGTTCAGAGCAGACAGAAGCAGGGTGGTGGCAC
CGTTGAAAGGCAGAAAGAGCCAGGAGAAAGCTGATGGAGCCAGGACAGAGATCTGGTTCCAGCTTTCAGCCACTA
GCTTCCTGTTGTGTGCGGGGTGTGGTGGAATTAAACAGCATTCATTGTGTGTCCCTGTGCCTGGCACACAGAATC
ATTCATACGTGTTCAAGTGATCAAGGGGTTTCATTTGCTCTTGGGGGATTAGGTATCATTTGGGGAGGAAGCATG
TGTTCTGTGAGGTTGTTCGGCTATGTCCAAGTGTCGTTTACTAATGTACCCCTGCTGTTTGCTTTTGGTAATGTG
ATGTTGATGTTCTCCCCCTACCCACAACCATGCCCTTGAGGGTAGCAGGGCAGCAGCATACCAAAGAGATGTGCT
GCAGGACTCCGGAGGCAGCCTGGGTGGGTGAGCCATGGGGCAGTTGACCTGGGTCTTGAAAGAGTCGGGAGTGAC
AAGCTCAGAGAGCATGAACTGATGCTGGCATGAAGGATTCCAGGAAGATCATGGAGACCTGGCTGGTAGCTGTAA
CAGAGATGGTGGAGTCCAAGGAAACAGCCTGTCTCTGGTGAATGGGACTTTCTTTGGTGGACACTTGGCACCAGC
TCTGAGAGCCCTTCCCCTGTGTCCTGCCACCATGTGGGTCAGATGTACTCTCTGTCACATGAGGAGAGTGCTAGT
TCATGTGTTCTCCATTCTTGTGAGCATCCTAATAAATCTGTTCCATTTTG

FIGURE 147

MTEADVNPKAYPLADAHLTKKLLDLVQQSCNYKQLRKGANEATKTLNRGISEFIVMAADAEPLEIILHLPLLCED
KNVPYVFVRSKQALGRACGVSRPVIACSVTIKEGSQLKQQIQSIQQSIERLLV

FIGURE 148

GCGGCGGCGGCAGCGGCGGCGACGGCGAC**ATG**GAGAGCGGGGCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCG
ACCTGCGGCGCTTCCTGACGCAGCCGCAGGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCT
CCTGCATCTATGGTGAGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGG
ATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGTGGTCGACGCGT
ATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTGACCTGCTCTTCTCAGCTCTCTGGA
CCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAACCAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGG
GGGCCGACTCTGTGAGGGCAGCCATCACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGG
CCTACCAGCGCTACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACTG
CCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAACGCGGAGACCACCG
AGGGCTACCAGCCGCCCCCTGTGTAC**TGA**GCGGCGGTTAGCGTGGGAAGGGGGACAGAGAGGGCCCTCCCCTCTG
CCCTGGACTTTCCCATGAGCCTCCTGGAACTGCCAGCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACAC
ACAGCTAAGGAGCCTCATAGCCTGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCCAGAGGGCTTCAG
TCAGCCGCTCACTCCTCCAGGGCATTTTTAGGAAAGGGTTTTCAGCTAGTGTTTTTCCTCGCTTTTAATGACCTC
AGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCTCAGCTTCCCCCCGGCCC
GGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAGACTCGTGGGGGCCATCACACCTGCCCTGTG
CAGCGGAGCCGGACCAGGCTCTTGTGTCCTCACTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGG
GCCACCACCCTGTGCCGGTGGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCC
TCCTTGCTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTCTGCAGTT
GTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTCTGTGCCGAGTGTATTATAAA
ATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACGGAATAAATGTTTTCTCATTCAGTA

FIGURE 149

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCVFNRNEDACRYGSAIG
VLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWFVGFCFLTNQWAVTNPKDVLVGADSVRAAIT
FSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTPDPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

FIGURE 150

GCCACACGGTCTTTGAGCTGAGTCGAGGTGGACCCTTTGAACGCAGTCGCCCTACAGCCGCTGATTCCCCCCGCA
TCGCCTCCCGTGGAAGCCCAGGCCCGCTTCGCAGCTTTCTCCCTTTGTCTCATAACC**ATG**TCCACCAACGAGAAT
GCTAATACACCAGCTGCCCGTCTTCACAGATTCAAGAACAAGGGAAAAGACAGTACAGAAATGAGGCGTCGCAGA
ATAGAGGTCAATGTGGAGCTGAGGAAAGCTAAGAAGGATGACCAGATGCTGAAGAGGAGAAATGTAAGCTCATTT
CCTGATGATGCTACTTCTCCGCTGCAGGAAAACCGCAACAACCAGGGCACTGTAAATTGGTCTGTTGATGACATT
GTCAAAGGCATAAATAGCAGCAATGTGGAAAATCAGCTCCAAGCTACTCAAGCTGCCAGGAAACTACTTTCCAGA
GAAAAACAGCCCCCCATAGACAACATAATCCGGGCTGGTTTGATTCCGAAATTTGTGTCCTTCTTGGGCAGAACT
GATTGTAGTCCCATTCAGTTTGAATCTGCTTGGGCACTCACTAACATTGCTTCTGGGACATCAGAACAAACCAAG
GCTGTGGTAGATGGAGGTGCCATCCCAGCATTCATTTCTCTGTTGGCATCTCCCCATGCTCACATCAGTGAACAA
GCTGTCTGGGCTCTAGGAAACATTGCAGGTGATGGCTCAGTGTTCCGAGACTTGGTTATTAAGTACGGTGCAGTT
GACCCACTGTTGGCTCTCCTTGCAGTTCCTGATATGTCATCTTTAGCATGTGGCTACTTACGTAATCTTACCTGG
ACACTTTCTAATCTTTGCCGCAACAAGAATCCTGCACCCCCGATAGATGCTGTTGAGCAGATTCTTCCTACCTTA
GTTCGGCTCCTGCATCATGATGATCCAGAAGTGTTAGCAGATACCTGCTGGGCTATTTCCTACCTTACTGATGGT
CCAAATGAACGAATTGGCATGGTGGTGAAAACAGGAGTTGTGCCCCAACTTGTGAAGCTTCTAGGAGCTTCTGAA
TTGCCAATTGTGACTCCTGCCCTAAGAGCCATAGGGAATATTGTCACTGGTACAGATGAACAGACTCAGGTTGTG
ATTGATGCAGGAGCACTCGCCGTCTTTCCCAGCCTGCTCACCAACCCCAAAACTAACATTCAGAAGGAAGCTACG
TGGACAATGTCAAACATCACAGCCGGCCGCCAGGACCAGATACAGCAAGTTGTGAATCATGGATTAGTCCCATTC
CTTGTCAGTGTTCTCTCTAAGGCAGATTTTAAGACACAAAAGGAAGCTGTGTGGGCCGTGACCAACTATACCAGT
GGTGGAACAGTTGAACAGATTGTGTACCTTGTTCACTGTGGCATAATAGAACCGTTGATGAACCTCTTAACTGCA
AAAGATACCAAGATTATTCTGGTTATCCTGGATGCCATTTCAAATATCTTTCAGGCTGCTGAGAAACTAGGTGAA
ACTGAGAAACTTAGTATAATGATTGAAGAATGTGGAGGCTTAGACAAAATTGAAGCTCTACAAAACCATGAAAAT
GAGTCTGTGTATAAGGCTTCGTTAAGCTTAATTGAGAAGTATTTCTCTGTAGAGGAAGAGGAAGATCAAAACGTT
GTACCAGAAACTACCTCTGAAGGCTACACTTTCCAAGTTCAGGATGGGGCTCCTGGGACCTTTAACTTT**TAG**ATC
ATGTAGCTGAGACATAAATTTGTTGTGTACTACGTTTGGTATTTTGTCTTATTGTTTCTCTACTAAGAACTCTTT
CTTAAATGTGGTTTGTTACTGTAGCACTTTTTACACTGAAACTATACTTGAACAGTTCCAACTGTACATACATAC
TGTATGAAGCTTGTCCTCTGACTAGGTTTCTAATTTCTATGTGGAATTTCCTATCTTGCAGCATCCTGTAAATAA
ACATTCAAGTCCACCCTTAAAAAAAA

FIGURE 151

MSTNENANTPAARLHRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSSFPDDATSPLQENRNNQGTVN
WSVDDIVKGINSSNVENQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRTDCSPIQFESAWALTNIASG
TSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGDGSVFRDLVIKYGAVDPLLALLAVPDMSSLACGY
LRNLTWTLSNLCRNKNPAPPIDAVEQILPTLVRLLHHDDPEVLADTCWAISYLTDGPNERIGMVVKTGVVPQLVK
LLGASELPIVTPALRAIGNIVTGTDEQTQVVIDAGALAVFPSLLTNPKTNIQKEATWTMSNITAGRQDQIQQVVN
HGLVPFLVSVLSKADFKTQKEAVWAVTNYTSGGTVEQIVYLVHCGIIEPLMNLLTAKDTKIILVILDAISNIFQA
AEKLGETEKLSIMIEECGGLDKIEALQNHENESVYKASLSLIEKYFSVEEEEDQNVVPETTSEGYTFQVQDGAPG
TFNF

FIGURE 152

TGTCGGGGACGGTAACCGGGACCCGTGCTCTGCTCCTGTCGCCTTCGCCTCCTGAATCCCTAGCCAT**ATG**CGTGA
GTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTGGGAGCTCTACTGCCTGGAACA
CGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTT
CAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGT
TCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTA
TGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTTGGACCGAATTCGCAAGCTGGCTGACCA
GTGCACCCGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTCACCTCCCTGCT
CATGGAACGCCTGTCAGTTGATTATGGCAAGAAATCCAAGCTGGAGTTCTCCATTTACCCGGCACCCCAGGTTTC
CACAGCTGTAGTTGAGCCCTACAACTCCATCCTCACCACCCACACCACCCTGGAGCACTCTGATTGTGCCTTCAT
GGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTCGATATCGAGCGCCCAACCTACACTAACCTTAA
CCGCCTTATTAGCCAGATTGTGTCCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGAC
AGAATTCCAGACCAACCTGGTCCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCCTGTCATCTCTGC
TGAGAAAGCCTACCATGAACAGCTTTCTGTAGCAGACATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGT
GAAATGTGACCCTGGCCATGGTAAATACATGGCTTGCTGCCTGTTGTACCGTGGTGACGTGGTTCCCAAAGATGT
CAATGCTGCCATTGCCACCATCAAAACCAAGCGCACGATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGT
TGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCT
GAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGC
CTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTCAGAGGCCCGTGAAGATATGGCTGCCCT
TGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATAC**TAA**TT
ATCCATTCCTTTTGGCCCTGCAGCATGTCATGCTCCCAGAATTTCAGCTTCAGCTTAACTGACAGATGTTAAAGC
TTTCTGGTTAGATTGTTTTCACTTGGTGATCATGTCTTTTCCATGTGTACCTGTAATATTTTTCCATCATATCTC
AAAGTAAAGTCATTAACATCA

FIGURE 153

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVI
DEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTRLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVADITNACFEPAN
QMVKCDPGHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVDSVEGEGEEEGEE
Y

FIGURE 154A

GGACGCACAGGCATTCCCCGCGCCCCTCCAGCCCTCGCCGCCCTCGCCACCGCTCCCGGCCGCCGCGCTCCGGTA
CACACAGGATCCCTGCTGGGCACCAACAGCTCCACC**ATG**GGGCTGGCCTGGGGACTAGGCGTCCTGTTCCTGATG
CATGTGTGTGGCACCAACCGCATTCCAGAGTCTGGCGGAGACAACAGCGTGTTTGACATCTTTGAACTCACCGGG
GCCGCCCGCAAGGGGTCTGGGCGCCGACTGGTGAAGGGCCCCGACCCTTCCAGCCCAGCTTTCCGCATCGAGGAT
GCCAACCTGATCCCCCCTGTGCCTGATGACAAGTTCCAAGACCTGGTGGATGCTGTGCGGGCAGAAAAGGGTTTC
CTCCTTCTGGCATCCCTGAGGCAGATGAAGAAGACCCGGGGCACGCTGCTGGCCCTGGAGCGGAAAGACCACTCT
GGCCAGGTCTTCAGCGTGGTGTCCAATGGCAAGGCGGGCACCCTGGACCTCAGCCTGACCGTCCAAGGAAAGCAG
CACGTGGTGTCTGTGGAAGAAGCTCTCCTGGCAACCGGCCAGTGGAAGAGCATCACCCTGTTTGTGCAGGAAGAC
AGGGCCCAGCTGTACATCGACTGTGAAAAGATGGAGAATGCTGAGTTGGACGTCCCCATCCAAAGCGTCTTCACC
AGAGACCTGGCCAGCATCGCCAGACTCCGCATCGCAAAGGGGGGCGTCAATGACAATTTCCAGGGGGTGCTGCAG
AATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAAGGCTGCTCCAGCTCTACCAGTGTC
CTCCTCACCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCACTAACTACATTGGCCACAAGACA
AAGGACTTGCAAGCCATCTGCGGCATCTCCTGTGATGAGCTGTCCAGCATGGTCCTGGAACTCAGGGGCCTGCGC
ACCATTGTGACCACGCTGCAGGACAGCATCCGCAAAGTGACTGAAGAGAACAAAGAGTTGGCCAATGAGCTGAGG
CGGCCTCCCCTATGCTATCACAACGGAGTTCAGTACAGAAATAACGAGGAATGGACTGTTGATAGCTGCACTGAG
TGTCACTGTCAGAACTCAGTTACCATCTGCAAAAAGGTGTCCTGCCCCATCATGCCCTGCTCCAATGCCACAGTT
CCTGATGGAGAATGCTGTCCTCGCTGTTGGCCCAGCGACTCTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGG
ACCTCCTGTTCTACGAGCTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGT
GAGGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTTAAACAGGATGGTGGCTGG
AGCCACTGGTCCCCGTGGTCATCTTGTTCTGTGACATGTGGTGATGGTGTGATCACAAGGATCCGGCTCTGCAAC
TCTCCCAGCCCCCAGATGAATGGGAAACCCTGTGAAGGCGAAGCGCGGGAGACCAAAGCCTGCAAGAAAGACGCC
TGCCCCATCAATGGAGGCTGGGGTCCTTGGTCACCATGGGACATCTGTTCTGTCACCTGTGGAGGAGGGGTACAG
AAACGTAGTCGTCTCTGCAACAACCCCGCACCCCAGTTTGGAGGCAAGGACTGCGTTGGTGATGTAACAGAAAAC
CAGATCTGCAACAAGCAGGACTGTCCAATTGATGGATGCCTGTCCAATCCCTGCTTTGCCGGCGTGAAGTGTACT
AGCTACCCTGATGGCAGCTGGAAATGTGGTGCTTGTCCCCCTGGTTACAGTGGAAATGGCATCCAGTGCACAGAT
GTTGATGAGTGCAAAGAAGTGCCTGATGCCTGCTTCAACCACAATGGAGAGCACCGGTGTGAGAACACGGACCCC
GGCTACAACTGCCTGCCCTGCCCCCCACGCTTCACCGGCTCACAGCCCTTCGGCCAGGGTGTCGAACATGCCACG
GCCAACAAACAGGTGTGCAAGCCCCGTAACCCCTGCACGGATGGGACCCACGACTGCAACAAGAACGCCAAGTGC
AACTACCTGGGCCACTATAGCGACCCCATGTACCGCTGCGAGTGCAAGCCTGGCTACGCTGGCAATGGCATCATC
TGCGGGGAGGACACAGACCTGGATGGCTGGCCCAATGAGAACCTGGTGTGCGTGGCCAATGCGACTTACCACTGC
AAAAAGGATAATTGCCCCAACCTTCCCAACTCAGGGCAGGAAGACTATGACAAGGATGGAATTGGTGATGCCTGT
GATGATGACGATGACAATGATAAAATTCCAGATGACAGGGACAACTGTCCATTCCATTACAACCCAGCTCAGTAT
GACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACTGTCCCTACAACCACAACCCAGATCAGGCAGACACA
GACAACAATGGGGAAGGAGACGCCTGTGCTGCAGACATTGATGGAGACGGTATCCTCAATGAACGGGACAACTGC
CAGTACGTCTACAATGTGGACCAGAGAGACACTGATATGGATGGGGTTGGAGATCAGTGTGACAATTGCCCCTTG
GAACACAATCCGGATCAGCTGGACTCTGACTCAGACCGCATTGGAGATACCTGTGACAACAATCAGGATATTGAT
GAAGATGGCCACCAGAACAATCTGGACAACTGTCCCTATGTGCCCAATGCCAACCAGGCTGACCATGACAAAGAT
GGCAAGGGAGATGCCTGTGACCACGATGATGACAACGATGGCATTCCTGATGACAAGGACAACTGCAGACTCGTG
CCCAATCCCGACCAGAAGGACTCTGACGGCGATGGTCGAGGTGATGCCTGCAAAGATGATTTTGACCATGACAGT
GTGCCAGACATCGATGACATCTGTCCTGAGAATGTTGACATCAGTGAGACCGATTTCCGCCGATTCCAGATGATT
CCTCTGGACCCCAAAGGGACATCCCAAAATGACCCTAACTGGGTTGTACGCCATCAGGGTAAAGAACTCGTCCAG
ACTGTCAACTGTGATCCTGGACTCGCTGTAGGTTATGATGAGTTTAATGCTGTGGACTTCAGTGGCACCTTCTTC
ATCAACACCGAAAGGGACGATGACTATGCTGGATTTGTCTTTGGCTACCAGTCCAGCAGCCGCTTTTATGTTGTG
ATGTGGAAGCAAGTCACCCAGTCCTACTGGGACACCAACCCCACGAGGGCTCAGGGATACTCGGGCCTTTCTGTG
AAAGTTGTAAACTCCACCACAGGGCCTGGCGAGCACCTGCGGAACGCCCTGTGGCACACAGGAAACACCCCTGGC
CAGGTGCGCACCCTGTGGCATGACCCTCGTCACATAGGCTGGAAAGATTTCACCGCCTACAGATGGCGTCTCAGC
CACAGGCCAAAGACGGGTTTCATTAGAGTGGTGATGTATGAAGGGAAGAAAATCATGGCTGACTCAGGACCCATC
TATGATAAAACCTATGCTGGTGGTAGACTAGGGTTGTTTGTCTTCTCTCAAGAAATGGTGTTCTTCTCTGACCTG

FIGURE 154B

AAATACGAATGTAGAGATCCC**TAA**TCATCAAATTGTTGATTGAAAGACTGATCATAAACCAATGCTGGTATTGCA
CCTTCTGGAACTATGGGCTTGAGAAAACCCCCAGGATCACTTCTCCTTGGCTTCCTTCTTTTCTGTGCTTGCATC
AGTGTGGACTCCTAGAACGTGCGACCTGCCTCAAGAAAATGCAGTTTTCAAAAACAGACTCATCAGCATTCAGCC
TCCAATGAATAAGACATCTTCCAAGCATATAAACAATTGCTTTGGTTTCCTTTTGAAAAAGCATCTACTTGCTTC
AGTTGGGAAGGTGCCCATTCCACTCTGCCTTTGTCACAGAGCAGGGTGCTATTGTGAGGCCATCTCTGAGCAGTG
GACTCAAAAGCATTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCCTGACATC
CTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCGAGACGATTGTATGAAGAA
AATATGGAGGAACTGTTACATGTTCGGTACTAAGTCATTTTCAGGGGATTGAAAGACTATTGCTGGATTTCATGA
TGCTGACTGGCGTTAGCTGATTAACCCATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGG
CTTCTGGACTTCCTCCCTGATCCCCACCCTTACTCATCACCTTGCAGTGGCCAGAATTAGGGAATCAGAATCAAA
CCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCATTCTAGATGTAGCTTGTG
CAGATGTAGCAGGAAAATAGGAAAACCTACCATCTCAGTGAGCACCAGCTGCCTCCCAAAGGAGGGGCAGCCGTG
CTTATATTTTTATGGTTACAATGGCACAAAATTATTATCAACCTAACTAAAACATTCCTTTTCTCTTTTTTTCCGT
AATTACTAGGTAGTTTTCTAATTCTCTCTTTTGGAAGTATGATTTTTTTAAAGTCTTTACGATGTAAAATATTTA
TTTTTTACTTATTCTGGAAGATCTGGCTGAAGGATTATTCATGGAACAGGAAGAAGCGTAAAGACTATCCATGTC
ATCTTTGTTGAGAGTCTTCGTGACTGTAAGATTGTAAATACAGATTATTTATTAACTCTGTTCTGCCTGGAAATT
TAGGCTTCATACGGAAAGTGTTTGAGAGCAAGTAGTTGACATTTATCAGCAAATCTCTTGCAAGAACAGCACAAG
GAAAATCAGTCTAATAAGCTGCTCTGCCCCTTGTGCTCAGAGTGGATGTTATGGGATTCCTTTTTTCTCTGTTTT
ATCTTTTCAAGTGGAATTAGTTGGTTATCCATTTGCAAATGTTTTAAATTGCAAAGAAAGCCATGAGGTCTTCAA
TACTGTTTTACCCCATCCCTTGTGCATATTTCCAGGGAGAAGGAAAGCATATACACTTTTTTCTTTCATTTTTCC
AAAAGAGAAAAAAATGACAAAAGGTGAAACTTACATACAAATATTACCTCATTTGTTGTGTGACTGAGTAAAGAA
TTTTTGGATCAAGCGGAAAGAGTTTAAGTGTCTAACAAACTTAAAGCTACTGTAGTACCTAAAAAGTCAGTGTTG
TACATAGCATAAAAACTCTGCAGAGAAGTATTCCCAATAAGGAAATAGCATTGAAATGTTAAATACAATTTCTGA
AAGTTATGTTTTTTTTCTATCATCTGGTATACCATTGCTTTATTTTTATAAATTATTTTCTCATTGCCATTGGAA
TAGAATATTCAGATTGTGTAGATATGCTATTTAAATAATTTATCAGGAAATACTGCCTGTAGAGTTAGTATTTCT
ATTTTTATATAATGTTTGCACACTGAATTGAAGAATTGTTGGTTTTTTCTTTTTTTTGTTTTTTTTTTTTTTTTT
TTTTTTTTTGCTTTTGACCTCCCATTTTTACTATTTGCCAATACCTTTTTCTAGGAATGTGCTTTTTTTTGTACA
CATTTTTATCCATTTTACATTCTAAAGCAGTGTAAGTTGTATATTACTGTTTCTTATGTACAAGGAACAACAATA
AATCATATGGAAATTTATATTT

FIGURE 155

MGLAWGLGVLFLMHVCGTNRIPESGGDNSVFDIFELTGAARKGSGRRLVKGPDPSSPAFRIEDANLIPPVPDDKF
QDLVDAVRAEKGFLLLASLRQMKKTRGTLLALERKDHSGQVFSVVSNGKAGTLDLSLTVQGKQHVVSVEEALLAT
GQWKSITLFVQEDRAQLYIDCEKMENAELDVPIQSVFTRDLASIARLRIAKGGVNDNFQGVLQNVRFVFGTTPED
ILRNKGCSSSTSVLLTLDNNVVNGSSPAIRTNYIGHKTKDLQAICGISCDELSSMVLELRGLRTIVTTLQDSIRK
VTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKKVSCPIMPCSNATVPDGECCPRCWPS
DSADDGWSPWSEWTSCSTSCGNGIQQRGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHWSPWSSCSVT
CGDGVITRIRLCNSPSPQMNGKPCEGEARETKACKKDACPINGGWGPWSPWDICSVTCGGGVQKRSRLCNNPAPQ
FGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGVKCTSYPDGSWKCGACPPGYSGNGIQCTDVDECKEVPDACF
NHNGEHRCENTDPGYNCLPCPPRFTGSQPFGQGVEHATANKQVCKPRNPCTDGTHDCNKNAKCNYLGHYSDPMYR
CECKPGYAGNGIICGEDTDLDGWPNENLVCVANATYHCKKDNCPNLPNSGQEDYDKDGIGDACDDDDDNDKIPDD
RDNCPFHYNPAQYDYDRDDVGDRCDNCPYNHNPDQADTDNNGEGDACAADIDGDGILNERDNCQYVYNVDQRDTD
MDGVGDQCDNCPLEHNPDQLDSDSDRIGDTCDNNQDIDEDGHQNNLDNCPYVPNANQADHDKDGKGDACDHDDDN
DGIPDDKDNCRLVPNPDQKDSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFRRFQMIPLDPKGTSQNDP
NWVVRHQGKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDDYAGFVFGYQSSSRFYVVMWKQVTQSYWDT
NPTRAQGYSGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRTLWHDPRHIGWKDFTAYRWRLSHRPKTGFIRVVM
YEGKKIMADSGPIYDKTYAGGRLGLFVFSQEMVFFSDLKYECRDP

FIGURE 156

GGCACGAGGGCGGCGGCGGCGGTAGAGGCGGCGGCGGCGGCGGCAGCGGGCTCGGAGGCAGCGGTTGGGCTCGCG
GCGAGCGGACGGGGTCGAGTCAGTGCGTTCGCGCGAGTTGGAATCGAAGCCTCTTAAA**ATG**GCAGATGACTTGGA
CTTCGAGACAGGAGATGCAGGGGCCTCAGCCACCTTCCCAATGCAGTGCTCAGCATTACGTAAGAATGGCTTTGT
GGTGCTCAAAGGCCGGCCATGTAAGATCGTCGAGATGTCTACTTCGAAGACTGGCAAGCACGGCCACGCCAAGGT
CCATCTGGTTGGTATTGACATCTTTACTGGGAAGAAATATGAAGATATCTGCCCGTCAACTCATAATATGGATGT
CCCCAACATCAAAAGGAATGACTTCCAGCTGATTGGCATCCAGGATGGGTACCTATCACTGCTCCAGGACAGCGG
GGAGGTACGAGAGGACCTTCGTCTCCCTGAGGGAGACCTTGGCAAGGAGATTGAGCAGAAGTACGACTGTGGAGA
AGAGATCCTGATCACGGTGCTGTCTGCCATGACAGAGGAGGCAGCTGTTGCAATCAAGGCCATGGCAAAA**TAA**CT
GGCTCCCAGGATGGCGGTGGTGGCAGCAGTGATCCTCTGAACCTGCAGAGGCCCCCTCCCCGAGCCTGGCCTGGC
TCTGGCCCGGTCCTAAGCTGGACTCCTCCTACACAATTTATTTGACGTTTTATTTTGGTTTTCCCCACCCCCTCA
ATCTGTCGGGGAGCCCCTGCCCTTCACCTAGCTCCCTTGGCCAGGAGCGAGCGAAGCTGTGGCCTTGGTGAAGCT
GCCCTCCTCTTCTCCCCTCACACTACAGCCCTGGTGGGGGAGAAGGGGGTGGGTGCTGCTTGTGGTTTAGTCTTT
TTTTTTTTTTTTTTTTTTTTTTAAATTCAATCTGGAATCAGAAAGCGGTGGATTCTGGCAAATGGTCCTTGTGC
CCTCCCCACTCATCCCTGGTCTGGTCCCCTGTTGCCCATAGCCCTTTACCCTGAGCACCACCCCAACAGACTGGG
GACCAGCCCCCTCGCCTGCCTGTGTCTCTCCCCAAACCCCTTTAGATGGGGAGGGAAGAGGAGGAGAGGGGAGGG
GACCTGCCCCCTCCTCAGGCATCTGGGAGGGCCCTGCCCCCATGGGCTTTACCCTTCCCTGCGGGCTCTCTCCCC
GACACATTTGTTAAAATCAAACCTGAATAAAACTACAAGTTTAATATGAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 157

MADDLDFETGDAGASATFPMQCSALRKNGFVVLKGRPCKIVEMSTSKTGKHGHAKVHLVGIDIFTGKKYEDICPS
THNMDVPNIKRNDFQLIGIQDGYLSLLQDSGEVREDLRLPEGDLGKEIEQKYDCGEEILITVLSAMTEEAAVAIK
AMAK

FIGURE 158

AGCGAGTCCTTCTTTTCCTGACTGCAGCTCTTTTCATTTTGCCATCCTTCTCCAGCTCC**ATG**ATGGTTCTGCAGG
TTTCTGCGGCCCCCCGGACAGTGGCTCTGACGGCGTTACTGATGGTGCTGCTCACATCTGTGGTCCAGGGCAGGG
CCACTCCAGAGAATTACGTGTACCAGGGACGGCAGGAATGCTACGCGTTTAATGGGACACAGCGCTTCCTGGAGA
GATACATCTACAACCGGGAGGAGTACGCGCGCTTCGACAGCGACGTGGGGGAGTTCCGGGCGGTGACGGAGCTGG
GGCGGCCTGCTGCGGAGTACTGGAACAGCCAGAAGGACATCCTGGAGGAGAAGCGGGCAGTGCCGGACAGGGTAT
GCAGACACAACTACGAGCTGGACGAGGCCGTGACCCTGCAGCGCCGAGTCCAGCCTAAGGTGAACGTTTCCCCCT
CCAAGAAGGGGCCCCTGCAGCACCACAACCTGCTTGTCTGCCACGTGACAGATTTCTACCCAGGCAGCATTCAAG
TCCGATGGTTCCTGAATGGACAGGAGGAAACAGCTGGGGTCGTGTCCACCAACCTGATCCGTAATGGAGACTGGA
CCTTCCAGATCCTGGTGATGCTGGAAATGACCCCCCAGCAGGGAGACGTCTACATCTGCCAAGTGGAGCACACCA
GCCTGGACAGTCCTGTCACCGTGGAGTGGAAGGCACAGTCTGATTCTGCCCAGAGTAAGACATTGACGGGAGCTG
GGGGCTTCGTGCTGGGGCTCATCATCTGTGGAGTGGGCATCTTCATGCACAGGAGGAGCAAGAAAGTTCAACGAG
GATCTGCA**TAA**ACAGGGTTCCTGACCTCACCGAAAAGACTAATGTGCCTTAGAACAAGCATTTGCTGTGTTTTGT
TAACACCTGGTTCCAGGACAGACCCTCAGCTTCCCAAGAGGATACTGCTGCCAAGAAGTTGCTCTGAAGTCAGTT
TCTATCGTTCTGCTCTTTGATTCAAAGCACTGTTTCTCTCACTGGGCCTCCAACCATGTTCCCTTCTTCTTAGCA
CCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAAAAATATGCATCAAATCGTCTCTCATTACTTT
TCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAATAAAGAAGTTCATTTTGGTTTACACGTAGGAAAGAAGAGAAG
CATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATT
TCAGTGAGCTGCCCCCAAATCAAGTTTAGTGCCCTCATCCATTTATGTCTCAGACCGCTATTCTTAACTATTCAA
TGGTGAGCAGACTGCAAATCTGCCTGATAGGACCCATATTCCCACAGCACTAATTCAACATATATCTTACTGAGA
GCATGTTTTATCATTACCATTAAGAAGTTAAATGAACATCAGAATTTAAAATCATAAATATAATCTAATACACTT
T

FIGURE 159

MMVLQVSAAPRTVALTALLMVLLTSVVQGRATPENYVYQGRQECYAFNGTQRFLERYIYNREEYARFDSDVGEFR
AVTELGRPAAEYWNSQKDILEEKRAVPDRVCRHNYELDEAVTLQRRVQPKVNVSPSKKGPLQHHNLLVCHVTDFY
PGSIQVRWFLNGQEETAGVVSTNLIRNGDWTFQILVMLEMTPQQGDVYICQVEHTSLDSPVTVEWKAQSDSAQSK
TLTGAGGFVLGLIICGVGIFMHRRSKKVQRGSA

FIGURE 160

GGCACGAGGGGCGGCCGGTGAGGGGGAAGCAAGTCTGGTCTCTGTGATTGAAGAAGTCGGCTCTGGGCTCCAGTG
CGGGAATCACACACATACCTCAGA**ATG**CCGGGTCTAAGTTGTAGATTTTATCAACACAAATTTCCTGAGGTGGAA
GATGTAGTGATGGTGAATGTCAGATCCATTGCTGAAATGGGGGCTTATGTCAGCTTGCTGGAATACAACAACATT
GAAGGCATGATTCTTCTTAGTGAATTATCCAGAAGGCGTATCCGTTCTATCAACAAACTCATCCGAATTGGCAGG
AATGAGTGTGTGGTTGTCATTAGGGTGGACAAAGAAAAAGGATATATTGATTTGTCAAAAAGAAGAGTTTCTCCA
GAGGAAGCAATCAAATGTGAAGACAAATTCACAAAATCCAAAACTGTTTATAGCATTCTTCGTCATGTTGCTGAG
GTGTTAGAATACACCAAGGATGAGCAGCTGGAAAGCCTATTCCAGAGGACTGCCTGGGTCTTTGATGACAAGTAC
AAGAGACCTGGATATGGTGCCTATGATGCATTTAAGCATGCAGTCTCAGACCCATCTATTTTGGATAGTTTAGAT
TTGAATGAAGATGAACGGGAAGTACTCATTAATAATATTAATAGGCGCTTGACCCCACAGGCTGTCAAAATTCGA
GCAGATATTGAAGTGGCTTGTTATGGTTATGAAGGCATTGATGCTGTAAAAGAAGCCCTAAGAGCAGGTTTGAAT
TGTTCTACAGAAAACATGCCCATTAAGATTAATCTAATAGCTCCTCCTCGGTATGTAATGACTACGACAACCCTG
GAGAGAACAGAAGGCCTTTCTGTCCTCAGTCAAGCTATGGCTGTTATCAAAGAGAAGATTGAGGAAAAGAGGGGT
GTGTTCAATGTTCAAATGGAGCCCAAAGTGGTCACAGATACAGATGAGACTGAACTTGCGAGGCAGATGGAGAGG
CTTGAAAGAGAAAATGCCGAAGTGGATGGAGATGATGATGCAGAAGAAATGGAAGCCAAAGCTGAAGAT**TAA**CTT
TGTGGGAAACAGAGTCCAATTTAAGGAACACAGAGCAGCGCTTCCTGGCTGTAAATCCTAGACTTGAAAGTTTTC
CAGTATTGAAAACTTCAAAGCTGAATATTTTTTATTTCTAAGTATTTAAATGTTCTAACAGATCAGAACATGAAA
TGCCCTCCTAAATGTCAGCTGTTGTCACACAGTAGCTCCAACACTTTGAGCATTTTTAAGGGAGTGGCCTCATTT
CACTAGAGACAAATCTTTAAGAATAGTTCTAAAATTGGGCTTGTGATTTCCATTTCTGATGTCTCCAGATTGGCA
CCCCTTTCTAGTTCAATGCCTCACGAGATTTGCCAGGGGCATCCAAGGCAAACAATCCCAATCTTTCTATATAAA
ATGTATTCAAGCAAACATCAAATAAATTTCTGGGATATTTAACTATAGGCTTCTTCCTTCTTGTCACCAGTTAAA
AGCATTTTAATACTAAGACCCTAATTCTTTTATCTTTATTTTAGTCTTGATGTGGAACTGTAGGAGCAGGTGAAT
AAAGGATCTCTATAACAGATCCTTTCAAAAGAAGAGTTTTAGAGAAAATAAATTTAACTTTAACCACAGTGAAAG
TTGACCCTTAGCGGGACAAAGCCTTAAAATGCATTGAAAGAATTAGATCGGTTCTGTGCCTTTTATCTATTTGAG
ATTGATGACAACCTGTGTGAGAGAATTTATCACACCACGTCCTTATTGGAATAATAAGCTACTTGCCTTGAGTTT
ATAATTCAGGGTGGTAAAGTATGTTTTTAAATTTTAAAAAGCAGCTGCATTTTTTATTTAGTTGGAATATCACCC
AATTTTTTATTTTTATTGCTATTAAAATATCCACTAGATGCCACCTAGAGCTCCAGTTCTTTATAACAAAACAGG
GATCTGTTTGAACACTTACTGTTGTTTTTTTTTTTTTACATGTTTCCATCATTTCTGTCTTTAAGAACTAATTCG
TACATAATAAGTTTCATAGGTAACACATTATATTCTCTTATGATACTTGAGGTACCAGTTGTATTTAATTTTATT
CATTATCCCTAGATAGCTATTAAGATACTTAGATTAGACCTAACCCACCATAGTCAATCCAAGACTAGACTACTC
AATATTAAAGGGTCTGGAAAATAGAAGAGTGTGTTGGGCAGGTAGTTTGTACCATTTATGAAGGTTTGTTCCTTT
GTTAAATTTAGCAGCCTGTACTAGCTTTTGAAATCCAGAAGTTTTAACTTCCAGTGGCTGGTTTCTGAGAGAGTG
CCATGATTGCTAGCCAGCATTCCATATTGGGAATATGTAGAGGAGAACCTGGATGTACTTAAGAGTGGCATATAA
TTTTCACTTCTGTCTGTTGAGGCAAAAAAAAAAACAAGTTTAGAAAGCTGGCAACATGAAGAATGCATTCAAAATA
TAACAGGTGCTTCTTTGTTGTACGCAGAGGAATTTTTTCTTTTGATTTTGTTTACTGAAATTTGTTATACTTCAA
AAGCCATAACTTGAAAAATACTGGTGGCGTCGATGGTGAGTGATTTTTATCCCACGTGGGCCTTTTGCTCAGTTC
CATGGCAATTTTGTAAATTGACCCTAGCCAGAGAATAGATCAGTATTTCACTGATACCACGAGGAAAAGAACAAA
CAAAACTTAAAAGTATTCATACACCTTGCTAACCTAAAAGACAGCAGGGACAAGATACATATGAGGACAAGGTAT
ACACCCAGTTCTGAATAACTTGAAGAACAGGCTTGGCAAAGAAGTAAGTTTATCCAAATCTTGAATTTCTGCCAG
GCATGGTAGCTCATGCCTGTAACCCTGGCACTTAAGGGGCCAAGGCAGGAGGATCACTTGAGGCCAGTGAGCTGT
GATCACTCCAGTGCACTCGAGCCTGGGTGACAGGGCAAGACCCTGTCTCAAAAAAAAAAAAAAAAAA

FIGURE 161

MPGLSCRFYQHKFPEVEDVVMVNVRSIAEMGAYVSLLEYNNIEGMILLSELSRRRIRSINKLIRIGRNECVVVIR
VDKEKGYIDLSKRRVSPEEAIKCEDKFTKSKTVYSILRHVAEVLEYTKDEQLESLFQRTAWVFDDKYKRPGYGAY
DAFKHAVSDPSILDSLDLNEDEREVLINNININRRLTPQAVKIRADIEVACYGYEGIDAVKEALRAGLNCSTENMPI
KINLIAPPRYVMTTTTLERTEGLSVLSQAMAVIKEKIEEKRGVFNVQMEPKVVTDTDETELARQMERLERENAEV
DGDDDAEEMEAKAED

FIGURE 162

AGGTCCGGCTTACCGTCGTTTACGACAGTGTCAGGATCGCGGGCTTGCTTTCCGGTAGCGTGGGCTGACGCCTCG
CTCAATTTCTCACAGGGCTGCGCAGGTTTCCCCCGTCTGCGAATGGACCACTGGAGGGGTTCAAAGGTTCGCGTC
CCAGTACGGGA**ATG**AGCCTCTTTGATCTCTTCCGGGGCTTTTTCGGCTTTCCTGGACCTCGGAGCCACAGAGATC
CCTTTTTTGGAGGGATGACTCGAGATGAAGATGATGATGAGGAAGAAGAAGAAGAAGGGGGCTCATGGGGCCGTG
GGAACCCAAGGTTCCATAGTCCTCAGCACCCCCCTGAGGAATTTGGCTTCGGCTTCAGCTTCAGCCCAGGAGGAG
GGATACGTTTCCACGATAACTTCGGCTTTGATGACCTAGTACGAGATTTCAATAGCATCTTCAGCGATATGGGGG
CCTGGACCTTGCCTTCCCATCCTCCTGAACTTCCAGGTCCTGAGTCAGAGACACCTGGTGAGAGACTACGGGAGG
GACAGACACTTCGGGACTCAATGCTTAAGTATCCAGATAGTCACCAGCCCAGGATCTTTGGGGGGGTCTTGGAGA
GTGATGCAAGAAGTGAATCCCCCCAACCAGCACCAGACTGGGGCTCCCAGAGGCCATTTCATAGGTTTGATGATG
TATGGCCTATGGACCCCCATCCTAGAACCAGAGAGGACAATGATCTTGATTCCCAGGTTTCCCAGGAGGGTCTTG
GCCCGGTTCTACAGCCCCAGCCCAAATCCTATTTCAAGAGCATCTCTGTGACCAAGATCACTAAACCAGATGGGA
TAGTGGAGGAGCGCCGGACTGTGGTGGACAGTGAGGGCCGGACAGAGACTACAGTAACCCGACACGAAGCAGATA
GCAGTCCTAGGGGTGATCCAGAATCACCAAGACCTCCAGCCCTGGATGATGCCTTTTCCATCCTGGACTTATTCC
TGGGACGTTGGTTCCGGTCCCGG**TAG**CCTTGTTAACCCTCAGAGGCCTTCAAGTCCTTTCCACCTCTCACCCATT
GCCCACCATTAATAAGCTTAGCTTCTCTTGCCACCTCAGGGGCTTGGATATGTGGAATAGTGAACTGGGGCCATG
TCAGTTTGTCACTCACCCAAACTGACCAATAAAACCTTTATTTATGCTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 163

MSLFDLFRGFFGFPGPRSHRDPFFGGMTRDEDDDEEEEEEGGSWGRGNPRFHSPQHPPEEFGFGFSFSPGGGIRF
HDNFGFDDLVRDFNSIFSDMGAWTLPSHPPELPGPESETPGERLREGQTLRDSMLKYPDSHQPRIFGGVLESDAR
SESPQPAPDWGSQRPFHRFDDVWPMDPHPRTREDNDLDSQVSQEGLGPVLQPQPKSYFKSISVTKITKPDGIVEE
RRTVVDSEGRTETTVTRHEADSSPRGDPESPRPPALDDAFSILDLFLGRWFRSR

FIGURE 164

GGACACCGGGCCATGCACGCCCCCAACTGAAGCTGCATCTCAAAGCCGAAGATTCCAGCAGCCCAGGGGATTTCA
AAGAGCTCAGACTCAGAGGAACATCTGCGGAGAGACCCCCGAAGCCCTCTCCAGGGCAGTCCTCATCCAGACGCT
CCGCTAGTGCAGACAGGAGCGCGCAGTGGCCCCGGCTCGCCGCGCC**ATG**GAGCGGATCCCCAGCGCGCAACCACC
CCCCGCCTGCCTGCCCAAAGCACCGGGACTGGAGCACGGAGACCTACCAGGGATGTACCCTGCCCACATGTACCA
AGTGTACAAGTCAAGACGGGGAATAAAGCGGAGCGAGGACAGCAAGGAGACCTACAAATTGCCGCACCGGCTCAT
CGAGAAAAAGAGACGTGACCGGATTAACGAGTGCATCGCCCAGCTGAAGGATCTCCTACCCGAACATCTCAAACT
TACAACTTTGGGTCACTTGGAAAAAGCAGTGGTTCTTGAACTTACCTTGAAGCATGTGAAAGCACTAACAAACCT
AATTGATCAGCAGCAGCAGAAAATCATTGCCCTGCAGAGTGGTTTACAAGCTGGTGAGCTGTCAGGGAGAAATGT
CGAAACAGGTCAAGAGATGTTCTGCTCAGGTTTCCAGACATGTGCCCGGGAGGTGCTTCAGTATCTGGCCAAGCA
CGAGAACACTCGGGACCTGAAGTCTTCGCAGCTTGTCACCCACCTCCACCGGGTGGTCTCGGAGCTGCTGCAGGG
TGGTACCTCCAGGAAGCCATCAGACCCAGCTCCCAAAGTGATGGACTTCAAGGAAAAACCCAGCTCTCCGGCCAA
AGGTTCGGAAGGTCCTGGGAAAAACTGCGTGCCAGTCATCCAGCGGACTTTCGCTCACTCGAGTGGGGAGCAGAG
CGGCAGCGACACGGACACAGACAGTGGCTATGGAGGAGAATCGGAGAAGGGCGACTTGCGCAGTGAGCAGCCGTG
CTTCAAAAGTGACCACGGACGCAGGTTCACGATGGGAGAAAGGATCGGCGCAATTAAGCAAGAGTCCGAAGAACC
CCCCACAAAAAAGAACCGGATGCAGCTTTCGGATGATGAAGGCCATTTCACTAGCAGTGACCTGATCAGCTCCCC
GTTCCTGGGCCCACACCCACACCAGCCTCCTTTCTGCCTGCCCTTCTACCTGATCCCACCTTCAGCGACTGCCTA
CCTGCCCATGCTGGAGAAGTGCTGGTATCCCACCTCAGTGCCAGTGCTATACCCAGGCCTCAACGCCTCTGCCGC
AGCCCTCTCTAGCTTCATGAACCCAGACAAGATCTCGGCTCCCTTGCTCATGCCCCAGAGACTCCCTTCTCCCTT
GCCAGCTCATCCGTCCGTCGACTCTTCTGTCTTGCTCCAAGCTCTGAAGCCAATCCCCCCTTTAAACTTAGAAAC
CAAAGAC**TAA**ACTCTCTAGGGGATCCTGCTGCTTTGCTTTCCTTCCTCGCTACTTCCTAAAAAGCAACAAAAAAG
TTTTTGTGAATGCTGCAAGATTGTTGCATTGTGTATACTGAGATAATCTGAGGCATGGAGAGCAGATTCAGGGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTATGTGCGTGTGCGTGCACATGTGTGCCTGCGTGTTGGTATAGGACTTT
AAAGCTCCTTTTGGCATAGGGAAGTCACGAAGGATTGCTTGACATCAGGAGACTTGGGGGGGATTGTAGCAGACG
TCTGGGCTTTTCCCCACCCAGAGAATAGCCCCCTTCGATACACATCAGCTGGATTTTCAAAAGCTTCAAAGTCTT
GGTCTGTGAGTCACTCTTCAGTTTGGGAGCTGGGTCTGTGGCTTTGATCAGAAGGTACTTTCAAAAGAGGGCTTT
CCAGGGCTCAGCTCCCAACCAGCTGTTAGGACCCCACCCTTTTGCCTTTATTGTCGACGTGACTCACCAGACGTC
GGGGAGAGAGAGCAGTCAGACCGAGCTTTCTGCTAACATGGGGAGGTAGCAGGCACTGGCATAGCACGGTAGTGG
TTTGGGGAGGTTTCCGCAGGTCTGCTCCCCACCCCTGCCTCGGAAGAATAAAGAGAATGTAGTTCCCTACTCAGG
CTTTCGTAGTGATTAGCTTACTAAGGAACTGAAAATGGGCCCCTTGTACAAGCTGAGCTGCCCCGGAGGGAGGGA
GGAGTTCCCTGGGCTTCTGGCACCTGTTTCTAGGCCTAACCATTAGTACTTACTGTGCAGGGAACCAAACCAAGG
TCTGAGAAATGCGGACACCCCGAGCGAGCACCCCAAAGTGCACAAAGCTGAGTAAAAAGCTGCCCCCTTCAAACA
GAACTAGACTCAGTTTTCAATTCCATCCTAAAACTCCTTTTAACCAAGCTTAGCTTCTCAAAGGCCTAACCAAGC
CTTGGCACCGCCAGATCCTTTCTGTAGGCTAATTCCTCTTGCCCAACGGCATATGGAGTGTCCTTATTGCTAAAA
AGGATTCCGTCTCCTTCAAAGAAGTTTTATTTTTGGTCCAGAGTACTTGTTTTCCCGATGTGTCCAGCCAGCTCC
GCAGCAGCTTTTCAAGATGCACTATGCCTGATTGCTGATCGTGTTTTAACTTTTTCTTTTCCTGTTTTTATTTTG
GTATTAAGTCGTTGCCTTTATTTGTAAAGCTGTTATAAATATATATTATATAAATATATTAAAAAGGAAAATGTT
TCAGATGTTTATTTGTATAATTACTTGATTCACACAGTGAGAAAAAATGAATGTATTCCTGTTTTTGAAGAGAAG
AATAATTTTTTTTTCTCTAGGGAGAGGTACAGTGTTTATATTTTGGAGCCTTCCTGAAGGTGTAAAATTGTAAAT
ATTTTTATCTATGAGTAAATGTTAAGTAGTTGTTTTAAAATACTTAATAAAATAATTCTTTTCCTGTGGAAG

FIGURE 165

MERIPSAQPPPACLPKAPGLEHGDLPGMYPAHMYQVYKSRRGIKRSEDSKETYKLPHRLIEKKRRDRINECIAQL
KDLLPEHLKLTTLGHLEKAVVLELTLKHVKALTNLIDQQQQKIIALQSGLQAGELSGRNVETGQEMFCSGFQTCA
REVLQYLAKHENTRDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAPKVMDFKEKPSSPAKGSEGPGKNCVPVIQR
TFAHSSGEQSGSDTDTDSGYGGESEKGDLRSEQPCFKSDHGRRFTMGERIGAIKQESEEPPTKKNRMQLSDDEGH
FTSSDLISSPFLGPHPHQPPFCLPFYLIPPSATAYLPMLEKCWYPTSVPVLYPGLNASAAALSSFMNPDKISAPL
LMPQRLPSPLPAHPSVDSSVLLQALKPIPPLNLETKD

FIGURE 166A

GTCCTTTCACGCGTGTCTTCGTGTTGGTGCGCTTTTCACTGGTCATAAAGTGCTGCTCACGGCCGTGAACTGCTA
CAGCGTGAAGGCCGCCACCCGGGTCCAGGATGCTTTTGCCGCCGCCAAGCTCCTGGCCCTGGCCCTGATCATCCT
GCTGGGCTTCGTCCAGATCGGGAAGGGTGATGTGTCCAATCTAGATCCCAAGTTCTCATTTGAAGGCACCAAACT
GGATGTGGGGAACATTGTGCTGGCATTATACAGCGGCCTCTTTGCCTATGGAGGATGGAATTACTTGAATTTCGT
CACAGAGGAA**ATG**ATCAACCCCTACAGAAACCTGCCCCTGGCCATCATCATCTCCCTGCCCATCGTGACGCTGGT
GTACGTGCTGACCAACCTGGCCTACTTCACCACCCTGTCCACCGAGCAGATGCTGTCGTCCGAGGCCGTGGCCGT
GGACTTCGGGAACTATCACCTGGGCGTCATGTCCTGGATCATCCCCGTCTTCGTGGGCCTGTCCTGCTTTGGCTC
CGTCAATGGGTCCCTGTTCACATCCTCCAGGCTCTTCTTCGTGGGGTCCCGGGAAGGCCACCTGCCCTCCATCCT
CTCCATGATCCACCCACAGCTCCTCACCCCCGTGCCGTCCCTCGTGTTCACGTGTGTGATGACGCTGCTCTACGC
CTTCTCCAAGGACATCTTCTCCGTCATCAACTTCTTCAGCTTCTTCAACTGGCTCTGCGTGGCCCTGGCCATCAT
CGGCATGATCTGGCTGCGCCACAGAAAGCCTGAGCTTGAGCGGCCCATCAAGGTGAACCTGGCCCTGCCTGTGTT
CTTCATCCTGGCCTGCCTCTTCCTGATCGCCGTCTCCTTCTGGAAGACACCCGTGGAGTGTGGCATCGGCTTCAC
CATCATCCTCAGCGGGCTGCCCGTCTACTTCTTCGGGGTCTGGTGGAAAAACAAGCCCAAGTGGCTCCTCCAGGG
CATCTTCTCCACGACCGTCCTGTGTCAGAAGCTCATGCAGGTGGTCCCCCAGGAGACA**TAG**CCAGGAGGCCGAGT
GGCTGCCGGAGGAGCATGCGCAGAGGCCAGTTAAAGTAGATCACCTCCTCGAACCCACTCCGGTTCCCCGCAACC
CACAGCTCAGCTGCCCATCCCAGTCCTCGCCGTCCCTCCCAGGTCGGGCAGTGGAGGCTGCTGTGAAAACTCTGG
TACGAATCTCATCCCTCAACTGAGGGCCAGGGACCCAGGTGTGCCTGTGCTCCTGCCCAGGAGCAGCTTTTGGTC
TCCTTGGGCCCTTTTTCCCTTCCCTCCTTTGTTTACTTATATATATATTTTTTTTAAACTTAAATTTTGGGTCAA
CTTGACACCACTAAGATGATTTTTTAAGGAGCTGGGGGAAGGCAGGAGCCTTCCTTTCTCCTGCCCCAAGGGCCC
AGACCCTGGGCAAACAGAGCTACTGAGACTTGGAACCTCATTGCTACCACAGACTTGCACTGAAGCCAGACAGCT
GCCCAGACACATGGGCTTGTGACATTCGTGAAAACCAACCCTGTGGGCTTATGTCTCTGCCTTAGGGTTTGCAGA
GTGGAAACTCAGCCGTAGGGTGGCACTGGGAGGGGGTGGGGGATCTGGGCAAGGTGGGTGATTCCTCCCAGGAGG
TGCTTGAGGCCCCGATGGACTCCTGACCATAATCCTAGCCCCGAGACACCATCCTGAGCCAGGGAACAGCCCCAG
GGTTGGGGGGGTGCCGGCATCTCCCCTAGCTCACCAGGCCTGGCCTCTGGGCAGTGTGGCCTCTTGGCTATTTCTG
TTCCAGTTTTGGAGGCTGAGTTCTGGTTCATGCAGACAAAGCCCTGTCCTTCAGTCTTCTAGAAACAGAGACAAG
AAAGGCAGACACACCGCGGCCAGGCACCCATGTGGGCGCCCACCCTGGGCTCCACACAGCAGTGTCCCCTGCCCC
AGAGGTCGCAGCTACCCTCAGCCTCCAATGCATTGGCCTCTGTACCGCCCGGCAGCCCCTTCTGGCCGGTGCTGG
GTTCCCACTCCCGGCCTAGGCACCTCCCCGCTCTCCCTGTCACGCTCATGTCCTGTCCTGGTCCTGATGCCCGTT
GTCTAGGAGACAGAGCCAAGCACTGCTCACGTCTCTGCCGCCTGCGTTTGGAGGCCCCTGGGCTCTCACCCAGTC
CCCACCCGCCTGCAGAGAGGGAACTAGGGCACCCCTTGTTTCTGTTGTTCCCGTGAATTTTTTTCGCTATGGGAG
GCAGCCGAGGCCTGGCCAATGCGGCCCACTTTCCTGAGCTGTCGCTGCCTCCATGGCAGCAGCCAAGGACCCCCA
GAACAAGAAGACCCCCCCGCAGGATCCCTCCTGAGCTCGGGGGGCTCTGCCTTCTCAGGCCCCGGGCTTCCCTTC
TCCCCAGCCAGAGGTGGAGCCAAGTGGTCCAGCGTCACTCCAGTGCTCAGCTGTGGCTGGAGGAGCTGGCCTGTG
GCACAGCCCTGAGTGTCCCAAGCCGGGAGCCAACGAAGCCGGACACGGCTTCACTGACCAGCGGCTGCTCAAGCC
GCAAGCTCTCAGCAAGTGCCCAGTGGAGCCTGCCGCCCCCACCTGGGCACCGGGACCCCCTCACCATCCAGTGGG
CCCGGAGAAACCTGATGAACAGTTTGGGGACTCAGGACCAGATGTCCGTCTCTCTTGCTTGAGGAATGAAGACCT
TTATTCACCCCTGCCCCGTTGCTTCCCGCTGCACATGGACAGACTTCACAGCGTCTGCTCATAGGACCTGCATCC
TTCCTGGGGACGAATTCCACTCGTCCAAGGGACAGCCCACGGTCTGGAGGCCGAGGACCACCAGCAGGCAGGTGG
ACTGACTGTGTTGGGCAAGACCTCTTCCCTCTGGGCCTGTTCTCTTGGCTGCAAATAAGGACAGCAGCTGGTGCC
CCACCTGCCTGGTGCATTGCTGTGTGAATCCAGGAGGCAGTGGACATCGTAGGCAGCCACGGCCCCAGGTCCAGG
AGAAGTGCTCCCTGGAGGCACGGACCACTGCTTCCCACTGGGGCCGGCGGGGCCCACGCACGACGTCAGCCTCTT
ACCTTCCCGCCTCGGCTAGGGGTCCTCGGGATGCCGTTCTGTTCCAACCTCCTGTTCTGGGAGGTGGACATGCCT
CAAGGATACAGGGAGCCGGCGGCCTCTCGACGGCACGCACTTCCTGTTGGCTGCTGCGGCTGTGGGCGAGCATGG
GGGCTGCCAGCGTCTGTTGTGGAAAGTAGCTGCTAGTGAAATGGCTGGGGCCGCTGGGGTCCGTCTTCACACTGC
GCAGGTCTCTTCTGGGCGTCTGAGCTGGGGTGGGAGCTCCTCCGCAGAAGGTTGGTGGGGGGTCCAGTCTGTGAT
CCTTGGTGCTGTGTGCCCCACTCCAGCCTGGGGACCCCACTTCAGAAGGTAGGGGCCGTGTCCCGCGGTGCTGAC
TGAGGCCTGCTTCCCCCTCCCCCTCCTGCTGTGCTGGAATTCCACAGGGACCAGGGCCACCGCAGGGGACTGTCT
CAGAAGACTTGATTTTTCCGTCCCTTTTTCTCCACACTCCACTGACAAACGTCCCCAGCGGTTTCCACTTGTGGG

FIGURE 166B

CTTCAGGTGTTTTCAAGCACAACCCACCACAACAAGCAAGTGCATTTTCAGTCGTTGTGCTTTTTTGTTTTGTGC
TAACGTCTTACTAATTTAAAGATGCTGTCGGCACCATGTTTATTTATTTCCAGTGGTCATGCTCAGCCTTGCTGC
TCTGCGTGGCGCAGGTGCCATGCCTGCTCCCTGTCTGTGTCCCAGCCACGCAGGGCCATCCACTGTGACGTCGGC
CGACCAGGCTGGACACCCTCTGCCGAGTAATGACGTGTGTGGCTGGGACCTTCTTTATTCTGTGTTAATGGCTAA
CCTGTTACACTGGGCTGGGTTGGGTAGGGTGTTCTGGCTTTTTTGTGGGGTTTTTATTTTTAAAGAAACACTCAA
TCATCCTAG

FIGURE 167

MINPYRNLPLAIIISLPIVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDFGNYHLGVMSWIIPVFVGLSCFGSVNG
SLFTSSRLFFVGSREGHLPSILSMIHPQLLTPVPSLVFTCVMTLLYAFSKDIFSVINFFSFFNWLCVALAIIGMI
WLRHRKPELERPIKVNLALPVFFILACLFLIAVSFWKTPVECGIGFTIILSGLPVYFFGVWWKNKPKWLLQGIFS
TTVLCQKLMQVVPQET

FIGURE 168

TGAACTGAGCGGCCCCTGAGCTGACAGATACACTGCGCAGTGGAACGGCGAGCGAGCCGACGGGCGAGTGAGGGG
CGCAC**ATG**ATCACCTCGGCCGCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTGCAC
TACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTTTAT
ACGAAGATGAAGGTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGGCTT
TTGAGGAGTCTCTGAATTATGCTCTTGGAGCAAGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGGAAA
CTATTATAGCAAAATGCATTGATCACTACACCAAACAATGTGTGGAAAATGCAGATTTGCCTGAAGGAGAAAAAA
AACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATAAAC
AGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGTCTTTGAAAAGACCATACTGGAGTCGAATGATGTCC
CAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTCGGAATAAAGTACTAA
GAGTTCTAGTTAAAATCTACATGAACTTGGAGAAACCTGATTTCATCAATGTTTGTCAGTGCTTAATTTTCTTAG
ATGATCCTCAGGCTGTGAGTGATATCTTAGAGAAACTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGATTT
GTTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTCATCTGTAATCCAGAATCTTCGAACTGTTGGCACCC
CTATTGCTTCTGTGCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAGACAGTGACTCGATGGAAA
CAGAAGAAAAGACAAGCAGTGCATTTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTTTGA
AAATGATTAAAATTTTAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATACAG
ACCTCATGATTCTAAAAAACACAAAGGATGCAGTACGGAATTCTGTATGTCATACTGCAACCGTTATAGCAAACT
CTTTTATGCACTGTGGGACAACCAGTGACCAGTTTCTTAGAGATAATTTGGAATGGTTAGCCAGAGCCACTAACT
GGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAAGAAGCATTACAGTTAATGG
CAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTCTTA
TTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAACGCCAGCAATGATATCGTTA
GACACGGTGGCAGTCTGGGCCTTGGTTTGGCAGCCATGGGAACTGCACGTCAAGATGTTTATGATTTGCTAAAAA
CAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCTGGCCCTAGGTTTGGTTATGTTGGGCTCTA
AAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAAACTCAACATGAGAAGATTCTGCGTGGTCTTG
CAGTTGGCATAGCTTTAGTAATGTATGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTCGTGACA
AGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTATTGTGGCTCTGGTAACAACAAAGCAA
TTCGACGCCTGCTACATGTGGCTGTAAGTGATGTGAATGATGATGTCAGGAGTGCAGCAGTAGAATCACTTGGGT
TCATTCTATTCAGAACCCCTGAACAGTGCCCAAGTGTTGTCTCTTTGTTGTCAGAGAGTTACAACCCTCATGTGC
GCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAAACAAGGAAGCCATTAATTTGCTAGAAC
CAATGACAAACGACCCCGTGAACTACGTGAGGCAAGGGGCACTCATAGCTTCAGCTCTCATCATGATCCAGCAGA
CTGAAATCACTTGTCCAAAGGTGAATCAGTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATGATG
TCATGGCCAAGTTTGGCGCTATTCTGGCCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCTTGC
AGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCCTTGTATTTACCCAGTTTTGGTTCTGGTTTC
CTCTTTCACACTTCCTGTCATTGGCTTATACCCCTACCTGTGTCATTGGCCTTAACAAGGACTTAAAGATGCCGA
AAGTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCCTCTGGAAGTACCAAAAGAAAAAG
AAAAGGAAAAGGTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAGGAAAAAA
AGGAGGAGGAGAAAATGGAAGTGGATGAGGCAGAGAAAAAGGAGGAAAAAGAGAAGAAAAAAGAACCTGAGCCAA
ACTTCCAGTTATTGGATAACCCAGCCCGAGTTATGCCTGCCCAGCTTAAGGTCCTAACCATGCCGGAGACCTGTA
GATACCAGCCTTTCAAACCACTCTCTATTGGAGGCATCATCATTCTGAAGGATACCAGTGAAGACATTGAGGAGC
TGGTGGAACCTGTGGCAGCACATGGCCCAAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCCAGAACCATTTG
AGTATATTGATGAT**TAA**GGACCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGGAAT
GCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAACCC
TGTCTCCAAGTCTTTGGTTGAAGAGAAGATATATGACTGTTGAGTGTGCTCTTTCACAGAACTTGGTTTTCAAAT
AAATATAAGATCTCCAGATGGACAAG

FIGURE 169

MITSAAGIISLLDEDEPQLKEFALHKLNAVVNDFWAEISESVDKIEVLYEDEGFRSRQFAALVASKVFYHLGAFE
ESLNYALGARDLFNVVNDNSEYVETIIAKCIDHYTKQCVENADLPEGEKKPIDQRLEGIVNKMFQRCLDDHKYKQA
IGIALETRRLDVFEKTILESNDVPGMLAYSLKLCMSLMQNKQFRNKVLRVLVKIYMNLEKPDFINVCQCLIFLDD
PQAVSDILEKLVKEDNLLMAYQICFDLYESASQQFLSSVIQNLRTVGTPIASVPGSTNTGTVPGSEKDSDSMETE
EKTSSAFVGKTPEASPEPKDQTLKMIKILSGEMAIELHLQFLIRNNNTDLMILKNTKDAVRNSVCHTATVIANSF
MHCGTTSDQFLRDNLEWLARATNWAKFTATASLGVIHKGHEKEALQLMATYLPKDTSPGSAYQEGGGLYALGLIH
ANHGGDIIDYLLNQLKNASNDIVRHGGSLGLGLAAMGTARQDVYDLLKTNLYQDDAVTGEAAGLALGLVMLGSKN
AQAIEDMVGYAQETQHEKILRGLAVGIALVMYGRMEEADALIESLCRDKDPILRRSGMYTVAMAYCGSGNNKAIR
RLLHVAVSDVNDDVRSAAVESLGFILFRTPEQCPSVVSLLSESYNPHVRYGAAMALGICCAGTGNKEAINLLEPM
TNDPVNYVRQGALIASALIMIQQTEITCPKVNQFRQLYSKVINDKHDDVMAKFGAILAQGILDAGGHNVTISLQS
RTGHTHMPSVVGVLVFTQFWFWFPLSHFLSLAYTPTCVIGLNKDLKMPKVQYKSNCKPSTFAYPAPLEVPKEKEK
EKVSTAVLSITAKAKKKEKEKEKKEEEKMEVDEAEKKEEKEKKKEPEPNFQLLDNPARVMPAQLKVLTMPETCRY
QPFKPLSIGGIIILKDTSEDIEELVEPVAAHGPKIEEEEQEPEPPEPFEYIDD

FIGURE 170A

TAGAATACTTGGGTGACATCTGCCTGAGAGATCTCCAAGAATTACAGAAGACAAAAATACTAATGCATTTGAGAA
AGCGGTAGTTTTGGGGGGAGGGGGAAAAAGCAACTGCTTTCCTGATCTGCAACTTGGCTGGATGCTAAG**ATG**TCA
GTGGACATGAATAGCCAGGGGTCTGACAGCAATGAAGAGGACTATGACCCAAATTGTGAGGAAGAGGAAGAAGAA
GAAGAAGACGACCCTGGGGACATAGAGGACTATTACGTGGGAGTAGCCAGCGATGTGGAGCAGCAGGGGGCTGAT
GCCTTTGATCCCGAGGAGTACCAGTTCACTTGCTTGACCTACAAGGAATCTGAGGGTGCCCTCAATGAGCACATG
ACCAGCTTAGCTTCTGTCCTAAAGGTATCTCATTCAGTTGCTAAACTTATATTAGTTAATTTCCACTGGCAAGTT
TCAGAGATATTGGACAGATACAAGTCCAATTCTGCTCAACTGCTTGTTGAGGCTCGAGTTCAGCCTAATCCATCA
AAACATGTTCCCACATCCCATCCCCCTCACCACTGTGCAGTGTGTATGCAGTTTGTGCGAAAGGAAAACCTACTC
TCTCTGGCCTGTCAGCACCAGTTTTGCCGCAGCTGCTGGGAGCAGCACTGCTCAGTTCTCGTCAAGGACGGCGTG
GGCGTGGGAGTCTCTTGCATGGCTCAGGACTGTCCACTCCGTACACCAGAGGACTTTGTGTTTCCATTGCTTCCC
AATGAAGAATTGAGAGAGAAATACAGGCGCTACCTCTTCAGGGACTATGTGGAGAGTCATTACCAGCTCCAGCTG
TGCCCTGGTGCAGACTGCCCCATGGTTATTCGGGTACAGGAGCCTAGAGCTCGCCGAGTACAGTGCAATCGGTGC
AACGAGGTCTTCTGTTTCAAGTGTCGTCAGATGTATCACGCACCCACAGACTGTGCCACAATCCGGAAATGGCTC
ACGAAGTGTGCAGACGACTCTGAAACAGCCAACTACATTAGTGCTCACACTAAAGACTGTCCCAAGTGCAACATC
TGCATTGAGAAGAATGGAGGCTGCAATCACATGCAATGCTCCAAATGTAAACACGACTTCTGCTGGATGTGTCTA
GGAGATTGGAAGACTCATGGCAGTGAATACTATGAGTGCAGTCGTTACAAGGAGAATCCTGACATCGTGAACCAG
AGCCAACAAGCCCAGGCGAGGGAAGCCCTCAAGAAGTACTTATTCTACTTTGAGAGGTGGGAAAACCACAATAAA
AGCTTGCAGCTAGAGGCACAGACATACCAGCGGATTCACGAGAAGATTCAGGAGAGGGTCATGAACAATCTGGGG
ACATGGATCGACTGGCAGTACCTACAGAATGCTGCCAAGCTCTTGGCCAAGTGTCGATACACCCTGCAATACACC
TACCCATATGCATATTACATGGAGTCCGGACCCAGGAAGAAGCTGTTTGAATACCAGCAGGCTCAGCTGGAGGCT
GAGATCGAAAACCTCTCATGGAAAGTGGAGCGTGCAGACAGCTATGACAGAGGGGACTTGGAGAACCAGATGCAT
ATAGCGGAGCAGCGGAGGAGAACCCTGCTGAAAGATTTCCATGACACC**TAA**GTTGGGATGTGGATGTGCCGGGGT
GAGGAAGATGTGGCTGCAAGGTCTCCCGGCTGCCATACTGCATGCTGCAGGCTCTGCCTTTCATGACCCCAGGCA
ACAGCCAGGGCCCCACTCCTGAGAGACACTGGCAACACCTCTTAGTTGATTTCTGTTTTCTTCTCTTTTCACTTT
TTGTTTCTACCAGGGTAGAGGCCATGTTGAACTGGCCTCTTTTCAGGACTTTTATTTCCCCCTGGATGGTTGTTG
GGAGGGAGGGAAAGTGTTTTCTGAATGGCTATTAATAGTATTAGATCATTACAACTTATGTAACTTTCAAAGGTT
GTACAATTATACAAAAAAAAAAAAAAAGGCAAACTATAGGATAACACAGAGCCCTTTTTGAAAATAAATTGGCAT
TGGAGTGTTTTACCCTCTAGCTGTTTTACTTAGAATGTAACATATGCTGCCTACCCACCTCAAAATGTCTGTACT
GCAAGAGGGCCCTGGGCCTCTGCTTTCCATATTCACGTTTGGCCAGAGTTGTAGTCCCAAAGAAGAGCATGGGTG
GCAGATGGTAGGGAATTGAACTGGCCTGTGCAATGGGCATGGAGCACAAGGGGTCACAGCATGCCTCCTGCCTTA
CCGTGGCAGTACGGAGACAGTCCAGAACATGGTCTTCTTGCCACGGGGTGTTGTTGTCTCTGGTGGTGCTGCATG
TCTGTGGCTCACCTTTATTCTTGAAACTGAGGTTTACCTGGATCTGGCTACTGAGGCTAGAGCCCACAGCAGAAT
GGGGTTGGGCCTGTGGCCCCCAAACTAGGGGGTGTGGGTTCATCACAGTGTTGCCTTTTGTCTCCTAAAGATAGG
GATCTACTTTTGAAGGGAATTGTTCCTCCCAAATAAATTTGCTTTACCTTGGTCCTTTCTTTTGTGCCAGTATTC
AAGTGGTATAGCTCTGAGCAGGGTCACATTTGGCCAAACCTGACACTGTCTTGCTGCATTCTCCTTTGGCAAACA
TCAGGGTCAGAATTCAGGATAGCCCTTCCTAGGGCACTGGACTTTCTGGCATGGGGGCTGTGTTTGCACAAGTTA
TTTTCATGTTACCTGGAGAGTGTCCAGAGGCTGCTCTGAGGCTGAGGTGTGTTCCCCCTTGCCTGGTTCCAGCTG
TCAGAGGGATACCATCCTAGGGTCTGGGAATCCAAGGCCACGAGACTCCTTGGTTTGTGGTCCGAGATCCTGTAC
TAAGGAGGGTCTGGCCAGAGGAACAGACCAGCTTTTGCACAATGAAGCGCAAGGGAACAAGTGGTTTGCCTGGTG
TCCTACCTGTCCTGAACCTGGTCCTGTGGGCCATTGAAAAGTTAGATCTGTGATCTCTGGGGTTTTTGTGGCTTT
GTTCAATGCTTCCACTCTAGGGCAGGCAGAGCAGTCTATACTCTCCCAAGCCTGCTTGACCTCCAAGTAGAGCTG
ATACAGAGATCTGTGAATATTGTGATAGAAATTCTTTGGTATTCATACATTTCAGCTGCAAGTCAGCAATTTCCC
AGGTACCATGTAAGCTATAAAACAGTCATTCTTAAAGACAGAGGATAGCTGTGACTCATGGGATCATGAGGTCCA
TGGCTGGTTGCAGGTTCCCTTTTTCCTTCCTCAGGTTTTGTCTCTTCCTGTGTTGTCCCCAGCAAGGGAGAGACT
GTGGGGTGGATTGGGAGAACAGATTAGGAGTATAGCAAATGAACCCAGAATGGAACAGTGGGGAGCTAACTGTGA
ATGAGGAGAGTACCTGCTGCAGGACCTGGAGGTCAGGTGTGAATGCTGTATTGGCACAGGGAATAAATATCCTGG
CGTCTGGAGCCTTCACCTCTCCGTCAAGTCCTTCCTGTGATACTGCCATGGCACAGGATCTGAGTTGCAGCTCTG
CACCCTAAATCACACCCTGGGCATTGTCTGGGCTGCAGGGCTGCCAGGTTCTGTACTTGTGTCCAGCTGTGGCCC

FIGURE 170B

TGGATGCTGGAGCTGGAGGGTTTTCTGTGCTCAGACTGTAGCCTGTAGCTCTTGGCCTGTGTAGAGCCCCCTCCT
GTGCCCTCAGTGGCTGTCGTTTGTTAACATCATCAGGAAGATGGGAAAGGTCAGGCAGAATTTTTCTGCCCTACA
AAGGGTGGAAGAGAAAGGACACAGTATTTTCATGAATTTACCATATATCTTTGTTTTTCTTCAACGAAAAAGTTA
ATTGAGGCAATGTCATCTGCTCAAAGTTGAGTGGTTTATTCACAATAAACTGTAAGTTTCTGATTAT

FIGURE 171

MSVDMNSQGSDSNEEDYDPNCEEEEEEEEDDPGDIEDYYVGVASDVEQQGADAFDPEEYQFTCLTYKESEGALNE
HMTSLASVLKVSHSVAKLILVNFHWQVSEILDRYKSNSAQLLVEARVQPNPSKHVPTSHPPHHCAVCMQFVRKEN
LLSLACQHQFCRSCWEQHCSVLVKDGVGVGVSCMAQDCPLRTPEDFVFPLLPNEELREKYRRYLFRDYVESHYQL
QLCPGADCPMVIRVQEPRARRVQCNRCNEVFCFKCRQMYHAPTDCATIRKWLTKCADDSETANYISAHTKDCPKC
NICIEKNGGCNHMQCSKCKHDFCWMCLGDWKTHGSEYYECSRYKENPDIVNQSQQAQAREALKKYLFYFERWENH
NKSLQLEAQTYQRIHEKIQERVMNNLGTWIDWQYLQNAAKLLAKCRYTLQYTYPYAYYMESGPRKKLFEYQQAQL
EAEIENLSWKVERADSYDRGDLENQMHIAEQRRRTLLKDFHDT

FIGURE 172

TAGCTAGGCAGGAAGTCGGCGCGGGCGGCGCGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTCACCTCGGTGTCTGCAGCACCCTCCGCTTCCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAGTTCAC
C**ATG**TCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCACTGTTGAGGTTGATCTCTT
CACCTCAAAAGGTCTCTTCAGAGCTGCTGTGCCCAGTGGTGCTTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAAACTATTGCGCC
TGCCCTGGTTAGCAAGAAACTGAACGTCACAGAACAAGAGAAGATTGACAAACTGATGATCGAGATGGATGGAAC
AGAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCCTTGCCGTCTGCAAAGCTGGTGCCGTTGA
GAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCCTGCCAGTCCCGGCGTT
CAATGTCATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTCATGATCCTCCCAGTCGGTGC
AGCAAACTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCTGGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGCAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACCAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACTTCAGAAACCCCTTGGCCAAG**TAA**GCTGTGGGCAGGCAAGCCCTTCGGTCACCTGTTGGCTACACAGA
CCCCTCCCCTCGTGTCAGCTCAGGCAGCTCGAGGCCCCCGACCAACACTTGCAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAACTTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTTCTCGCCTCACTTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTCATCTCCGGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAAATAAAAAGCCTCA
GTGACCCATGAG

FIGURE 173

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALELRDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLNVTEQEKIDKLMIEMDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPAF
NVINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIKDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGVMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEELGSKAKFAGRNFRNPLAK

FIGURE 174

GGCTGAGGCAGTGGCTCCTTGCACAGCAGCTGCACGCGCCGTGGCTCCGGATCTTCTTCGTCTTTGCAGCGTAGC
CCGAGTCGGTCAGCGCCAGAGGACCTCAGCAGCC**ATG**TCGAAGCCCCATAGTGAAGCCGGGACTGCCTTCATTCA
GACCCAGCAGCTGCACGCAGCCATGGCTGACACATTCCTGGAGCACATGTGCCGCCTGGACATTGATTCACCACC
CATCACAGCCCGGAACACTGGCATCATCTGTACCATTGGCCCAGCTTCCCGATCAGTGGAGACGTTGAAGGAGAT
GATTAAGTCTGGAATGAATGTGGCTCGTCTGAACTTCTCTCATGGAACTCATGAGTACCATGCGGAGACCATCAA
GAATGTGCGCACAGCCACGGAAAGCTTTGCTTCTGACCCCATCCTCTACCGGCCCGTTGCTGTGGCTCTAGACAC
TAAAGGACCTGAGATCCGAACTGGGCTCATCAAGGGCAGCGGCACTGCAGAGGTGGAGCTGAAGAAGGGAGCCAC
TCTCAAAATCACGCTGGATAACGCCTACATGGAAAAGTGTGACGAGAACATCCTGTGGCTGGACTACAAGAACAT
CTGCAAGGTGGTGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCTCCAGGTGAAGCAGAAAGG
TGCCGACTTCCTGGTGACGGAGGTGGAAAATGGTGGCTCCTTGGGCAGCAAGAAGGGTGTGAACCTTCCTGGGGC
TGCTGTGGACTTGCCTGCTGTGTCGGAGAAGGACATCCAGGATCTGAAGTTTGGGGTCGAGCAGGATGTTGATAT
GGTGTTTGCGTCATTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGAAGGTCCTGGGAGAGAAGGGAAAGAA
CATCAAGATTATCAGCAAAATCGAGAATCATGAGGGGGTTCGGAGGTTTGATGAAATCCTGGAGGCCAGTGATGG
GATCATGGTGGCTCGTGGTGATCTAGGCATTGAGATTCCTGCAGAGAAGGTCTTCCTTGCTCAGAAGATGATGAT
TGGACGGTGCAACCGAGCTGGGAAGCCTGTCATCTGTGCTACTCAGATGCTGGAGAGCATGATCAAGAAGCCCCG
CCCCACTCGGGCTGAAGGCAGTGATGTGGCCAATGCAGTCCTGGATGGAGCCGACTGCATCATGCTGTCTGGAGA
AACAGCCAAAGGGGACTATCCTCTGGAGGCTGTGCGCATGCAGAACCTGATTGCCCGTGAGGCAGAGGCTGCCAT
CTACCACTTGCAATTATTTGAGGAACTCCGCCGCCTGGCGCCCATTACCAGCGACCCCACAGAAGCCACCGCCGT
GGGTGCCGTGGAGGCCTCCTTCAAGTGCTGCAGTGGGGCCATAATCGTCCTCACCAAGTCTGGCAGGTCTGCTCA
CCAGGTGGCCAGATACCGCCCACGTGCCCCCATCATTGCTGTGACCCGGAATCCCCAGACAGCTCGTCAGGCCCA
CCTGTACCGTGGCATCTTCCCTGTGCTGTGCAAGGACCCAGTCCAGGAGGCCTGGGCTGAGGACGTGGACCTCCG
GGTGAACTTTGCCATGAATGTTGGCAAGGCCCGAGGCTTCTTCAAGAAGGGAGATGTGGTCATTGTGCTGACCGG
ATGGCGCCCTGGCTCCGGCTTCACCAACACCATGCGTGTTGTTCCTGTGCCG**TGA**TGGACCCCAGAGCCCCTCCT
CCAGCCCCTGTCCCACCCCCTTCCCCCAGCCCATCCATTAGGCCAGCAACGCTTGTAGAACTCACTCTGGGCTGT
AACGTGGCACTGGTAGGTTGGGACACCAGGGAAGAAGATCAACGCCTCACTGAAACATGGCTGTGTTTGCAGCCT
GCTCTAGTGGGACAGCCCAGAGCCTGGCTGCCCCATCATGTGGCCCCACCCAATCAAGGGAAGAAGGAGGAATGC
TGGACTGGAGGCCCCTGGAGCCAGATGGCAAGAGGGTGACAGCTTCCTTTCCTGTGTGTACTCTGTCCAGTTCCT
TTAGAAAAAATGGATGCCCAGAGGACTCCCAACCCTGGCTTGGGGTCAAGAAACAGCCAGCAAGAGTTAGGGGCC
TTAGGGCACTGGGCTGTTGTTCCATTGAAGCCGACTCTGGCCCTGGCCCTTACTTGCTTCTCTAGCTCTCTAGGC
CTCTCCAGTTTGCACCTGTCCCCACCCTCCACTCAGCTGTCCTGCAGCAAACACTCCACCCTCCACCTTCCATTT
TCCCCCACTACTGCAGCACCTCCAGGCCTGTTGCCGC

FIGURE 175

MSKPHSEAGTAFIQTQQLHAAMADTFLEHMCRLDIDSPPITARNTGIICTIGPASRSVETLKEMIKSGMNVARLN
FSHGTHEYHAETIKNVRTATESFASDPILYRPVAVALDTKGPEIRTGLIKGSGTAEVELKKGATLKITLDNAYME
KCDENILWLDYKNICKVVEVGSKIYVDDGLISLQVKQKGADFLVTEVENGGSLGSKKGVNLPGAAVDLPAVSEKD
IQDLKFGVEQDVDMVFASFIRKASDVHEVRKVLGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIE
IPAEKVFLAQKMMIGRCNRAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAV
RMQNLIAREAEAAIYHLQLFEELRRLAPITSDPTEATAVGAVEASFKCCSGAIIVLTKSGRSAHQVARYRPRAPI
IAVTRNPQTARQAHLYRGIFPVLCKDPVQEAWAEDVDLRVNFAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTM
RVVPVP

FIGURE 176

GGCTTGGTCACT**ATG**GAGGAGATAGGCATCTTGGTGGAGAAGGCTCAGGATGAGATCCCAGCACTGTCCGTGTCC
CGGCCCCAGACCGGCCTGTCCTTCCTGGGCCCTGAGCCTGAGGACCTGGAGGACCTGTACAGCCGCTACAAGAAG
CTGCAGCAAGAGCTGGAGTTCCTGGAGGTGCAGGAGGAATACATCAAAGATGAGCAAAAGAACCTGAAAAAGGAA
TTTCTCCATGCCCAGGAGGAGGTGAAGCGAATCCAAAGCATCCCGCTGGTCATCGGACAATTTCTGGAGGCTGTG
GATCAGAATACAGCCATCGTGGGCTCTACCACAGGCTCCAACTATTATGTGCGCATCCTGAGCACCATCGATCGG
GAGCTGCTCAAGCCCAACGCCTCAGTGGCCCTCCACAAGCACAGCAATGCACTGGTGGACGTGCTGCCCCCCGAA
GCCGACAGCAGCATCATGATGCTCACCTCAGACCAGAAGCCAGATGTGATGTACGCGGACATCGGAGGCATGGAC
ATCCAGAAGCAGGAGGTGCGGGAGGCCGTGGAGCTCCCGCTCACGCATTTCGAGCTCTACAAGCAGATCGGCATC
GATCCCCCCCGAGGCGTCCTCATGTATGGCCCACCTGGCTGTGGGAAGACCATGTTGGCAAAGGCGGTGGCACAT
CACACAACAGCTGCATTCATCCGGGTCGTGGGCTCGGAGTTTGTACAGAAGTATCTGGGTGAGGGCCCCCGCATG
GTCCGGGATGTGTTCCGCCTGGCCAAGGAGAATGCACCTGCCATCATCTTCATAGACGAGATTGATGCCATCGCC
ACCAAGAGATTCGATGCTCAGACAGGGGCCGACAGGGAGGTTCAGAGGATCCTGCTGGAGCTGCTGAATCAGATG
GATGGATTTGATCAGAATGTCAATGTCAAGGTAATCATGGCCACAAACAGAGCAGACACCCTGGATCCGGCCCTG
CTACGGCCAGGACGGCTGGACCGTAAAATTGAATTTCCACTTCCTGACCGCCGCCAGAAGAGATTGATTTTCTCC
ACTATCACTAGCAAGATGAACCTCTCTGAGGAGGTTGACTTGGAAGACTATGTGGCCCGGCCAGATAAGATTTCA
GGAGCTGATATCAACTCCATCTGTCAGGAGAGTGGAATGTTGGCTGTCCGTGAAAACCGCTACATTGTCCTGGCC
AAGGACTTCGAGAAAGCATACAAGACTGTCATCAAGAAGGACGAGCAGGAGCATGAGTTTTACAAG**TGA**CCCTTC
CCTTCCCTCCACCACACCACTCAGGGGCTGGGGCTTCTCTCGCACCCCCAGCACCTCTGTCCCAAAACCTCATTC
CCTTTTTTCTTTACCCAGGATTGGTTTCTTCAATAAATAGATAAGATCGAATCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 177

MEEIGILVEKAQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSRYKKLQQELEFLEVQEEYIKDEQKNLKKEFLHA
QEEVKRIQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSS
IMMLTSDQKPDVMYADIGGMDIQKQEVREAVELPLTHFELYKQIGIDPPRGVLMYGPPGCGKTMLAKAVAHHTTA
AFIRVVGSEFVQKYLGEGPRMVRDVFRLAKENAPAIIFIDEIDAIATKRFDAQTGADREVQRILLELLNQMDGFD
QNVNVKVIMATNRADTLDPALLRPGRLDRKIEFPLPDRRQKRLIFSTITSKMNLSEEVDLEDYVARPDKISGADI
NSICQESGMLAVRENRYIVLAKDFEKAYKTVIKKDEQEHEFYK

FIGURE 178

CCGAGGCCAAGTCCCGGGCGCTAGCCCACCTCCCACCCGCCTCTTGGCTCCTCTCCTCTAGGCCGTCGCTTTCGG
GTTCTCTCATCGCTTCGTCGTTCGCCAATGTTTGAGGAGAAGGCCAGCAGTCCTTCAGGGAAG**ATG**GGAGGCGAG
GAGAAGCCGATTGGTGCTGGTGAAGAGAAGCAAAAGGAAGGAGGCAAAAAGAAGAACAAAGAAGGATCTGGAGAT
GGAGGTCGAGCTGAGTTGAATCCTTGGCCTGAATATATTTACACACGTCTTGAGATGTATAATATACTAAAAGCA
GAACATGATTCCATTCTGGCAGAAAAGGCAGAAAAAGATAGCAAGCCAATTAAAGTCACTTTGCCTGATGGTAAA
CAGGTTGATGCGGAATCTTGGAAAACTACACCATATCAAATTGCCTGTGGAATTAGTCAAGGCCTGGCCGACAAC
ACCGTTATTGCTAAAGTAAATAATGTTGTGTGGGACCTGGACCGCCCTCTGGAAGAAGATTGTACCTTGGAGCTT
CTCAAGTTTGAGGATGAGGAAGCTCAGGCAGTGTATTGGCACTCTAGTGCTCACATAATGGGTGAAGGCATGGAA
AGAGTCTATGGTGGATGTTTATGCTACGGTCCGCCAATAGAAAATGGATTCTATTATGACATGTACCTCGAAGAA
GGGGGTGTGTCTAGCAATGATTTCTCTTCTCTGGAGGCTTTGTGTAAGAAAATCATTAAAGAAAAACAAGCTTTT
GAAAGACTGGAAGTTAAGAAAGAAACTTTACTGGCAATGTTTAAGTACAACAAGTTCAAATGCCGGATATTGAAT
GAAAAGGTGAATACTCCAACTACCACAGTCTATAGATGTGGCCCTTTGATAGATCTCTGCCGGGGTCCTCATGTT
AGACACACGGGCAAAATTAAGGCTTTAAAAATACACAAAAATTCCTCCACGTACTGGGAAGGCAAAGCAGATATG
GAGACTCTCCAGAGAATTTATGGCATTTCATTCCCAGATCCTAAAATGTTGAAAGAGTGGGAGAAGTTCCAAGAG
GAAGCTAAAAACCGAGATCATAGGAAAATTGGCAGGGACCAAGAACTATATTTCTTTCATGAACTCAGCCCTGGA
AGTTGCTTTTTTCTGCCAAAAGGAGTCTATATTTATAATGCACTTATTGAATTCATTAGGAGCGAATATAGGAAA
AGAGGATTCCAGGAGGTAGTCACCCCAAACATCTTCAACAGCCGACTCTGGATGACCTCGGGCCACTGGCAGCAC
TACAGCGAGAACATGTTCTCCTTTGAGGTGGAGAAGGAGCTGTTTGCCCTGAAACCCATGAACTGCCCAGGACAC
TCCCTTATGTTTGATCATCGGCCAAGGTCCTGGCGAGAACTGCCTCTGCGGCTAGCTGATTTTGGGGGTCTTCAT
AGGAACGAGCTGTCTGGAGCACTCACAGGACTCACCCGGGTACGAAGATTCCAACAGGATGATGCTCACATATTC
TGTGCCATGGAGCAGATTGAAGATGAAATAAAAGGTTGTTTGGATTTTCTACGTACGGTATATAGCGTATTTGGA
TTTTCTTTTAAACTAAACCTTTCTACTCGCCCGGAAAAATTCCTTGGAGATATCGAAGTATGGGATCAAGCTGAG
AAACAACTTGAAAACAGTCTGAATGAATTTGGTGAAAAGTGGGAGTTAAACTCTGGAGATGGAGCTTTCTATGGC
CCAAAGATTGACATACAGATTAAAGATGCGATTGGGCGGTACCACCAGTGTGCAACCATCCAGCTGGATTTCCAG
TTGCCCATCAGATTTAATCTTACTTATGTAAGCCATGATGGTGAGGATAAGAAAAGGCCAGTGATTGTTCATCGA
GCCATCTTGGGATCAGTGGAAAGAATGATTGCTATCCTCACAGAAAACTATGGGGGCAAATTGGCCCCCTTTTGG
CTGTCCCCTCGCCAGGTAATGGTAGTTCCAGTGGGACCAACCTGTGATGAATATGCCCAAAACGTACGACAACAA
TTCCACGATGCCAAATTCATGGCAGACATTGATCTGGATCCAGGCTGTACATTGAATAAAAAGATTCGAAATGCA
CAGTTAGCACAGTATAACTTCATTTTAGTTGTTGGTGAAAAAGAGAAAATCACTGGCACTGTTAATATCCGCACA
AGAGACAATAAGGTCCACGGGGAACGCACCATTTCTGAAACTATCGAGCGGCTACAGCAGCTCAAAGAGTTCCGC
AGCAAACAGGCAGAAGAAGAATTT**TAA**TGAAAAAATTACCCAGATTGGCTCCATGGAAAAGGAGGAACAGCGTTT
CCGTAAAATTGACTTTGTACTCGAAAACGTCAATTTATATTGAACTTGGAGGAGGAGTTTGGCAAAGTCTGAAAT
AGGTCAACCTGCAGGCGTAACTATTTTTGACCTAGTCAGTTTTTAAACAATGTGCATTTGAAGGAGTTAATTAAA
AGAGAGCCAATAAAATGATTTTACTCATTCAGTATCTGAGTACTGGAAGTGAAACATGAGGAATGCTTTAGTGTA
ATGTGGGAGAACTTTTTTGTAAATTTAATGCAATTGAAAAAGTTTTCAAATTCAATTAAGATAACTAGAATTGGT
TATGGTGTAACCCGAATTC

FIGURE 179

MGGEEKPIGAGEEKQKEGGKKKNKEGSGDGGRAELNPWPEYIYTRLEMYNILKAEHDSILAEKAEKDSKPIKVTL
PDGKQVDAESWKTTPYQIACGISQGLADNTVIAKVNNVVWDLDRPLEEDCTLELLKFEDEEAQAVYWHSSAHIMG
EGMERVYGGCLCYGPPIENGFYYDMYLEEGGVSSNDFSSLEALCKKIIKEKQAFERLEVKKETLLAMFKYNKFKC
RILNEKVNTPTTTVYRCGPLIDLCRGPHVRHTGKIKALKIHKNSSTYWEGKADMETLQRIYGISFPDPKMLKEWE
KFQEEAKNRDHRKIGRDQELYFFHELSPGSCFFLPKGVYIYNALIEFIRSEYRKRGFQEVVTPNIFNSRLWMTSG
HWQHYSENMFSFEVEKELFALKPMNCPGHSLMFDHRPRSWRELPLRLADFGGLHRNELSGALTGLTRVRRFQQDD
AHIFCAMEQIEDEIKGCLDFLRTVYSVFGFSFKLNLSTRPEKFLGDIEVWDQAEKQLENSLNEFGEKWELNSGDG
AFYGPKIDIQIKDAIGRYHQCATIQLDFQLPIRFNLTYVSHDGEDKKRPVIVHRAILGSVERMIAILTENYGGKL
APFWLSPRQVMVVPVGPTCDEYAQNVRQQFHDAKFMADIDLDPGCTLNKKIRNAQLAQYNFILVVGEKEKITGTV
NIRTRDNKVHGERTISETIERLQQLKEFRSKQAEEEF

FIGURE 180

GGCACGAGGATTCGCTGCTCCGCAGCACGGCCGGAGCTGGTCCGGTCAAGAGTCGGGATTTGTGGGGAGAGGTTT
TCCACTGGTCAAGAGAAGGCTTTAAGAAAGACGGTATTAATCTCCCGTTGCGGCTCCCGCCTGGTCCCATCTTCT
GCCCGCTCCTCCAGGAA**ATG**AATCTGCTGCCGAATATTGAGAGTCCAGTGACTCGGCAGGAGAAGATGGCGACCG
TGTGGGATGAGGCCGAGCAAGATGGAATTGGGGAGGAGGTGCTCAAGATGTCCACGGAGGAGATCATCCAGCGCA
CACGGCTGCTGGACAGTGAGATCAAGATCATGAAGAGTGAAGTGTTGAGAGTCACCCATGAGCTCCAAGCCATGA
AGGACAAGATAAAAGAGAACAGTGAGAAAATCAAAGTGAACAAGACCCTGCCGTACCTTGTCTCCAACGTCATCG
AGCTCCTGGATGTTGATCCTAATGACCAAGAGGAGGATGGTGCCAATATTGACCTGGACTCCCAGAGGAAGGGCA
AGTGTGCTGTGATCAAAACCTCTACACGACAGACGTACTTCCTTCCTGTGATTGGGTTGGTGGATGCTGAAAAGC
TAAAGCCAGGAGACCTGGTGGGTGTGAACAAAGACTCCTATCTGATCCTGGAGACGCTGCCCACAGAGTATGACT
CGCGGGTGAAGGCCATGGAGGTAGACGAGAGGCCCACGGAGCAATACAGTGACATTGGGGGTTTGGACAAGCAGA
TCCAGGAGCTGGTGGAGGCCATTGTCTTGCCAATGAACCACAAGGAGAAGTTTGAGAACTTGGGGATCCAACCTC
CAAAAGGGGTGCTGATGTATGGGCCCCCAGGGACGGGGAAGACCCTCCTGGCCCGGGCCTGTGCCGCACAGACTA
AGGCCACCTTCCTAAAGCTGGCTGGCCCCCAGCTGGTGCAGATGTTCATTGGAGATGGTGCCAAGCTAGTCCGGG
ATGCCTTTGCCCTGGCCAAGGAGAAAGCGCCCTCTATCATCTTCATTGATGAGTTGGATGCCATCGGCACCAAGC
GCTTTGACAGTGAGAAGGCTGGGGACCGGGAGGTGCAGAGGACAATGCTGGAGCTTCTGAACCAGCTGGATGGCT
TCCAGCCCAACACCCAAGTTAAGGTAATTGCAGCCACAAACAGGGTGGACATCCTGGACCCCGCCCTCCTCCGCT
CGGGCCGCCTTGACCGCAAGATAGAGTTCCCGATGCCCAATGAGGAGGCCCGGGCCAGAATCATGCAGATCCACT
CCCGAAAGATGAATGTCAGTCCTGACGTGAACTACGAGGAGCTGGCCCGCTGCACAGATGACTTCAATGGGGCCC
AGTGCAAGGCTGTGTGTGTGGAGGCGGGCATGATCGCACTGCGCAGGGGTGCCACGGAGCTCACCCACGAGGACT
ACATGGAAGGCATCCTGGAGGTGCAGGCCAAGAAGAAAGCCAACCTACAATACTACGCC**TAG**GGCACACAGGCCA
GCCCCAGTCTCACGGCTGAAGTGCGCAATAAAAGATGGTTTAGGGTCCCTGCCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 181

MNLLPNIESPVTRQEKMATVWDEAEQDGIGEEVLKMSTEEIIQRTRLLDSEIKIMKSEVLRVTHELQAMKDKIKE
NSEKIKVNKTLPYLVSNVIELLDVDPNDQEEDGANIDLDSQRKGKCAVIKTSTRQTYFLPVIGLVDAEKLKPGDL
VGVNKDSYLILETLPTEYDSRVKAMEVDERPTEQYSDIGGLDKQIQELVEAIVLPMNHKEKFENLGIQPPKGVLM
YGPPGTGKTLLARACAAQTKATFLKLAGPQLVQMFIGDGAKLVRDAFALAKEKAPSIIFIDELDAIGTKRFDSEK
AGDREVQRTMLELLNQLDGFQPNTQVKVIAATNRVDILDPALLRSGRLDRKIEFPMPNEEARARIMQIHSRKMNV
SPDVNYEELARCTDDFNGAQCKAVCVEAGMIALRRGATELTHEDYMEGILEVQAKKKANLQYYA

FIGURE 182

GGCACCGCGCGGGACGGAGCTTGGCTGTTGGTCGGTGGGTTCCCGTGCGGCGGCGGCCAAGGAGGAGGAGACACA
GTTGGAGCAGCTCCGTGGGCTGACTGGGGCGAGGCCTCAGCAGCGCGAGCTTGAGTGCGGCCGAGCCTGCGGCGC
CTTCCCCTGCGGGTGGGGACGAGCGGGCCCCGCGGCGTCATCGGCGGCGAGGAGCCGCCGCGCCTCGGCCTAGC**A**
TGTCGGAAGCGGGCGAGGAGCAGCCCATGGAGACGACGGGCGCCACCGAGAACGGACATGAGGCCGTCCCCGAAG
CGAGTCGCGGCCGGGGCTGGACGGGCGCCGCGGCGGGGCTGGAGGCGCGACCGCCGCGCCCCCGAGCGGGAATCA
GAACGGCGCCGAGGGACCAGATCAACGCCAGCAAGAACGAGGAGGACGCGGGAAAAATGTTCGTTGGTGGCCTGA
GCTGGGATACTAGCAAAAAAGATTTAAAAGACTATTTTACTAAATTTGGAGAGGTCGTTGACTGTACAATAAAAA
TGGATCCCAACACTGGACGGTCAAGAGGGTTTGGGTTTATCCTGTTCAAAGATGCAGCCAGTGTGGAGAAGGTCC
TAGACCAGAAGGAGCACAGGCTGGATGGCCGTGTCATTGACCCTAAAAAGGCCATGGCTATGAAGAAGGACCCGG
TCAAGAAAATCTTCGTTGGGGGTCTGAATCCTGAAAGTCCCACTGAGGAAAAGATCAGGGAGTACTTTGGCGAGT
TTGGGGAGATTGAGGCCATTGAATTGCCAATGGATCCAAAGTTGAACAAAAGACGAGGTTTTGTGTTTATCACCT
TTAAAGAAGAAGAACCCGTGAAGAAGGTTCTGGAGAAAAAGTTCCATACTGTCAGTGGAAGCAAGTGTGAGATCA
AGGTGGCCCAGCCCAAAGAAGTCTATCAGCAGCAGCAGTATGGCTCTGGGGGCCGTGGAAACCGCAACCGAGGGA
ACCGAGGCAGCGGAGGTGGTGGTGGAGGTGGAGGTCAGAGTCAGAGTTGGAATCAGGGCTACGGCAACTACTGGA
ACCAGGGCTACGGCTACCAGCAGGGCTACGGGCCTGGCTATGGCGGCTACGACTACTCGCCCTATGGCTATTACG
GCTACGGCCCCGGCTACGACTACAGTCAGGGTAGTACAAACTACGGCAAGAGCCAGCGACGTGGTGGCCATCAGA
ATAACTACAAGCCATAC**TGA**GGCGGCCAAGGGAGCGACCAACTGATCGCACACATGCTTTGTTTGGATATGGAGT
GAACACAATTATGTACCAAATTTAACTTGGCAAACTTTCTATTGCCTGTCCCATGTGCATCTTATTTAAAATTTC
CCCCATGGAAATCACTCTCCTGTTGACTATTTCCAGAGCTCTAGGTGTTTAGGCAGCGTGTGGTGTCTGAGAGGC
CATAGCGCCATCATGGGCTGATTTTTATTACCAGGTCCCCCAGAAGCAGGTGAGAGGCTCTGCTTCCTGCTGCCG
CTCTGCAGCCTGGACCTGTGGACCCTGGTTGTAAAGAGTAAATTGTATCTTAGGAAACCAGTGTCACCTTTTTTT
CACCTTTTAATTTTATATTATTTGCGTCATACATTTCCTGTAACGGAAGTGTTAATTTTACTGTACTTTTTGGTA
CCCCTTTTGGGAATCTAATGTATTGTAAGGTATTTTACACGTGTCCTGATTTTGCCACAACCTGGATATTGAAGC
TATCCAAGCTTTTGAAATAAAATTTAAAAACCCCAAGCCTGGGTGAGTGTGGGAAAAAAAAAAAAAAAA

FIGURE 183

MSEAGEEQPMETTGATENGHEAVPEASRGRGWTGAAAGLEARPPRPRAGIRTAPRDQINASKNEEDAGKMFVGGL
SWDTSKKDLKDYFTKFGEVVDCTIKMDPNTGRSRGFGFILFKDAASVEKVLDQKEHRLDGRVIDPKKAMAMKKDP
VKKIFVGGLNPESPTEEKIREYFGEFGEIEAIELPMDPKLNKRRGFVFITFKEEEPVKKVLEKKFHTVSGSKCEI
KVAQPKEVYQQQQYGSGGRGNRNRGNRGSGGGGGGGGQSQSWNQGYGNYWNQGYGYQQGYGPGYGGYDYSPYGYY
GYGPGYDYSQGSTNYGKSQRRGGHQNNYKPY

FIGURE 184

TAGCTGGATTCCAGCCATTGCTGCAGCTGCTCCACAGCCCTTTTCAGGACCCAAACAACCGCAGCCGCTGTTCCC
AGG**ATG**GTGATCCGTGTATATATTGCATCTTCCTCTGGCTCTACAGCGATTAAGAAGAAACAACAAGATGTGCTT
GGTTTCCTAGAAGCCAACAAAATAGGATTTGAAGAAAAAGATATTGCAGCCAATGAAGAGAATCGGAAGTGGATG
AGAGAAAATGTACCTGAAAATAGTCGACCAGCCACAGGTTACCCCCTGCCACCTCAGATTTTCAATGAAAGCCAG
TATCGCGGGGACTATGATGCCTTCTTTGAAGCCAGAGAAAATAATGCAGTGTATGCCTTCTTAGGCTTGACAGCC
CCACCTGGTTCAAAGGAAGCAGAAGTGCAAGCAAAGCAGCAAGCA**TGA**ACCTTAAGCACTGTGCTTTAAGCATCC
TGAAAAATGAGTCTCCATTGCTTTTATAAAATAGCAGAATTAGCTTTGCTTCAAAAGAAATAGGCTTAATGTTGA
AATAATAGATTAGTTGGGTTTTCACATGCAAACATTCAAAATGAATACAAAATTAAAATTTGAACATTATGGTGA
TTATGGTGAGGAGAATGGGATATTAACATAAAATTATATTAATAAGTAGATATCGTAGAAATAGTGTTGTTACCT
GCCAAGCCATCCTGTATACACCAATGATTTTACAAAGAAAACACCCTTCCCTCCTTCTGCCATTACTATGGCAAC
TTAAGTGTATCTGCAGCTCTACATTAAAAAGGAGAAAGAGAAATAACCTGTCTCTCATTCCTAAGTTGCCTCATT
AATTTTCATGAACAAGAATATGTACCTTTTTGATGCTATATTACTGCGATTAAAAAAGTTCTTGCAGGTAATGTT
TATGTATAGTTAAACGTTGTAATTTCTTATCGTAATTATAACATTCCCATTCTTTGTAGATGAAACTCTACATAT
GAACCACAGATTTTCTGAGCTTCTAAATGTAGCCTTTCATTGCACATTTCAGTGATCAGAATAGATATCCTTTTA
CACGCACAAAAGCAATAGATTCATTCAGTGGACAAGTTCCTTGTTTAACTACACAGCTATGATGGAATCATATAT
CCAAGTTCCTTGCCTCAGTGAAATATGCATATGTATATCATGAAGTGGGATGCCAAGTAAGCTTAAAATGCATTC
TCTAGCAAAGAGATTAGACTTTTAAATAACTCTTATAAAACAGGTTGGCGATCATTTCCCAAGATTGGTTTCCCT
TGAGTTTTTGTTAAAACAAATCTTAGTAGTTTTGCCCGTTTAAAACAACTCACAATCGTAAATGCTACTATTCCT
AAGATATCTTACCTTTTTATTTCAGTTTAGCCATGTATTGTATGAGTGTATTAGTCTAAGCAGTGAGAATCTTTT
CTATGCCTCTATTCCAGCAAAAAGTAGAAGTATCAAATAAAAAGGGCAACTTTTAAAATATTAAGCCTGAAGACT
TCTAAAAAGACAAGAAACATGGCCTAAATAACCAACATAGATTTACATAGTAAGTTTCACACTACCTTATTACCA
AAAGCAAACACCTCTTACTTTAAACTACATTATCATGTATATCTATTGTATGCTGGTCTTTACTTTTTGCCAAAA
TCAACATATAATGAAGAGATGCCTTTGTTTGATGAGATTCAAACTTGATGCTATGCTTTAAAATAAACTCAGTAC
TTTTAGAAACATAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 185

MVIRVYIASSSGSTAIKKKQQDVLGFLEANKIGFEEKDIAANEENRKWMRENVPENSRPATGYPLPPQIFNESQY
RGDYDAFFEARENNAVYAFLGLTAPPGSKEAEVQAKQQA

FIGURE 186

ATGGCGGAGCGCGGGTACAGCTTTTCGCTGACTACATTCAGCCCGTCTGGTAAACTTGTCCAGATTGAATATGCT
TTGGCTGCTGTAGCTGGAGGAGCCCCGTCCGTGGGAATTAAAGCTGCAAATGGTGTGGTATTAGCAACTGAGAAA
AAACAGAAATCCATTCTGTATGATGAGCGAAGTGTACACAAAGTAGAACCAATTACCAAGCATATAGGTTTGGTG
TACAGTGGCATGGGCCCCGATTACAGAGTGCTTGTGCACAGAGCTCGAAAACTAGCTCAACAATACTATCTTGTG
TACCAAGAACCCATTCCTACAGCTCAGCTGGTACAGAGAGTAGCTTCTGTGATGCAAGAATATACTCAGTCAGGT
GGTGTTCGTCCATTTGGAGTTTCTTTACTTATTTGTGGTTGGAATGAGGGACGACCATATTTATTTCAGTCAGAT
CCATCTGGAGCTTACTTTGCCTGGAAAGCTACAGCAATGGGAAAGAACTATGTGAATGGGAAGACTTTCCTTGAG
AAAAGATATAATGAAGATCTGGAACTTGAAGATGCCATTCATACAGCCATCTTAACCCTAAAGGAAAGCTTTGAA
GGGCAAATGACAGAGGATAACATAGAAGTTGGAATCTGCAATGAAGCTGGATTTAGGAGGCTTACTCCAACTGAA
GTTAAGGATTACTTGGCTGCCATAGCA**TAA**CAATGAAGTGACTGAAAAATCCAGAATTTCAGATAATCTATCTAC
TTAAACATGTTTAAAGTATGTTTTGTTTTGCAGACTTTTTGCATACTTATTTCTACATGGTTTAAATCGACTGTT
TTTAAAATGACACTTATAAATCCTAATAAACTGTTAAACCC

FIGURE 187

MAERGYSFSLTTFSPSGKLVQIEYALAAVAGGAPSVGIKAANGVVLATEKKQKSILYDERSVHKVEPITKHIGLV
YSGMGPDYRVLVHRARKLAQQYYLVYQEPIPTAQLVQRVASVMQEYTQSGGVRPFGVSLLICGWNEGRPYLFQSD
PSGAYFAWKATAMGKNYVNGKTFLEKRYNEDLELEDAIHTAILTLKESFEGQMTEDNIEVGICNEAGFRRLTPTE
VKDYLAAIA

FIGURE 188

GCGATTCGGTGGCACGTGGAGCCACGGCGTGGGAGTAGGGGGCTGAAGGCAGGCAGCAGCGGCCAGGGCCGCCCT
CTGCTAGCCGCTTGGGTCTCGGGATACCCCGTTTCTTCCTGTAGGTGTGGGACGTGCGTGCGGCGAG**ATG**GACAC
TCCCCCGCTCTCGGATTCGGAGTCGGAATCCGATGAATCCCTTGTCACAGACAGAGAGTTGCAGGATGCGTTTTC
CCGAGGGCTTCTGAAGCCAGGCCTCAATGTCGTGCTAGAGGGGCCGAAGAAGGCCGTGAACGACGTGAATGGCCT
GAAGCAATGTTTGGCAGAATTCAAGCGGGATCTGGAATGGGTTGAAAGGCTCGATGTGACACTGGGTCCGGTACC
GGAGATCGGTGGATCTGAGGCGCCAGCACCTCAGAACAAGGACCAGAAAGCTGTTGATCCAGAAGACGACTTCCA
GCGAGAGATGAGTTTCTATCGCCAAGCCCAGGCCGCAGTGCTTGCAGTCTTACCCCGCCTCCATCAGCTCAAAGT
CCCTACGAAGCGACCCACTGATTATTTTGCGGAAATGGCCAAATCTGATCTGCAGGTGCAGAAGATTCGACAGAA
GCTGCAGACTAAACAGGCTGCCATGGAGAGGTCTGAAAAAGCTAAGCAACTGCGAGCACTTAGGAAATACGGGAA
GAAGGTGCAAACGGAGGTTCTTCAGAAGAGGCAGCAGGAGAAAGCCCATATGATGAATGCTATTAAGAAATATCA
GAAAGGCTTCTCTGATAAACTGGATTTCCTTGAGGGAGATCAGAAACCTCTGGCACAGCGCAAGAAGGCAGGAGC
CAAAGGCCAGCAGATGAGGAAGGGGCCCAGTGCTAAACGACGGTATAAAAACCAGAAGTTTGGTTTTGGTGGAAA
GAAGAAAGGCTCAAAGTGGAACACTCGGGAGAGCTATGATGATGTATCTAGCTTCCGGGCCAAGACAGCTCATGG
CAGAGGCCTCAAGAGGCCTGGCAAGAAAGGGTCAAATAAGAGACCTGGAAAACGAACAAGAGAGAAGATGAAGAA
CAGAACACAC**TAA**ATAGCATCTTTGAATACAAAGAACCAAGAAAAAGGAATGAAGACTCGCAATTTCACGACACA
CTTTGATCCCTTCTGTTGGTGTCATGTTGTAAACATTTCTTTCAATAAACTAAAGAAAAATTATTAAAGGAACAC
ATACCTTTGGTTAAATAGTCTAGACTAAAAGATTGAGAAGTTACTTTCCATTGCTATCTATTGATAATTTAGACA
TTGAGTTCAAATTGCCTTCATTTTATGATAAATAATGATTTAACTGAAAA

FIGURE 189

MDTPPLSDSESESDESLVTDRELQDAFSRGLLKPGLNVVLEGPKKAVNDVNGLKQCLAEFKRDLEWVERLDVTLG
PVPEIGGSEAPAPQNKDQKAVDPEDDFQREMSFYRQAQAAVLAVLPRLHQLKVPTKRPTDYFAEMAKSDLQVQKI
RQKLQTKQAAMERSEKAKQLRALRKYGKKVQTEVLQKRQQEKAHMMNAIKKYQKGFSDKLDFLEGDQKPLAQRKK
AGAKGQQMRKGPSAKRRYKNQKFGFGGKKKGSKWNTRESYDDVSSFRAKTAHGRGLKRPGKKGSNKRPGKRTREK
MKNRTH

FIGURE 190

GCCGCGCCGGCTCTGGGCACTCAGCATCGTTTCCTTTTCCTCCGCTGGAGCAGCT**ATG**GCGGCGGTGAAGACCCT
GAACCCCAAGGCCGAGGTGGCCCGAGCGCAGGCGGCGCTGGCGGTCAACATCAGCGCAGCGCGGGGTCTGCAGGA
CGTGCTAAGGACCAACCTGGGGCCCAAGGGCACCATGAAGATGCTCGTTTCTGGCGCTGGAGACATCAAACTTAC
TAAAGACGGCAATGTGCTGCTTCACGAAATGCAAATTCAACACCCAACAGCTTCCTTAATAGCAAAGGTAGCAAC
AGCCCAGGATGATATAACTGGTGATGGTACGACTTCTAATGTCCTAATCATTGGAGAGCTGCTGAAACAGGCGGA
TCTCTACATTTCTGAAGGCCTTCATCCTAGAATAATCACTGAAGGATTTGAAGCTGCAAAGGAAAAGGCCCTTCA
GTTTTTGGAAGAAGTCAAAGTAAGCAGAGAGATGGACAGGGAAACACTTATAGATGTGGCCAGAACATCTCTTCG
TACTAAAGTTCATGCTGAACTTGCAGATGTCTTAACAGAGGCTGTAGTGGACTCCATTTTGGCCATTAAAAAGCA
AGATGAACCTATTGATCTCTTCATGATTGAGATCATGGAGATGAAACATAAATCTGAAACTGATACAAGCTTAAT
CAGAGGGCTTGTTTTGGACCACGGAGCACGGCATCCTGATATGAAGAAAAGGGTGGAGGATGCATACATCCTCAC
TTGTAACGTGTCATTAGAGTATGAGAAAACAGAAGTGAATTCTGGCTTTTTTTACAAGAGTGCAGAAGAGAGAGA
AAAACTCGTGAAAGCTGAAAGAAAATTCATTGAAGATAGGGTTAAAAAAATAATAGAACTGAAAAGGAAAGTCTG
TGGCGATTCAGATAAAGGATTTGTTGTTATTAATCAAAAGGGAATTGACCCCTTTTCCTTAGATGCTCTTTCAAA
AGAAGGCATAGTCGCTCTGCGCAGAGCTAAAAGGAGAAATATGGAGAGGCTGACTCTTGCTTGTGGTGGGGTAGC
CCTGAATTCTTTTGACGACCTAAGTCCTGACTGCTTGGGACATGCAGGACTTGTATATGAGTATACATTGGGAGA
AGAGAAGTTTACCTTTATTGAGAAATGTAACAACCCTCGTTCTGTCACATTATTGATCAAAGGACCAAATAAGCA
CACACTCACTCAGATCAAAGATGCAGTGAGGGACGGCTTGAGGGCTGTCAAAAATGCTATTGATGATGGCTGTGT
GGTTCCAGGTGCTGGTGCCGTGGAAGTGGCAATGGCAGAAGCCCTGATTAAACATAAGCCCAGTGTAAAGGGCAG
GGCACAGCTTGGAGTCCAAGCATTTGCTGATGCATTGCTCATTATTCCCAAGGTTCTTGCTCAGAACTCTGGTTT
TGACCTTCAGGAAACATTAGTTAAAATTCAAGCAGAACATTCAGAATCAGGTCAGCTTGTGGGTGTGGACCTGAA
CACAGGTGAGCCAATGGTGGCAGCAGAAGTAGGCGTATGGGATAACTATTGTGTAAAGAAACAGCTTCTTCACTC
CTGCACTGTGATTGCCACCAACATTCTCTTGGTTGATGAGATCATGCGAGCTGGAATGTCTTCTCTGAAAGGT**TG**
AATTGAAGCTTCCTCTGTATCTGAATCTTGAAGACTGCAAAGTGATCCTGAGGATTACAGCTGTGGAATTTTTGT
CCAAGCTTCAAATAATTTTGAAAGAAATTTTCCCATATGAAAAAAGGAGAGAACACTGGCATCTGTTGAAATTTG
GAAGTTCTGAAATTATAGTATTTTTAAAAATTGCACTGAAGTGTATACACATAAAGCAGGTCTTTTATCCAGTGA
ACAGGATGTTTTGCTTTAGCAGCAGTGACATAAAATTCCATGTTAGATAAGCATATGTTACTTACCTTGTTATTA
AATATTTCTTGAAAAGCAAATTTTAATGGTTAATTTTATGTGGACGTATGTTAAATTATCCAAACTACCCTATTG
TTAAGCATTTGGTTTTAAAATTTTTATGCTAATATAAATGCTCAAGTAATTTAAAATATTGAAAGCATCCCTGTT
GGTATAAATTTCTGAGTAAATGCATTGGATCAGTTGGACTTTGAACGCCCTTTGAAATGGCTTTGCTAAAATGCT
CCCGCCACAAAGTTGTAGGAAATGGGAAGAGGAGTCAACTAGAGGCAAGGGAGTTGAGAGAGCTGCAACTGTAAA
GGGCAAGAACAGGCAGAGGTAAAAAGATGATGGAAGGTGTGGTGACTAAGGGCCACGGTTATTGGGTGAAATTTG
AGATGTAGGCCAACTGTATTTTCAAGCTTCTGAACTTAAGGCAAAATATTCATCGCAAAGTCTCTAGCGTCATAT
TTTTCTCACCCAAATTACGTTTCCACGAGTTATTATATATAGTTGGTCTATCTCTGCAGTCCTTGAAGGTGAAGT
TGTGTGTTACTAGGCTGTGTTTTGGGATGTCAGCAGTGGCCTGAAGTGAGTTGTGCAATAAATGTTAAGTTGAAA
CCTCAAAAAAAA

FIGURE 191

MAAVKTLNPKAEVARAQAALAVNISAARGLQDVLRTNLGPKGTMKMLVSGAGDIKLTKDGNVLLHEMQIQHPTAS
LIAKVATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPRIITEGFEAAKEKALQFLEEVKVSREMDRETLID
VARTSLRTKVHAELADVLTEAVVDSILAIKKQDEPIDLFMIEIMEMKHKSETDTSLIRGLVLDHGARHPDMKKRV
EDAYILTCNVSLEYEKTEVNSGFFYKSAEEREKLVKAERKFIEDRVKKIIELKRKVCGDSDKGFVVINQKGIDPF
SLDALSKEGIVALRRAKRRNMERLTLACGGVALNSFDDLSPDCLGHAGLVYEYTLGEEKFTFIEKCNNPRSVTLL
IKGPNKHTLTQIKDAVRDGLRAVKNAIDDGCVVPGAGAVEVAMAEALIKHKPSVKGRAQLGVQAFADALLIIPKV
LAQNSGFDLQETLVKIQAEHSESGQLVGVDLNTGEPMVAAEVGVWDNYCVKKQLLHSCTVIATNILLVDEIMRAG
MSSLKG .

FIGURE 192

GCCGCGCCGGCTCTGGGCACTCAGCATCGTTTCCTTTTCCTCCGCTGGAGCAGCT**ATG**GCGGCGGTGAAGACCCT
GAACCCCAAGGCCGAGGTGGCCCGAGCGCAGGCGGCGCTGGCGGTCAACATCAGCGCAGCGCGGGGTCTGCAGGA
CGTGCTAAGGACCAACCTGGGGCCCAAGGGCACCATGAAGATGCTCGTTTCTGGCGCTGGAGACATCAAACTTAC
TAAAGACGGCAATGTGCTGCTTCACGAAATGCAAATTCAACACCCAACAGCTTCCTTAATAGCAAAGGTAGCAAC
AGCCCAGGATGATATAACTGGTGATGGTACGACTTCTAATGTCCTAATCATTGGAGAGCTGCTGAAACAGGCGGA
TCTCTACATTTCTGAAGGCCTTCATCCTAGAATAATCACTGAAGGATTTGAAGCTGCAAAGGAAAAGGCCCTTCA
GTTTTTGGAAGAAGTCAAAGTAAGCAGAGAGATGGACAGGGAAACACTTATAGATGTGGCCAGAACATCTCTTCG
TACTAAAGTTCATGCTGAACTTGCAGATGTCTTAACAGAGGCTGTAGTGGACTCCATTTTGGCCATTAAAAAGCA
AGATGAACCTATTGATCTCTTCATGATTGAGATCATGGAGATGAAACATAAATCTGAAACTGATACAAGCTTAAT
CAGAGGGCTTGTTTTGGACCACGGAGCACGGCATCCTGATATGAAGAAAAGGGTGGAGGATGCATACATCCTCAC
TTGTAACGTGTCATTAGAGTATGAGAAAACAGAAGTGAATTCTGGCTTTTTTTACAAGAGTGCAGAAGAGAGAGA
AAAACTCGTGAAAGCTGAAAGAAAATTCATTGAAGATAGGGTTAAAAAAATAATAGAACTGAAAAGGAAAGTCTG
TGGCGATTCAGATAAAGGATTTGTTGTTATTAATCAAAAGGGAATTGACCCCTTTTCCTTAGATGCTCTTTCAAA
AGAAGGCATAGTCGCTCTGCGCAGAGCTAAAAGGAGAAATATGGAGAGGCTGACTCTTGCTTGTGGTGGGGTAGC
CCTGAATTCTTTTGACGACCTAAGTCCTGACTGCTTGGGACATGCAGGACTTGTATATGAGTATACATTGGGAGA
AGAGAAGTTTACCTTTATTGAGAAATGTAACAACCCTCGTTCTGTCACATTATTGATCAAAGGACCAAATAAGCA
CACACTCACTCAGATCAAAGATGCAGTGAGGGACGGCTTGAGGGCTGTCAAAAATGCTATTGATGATGGCTGTGT
GGTTCCAGGTGCTGGTGCCGTGGAAGTGGCAATGGCAGAAGCCCTGATTAAACATAAGCCCAGTGTAAAGGGCAG
GGCACAGCTTGGAGTCCAAGCATTTGCTGATGCATTGCTCATTATTCCCAAGGTTCTTGCTCAGAACTCTGGTTT
TGACCTTCAGGAAACATTAGTTAAAATTCAAGCAGAACATTCAGAATCAGGTCAGCTTGTGGGTGTGGACCTGAA
CACAGGTGAGCCAATGGTGGCAGCAGAAGTAGGCGTATGGGATAACTATTGTGTAAAGAAACAGCTTCTTCACTC
CTGCACTGTGATTGCCACCAACATTCTCTTGGTTGATGAGATCATGCGAGCTGGAATGTCTTCTCTGAAAGGT**TG**
AATTGAAGCTTCCTCTGTATCTGAATCTTGAAGACTGCAAAGTGATCCTGAGGATTACAGCTGTGGAATTTTTGT
CCAAGCTTCAAATAATTTTGAAAGAAATTTTCCCATATGAAAAAAGGAGAGAACACTGGCATCTGTTGAAATTTG
GAAGTTCTGAAATTATAGTATTTTTAAAAATTGCACTGAAGTGTATACACATAAAGCAGGTCTTTTATCCAGTGA
ACAGGATGTTTTGCTTTAGCAGCAGTGACATAAAATTCCATGTTAGATAAGCATATGTTACTTACCTTGTTATTA
AATATTTCTTGAAAAGCAAATTTTAATGGTTAATTTTATGTGGACGTATGTTAAATTATCCAAACTACCCTATTG
TTAAGCATTTGGTTTTAAAATTTTTATGCTAATATAAATGCTCAAGTAATTTAAAATATTGAAAGCATCCCTGTT
GGTATAAATTTCTGAGTAAATGCATTGGATCAGTTGGACTTTGAACGCCCTTTGAAATGGCTTTGCTAAAATGCT
CCCGCCACAAAGTTGTAGGAAATGGGAAGAGGAGTCAACTAGAGGCAAGGGAGTTGAGAGAGCTGCAACTGTAAA
GGGCAAGAACAGGCAGAGGTAAAAAGATGATGGAAGGTGTGGTGACTAAGGGCCACGGTTATTGGGTGAAATTTG
AGATGTAGGCCAACTGTATTTTCAAGCTTCTGAACTTAAGGCAAAATATTCATCGCAAAGTCTCTAGCGTCATAT
TTTTCTCACCCAAATTACGTTTCCACGAGTTATTATATATAGTTGGTCTATCTCTGCAGTCCTTGAAGGTGAAGT
TGTGTGTTACTAGGCTGTGTTTTGGGATGTCAGCAGTGGCCTGAAGTGAGTTGTGCAATAAATGTTAAGTTGAAA
CCTCAAAAAAAA

FIGURE 193

MAAVKTLNPKAEVARAQAALAVNISAARGLQDVLRTNLGPKGTMKMLVSGAGDIKLTKDGNVLLHEMQIQHPTAS
LIAKVATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPRIITEGFEAAKEKALQFLEEVKVSREMDRETLID
VARTSLRTKVHAELADVLTEAVVDSILAIKKQDEPIDLFMIEIMEMKHKSETDTSLIRGLVLDHGARHPDMKKRV
EDAYILTCNVSLEYEKTEVNSGFFYKSAEEREKLVKAERKFIEDRVKKIIELKRKVCGDSDKGFVVINQKGIDPF
SLDALSKEGIVALRRAKRRNMERLTLACGGVALNSFDDLSPDCLGHAGLVYEYTLGEEKFTFIEKCNNPRSVTLL
IKGPNKHTLTQIKDAVRDGLRAVKNAIDDGCVVPGAGAVEVAMAEALIKHKPSVKGRAQLGVQAFADALLIIPKV
LAQNSGFDLQETLVKIQAEHSESGQLVGVDLNTGEPMVAAEVGVWDNYCVKKQLLHSCTVIATNILLVDEIMRAG
MSSLKG

FIGURE 194A

GGCCCCA**ATG**AGTGGCACACAGTCTACTATCACCGACAGGTTTCCCCTCAAAAAACCTATAAGGCATGGAAGTAT
TTTGAACCGAGAGTCACCAACAGATAAGAAGCAGAAAGTTGAGCGCATTGCATCACATGATTTTGACCCCACAGA
TAGCTCCTCCAAGAAGACAAAGTCTAGTTCAGAGGAGAGTAGATCCGAGATATATGGTCTTGTTCAGCGTTGCGT
AATCATCCAGAAAGATGACAATGGATTTGGGCTGACGGTCAGTGGAGACAATCCAGTCTTCGTACAGTCTGTCAA
AGAAGATGGAGCAGCCATGCGGGCTGGAGTACAGACAGGTGATCGAATCATCAAGGTGAATGGAACTCTGGTGAC
TCATTCAAATCATCTGGAGGTGGTGAAGCTAATCAAATCTGGTTCCTATGTAGCTCTCACTGTTCAGGGACGCCC
ACCTGGGTCGCCCCAGATTCCACTTGCCGACTCTGAAGTAGAGCCGTCAGTCATTGGACATATGTCTCCCATCAT
GACATCTCCTCATTCACCTGGAGCATCTGGGAATATGGAGAGAATCACTAGTCCTGTGCTCATGGGGGAGGAAAA
CAATGTGGTTCATAACCAGAAAGTAGAAATTCTGAGAAAAATGTTACAGAAAGAACAGGAACGGCTACAGTTATT
GCAGGAAGATTACAACCGAACACCTGCCCAAAGATTGCTAAAAGAGATCCAAGAGGCCAAGAAACACATTCCTCA
GCTGCAAGAGCAGTTATCCAAAGCCACAGGCTCTGCTCAGGATGGAGCTGTAGTTACACCCTCCAGACCTTTAGG
GGACACCCTAACAGTCAGTGAGGCAGAAACAGATCCTGGAGATGTACTGGGCAGGACTGACTGTAGCAGTGGAGA
TGCTTCTCGGCCCAGTAGTGACAATGCAGATAGTCCCAAGAGTGGCCCAAAAGAGAGAATTTATCTAGAGGAAAA
CCCAGAGAAAAGTGAAACAATTCAGGACACTGACACTCAATCACTTGTCGGAAGTCCCTCAACCCGTATAGCACC
TCATATTATTGGAGCAGAAGATGATGATTTTGGTACTGAACATGAACAGATCAATGGACAGTGCAGCTGTTTCCA
GAGCATTGAATTACTAAAATCTCGCCCGGCTCATTTGGCTGTTTTCTTACACCATGTAGTTTCACAATTTGACCC
TGCGACTTTGCTCTGTTATCTCTATTCAGACCTGTATAAACATACCAATTCCAAAGAAACTCGTCGCATCTTCCT
TGAGTTTCATCAGTTCTTTCTAGATCGATCAGCACACCTGAAAGTTTCTGTTCCTGATGAAATGTCTGCAGATCT
AGAAAAGAGAAGACCTGAGCTCATTCCTGAGGATCTGCATCGCCACTATATCCAAACTATGCAAGAAAGAGTCCA
TCCAGAAGTTCAAAGGCACTTAGAAGATTTTCGGCAGAAACGTAGTATGGGACTGACCTTGGCTGAAAGCGAGCT
GACTAAACTTGATGCAGAGCGAGACAAGGACCGATTGACTTTGGAGAAGGAGCGGACATGTGCAGAACAGATTGT
TGCCAAAATTGAAGAAGTATTGATGACTGCTCAGGCTGTAGAGGAAGATAAGAGCTCCACCATGCAGTATGTTAT
TCTCATGTATATGAAGCATTTGGGAGTAAAAGTGAAAGAGCCTCGAAATTTGGAGCACAAACGGGGTCGGATTGG
ATTTCTTCCCAAAATCAAGCAAAGTATGAAGAAAGATAAAGAAGGGGAAGAAAAAGGGAAGCGAAGAGGATTCCC
CAGCATCCTGGGACCCCCACGGAGACCAAGCCGTCATGACAACAGTGCAATTGGCAGAGCCATGGAACTACAGAA
GGCGCGCCACCCTAAGCACTTATCCACACCCTCATCTGTGAGTCCTGAACCTCAGGACTCTGCCAAGTTGCGCCA
GAGTGGGTTAGCAAATGAAGGAACAGACGCTGGATACCTGCCTGCCAATTCCATGTCTTCTGTAGCTTCAGGGGC
CTCTTTTTCCCAGGAAGGAGGGAAAGAGAATGATACAGGATCAAAGCAAGTTGGAGAAACATCAGCACCTGGAGA
CACCTTAGATGGCACACCTCGTACTCTCAATACTGTCTTTGATTTCCCACCACCTCCATTAGACCAAGTGCAGGA
GGAGGAATGTGAAGTAGAAAGGGTGACTGAACATGGGACACCAAAGCCCTTTCGAAAGTTTGACAGTGTAGCTTT
TGGAGAAAGTCAAAGTGAGGATGAACAATTTGAAAATGACTTAGAGACAGACCCACCCAACTGGCAGCAGCTTGT
TAGTCGAGAAGTGTTACTGGGACTAAAACCTTGTGAAATCAAAAGACAGGAAGTGATTAATGAATTGTTCTACAC
TGAAAGAGCTCATGTTCGAACACTGAAGGTTCTTGATCAAGTGTTCTATCAGCGAGTATCCAGAGAAGGAATTCT
GTCACCCTCAGAGCTACGGAAAATTTTTTCAAACTTGGAAGATATTCTTCAACTTCATATTGGATTGAATGAACA
AATGAAGGCTGTTCGAAAGAGAAATGAGACCTCTGTTATCGATCAGATTGGGGAAGATTTGCTGACATGGTTCAG
CGGACCAGGAGAGGAGAAATTGAAACATGCTGCTGCTACCTTTTGCAGTAACCAACCTTTCGCCCTGGAAATGAT
CAAATCTCGTCAGAAAAAGGATTCTCGATTTCAGACTTTTGTGCAAGATGCTGAAAGTAATCCACTGTGTCGTCG
TCTTCAACTGAAGGATATTATTCCCACTCAAATGCAAAGGCTTACTAAGTACCCACTTCTGTTGGATAATATTGC
CAAATACACAGAATGGCCAACAGAAAGGGAGAAGGTGAAGAAAGCTGCAGATCACTGTCGTCAGATCTTAAATTA
TGTAAATCAGGCTGTCAAGGAGGCAGAAAACAAGCAGCGCCTAGAAGATTATCAGCGTCGCCTTGATACCTCCAG
CCTGAAGTTGTCAGAGTACCCAAATGTTGAAGAGCTCAGGAATTTGGATTTAACAAAAAGGAAGATGATTCATGA
AGGGCCATTGGTTTGGAAGGTGAATAGAGATAAAACTATTGATTTATACACGTTGCTGCTGGAAGACATTCTTGT
ATTGTTACAAAAGCAGGATGATAGACTGGTTTTAAGGTGTCATAGTAAGATTCTGGCATCTACAGCTGATAGCAA
ACACACGTTTAGCCCTGTCATTAAGTTGAGTACAGTGTTGGTTCGACAAGTGGCAACAGATAACAAAGCTTTATT
CGTCATTTCCATGTCAGACAATGGCGCTCAGATTTATGAACTGGTGGCACAGACAGTTTCTGAAAAGACTGTCTG
GCAGGACCTAATCTGTCGGATGGCTGCATCAGTGAAGGAGCAATCCACAAAGCCAATTCCATTACCACAGTCAAC
ACCTGGCGAAGGAGATAATGATGAAGAAGATCCTTCAAAATTAAAAGAGGAGCAGCATGGCATTTCAGTCACTGG
TTTGCAGAGTCCAGACAGAGATTTGGGATTAGAATCTACCTTAATATCGTCAAAACCTCAGTCTCATTCACTGAG

FIGURE 194B

TACCTCTGGGAAATCAGAGGTACGTGATCTGTTTGTGGCTGAGAGACAGTTTGCAAAGGAACAACATACAGATGG
GACACTAAAGGAAGTTGGAGAAGATTATCAAATCGCAATCCCAGATTCACACCTGCCTGTCTCAGAAGAACGGTG
GGCATTGGATGCACTAAGAAATTTGGGTTTGTTGAAGCAGTTGCTGGTGCAACAGCTAGGTTTGACTGAGAAGAG
CGTTCAGGAAGACTGGCAACATTTCCCAAGATACAGAACAGCCTCTCAGGGGCCGCAGACAGACAGTGTCATCCA
GAACTCTGAAAATATTAAGGCCTATCATTCTGGTGAAGGACATATGCCCTTTAGAACTGGAACTGGTGACATTGC
AACTTGTTACAGTCCACGGACTTCAACTGAATCTTTTGCTCCACGGGATTCAGTGGGACTGGCACCCCAGGATAG
CCAGGCAAGTAACATTTTAGTAATGGACCACATGATTATGACCCCAGAGATGCCTACCATGGAGCCAGAAGGGGG
TCTTGATGACAGTGGAGAGCACTTTTTTGATGCCCGTGAAGCACATAGTGATGAGAATCCATCAGAAGGTGATGG
AGCAGTTAACAAGGAAGAGAAGGATGTTAATTTACGCATCTCAGGAAACTATTTGATCCTTGATGGCTATGACCC
AGTGCAGGAGAGTTCCACAGATGAGGAGGTTGCTTCCTCACTTACCCTGCAGCCCATGACAGGCATCCCTGCTGT
GGAATCCACCCACCAGCAGCAACATTCTCCTCAGAATACTCACTCCGATGGGGCAATTTCACCATTCACCCCCGA
ATTTCTGGTCCAGCAGCGCTGGGGAGCTATGGAGTATTCCTGTTTTGAGATCCAGAGTCCCTCCTCTTGTGCAGA
TTCACAGAGCCAGATCATGGAGTACATTCATAAGATAGAGGCTGACCTTGAACACTTAAAGAAGGTGGAGGAAAG
TTACACCATTCTTTGCCAAAGGCTGGCTGGATCAGCCCTCACAGACAAGCACTCAGATAAAAGT**TAG**AGCCGCAT
GTCCTGGAGGTGACTGCAGGTTGTTGGATTTGGAGTATCGGCCGTGTCTCACCACATCCTGGCTCCAGTGTGGAT
GCAGAGAGAGTGTGACAGAGGATCTGCCTGTGAACCACCTGGGATTAGTCAAGTCCCAAGGTGCCCAGAGTGGGA
CTAGTTCTTCACAGTGTGGCAGCTGCACTAATCTGTTTGTGAGGGAATATCCATTCCCTCACTCTACTCTCCTCA
CTATCGGAAATTCATTTTGATTCAGAATAAAAACCAAATGTATAGAGCTTTGGGTGTAGGATATGAAATTGTACT
TAGATTTAAGAAAAAGAGAAAATCAGATGTATTTATTTGACTTCATTCCGTATTTGAAAGCACATTTTAATTTTT
ATTTGCCTTGTTTTGTTTTAATTGAGTAGTGAGAGTTTTAGACCTTTGTCTTTAGTACACCCAAGGATCAACTGC
TCCTGAAGCAAAGAGGTCAGGATGGAGTATGCAGAAGTTGGGTAGAGAGGTTAAGAAGAGGAGGAAGTGAGACGG
GGAAGGGAGGAGCACCTTGCTTCACTATACAGTATTCCAAGCTCTCTGCTGTCCAGTAGGCTGCTTCTCTGAGGG
TCACCTCAAAGGTATGCTATGCCGTGTGGCTCTTATGTGCCCAGGTGGTGTGGTCAGAGAGTGGATGGGCTTCCT
CCCGCCCTGAGGCAAGCACCTCTTCTCTGTAGCTGGGATCAACCACAATTAATAGGAATCCTCAACATACTAAAT
AGCAGGCACTTGAAAATGGGTGTGTTTTCTTCCATTGTCGTCTTTTCTATTGAGGGTTGGGATTTGGGTGGGAGA
GGAAAGCAAATTTTATTTTCTTGACTATAAATTTGTTATTCTTGGTATCATTTCATTTTTATAATTATACATTAG
ACATTGGCACTTGTGTAAAACTGTCCCTGCAGATTGAGCAGGAAGTAAAAACAAATGGAAATGCTTCGGATAGTG
GCAGGGGTGGGGGTTGCTAAGGAAAGGGTGGGATGGGAGTGGGTAAAGAGTTTGGGAAGGTTATCTAACTGAATC
ACTACTGAGTTGAATCATGGCTATCATTAGCCACAGGTACTGCTGATTATAAGGCCAGTAAAATTTTAGTACCTG
GAGGTTTGACTCTAATTTTTGCACTGATGGTGCCAAAGGGCCCTGAGTCAAAAGGATAGCCAAGGGTGGAGTGGA
AAAAGATATGGTGAAGGCAGAACTGCTCACACCAGCTCCAGAAGCACGTCCTCTGACTTCACTGCCGCAGCTCTT
TCCACACGGGGCCGTGATTGACCCTAAAAATTGCAGACCAGCACATACACTGGACACTGCAGGCAAGGTGTTGGT
AACTGCCTGCTCTAGGATGAATAGTAGCGTTAGCAGCACCCTACAGAGGGTAAGTTTCAGAATTGTAATTTGAGA
ACTCCTTCAATTATATTGACTTTCTTTGGTTTTCCTTGTGCATTAGGTATATATTTTTTGAAGTATTTTTGCCAA
CTAAAATGAAGTCTGTAAATTCTGTTAATAAACAAGGAGTTCATCCGTTGCTCACATCTTTCATTGGTGCCCTCT
GAACTCTGTGGGTTGCTAGGATGTAATTTTAATGCTTCCCTGCAGTCCAAAGATGATTTTTTCACCACAAATGGT
AAGGGATGCCCACCTACTTTTATAAACACCACTGCAACTTAACAAGTTTATTTATCTATGTCCAGATTTCTGTTT
CTGTCCTAAATTGATCTGTGTTTTTAGGTGGATCAACTTGGATCTTTAGACCTCATCTATAAATTGAAATTATAT
TTTTAGTCATAAGCCAAGTACAATCTAACTCAGAATGGGATTAAAAATTTTAGAAGCAGAAGCTAATATATAAAT
GAAGTTTGGGATTTGGAACTTTCTGTATCTCTTAGGAGGAACAAGTAAAAACCAAATGGTTACATTGTGCTGCTA
GAAATAATGTCATTCTCAATTAAAAGGGTTACACCTGTAGCCACTTGACACTAACACCATCGAGGGCAATTAATC
AGGAGAAAAGTAAATATAAAAACTTTGCTCTTAACGTCACACACTACAGGGTAATTATGTAATTCTCTAGCACTC
AATTAAGAAGCTTGTAGGTTAGCAAAATTTCAGTTTCTCTAGTTCAGCCAGTGTCTTGTCCTTAGTAATTATTTG
CTTTCCCTGCAGTTCAATTTCTCCTTGGAACTCTAACAGGACTAACTGGAAAAATACTTTGACCATAGCTCTAGT
ACTTCCAAATAAATTCATATCTAGATTTTCAAACAAAGCCCCAAGATGAAGTCTAATTCTGAAAATATCTCACAA
TTTTTGAATGTTCTTTTTATCTTACCGACCTAACTTCTCTTTTCCCTCCCAACTTGGCCTCCCACACGTTCCATT
TCATTTTGGCCATTATAGTCACATCCGTTTGACTTTGGTTGTGACATCTTCCTTTCAGGATGATGGAATTAGATG
CAGTCTGTCTTTGAGTGAGACTGGTCACCATCAGAGGAGTTTTTTCTAAGTGACGTGACTAGAAGTTGAAATCTA

FIGURE 194C

CTTCCCTGCTAAAGGGCACAGGGGTGGTGTACAAAGAAAGCTACCTTCCCAGAGCAAGCAGGCTGCATTTTAGCT
ATGGAAGTGACCTGCTGTGACACTGTGCTCTCTTCTGTGGGCTTAATGGTTCCTTTGCTATGAAGTGGCAAATTA
CATGTAGAGTGTCTCCTTCCTTTTCAGAGAACAGTTAATCAAGGCAAATCAGCAAGCCCCCAAAGTGCTGTAATT
TAACATCATGATTACCACCTTCGAAGCTATATATTTTGCATACTTTAAAATCACCTAACTTGGACTGCTTGAATT
ACATTGGCTTTTAGAACCGAAATTGTAACTATGTATTGTATTTCATGGGAGGTATATTTTATGAGCTTTTTGGCT
TTCTTTTTTCCCACAGCAACTGCCAATGAAGGATGAATCCCCTTTTTAAAAAGTTGTTGTTGTTGTTTATTT
GATTTTGAGTTAGGAGGGATAATAGAGAAGTCCATTTAAAAATTATTTTTAGAAGCTAAAGAAAGTAATTATGCT
TCCTGTGAATTGTCTTTTACTGGCATCTTTGTTTTCCTCTTTGATGTTAGTAAATTTGGTGTAATACGTGGGGCT
TCCATATTTCAAAGTGGAAGCTTTCTTCTCTGAAGTCGATATATGGTTTTGAATTACTAGAGCTTTGGTCAGTAT
TTCCTTCCCTATATGTCACAGAGGGCACCACTGAGAACTGCGTGCATAGGACCTCAAAATACAAAATTAGCAGGG
CCTCACAGTCAGCTTCCTCATGGCTAGTTTTTCCCCCTTATATTACAATTTTTGTTTTATAAGTCATTTTTTTCC
TGATATTTCCACCACTTTTCAGAGTCATCTACAAAATTTTTCTTTCCTCAAGAAAAGAGTTCCTTTTGCCTTATT
CCTTATGCCTTCCCCACTGGTATTGAGGGTTTTGATAATAAATTGGTAGGAAAAAAAAGTACCTCCTAGAAGGAA
GCCTTCCCCACCATTTCCAGGTGCCAACTGCTAAGCAGATATATTCCAAAAATGGTAACTGTCATGTGCACACTG
TTGGTTATTTTTAATAAGCCTCTTCCTACTAGAACATTTTATTTTCCTTGTTCACCATACAATCATGTACTCTTT
AACAGAAATTGCTTTTAAAAAATATCTGGAACTATCTTTAAAAAAACTTTATTAATAATCATGTATTTTTACTGA
TCACATTTTGAAATGCCTAAAAGACTTTATTGTTCTAATTATCCAGATGTACCTTTGTAAAATAGCTCTTTTATG
AATTAGCTGATAAGGCTGTATGTTTCTGGAACAAAATATTGGTCATCTAAAAACTTTCTGTTTTCTGGGGTCTGG
GAAAATAGAAAATAAGATTTCAAATATTAAATAAGCTTAAAGGAACCAAGCATGTGACTTTTACTTTGTATTCTG
GTTGATTTGTCTTGTCCAAGTTATATTAGAAAAGTTGAGGAGTCGAGGAGCCTGTAATTAATTTTCCTGTCAGTG
ACTGTCAGACATCTTCCTGCTTATTAGAGCATCCCTAGCAACAAGGCTAAACCTTCATGACAGTGCTGGCAGGTG
GGCTTGCCCTAGCATGTGGGGCAGGTTTGTTGTTTTTTTAATAGCTTTATTGAGATATTCACATATCATATAATT
CATCCATTTAAAGTGTATAATCAGATGGGTTTTGGTATATTATTGATTTTTAATTGTGGTGAAATATATATATAA
CAAAATTTGCTATTGTAACTATTTTTAAGTATAAAGTTCAGTGAGGTAGGCCAGCTTTTATGACGCACCTGAAGA
TAACTTTGGTTTTAATCCTACCCTAAATGAAGCATATGCCTCTATTTTTCCTGTCCCCAGTGCTGGGCTTCTTCA
CATACCAACATTTCTGTGCTTTTACCAACAGCATTTTAGCTCAGAAGGCTCGCTTACTTTGGGCATTTGCTGTAT
TTTGGTTTTGAAATACTTGTAATTTGACTTATTCTTGGGATAATATTTTAGTTTTCAGTCATTCAAGGGCACATT
TGGCTGACGGAGCTAATAAGCGTAATAAAATGCTTAGTAGTTTATACCATCTTTTAGTTAAACATTTTAAAGATT
AAGACTATTCAAATGTACTTTGCGGAAATTAACCTGTTTGTATGCCTGGCTTTGTTTACAAACATATATCTATAT
CTATATATATAGATACAGATACAGATACATATCTGGTGGAACAAAGAAATACCTGTACCATTCCCACTTGCTCTT
TGATAGCCACCTCCTAGGAATGGAGACAATAAAACTCTGTATTTGCATGTG

FIGURE 195

MSGTQSTITDRFPLKKPIRHGSILNRESPTDKKQKVERIASHDFDPTDSSSKKTKSSSEESRSEIYGLVQRCVII
QKDDNGFGLTVSGDNPVFVQSVKEDGAAMRAGVQTGDRIIKVNGTLVTHSNHLEVVKLIKSGSYVALTVQGRPPG
SPQIPLADSEVEPSVIGHMSPIMTSPHSPGASGNMERITSPVLMGEENNVVHNQKVEILRKMLQKEQERLQLLQE
DYNRTPAQRLLKEIQEAKKHIPQLQEQLSKATGSAQDGAVVTPSRPLGDTLTVSEAETDPGDVLGRTDCSSGDAS
RPSSDNADSPKSGPKERIYLEENPEKSETIQDTDTQSLVGSPSTRIAPHIIGAEDDDFGTEHEQINGQCSCFQSI
ELLKSRPAHLAVFLHHVVSQFDPATLLCYLYSDLYKHTNSKETRRIFLEFHQFFLDRSAHLKVSVPDEMSADLEK
RRPELIPEDLHRHYIQTMQERVHPEVQRHLEDFRQKRSMGLTLAESELTKLDAERDKDRLTLEKERTCAEQIVAK
IEEVLMTAQAVEEDKSSTMQYVILMYMKHLGVKVKEPRNLEHKRGRIGFLPKIKQSMKKDKEGEEKGKRRGFPSI
LGPPRRPSRHDNSAIGRAMELQKARHPKHLSTPSSVSPEPQDSAKLRQSGLANEGTDAGYLPANSMSSVASGASF
SQEGGKENDTGSKQVGETSAPGDTLDGTPRTLNTVFDFPPPPLDQVQEEECEVERVTEHGTPKPFRKFDSVAFGE
SQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEIKRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSP
SELRKIFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSGPGEEKLKHAAATFCSNQPFALEMIKS
RQKKDSRFQTFVQDAESNPLCRRLQLKDIIPTQMQRLTKYPLLLDNIAKYTEWPTEREKVKKAADHCRQILNYVN
QAVKEAENKQRLEDYQRRLDTSSLKLSEYPNVEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDNKALFVISMSDNGAQIYELVAQTVSEKTVWQD
LICRMAASVKEQSTKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLGLESTLISSKPQSHSLSTS
GKSEVRDLFVAERQFAKEQHTDGTLKEVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLTEKSVQ
EDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMPFRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQA
SNILVMDHMIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNKEEKDVNLRISGNYLILDGYDPVQ
ESSTDEEVASSLTLQPMTGIPAVESTHQQQHSPQNTHSDGAISPFTPEFLVQQRWGAMEYSCFEIQSPSSCADSQ
SQIMEYIHKIEADLEHLKKVEESYTILCQRLAGSALTDKHSDKS

FIGURE 196

GAGTTCCAGCAGTCCGCGAGCTGCCGTCGGCTCCGCGGGGGGGGCGGGCCGGGCACCCCGGGGCGCGGAGGAGCG
CTCCTCGCTTCTCTCCTTCCCCCCTGCCGCACTCCGCCGGACCCTCCCGCCGGCCCGCGCCGCTGCACTCGCCCT
CTCCTCTCGCCCCCCGGCAAACTTTCGGCCCCTCCCCGCCCCTCGCCCGTTATTCGTCGTGGCTCAAGCCCGGCC
ACGCCGCCCCAAGGGCTCCTCCCGACCTCCCGGCCTGCCGCTCCGGCCACTGCGGGATCCAGAAAC**ATG**TCGACC
ACACTTCTGTCCGCCTTCTACGATGTCGACTTCTTGTGCAAGACAGAGAAATCCCTGGCCAACCTCAACCTGAAC
AACATGCTGGACAAGAAGGCGGTGGGGACGCCTGTGGCCGCCGCCCCCAGCTCGGGCTTCGCGCCGGGATTCCTC
CGACGGCACTCGGCCAGCAACCTGCATGCACTCGCCCACCCCGCGCCCAGCCCCGGCAGCTGCTCGCCCAAGTTC
CCGGGCGCCGCTAACGGCAGCAGCTGCGGCAGCGCGGCGGCCGGCGGTCCGACCTCCTACGGCACCCTTAAGGAG
CCGTCGGGGGGCGGCGGCACAGCCCTGCTCAACAAGGAGAACAAATTCCGGGACCGCTCGTTTAGCGAGAACGGC
GATCGCAGCCAGCACCTCCTGCACCTGCAGCAGCAGCAGAAGGGGGGCGGCGGCTCCCAGATCAACTCCACGCGC
TACAAGACCGAGCTGTGCCGGCCCTTCGAGGAGAGCGGCACGTGCAAGTACGGCGAAAAGTGCCAGTTCGCGCAT
GGCTTCCACGAGCTGCGCAGCCTGACTCGCCATCCGAAGTACAAGACCGAGCTGTGCCGCACCTTTCATACCATC
GGCTTCTGCCCCTATGGGCCGCGCTGCCACTTCATCCACAACGCGGACGAGCGGCGGCCCGCGCCGTCGGGGGGC
GCCTCCGGGGACCTGCGTGCCTTTGGCACGCGCGATGCGTTGCACCTGGGCTTCCCGCGGGAGCCGCGGCCCAAG
TTGCACCACAGCCTCAGCTTCTCGGGCTTCCCGTCGGGCCACCATCAGCCCCCGGGCGGCCTCGAGTCGCCGCTG
CTGCTCGACAGCCCCACGTCGCGCACGCCGCCGCCGCCCTCCTGCTCTTCGGCCTCGTCCTGCTCCTCCTCCGCC
TCCTCCTGTTCCTCGGCCTCCGCGGCCTCCACGCCCTCGGGCGCCCCGACATGCTGCGCCTCCGCGGCGGCCGCG
GCTGCGGCCGCTCTGCTGTACGGCACCGGGGGCGCCGAGGACCTGCTGGCGCCGGGGGCCCCGTGCGCGGCCTGC
TCGTCGGCCTCGTGCGCCAACAACGCCTTCGCCTTCGGTCCGGAGCTCAGCAGCCTCATCACGCCGCTCGCCATC
CAGACCCACAACTTTGCCGCCGTGGCCGCCGCCGCCTACTACCGCAGTCAGCAGCAGCAGCAGCAGCAGGGCCTG
GCGCCCCCCGCGCAGCCGCCGGCGCCGCCCAGCGCGACCCTCCCCGCCGGGGCCGCCGCACCTCCCTCGCCGCCC
TTCAGCTTCCAGCTGCCGCGCCGCCTGTCCGACTCGCCCGTGTTCGACGCGCCCCCCAGCCCCCCGGACTCGCTG
TCGGACCGCGACAGCTACCTAAGCGGCTCCCTGAGCTCCGGCAGCCTCAGCGGCTCTGAGTCTCCCAGCCTCGAC
CCTGGCCGCCGCCTGCCAATCTTCAGCCGCCTCTCCATCTCCGACGAC**TGA**GGCAAGAGGGCGCCAGTGAGGAGG
AAGGGAAGGCGGTTCAGAGATGTTGGAGGACACCCCTCGCCATCTCGCCCTTGCTGGGGGCACGGGAGTGGGGGG
GGTGACATGGGCCCTAGGCAGACTGCAAGCCCGACCGAGCACTTGGACTCGAACTCTGTGCCGGGAGGGGCCCCC
ACCCCTCCTTTTTCGGTTTCCTCTTGTCTTTTTTTTTTTATTTTTATTACGAAGTTTCATTCTTTTTGAGCAAAA
AAGTCGAACTTTTTCTGTTGAACAAAATATTCACAACAGGGCAGTTGTGATACGAATAGAACAAAAAAAAAAAAA
AAACACTTAAACTTTGTTAGGACTCCGATGAGTTTGGGACTTCAGGAAAAATCAACCCAGCACCAGCAGCTACCA
ACCACCATTCCATCTCTTCACTTGAACAGCATTAGTTAAGTCCAGATGTGGGAACCCTTCTCTTGGAAGAAGTTC
CTAATTGTGTCTCAGACCGGTGTAAACAAACCAGCCAGCCGCCACCTTGCTAAACCTATAAGCTTTTTAAAATCC
AATATATTCTGCCAAGAATATGCCTTGATAGTTAGCCCTCAGCCCATAGGTGTTTTTTGTTTTTTAACAGAATTA
TATATGTCTGGGGGTGAAAAAACCCTTGCATTCCAAAGGTCCATACTGGTTACTTGGTTTCATTGCCACCACTTA
GTGGATGTTCAGTTTAGAACCATTTTGTCTGCTCCCTCTGGAAGCCTTGCGCA

FIGURE 197

MSTTLLSAFYDVDFLCKTEKSLANLNLNNMLDKKAVGTPVAAAPSSGFAPGFLRRHSASNLHALAHPAPSPGSCS
PKFPGAANGSSCGSAAAGGPTSYGTLKEPSGGGGTALLNKENKFRDRSFSENGDRSQHLLHLQQQQKGGGGSQIN
STRYKTELCRPFEESGTCKYGEKCQFAHGFHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFIHNADERRPAP
SGGASGDLRAFGTRDALHLGFPREPRPKLHHSLSFSGFPSGHHQPPGGLESPLLLDSPTSRTPPPPSCSSASSCS
SSASSCSSASAASTPSGAPTCCASAAAAAAAALLYGTGGAEDLLAPGAPCAACSSASCANNAFAFGPELSSLITP
LAIQTHNFAAVAAAAYYRSQQQQQQQGLAPPAQPPAPPSATLPAGAAAPPSPPFSFQLPRRLSDSPVFDAPPSPP
DSLSDRDSYLSGSLSSGSLSGSESPSLDPGRRLPIFSRLSISDD

FIGURE 198A

CAGATTTACGAGGTTCTGTTCTAGTGCCAAAGGCTCTTGGTAGTAAATAGTGAGCAAAATAGATACCTGTCTCCT
GATGGATCTTGCCAGCCCCNTCCNTATTTTTTNTTAAGTTATTTATTAAAACCACACACACCTTGCAAAGAAAAA
GGGAAACTGGCAGTCTCTGTAGAGGAAGCCGGTGGCATCGCTCAGAGCCACAAACTGTATTTCTAAACAGCCCTT
TCCCTGGTTCCCTCTCTCCTGCCCCACTTTTTTTAAAATCCAGACTGTAAAAAACACATCTACTGACACTCACTT
TACTTTAAAAAAAGAAGAGAAAAAGTAAAGCGTTACAAGACTTTCCTCCTGGAAACTATAAACTGAAAAAAAAAT
CCATAAAAGATTAAATCCTGGCGGGTTGTGGGGTGGCGGGGGCCGGCGGGGAGGGGGCGCGGAGTGGAGATTGGC
TCTCTGAGGTGGTCAGGGGCCCTGTGACAGCTTGGGACTTTCAGCACCTGGTTTGGGGTCATTTATCTGCTCAAC
TGTCAGGACCCCCCACCCCCAAACCCCAGCCACCAACACAACCATCGTAGAAGGGAACACAACACAGAGGGTCTT
TTTTCATTTTTTTAAAAAATCGGTTTGGTTGTGTTTTTGTTTTCCATGGGGGAGCTTTAAAACTCATTATTGCAA
CACTAGTTCCATTTTTCGCCAGGGTTCCAATAACACGGCATCATAAAGGCAACGCAACCCACAGTTCTCAAGACA
TTTACCACGGTCACTACATCCGGCAGCGGGGTGGCCCCTAGCTCCTGCTGCCCCCCCGCCCTTTCTCCCCGCCCG
CCCCCGGAGCTCAGCCGATTTCTGAGGCTCCAACTCTACCCACTCCCTCCCCGGGCCGCCGCCGCCGCGCCTTCC
CCCATTCTTACTCCCTCGAGGAGAGCCACAGGTTGCAAATCCAACCAACCTCGCAATCTATTTTTGCAAAATCAC
TCACAAAGATCTCCCTTTCGCGCCCGCGCCCGCTCCTCCCGCGCCGGGTCCCCTCAGCCACGGCCACAAAGTGCC
CTTCTCTCCTCCTGAGTCTTGCACATAAGGAACGCGGGCTGGGGCTCTGTTCGTCTTTCTCCTCGCCCAAGGTAA
GGACCTCGGGAATCTGAAGCCTGGCGTCCACTACGCTCAGGCCCGCAGTTCCCTTTTTACAGAGCTTGCACCATG
GGAAAAAATAAAATAAAATTTAGGAAAGGGAGGCAACAGCCATTGGGAGCCAACACAGAGTCACGCAGCGCCCAA
AATACAAACACCGCAGCGGCCAGAAATCCCGCCACCTTTCTCGTTCTCCCAGGCTGTCCTGTCGAGGTTCCCTGA
GTCCCCCCCGCACACTGAAAGGCATCGCAGGTGCAGTGCGCACCCCTTTCCCACCCACCCCAAGAAGCCCTGTCCC
GCCATCAGTCTCTCTCCTCGGGATGAGCAGGGAGAGCGCGCGGAGGTTCCCGACTCCCTCGACTACAACCAAGAA
AGAATAATTTTCAAAGTGTTCAACATCCCCGCCCCCAAGCTCCCCAAAACACAGGGGCAGGGAACACCAAAACAC
TCGGCTCTCGTTAGGAAGATCACGGCTCTGAAAGGAAATAGTAGACACGATACTTCATCTCATCTGGATTTATGA
CCAAAAAAACAAAAACAAAAACCCAAAGAGTTCGCTTGCATTTTTTCCTTCCAAATCTCGGTTCGGCTCGAAGGC
AGGGAATCTAAAAGACCGAGGCCG**ATG**GAAGAGAGCCAGCGGGGCGAGCGAGCGGGCAGCCTCCCTTTTTGCCTC
CCGGAGTCACCCGTTATTCGTCGTGGCTCAAGCCCGGCCACGCCGCCCCAAGGGCTCCTCCCGACCTCCCGGCCT
GCCGCTCCGGCCACTGCGGGATCCAGAAACATGTCGACCACACTTCTGTCCGCCTTCTACGATGTCGACTTCTTG
TGCAAGACAGAGAAATCCCTGGCCAACCTCAACCTGAACAACATGCTGGACAAGAAGGCGGTGGGGACGCCTGTG
GCCGCCGCCCCCAGCTCGGGCTTCGCGCCGGGATTCCTCCGACGGCACTCGGCCAGCAACCTGCATGCACTCGCC
CACCCCGCGCCCAGCCCCGGCAGCTGCTCGCCCAAGTTCCCGGGCGCCGCTAACGGCAGCAGCTGCGGCAGCGCG
GCGGCCGGCGGTCCGACCTCCTACGGCACCCTTAAGGAGCCGTCGGGGGGCGGCGGCACAGCCCTGCTCAACAAG
GAGAACAAATTCCGGGACCGCTCGTTTAGCGAGAACGGCGATCGCAGCCAGCACCTCCTGCACCTGCAGCAGCAG
CAGAAGGGGGGCGGCGGCTCCCAGATCAACTCCACGCGCTACAAGACCGAGCTGTGCCGGCCCTTCGAGGAGAGC
GGCACGTGCAAGTACGGCGAAAAGTGCCAGTTCGCGCATGGCTTCCACGAGCTGCGCAGCCTGACTCGCCATCCG
AAGTACAAGACCGAGCTGTGCCGCACCTTTCATACCATCGGCTTCTGCCCCTATGGGCCGCGCTGCCACTTCATC
CACAACGCGGACGAGCGGCGGCCCGCGCCGTCGGGGGGCGCCTCCGGGGACCTGCGTGCCTTTGGCACGCGCGAT
GCGTTGCACCTGGGCTTCCCGCGGGAGCCGCGGCCCAAGTTGCACCACAGCCTCAGCTTCTCGGGCTTCCCGTCG
GGCCACCATCAGCCCCCGGGCGGCCTCGAGTCGCCGCTGCTGCTCGACAGCCCCACGTCGCGCACGCCGCCGCCG
CCCTCCTGCTCTTCGGCCTCGTCCTGCTCCTCCTCCGCCTCCTCCTGTTCCTCGGCCTCCGCGGCCTCCACGCCC
TCGGGCGCCCCGACATGCTGCGCCTCCGCGGCGGCCGCGGCTGCGGCCGCTCTGCTGTACGGCACCGGGGGCGCC
GAGGACCTGCTGGCGCCGGGGGCCCCGTGCGCGGCCTGCTCGTCGGCCTCGTGCGCCAACAACGCCTTCGCCTTC
GGTCCGGAGCTCAGCAGCCTCATCACGCCGCTCGCCATCCAGACCCACAACTTTGCCGCCGTGGCCGCCGCCGCC
TACTACCGCAGTCAGCAGCAGCAGCAGCAGCAGGGCCTGGCGCCCCCCGCGCAGCCGCCGGCGCCGCCCAGCGCG
ACCCTCCCCCGCCGGGGCCGCCGCACCTCCCTCGCCGCCCTTCAGCTTCCAGCTGCCGCGCCGCCTGTCCGACTCG
CCCGTGTTCGACGCGCCCCCCCAGCCCCCCCGGACTCGCTGTCGGACCGCGACAGCTACCTAAGCGGCTCCCTGAGC
TCCGGCAGCCTCAGCGGCTCTGAGTCTCCCAGCCTCGACCCTGGCCGCCGCCTGCCAATCTTCAGCCGCCTCTCC
ATCTCCGACGAC**TGA**GGCAAGAGGGCGCCAGTGAGGAGGAAGGGAAGGCGGTTCAGAGATGTTGGAGGACACCCC
TCGCCATCTCGCCCTTGCTGGGGGCACGGGAGTGGGGGGGGTGACATGGGCCCTAGGCAGACTGCAAGCCCGACC
GAGCACTTGGACTCGAACTCTGTGCCGGGAGGGGCCCCCACCCCTCCTTTTTCGGTTTCCTCTTGTCTCTTTTTT

FIGURE 198B

TTTATTTTTATTACGAAGTTTCATTCTTTTTGAGCAAAAAAGTCGAACTTTTTCTGTTGAACAAAATATTCACAA
CAGGGCAGTTGTGATACGAATAGAACAAAAAAGAAAAAAAAAACACTTAAACTTTGTTAGGACTCCGATGAGTTT
GGGACTTCAGGAAAAATCAACCCAGCACCAGCAGCTACCAACCACCATTCCATCTCTTCACTTGAACAGCATTAG
TTAAGTCCAGATGTGGGAACCCTTCTCTTGGAAGAAGTTCCTAATTGTGTCTCAGACCGGTGTAAACAAACCAGC
CAGCCGCCACCTTGCTAAACCTATAAGCTTTTTAAAATCCAATATATTCTGCCAAGAATATGCCTTGATAGTTAG
CCCTCAGCCCATAGGTGTTTTTTGTTTTTTAACAGAATTATATATGTCTGGGGGTGAAAAAACCCTTGCATTCCA
AAGGTCCATACTGGTTACTTGGTTTCATTGCCACCACTTAGTGGATGTTCAGTTTAGAACCATTTTGTCTGCTCC
CTCTGGAAGCCTTGCGCAGAGCTTACTTTGTAATTGTTGGAGAATAACTGCTGAATTTTTAGCTGTTTTGAGTTG
ATTCGCACCACTGCACCACAACTCAATATGAAAACTATTTAACTTATTTATTATCTTGTGAAAAGTATACAATGA
AAATTTTGTTCATACTGTATTTATCAAGTATGATGAAAAGCAATAGATATATATTCTTTTATTATGTTAAATTAT
GATTGCCATTATTAATCGGCAAAATGTGGAGTGTATGTTCTTTTCACAGTAATATATGCCTTTTGTAACTTCACT
TGGTTATTTTATTGTAAATGAGTACAAAATTCTTAATTTAAGAGATTGTATGTAATATTTATTTCATTAATTTCT
TTCCTTGTTTACGTAAATTTTGAAAGATTGCATGATTTCTTGACAGAAATCGATCTTGATGCTGTGGAAGTAGTT
TGAGGAACATCCTATGAGTTTTCTTAGAATGTATAAAGGTTGTAGCCCATCCAACTTCAAAGAAAAAAATGACCA
CATACTTTGCAATCAGGCTGAAATGTGGCATGCTTTTCTAATTCCAACTTTATAAACTAGCAAAAAAGTGTTTGC
TTATTCCACCAGTTCTACTGTGACATACTCGAGTATAAAGACATGTAGCAATAACGGGGAGTGGGGGGGGAGTCT
CACAGTGCCTTTGGAAGGGCCCGAACTTGCCTTAAATCTTCCTCAACCAAATAAGTATTTTATTAGTGCTTGAGA
GAATCTGAATGTAGGATGGGTTCAACTGCACAAAAGGAAAAGATTTTTACCACTTTTTTTATATAGATATAAAGT
GAAGCAACCGCCTTAGTGCTGAAATATGTAGTACATGAATATGCCTTGTTTAATTACAGAAAATTCCAAAACTTG
TACTATTTTTTTTTTCCATGTAGAAAGGCAGGAATGTCTCCTAAGCTTTCCTGGACAGCAGATGAATGAGCGGTA
GCTTTAGTTTGTACGTAGGTACAGTTGGAGCACTATATGTACTCTCTGGACTACTTTGGACAGAAGTAGGTTTTT
GAATGTAACAAGATAAGTCAACTTGAGTTGTAATATATTTTGGGGAATCAGCTCACTACAAATTGTGACTGTAAA
CATTGTACTGTAAATGTTTTGTAGTTTTCCCCCAATAAAATTTTTGGGAAAAAAAGGTATTAACATGTAAGAGCT
TTCTTTTTAAACAGGAATGTCTTAGCTTTCTAGCTTCCCAGCTAACCATGTCTGCCATTCCCCAGGTCTTGGCAT
GGTGGGGGAGGACTTGGAGAGCTGGCAGAGCCAGAGTTCAGAAGAGCCTGCGTCCTCTCAGCCCGTATATATTTT
ATAAGCAAGTTCTTCTAATGAAAGAAAGTAATTATTTGGACTGTCAAGGGCATTAGTT

FIGURE 199

MEESQRGERAGSLPFCLPESPVIRRGSSPATPPQGLLPTSRPAAPATAGSRNMSTTLLSAFYDVDFLCKTEKSLA
NLNLNNMLDKKAVGTPVAAAPSSGFAPGFLRRHSASNLHALAHPAPSPGSCSPKFPGAANGSSCGSAAAGGPTSY
GTLKEPSGGGGTALLNKENKFRDRSFSENGDRSQHLLHLQQQQKGGGGSQINSTRYKTELCRPFEESGTCKYGEK
CQFAHGFHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFIHNADERRPAPSGGASGDLRAFGTRDALHLGFPR
EPRPKLHHSLSFSGFPSGHHQPPGGLESPLLLDSPTSRTPPPPSCSSASSCSSSASSCSSASAASTPSGAPTCCA
SAAAAAAAALLYGTGGAEDLLAPGAPCAACSSASCANNAFAFGPELSSLITPLAIQTHNFAAVAAAAYYRSQQQQ
QQQGLAPPAQPPAPPSATLPAGAAAPPSPPFSFQLPRRLSDSPVFDAPPSPPDSLSDRDSYLSGSLSSGSLSGSE
SPSLDPGRRLPIFSRLSISDD

FIGURE 200

GTCGTGGAAGCAGGACTGCGCCGCGTCTTCCTCAAGGTGGGGTTCGGGGGGCCACCGAATCGCTGTCACGCCGGC
AGGTTGAGAACAAAAACATGCACCTGGAGTTTCCCCGGAGCCCTCTGCGTGGTTGAGCTTCGGTGGAATTTCGGG
GCTCTTGGCTGCCAGCCGCGCTTGCCTGGTAGCAACAGAAACCAGTCCTGCTCTCCTCCGTGGACATTTCATTAC
CATCCAGAAGTGTCTCCCACTGAAGGCATCCGTGGTTGTTTTTAAGCCACAAAAAAGCCACACCCAAGATCACCT
GACACCCACCCTGACAAGTGTCC**ATG**ATGCTGGGCCCTGAGGGAGGTGAAGGCTTTGTGGTCAAGCTCCGTGGCC
TGCCCTGGTCCTGCTCTGTTGAGGACGTGCAGAACTTCCTCTCTGACTGCACGATTCATGATGGGGCCGCAGGTG
TCCATTTCATCTACACTAGAGAGGGCAGGCAGAGTGGTGAGGCTTTTGTTGAACTTGGATCAGAAGATGATGTAA
AAATGGCCCTGAAAAAAGACAGGGAAAGCATGGGACACCGGTACATTGAGGTGTTCAAGTCCCACAGAACCGAGA
TGGATTGGGTGTTGAAGCACAGTGGTCCCAACAGTGCCGACAGCGCCAACGATGGCTTCGTGCGGCTTCGAGGAC
TCCCATTTGGATGCACAAAGGAAGAAATTGTTCAGTTCTTCTCAGGGTTGGAAATTGTGCCAAACGGGATCACAT
TGCCTGTGGACCCCGAAGGCAAGATTACAGGGGAAGCGTTCGTGCAGTTTGCCTCGCAGGAGTTAGCTGAGAAGG
CTCTAGGGAAACACAAGGAGAGGATAGGGCACAGGTACATTGAGGTGTTTAAGAGCAGCCAGGAGGAAGTTAGGT
CATACTCAGATCCCCCTCTGAAGTTCATGTCCGTGCAGCGGCCAGGGCCCTATGACCGGCCCGGGACTGCCAGGA
GGTACATTGGCATCGTGAAGCAGGCAGGCCTGGAAAGGATGAGGCCTGGTGCCTACAGCACAGGCTACGGGGGCT
ACGAGGAGTACAGTGGCCTCAGTGATGGCTACGGCTTCACCACCGACCTGTTCGGGAGAGACCTCAGCTACTGTC
TCTCCGGGATGTATGACCACAGATACGGCGACAGTGAGTTCACAGTGCAGAGCACCACAGGCCACTGTGTCCACA
TGAGGGGCCTGCCGTACAAAGCGACCGAGAACGACATTTACAACTTCTTCTCTCCTCTCAACCCTGTGAGAGTCC
ATATTGAGATTGGCCCAGATGGAAGAGTGACGGGTGAAGCAGATGTTGAGTTTGCTACTCATGAAGAAGCTGTGG
CAGCTATGTCCAAAGACAGGGCCAATATGCAGCACAGATATATAGAACTCTTCTTGAATTCAACAACAGGGGCCA
GCAATGGGGCGTATAGCAGCCAGGTGATGCAAGGCATGGGGGTGTCTGCTGCCCAGGCCACTTACAGTGGCCTGG
AGAGCCAGTCAGTGAGTGGCTGTTACGGGGCCGGCTACAGTGGGCAGAACAGCATGGGTGGCTATGAC**TAG**TTTT
GTTAGGAACATTTGAGTTACTTCAATCATTTTCACAGGCAGCCAACAAGCAATTAAGAGCAGTTATAATAGAGGA
AGCTGGGGGACCCATTTTGCACCATGAGTTTGTGAAAAATCTGGATTAAAAAATTACCTCTTCAGTGTTTTCTCA
TGCAAAATTTTCTTCTAGCATGTGATAATGAGTAAACTAAAACTATTTTCAGCTTTTCTCAATTAACATTTTGGT
AGTATACTTCAGAGTGATGTTATCTAAGTTTAAGTAGTTTAAGTATGTTAAATGTGGATCTTTTACACCACATCA
CAGTGAACACACTGGGGAGACGTGCTTTTTTGGAAAACTCAAAGGTGCTAGCTCCCTGATTCAAAGAAATATTTC
TCATGTTTGTTCATTCTAGTTTATATTTTCATTTAAAATCCTTTAGGTTAAGTTTAAGCTTTTTAAAAGTTAGTT
TTGAGAATTGAGACACAATACTAATACTGTAGGAATTGGTGAGGCCTTGACTTAAAACTTTCTTTGTACTGTGAT
TTCCTTTTGGGTGTATTTTGCTAAGTGAAACTTGTTAAATTTTTTGTTAACTAAATTTTTTTCTTAAAATAAAGA
CTTTTTCACAATGACTGGCACAGATTACTCAGCAAAAGATAGCAAAACGGGTGGTTGAAGATAATTCATTTTAAT
CGTAATGTATTTTAGTGTGAATTTAAAAATTTCATACATCAAATCTATGATCTCCCTTATATTCTTATGATGAGG
CTAAATAAAAGTCTAATAAAAATGTTAAATATGTGAATGGTGGAAATGGTGACTAGCAGCACACATTCTGGGAAG
CATCAAATAGACACACGGCCCCAGCCACCTGCAACTTATGTGCACTGTTGTAAACCATTCAGAATTTTCCTGCTA
GGCCCTTGATGCTGGAGTCACATCTGTTGATAGCTGGAGAACTTTAGTTTCAAGTACTACATTGTGAAAGCAATT
ATTTTGTTTCTCGTTTTTATAAAATGCTGACTTAAACTTTT

FIGURE 201

MMLGPEGGEGFVVKLRGLPWSCSVEDVQNFLSDCTIHDGAAGVHFIYTREGRQSGEAFVELGSEDDVKMALKKDR
ESMGHRYIEVFKSHRTEMDWVLKHSGPNSADSANDGFVRLRGLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK
ITGEAFVQFASQELAEKALGKHKERIGHRYIEVFKSSQEEVRSYSDPPLKFMSVQRPGPYDRPGTARRYIGIVKQ
AGLERMRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGRDLSYCLSGMYDHRYGDSEFTVQSTTGHCVHMRGLPYKA
TENDIYNFFSPLNPVRVHIEIGPDGRVTGEADVEFATHEEAVAAMSKDRANMQHRYIELFLNSTTGASNGAYSSQ
VMQGMGVSAAQATYSGLESQSVSGCYGAGYSGQNSMGGYD

FIGURE 202

GGCACGAGGCG**ATG**GAGCCGGGGCGCCGGGGGGCCGCGGCGCTGCTAGCGCTGCTGTGCGTGGCCTGCGCGCTGC
GCGCCGGGCGCGCCCAATACGAACGCTACAGCTTCCGCAGCTTCCCACGGGACGAGCTGATGCCGCTCGAGTCGG
CCTACCGGCACGCGCTGGACAAGTACAGCGGCGAGCACTGGGCCGAGAGCGTGGGCTACCTGGAGATCAGCCTGC
GGCTGCACCGCTTGCTGCGCGACAGCGAGGCCTTCTGCCACCGCAACTGCAGCGCCGCGCCGCAGCCCGAGCCCG
CCGCCGGCCTCGCCAGCTATCCCGAGCTGCGCCTCTTCGGGGGCCTGCTGCGCCGCGCGCACTGCCTCAAGCGCT
GCAAGCAGGGCCTGCCAGCCTTCCGCCAGTCCCAGCCCAGCCGCGAGGTGCTGGCGGACTTCCAGCGCCGCGAGC
CCTACAAGTTCCTGCAGTTCGCTTACTTCAAGGCAAATAATCTCCCCAAAGCCATCGCCGCTGCTCACACCTTTC
TACTGAAGCATCCTGATGACGAAATGATGAAGAGGAACATGGCATATTATAAGAGCCTGCCTGGTGCCGAGGACT
ACATTAAAGACCTGGAAACCAAGTCATATGAAAGCCTGTTCATCCGAGCAGTGCGGGCATACAACGGTGAGAACT
GGAGAACATCCATCACAGACATGGAGCTGGCCCTTCCCGACTTCTTCAAAGCCTTTTACGAGTGTCTCGCAGCCT
GCGAGGGTTCCAGGGAGATCAAGGACTTCAAGGATTTCTACCTTTCCATAGCAGATCATTATGTAGAAGTTCTGG
AATGCAAAATACAGTGTGAAGAGAACCTCACCCCAGTTATAGGAGGCTATCCGGTTGAGAAATTTGTGGCTACCA
TGTATCATTACTTGCAGTTTGCCTATTATAAGTTGAACGACCTGAAGAATGCAGCCCCCTGTGCAGTCAGCTATC
TGCTCTTTGATCAGAATGACAAGGTCATGCAGCAGAACCTGGTGTATTACCAGTACCACAGGGACACTTGGGGCC
TCTCGGATGAGCACTTCCAGCCCAGACCTGAAGCAGTTCAGTTCTTTAATGTGACCACACTCCAGAAGGAGCTGT
ATGACTTTGCTAAGGAAAATATAATGGATGATGATGAGGGAGAAGTTGTGGAATATGTGGATGACCTCTTGGAAC
TGGAGGAGACCAGC**TAG**CCCACAGCAACCAAAGAGACTTCCTCTTGGCGTTCAGGAAACACAGATTCTTTGTCCT
TTTCCCAACAGCCCAGGCTGTTGATACCTCAGAGCCTTCTCTTTACTCTCCAAAGTGAAAGGGAAGCCCCCGTCT
CTCTAACTGCATGTCATCAGGGGTGAGCCTGCCTTTCCTATCTTCACACCTGCCACCTCATGTTCACACCTATCT
TTCTCACCTTTTTTTTGAGATGGAGTCTCGCTCTCTTGCCCAGGCTGGAGTGCAATGGCACGTTCTCAGCTCACT
GCAACCTCCGCCTCTTGGGTTCAAGCAATTCTGCTGCATCAGCCTCCCGAGTACCTGGGATTACAGGCATGTGCC
ACCACGCCCGGCTAATTTTGTATTTTTAAGTAAGAGACGGGGTTTTGCCATGTTGGCCAGGCTGGTCTCGAACTC
TTGACTTCAGATGATCCATCTGCCTTGGGCCTCCCACAGTGCTGGGATTACAGGCGTGAGCCACCATGCCCGGCC
TCTTTCTCACCTTTACACCTGTCTTCTTATCCTCACATCTGTTTTCACACCTTCATCCCTGTCTTCCTCATGTTC
ACACTTGTCTTCCCCATGTTCATAGCTGCCTTTCTTACCATTTTGGTTTGAAGGGCAGTCTTCTCTGGCTTGTTT
TTTTGTTTTTCCCAGAAAATCAGTATTATTTTTTAAATAAGAAAAACATTCCTAGAAGATGATAATTGTGAAAAC
CTCCTTTGGCTTATTTGCTTTTCCAGATTTTAGTCTCCTTTCTCCCCATCCGGGAAAGATGGTGGAAGACATAGG
CTAAATTTCTCCAGCCTCACAATGGTCTTCACTTGGTCTGACTTGTACCAATTCTAGCACCCACTGAAAAACAAG
TTGAGTAGAGAGTGTAGAGTGCAGAAATGTGGCTTTTGCCCCACTTTGCATCTCCAAAATTACAACGGTTGGCCG
ATCCCATTTGAGGACAATGCTTAGTTATAAGTCTCCGAGTTGGAAAAGGAAGAAAGCCAGAGCTGTCTAGTTTCA
TTCATTCTTTCAGTAAATATTTATTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 203

MEPGRRGAAALLALLCVACALRAGRAQYERYSFRSFPRDELMPLESAYRHALDKYSGEHWAESVGYLEISLRLHR
LLRDSEAFCHRNCSAAPQPEPAAGLASYPELRLFGGLLRRAHCLKRCKQGLPAFRQSQPSREVLADFQRREPYKF
LQFAYFKANNLPKAIAAAHTFLLKHPDDEMMKRNMAYYKSLPGAEDYIKDLETKSYESLFIRAVRAYNGENWRTS
ITDMELALPDFFKAFYECLAACEGSREIKDFKDFYLSIADHYVEVLECKIQCEENLTPVIGGYPVEKFVATMYHY
LQFAYYKLNDLKNAAPCAVSYLLFDQNDKVMQQNLVYYQYHRDTWGLSDEHFQPRPEAVQFFNVTTLQKELYDFA
KENIMDDDEGEVVEYVDDLLELEETS

FIGURE 204

CTCGTCGCCGCCGCCATTTTAGCTGTTGGTTCCGGCCGCACCGTGTGGGCTGTAGTAGCGGGAGGGGTGGGGGTC
CTCCAGAGTTAAGTGGCTGTCCTCGACTGTGCCCATACAGCAGCCAGCTTTCTTCCTTAATAACTGCCCGTTCGA
AGAGTGCGAGG**ATG**TCCAAGCGGCACCGGTTGGACCTAGGGGAGGATTACCCCTCTGGCAAGAAGCGTGCGGGGA
CCGATGGGAAGGATCGAGATCGAGACCGGGATCGTGAAGATCGGTCTAAAGATCGAGACCGAGAACGTGATAGAG
GAGATAGAGAGCGAGAGAGGGAGAAAGAAAAGGAGAAGGAGTTGCGAGCTTCAACAAATGCTATGCTTATCAGTG
CTGGATTACCACCCCTGAAAGCTTCCCATTCAGCTCACTCAACCCACTCAGCACATTCAACGCATTCTACACATT
CTGCTCATTCAACGCATGCCGGACATGCAGGTCACACGTCACTTCCACAGTGCATTAATCCGTTCACCAACTTAC
CCCATACTCCTCGATACTATGATATTCTAAAGAAACGTCTTCAGCTCCCTGTTTGGGAATACAAGGATAGGTTTA
CAGATATTCTGGGTAGACATCAGTCCTTTGTACTGGTTGGTGAGACTGGGTCTGGTAAAACAACACAAATTCCAC
ACCGGTGTGTGGAGTACATGCGATCATTACCAGGACCCAAGAGAGGAGTTGCCTGTACCCAACCCAGGAGAGTGG
CTGCAATGAGTGTGGCTCAGAGAGTTGCTGATGAGATGGATGTGATGTTGGGCCAGGAAGTTGGTTACTCCATTC
GATTTGAAGACTGCAGTAGTGCAAAAACATTTTTTATGTATATGACTGATGGGATGTTACTTCGTGAAGCTATGA
ATGATCCCCTCCTGGAGCGTTATGGTGTAATAATTCTTGATGAGGCTCATGAGAGGACACTGGCTACAGATATTC
TAATGGGTGTTCTGAAGGAAGTTGTAAGACAGAGATCAGATTTAAAGGTTATAGTTATGAGCGCTACTCTAGATG
CAGGAAAATTCCAGATTTACTTTGATAACTGTCCTCTCCTAACTATTCCTGGGCGTACACATCCTGTTGAGATCT
TCTATACTCCAGAACCAGAGAGAGATTATCTTGAAGCAGCAATTCGAACAGTTATCCAGATTCATATGTGTGAAG
AGGAAGAGGGAGATCTTCTTCTTTTCTTAACTGGTCAAGAGGAAATTGATGAAGCCTGTAAGAGAATAAAGCGTG
AAGTTGATGATTTGGGCCCTGAAGTTGGTGACATTAAAATCATTCCATTGTATTCTACACTTCCACCTCAGCAGC
AGCAACGCATTTTTGAGCCTCCACCTCCCAAAAAACAGAATGGAGCAATTGGAAGAAAGGTAGTTGTGTCAACTA
ACATAGCAGAGACGTCTTTGACAATAGATGGTGTGGTGTTTGTGATTGATCCTGGATTTGCGAAACAGAAGGTCT
ACAATCCTCGAATCAGAGTTGAGTCCCTTTTGGTGACAGCTATTAGTAAAGCTTCAGCTCAGCAAAGGGCTGGTC
GAGCTGGACGTACCAGACCTGGAAAATGCTTCAGACTTTACACAGAGAAAGCTTATAAAACAGAAATGCAGGATA
ACACCTATCCTGAGATTTTGCGTTCTAATTTAGGATCAGTTGTGTTACAATTGAAGAAACTTGGTATTGATGACT
TGGTACATTTTGATTTTATGGATCCACCAGCTCCTGAAACTCTGATGAGAGCCCTGGAACTTTTGAATTACCTGG
CTGCTTTAAATGATGATGGAGATCTGACTGAATTGGGATCCATGATGGCAGAGTTTCCTCTAGATCCACAGCTCG
CAAAAATGGTTATTGCAAGTTGTGACTACAACTGTTCTAATGAGGTCCTATCTATTACTGCTATGTTGTCAGTCC
CACAGTGTTTTGTTCGCCCCACGGAGGCCAAGAAAGCCGCAGATGAGGCCAAGATGAGATTTGCCCACATAGATG
GAGATCATCTGACACTGCTGAACGTCTACCATGCTTTTAAACAAAATCATGAATCGGTTCAGTGGTGTTATGACA
ACTTCATTAACTACAGGTCCCTGATGTCCGCGGACAATGTACGCCAGCAGCTATCTCGAATTATGGACAGATTTA
ATTTGCCTCGTCGAAGTACTGACTTTACAAGCAGGGACTATTATATTAATATAAGAAAAGCTTTGGTTACTGGGT
ATTTTATGCAGGTGGCACATTTAGAACGAACAGGGCATTACTTAACTGTGAAAGATAACCAGGTGGTTCAGTTGC
ATCCCTCTACTGTTCTTGACCACAAACCTGAATGGGTGCTTTATAATGAGTTTGTTCTAACAACAAAGAATTACA
TCCGGACATGTACAGACATCAAGCCAGAATGGTTGGTGAAAATTGCCCCTCAATATTATGACATGAGCAATTTCC
CACAGTGTGAAGCAAAGAGACAGTTGGACCGCATCATTGCCCAAACTTCAATCCAAGGAATATTCACAGTACTGA
ATTCAGTGCTTAGAACTGAAGTTATTGAGAGGACAGCTTTAAAAGATGAA**TGA**ACTCAAAAGTTCGAGTTGTGCT
CTTCACGTTGGTTCGATAATGGCCTTTATTTGAAAGCTTTTTAATTTTTCTTTACAGTAAATATTCCATTCTGAT
TTCATAAATTAAACATTTATGCCTCCCTTTTGTGTTGACACTGTAGCTCATACTGGAAAAGTCGATCAATGTTTT
GCAGTTTATTGAAAGTAGTTCTATATATAACAATGTTATAAGCATTTCTTTAGAAATGGTTGAAAATGCTTCTAA
AATGTGATTATCGACCATGGTATGCATGATCGTTGTAATTGTTGACATTCCTTTTAGAAGTTGTGAAATGTTACA
ACTTGTGCTTATGTAGACACAATTTTTTGTTTCAGTACCAGAGGCACTGACTTCAATAAAGTTTATTTATACGGA
AAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 205

MSKRHRLDLGEDYPSGKKRAGTDGKDRDRDRDREDRSKDRDRERDRGDREREREKEKEKELRASTNAMLISAGLP
PLKASHSAHSTHSAHSTHSTHSAHSTHAGHAGHTSLPQCINPFTNLPHTPRYYDILKKRLQLPVWEYKDRFTDIL
GRHQSFVLVGETGSGKTTQIPHRCVEYMRSLPGPKRGVACTQPRRVAAMSVAQRVADEMDVMLGQEVGYSIRFED
CSSAKTFFMYMTDGMLLREAMNDPLLERYGVIILDEAHERTLATDILMGVLKEVVRQRSDLKVIVMSATLDAGKF
QIYFDNCPLLTIPGRTHPVEIFYTPEPERDYLEAAIRTVIQIHMCEEEEGDLLLFLTGQEEIDEACKRIKREVDD
LGPEVGDIKIIPLYSTLPPQQQQRIFEPPPPKKQNGAIGRKVVVSTNIAETSLTIDGVVFVIDPGFAKQKVYNPR
IRVESLLVTAISKASAQQRAGRAGRTRPGKCFRLYTEKAYKTEMQDNTYPEILRSNLGSVVLQLKKLGIDDLVHF
DFMDPPAPETLMRALELLNYLAALNDDGDLTELGSMMAEFPLDPQLAKMVIASCDYNCSNEVLSITAMLSVPQCF
VRPTEAKKAADEAKMRFAHIDGDHLTLLNVYHAFKQNHESVQWCYDNFINYRSLMSADNVRQQLSRIMDRFNLPR
RSTDFTSRDYYINIRKALVTGYFMQVAHLERTGHYLTVKDNQVVQLHPSTVLDHKPEWVLYNEFVLTTKNYIRTC
TDIKPEWLVKIAPQYYDMSNFPQCEAKRQLDRIIAQTSIQGIFTVLNSVLRTEVIERTALKDE

FIGURE 206

GAATTCGCGGCCGCTGGTTTGCAGCTGCTCCGTCATCGTGCGGCCCGACGCTATCTCGCGCTCGTGTGCAGGCCC
GGCTCGGCTCCTGGTCCCCGGTGCGAGGGTTAACGCGAGGCCCCGGCCTCGGTCCCCGGACTAGGCCGTGACCCC
GGGTGCC**ATG**AAGCAGGAGGGCTCGGCGCGGCGCCGCGGCGCGGACAAGGCGAAACCGCCGCCCGGCGGAGGAGA
ACAAGAACCCCCACCGCCGCCGGCCCCCCAGGATGTGGAGATGAAAGAGGAGGCAGCGACGGGTGGCGGGTCAAC
GGGGGAGGCAGACGGCAAGACGGCGGCGGCAGCGGTTGAGCACTCCCAGCGAGAGCTGGACACAGTCACCTTGGA
GGACATCAAGGAGCACGTGAAACAGCTAGAGAAAGCGGTTTCAGGCAAGGAGCCGAGATTCGTGCTGCGGGCCCT
GCGGATGCTGCCTTCCACATCACGCCGCCTCAACCACTATGTTCTGTATAAGGCTGTGCAGGGCTTCTTCACTTC
AAATAATGCCACTCGAGACTTTTTGCTCCCCTTCCTGGAAGAGCCCATGGACACAGAGGCTGATTTACAGTTCCG
TCCCCGCACGGGAAAAGCTGCGTCGACACCCCTCCTGCCTGAAGTGGAAGCCTATCTCCAACTCCTCGTGGTCAT
CTTCATGATGAACAGCAAGCGCTACAAAGAGGCACAGAAGATCTCTGATGATCTGATGCAGAAGATCAGTACTCA
GAACCGCCGGGCCCTAGACCTTGTAGCCGCAAAGTGTTACTATTATCACGCCCGGGTCTATGAGTTCCTGGACAA
GCTGGATGTGGTGCGCAGCTTCTTGCATGCTCGGCTCCGGACAGCTACGCTTCGGCATGACGCAGACGGGCAGGC
CACCCTGTTGAACCTCCTGCTGCGGAATTACCTACACTACAGCTTGTACGACCAGGCTGAGAAGCTGGTGTCCAA
GTCTGTGTTCCCAGAGCAGGCCAACAACAATGAGTGGGCCAGGTACCTCTACTACACAGGGCGAATCAAAGCCAT
CCAGCTGGAGTACTCAGAGGCCCGGAGAACGATGACCAACGCCCTTCGCAAGGCCCCTCAGCACACAGCTGTCGG
CTTCAAACAGACGGTGCACAAGCTTCTCATCGTGGTGGAGCTGTTGCTGGGGGAGATCCCTGACCGGCTGCAGTT
CCGCCAGCCCTCCCTCAAGCGCTCACTCATGCCCTATTTCCTTCTGACTCAAGCTGTCAGGACAGGAAACCTAGC
CAAGTTCAACCAGGTCCTGGATCAGTTTGGGGAGAAGTTTCAAGCAGATGGGACCTACACCCTAATTATCCGGCT
GCGGCACAACGTGATTAAGACAGGTGTACGCATGATCAGCCTCTCCTATTCCCGAATCTCCTTGGCTGACATCGC
CCAGAAGCTGCAGTTGGATAGCCCCGAAGATGCAGAGTTCATTGTTGCCAAGGCCATCCGGGATGGTGTCATTGA
GGCCAGCATCAACCACGAGAAGGGCTATGTCCAATCCAAGGAGATGATTGACATCTATTCCACCCGAGAGCCCCA
GCTAGCCTTCCACCAGCGCATCTCCTTCTGCCTAGATATCCACAACATGTCTGTCAAGGCCATGAGGTTTCCTCC
CAAATCGTACAACAAGGACTTGGAGTCTGCAGAGGAACGGCGTGAGCGAGAACAGCAGGACTTGGAGTTTGCCAA
GGAGATGGCAGAAGATGATGATGACAGCTTCCCT**TGA**GCTGGGGGGCTGGGGAGGGGTAGGGGGAATGGGGACAG
GCTCTTTCCCCCTTGGGGGTCCCCTGCCCAGGGCACTGTCCCCATTTTCCCACACACAGCTCATATGCTGCATTC
GTGCAGGGGGTGGGGGTGCTGGGAGCCAGCCACCCTGACCTCCCCCAGGGCTCCTCCCCAGCCGGTGACTTACTG
TACAGCAGGCAGGAGGGTGGGCAGGCAACCTCCCCGGGCAGGGTCCTGGCCAGCAGTGTGGGAGCAGGAGGGGAA
GGATAGTTCTGTGTACTCCTTTAGGGAGTGGGGGACTAGAACTGGGATGTCTTGGCTTGTATGTTTTTTGAAGCT
TCGATTATGATTTTTAAACAATAAAAAGTTCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCGCGAAT
TC

FIGURE 207

MKQEGSARRRGADKAKPPPGGGEQEPPPPPAPQDVEMKEEAATGGGSTGEADGKTAAAAVEHSQRELDTVTLEDI
KEHVKQLEKAVSGKEPRFVLRALRMLPSTSRRLNHYVLYKAVQGFFTSNNATRDFLLPFLEEPMDTEADLQFRPR
TGKAASTPLLPEVEAYLQLLVVIFMMNSKRYKEAQKISDDLMQKISTQNRRALDLVAAKCYYYHARVYEFLDKLD
VVRSFLHARLRTATLRHDADGQATLLNLLLRNYLHYSLYDQAEKLVSKSVFPEQANNNEWARYLYYTGRIKAIQL
EYSEARRTMTNALRKAPQHTAVGFKQTVHKLLIVVELLLGEIPDRLQFRQPSLKRSLMPYFLLTQAVRTGNLAKF
NQVLDQFGEKFQADGTYTLIIRLRHNVIKTGVRMISLSYSRISLADIAQKLQLDSPEDAEFIVAKAIRDGVIEAS
INHEKGYVQSKEMIDIYSTREPQLAFHQRISFCLDIHNMSVKAMRFPPKSYNKDLESAEERREREQQDLEFAKEM
AEDDDDSFP

FIGURE 208A

CAGGACAGGGAAGAGCGGGCGCT**ATG**GGGAGCCGGACGCCAGAGTCCCCTCTCCACGCCGTGCAGCTGCGCTGGG
GCCCCCGGCGCCGACCCCCGCTCGTGCCGCTGCTGTTGCTGCTCGTGCCGCCGCCACCCAGGGTCGGGGGCTTCA
ACTTAGACGCGGAGGCCCCAGCAGTACTCTCGGGGCCCCCGGGCTCCTTCTTCGGATTCTCAGTGGAGTTTTACC
GGCCGGGAACAGACGGGGTCAGTGTGCTGGTGGGAGCACCCAAGGCTAATACCAGCCAGCCAGGAGTGCTGCAGG
GTGGTGCTGTCTACCTCTGTCCTTGGGGTGCCAGCCCCACACAGTGCACCCCCATTGAATTTGACAGCAAAGGCT
CTCGGCTCCTGGAGTCCTCACTGTCCAGCTCAGAGGGAGAGGAGCCTGTGGAGTACAAGTCCTTGCAGTGGTTCG
GGGCAACAGTTCGAGCCCATGGCTCCTCCATCTTGGCATGCGCTCCACTGTACAGCTGGCGCACAGAGAAGGAGC
CACTGAGCGACCCCGTGGGCACCTGCTACCTCTCCACAGATAACTTCACCCGAATTCTGGAGTATGCACCCTGCC
GCTCAGATTTCAGCTGGGCAGCAGGACAGGGTTACTGCCAAGGAGGCTTCAGTGCCGAGTTCACCAAGACTGGCC
GTGTGGTTTTAGGTGGACCAGGAAGCTATTTCTGGCAAGGCCAGATCCTGTCTGCCACTCAGGAGCAGATTGCAG
AATCTTATTACCCCGAGTACCTGATCAACCTGGTTCAGGGGCAGCTGCAGACTCGCCAGGCCAGTTCCATCTATG
ATGACAGCTACCTAGGATACTCTGTGGCTGTTGGTGAATTCAGTGGTGATGACACAGAAGACTTTGTTGCTGGTG
TGCCCAAAGGGAACCTCACTTACGGCTATGTCACCATCCTTAATGGCTCAGACATTCGATCCCTCTACAACTTCT
CAGGGGAACAGATGGCCTCCTACTTTGGCTATGCAGTGGCCGCCACAGACGTCAATGGGGACGGGCTGGATGACT
TGCTGGTGGGGGCACCCCTGCTCATGGATCGGACCCCTGACGGGCGGCCTCAGGAGGTGGGCAGGGTCTACGTCT
ACCTGCAGCACCCAGCCGGCATAGAGCCCACGCCCACCCTTACCCTCACTGGCCATGATGAGTTTGGCCGATTTG
GCAGCTCCTTGACCCCCCTGGGGGACCTGGACCAGGATGGCTACAATGATGTGGCCATCGGGGCTCCCTTTGGTG
GGGAGACCCAGCAGGGAGTAGTGTTTGTATTTCCTGGGGGCCCAGGAGGGCTGGGCTCTAAGCCTTCCCAGGTTC
TGCAGCCCCTGTGGGCAGCCAGCCACACCCCAGACTTCTTTGGCTCTGCCCTTCGAGGAGGCCGAGACCTGGATG
GCAATGGATATCCTGATCTGATTGTGGGGTCCTTTGGTGTGGACAAGGCTGTGGTATACAGGGGCCGCCCCATCG
TGTCCGCTAGTGCCTCCCTCACCATCTTCCCCGCCATGTTCAACCCAGAGGAGCGGAGCTGCAGCTTAGAGGGGA
ACCCTGTGGCCTGCATCAACCTTAGCTTCTGCCTCAATGCTTCTGGAAAACACGTTGCTGACTCCATTGGTTTCA
CAGTGGAACTTCAGCTGGACTGGCAGAAGCAGAAGGGAGGGGTACGGCGGGCACTGTTCCTGGCCTCCAGGCAGG
CAACCCTGACCCAGACCCTGCTCATCCAGAATGGGGCTCGAGAGGATTGCAGAGAGATGAAGATCTACCTCAGGA
ACGAGTCAGAATTTCGAGACAAACTCTCGCCGATTCACATCGCTCTCAACTTCTCCTTGGACCCCCAAGCCCCAG
TGGACAGCCACGGCCTCAGGCCAGCCCTACATTATCAGAGCAAGAGCCGGATAGAGGACAAGGCTCAGATCTTGC
TGGACTGTGGAGAAGACAACATCTGTGTGCCTGACCTGCAGCTGGAAGTGTTTGGGGAGCAGAACCATGTGTACC
TGGGTGACAAGAATGCCCTGAACCTCACTTTCCATGCCCAGAATGTGGGTGAGGGTGGCGCCTATGAGGCTGAGC
TTCGGGTCACCGCCCCTCCAGAGGCTGAGTACTCAGGACTCGTCAGACACCCAGGGAACTTCTCCAGCCTGAGCT
GTGACTACTTTGCCGTGAACCAGAGCCGCCTGCTGGTGTGTGACCTGGGCAACCCCATGAAGGCAGGAGCCAGTC
TGTGGGGTGGCCTTCGGTTTACAGTCCCTCATCTCCGGGACACTAAGAAAACCATCCAGTTTGACTTCCAGATCC
TCAGCAAGAATCTCAACAACTCGCAAAGCGACGTGGTTTCCTTTCGGCTCTCCGTGGAGGCTCAGGCCCAGGTCA
CCCTGAACGGTGTCTCCAAGCCTGAGGCAGTGCTATTCCCAGTAAGCGACTGGCATCCCCGAGACCAGCCTCAGA
AGGAGGAGGACCTGGGACCTGCTGTCCACCATGTCTATGAGCTCATCAACCAAGGCCCCAGCTCCATTAGCCAGG
GTGTGCTGGAACTCAGCTGTCCCCAGGCTCTGGAAGGTCAGCAGCTCCTATATGTGACCAGAGTTACGGGACTCA
ACTGCACCACCAATCACCCCATTAACCCAAAGGGCCTGGAGTTGGATCCCGAGGGTTCCCTGCACCACCAGCAAA
AACGGGAAGCTCCAAGCCGCAGCTCTGCTTCCTCGGGACCTCAGATCCTGAAATGCCCGGAGGCTGAGTGTTTCA
GGCTGCGCTGTGAGCTCGGGCCCCTGCACCAACAAGAGAGCCAAAGTCTGCAGTTGCATTTCCGAGTCTGGGCCA
AGACTTTCTTGCAGCGGGAGCACCAGCCATTTAGCCTGCAGTGTGAGGCTGTGTACAAAGCCCTGAAGATGCCCT
ACCGAATCCTGCCTCGGCAGCTGCCCCAAAAAGAGCGTCAGGTGGCCACAGCTGTGCAATGGACCAAGGCAGAAG
GCAGCTATGGCGTCCCACTGTGGATCATCATCCTAGCCATCCTGTTTGGCCTCCTGCTCCTAGGTCTACTCATCT
ACATCCTCTACAAGCTTGGATTCTTCAAACGCTCCCTCCCATATGGCACCGCCATGGAAAAAGCTCAGCTCAAGC
CTCCAGCCACCTCTGATGCC**TGA**GTCCTCCCAATTTCAGACTCCCATTCCTGAAGAACCAGTCCCCCCACCCTCA
TTCTACTGAAAAGGAGGGGTCTGGGTACTTCTTGAAGGTGCTGACGGCCAGGGAGAAGCTCCTCTCCCCAGCCCA
GAGACATACTTGAAGGGCCAGAGCCAGGGGGGTGAGGAGCTGGGGATCCCTCCCCCCCATGCACTGTGAAGGACC
CTTGTTTACACATACCCTCTTCATGGATGGGGGAACTCAGATCCAGGGACAGAGGCCCAGCCTCCCTGAAGCCTT
TGCATTTTGGAGAGTTTCCTGAAACAACTGGAAAGATAACTAGGAAATCCATTCACAGTTCTTTGGGCCAGACAT
GCCACAAGGACTTCCTGTCCAGCTCCAACCTGCAAAGATCTGTCCTCAGCCTTGCCAGAGATCCAAAAGAAGCCC

FIGURE 208B

CCAGTAAGAACCTGGAACTTGGGGAGTTAAGACCTGGCAGCTCTGGACAGCCCCACCCTGGTGGGCCAACAAAGA
ACACTAACTATGCATGGTGCCCCAGGACCAGCTCAGGACAGATGCCACAAGGATAGATGCTGGCCCAGGGCCAGA
GCCCAGCTCCAAGGGGAATCAGAACTCAAATGGGGCCAGATCCAGCCTGGGGTCTGGAGTTGATCTGGAACCCAG
ACTCAGACATTGGCACCAATCCAGGCAGATCCAGGACTATATTTGGGCCTGCTCCAGACCTGATCCTGGAGGCCC
AGTTCACCCTGATTTAGGAGAAGCCAGGAATTTCCCAGGACCTGAAGGGGCCATGATGGCAACAGATCTGGAACC
TCAGCCTGGCCAGACACAGGCCCTCCCTGTTCCCCAGAGAAAGGGGAGCCCACTGTCCTGGGCCTGCAGAATTTG
GGTTCTGCCTGCCAGCTGCACTGATGCTGCCCCTCATCTCTCTGCCCAACCCTTCCCTCACCTTGGCACCAGACA
CCCAGGACTTATTTAAACTCTGTTGCAAGTGCAATAAATCTGACCCAGTGCCCCCACTGACCAGAACTAGAAAAA
AAAA

FIGURE 209

MGSRTPESPLHAVQLRWGPRRRPPLVPLLLLLVPPPPRVGGFNLDAEAPAVLSGPPGSFFGFSVEFYRPGTDGVS
VLVGAPKANTSQPGVLQGGAVYLCPWGASPTQCTPIEFDSKGSRLLESSLSSSEGEEPVEYKSLQWFGATVRAHG
SSILACAPLYSWRTEKEPLSDPVGTCYLSTDNFTRILEYAPCRSDFSWAAGQGYCQGGFSAEFTKTGRVVLGGPG
SYFWQGQILSATQEQIAESYYPEYLINLVQGQLQTRQASSIYDDSYLGYSVAVGEFSGDDTEDFVAGVPKGNLTY
GYVTILNGSDIRSLYNFSGEQMASYFGYAVAATDVNGDGLDDLLVGAPLLMDRTPDGRPQEVGRVYVYLQHPAGI
EPTPTLTLTGHDEFGRFGSSLTPLGDLDQDGYNDVAIGAPFGGETQQGVVFVFPGGPGGLGSKPSQVLQPLWAAS
HTPDFFGSALRGGRDLDGNGYPDLIVGSFGVDKAVVYRGRPIVSASASLTIFPAMFNPEERSCSLEGNPVACINL
SFCLNASGKHVADSIGFTVELQLDWQKQKGGVRRALFLASRQATLTQTLLIQNGAREDCREMKIYLRNESEFRDK
LSPIHIALNFSLDPQAPVDSHGLRPALHYQSKSRIEDKAQILLDCGEDNICVPDLQLEVFGEQNHVYLGDKNALN
LTFHAQNVGEGGAYEAELRVTAPPEAEYSGLVRHPGNFSSLSCDYFAVNQSRLLVCDLGNPMKAGASLWGGLRFT
VPHLRDTKKTIQFDFQILSKNLNNSQSDVVSFRLSVEAQAQVTLNGVSKPEAVLFPVSDWHPRDQPQKEEDLGPA
VHHVYELINQGPSSISQGVLELSCPQALEGQQLLYVTRVTGLNCTTNHPINPKGLELDPEGSLHHQQKREAPSRS
SASSGPQILKCPEAECFRLRCELGPLHQQESQSLQLHFRVWAKTFLQREHQPFSLQCEAVYKALKMPYRILPRQL
PQKERQVATAVQWTKAEGSYGVPLWIIILAILFGLLLLGLLIYILYKLGFFKRSLPYGTAMEKAQLKPPATSDA

FIGURE 210

GGGCGCGCCAGAGACGCAGCCGCGCTCCCACCACCCACACCCACCGCGCCCTCGTTCGCCTCTTCTCCGGGAGCC
AGTCCGCGCCACCGCCGCCGCCCAGGCCATCGCCACCCTCCGCAGCC**ATG**TCCACCAGGTCCGTGTCCTCGTCCT
CCTACCGCAGGATGTTCGGCGGCCCGGGCACCGCGAGCCGGCCGAGCTCCAGCCGGAGCTACGTGACTACGTCCA
CCCGCACCTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCCGGGCGGCG
TGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGTGCGGCTCCTGCAGGACTCGGTGG
ACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAAGAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGC
TGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGC
TCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTAGGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGC
AGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCC
TCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGAGGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGATG
TTGACAATGCGTCTCTGGCACGTCTTGACCTTGAACGCAAAGTGGAATCTTTGCAAGAAGAGATTGCCTTTTTGA
AGAAACTCCACGAAGAGGAAATCCAGGAGCTGCAGGCTCAGATTCAGGAACAGCATGTCCAAATCGATGTGGATG
TTTCCAAGCCTGACCTCACGGCTGCCCTGCGTGACGTACGTCAGCAATATGAAAGTGTGGCTGCCAAGAACCTGC
AGGAGGCAGAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGACGCCCTGC
GCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCTTAAAG
GAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCTAACTACCAAG
ACACTATTGGCCGCCTGCAGGATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAAG
ACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCTGCTGGAAGGCGAGGAGAGCA
GGATTTCTCTGCCTCTTCCAAACTTTTCCTCCCTGAACCTGAGGGAAACTAATCTGGATTCACTCCCTCTGGTTG
ATACCCACTCAAAAAGGACATTCCTGATTAAGACGGTTGAAACTAGAGATGGACAGGTTATCAACGAAACTTCTC
AGCATCACGATGACCTTGAA**TAA**AAATTGCACACACTCAGTGGCAGGCGATATATTACCCAGGCAAGAATAAAAA
AGAAATCCCATATCTTAAAGAAACAGCTTTCAAGTGCCTTTCTGCAGTTTTTCAGGAGCGCAAGATAGATTTGGA
ATAGGAATAAGCTCTAGTTCTTAACAACCGACACTCCTACAAGATTTAGAAAAAAGTTTACAACATAATCTAGTT
TACAGAAAAATCTTGTGCTAGAATACTTTTTAAAAGGTATTTTGAATACCATTAAAACTGCTTTTTTTTTTTCCAG
CAAGTATCCAACCAACTTGGTTCTGCTTCAATAAATCTTTGGAAAACTCCA

FIGURE 211

MSTRSVSSSSYRRMFGGPGTASRPSSSRSYVTTSTRTYSLGSALRPSTSRSLYASSPGGVYATRSSAVRLRSSVP
GVRLLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLEQQNKILLAELEQLKGQGKSRLGDLY
EEEMRELRRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVE
SLQEEIAFLKKLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVAAKNLQEAEEWYKSKFADLSE
AANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEENFAVEAANYQDTIGRLQDEIQNMKEE
MARHLREYQDLLNVKMALDIEIATYRKLLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSKRTFLIKTVETR
DGQVINETSQHHDDLE

FIGURE 212A

CAGTTTGGAGCTCAGTCTTCCACCAAAGGCCGTTCAGTTCTCCTGGGCTCCAGCCTCCTGCAAGGACTGCAAGAG
TTTTCCTCCGCAGCTCTGAGTCTCCACTTTTTTGGTGGAGAAAGGCTGCAAAAAGAAAAAGAGACGCAGTGAGTG
GGAAAAGTATGCATCCTATTCAAACCTAATTGAATCGAGGAGCCCAGGGACACACGCCTTCAGGTTTGCTCAGGG
GTTCATATTTGGTGCTTAGACAAATTCAAA**ATG**AGGAAACATCGGCACTTGCCCTTAGTGGCCGTCTTTTGCCTC
TTTCTCTCAGGCTTTCCTACAACTCATGCCCAGCAGCAGCAAGCAGATGTCAAAAATGGTGCGGCTGCTGATATA
ATATTTCTAGTGGATTCCTCTTGGACCATTGGAGAGGAACATTTCCAACTTGTTCGAGAGTTTCTATATGATGTT
GTAAAATCCTTAGCTGTGGGAGAAAATGATTTCCATTTTGCTCTGGTCCAGTTCAACGGAAACCCACATACCGAG
TTCCTGTTAAATACGTATCGTACTAAACAAGAAGTCCTTTCTCATATTTCCAACATGTCTTATATTGGGGGAACC
AATCAGACTGGAAAAGGATTAGAATACATAATGCAAAGCCACCTCACCAAGGCTGCTGGAAGCCGGGCCGGTGAC
GGAGTCCCTCAGGTTATCGTAGTGTTAACTGATGGACACTCGAAGGATGGCCTTGCTCTGCCCTCAGCGGAACTT
AAGTCTGCTGATGTTAACGTGTTTGCAATTGGAGTTGAGGATGCAGATGAAGGAGCGTTAAAAGAAATAGCAAGT
GAACCGCTCAATATGCATATGTTCAACCTAGAGAATTTTACCTCACTTCATGACATAGTAGGAAACTTAGTGTCC
TGTGTGCATTCATCCGTGAGTCCAGAAAGGGCTGGGGACACGGAAACCCTTAAAGACATCACAGCACAAGACTCT
GCTGACATTATTTTCCTTATTGATGGATCAAACAACACCGGAAGTGTCAATTTCGCAGTCATTCTCGACTTCCTT
GTAAATCTCCTTGAGAAACTCCCAATTGGAACTCAGCAGATCCGAGTGGGGGTGGTCCAGTTTAGCGATGAGCCC
AGAACCATGTTTTCCTTGGACACCTACTCCACCAAGGCCCAGGTTCTGGGTGCAGTGAAAGCCCTCGGGTTTGCT
GGTGGGGAGTTGGCCAATATCGGCCTCGCCCTTGATTTCGTGGTGGAGAACCACTTCACCCGGGCAGGGGGCAGC
CGCGTGGAGGAAGGGGTTCCCCAGGTGCTGGTCCTCATAAGTGCCGGGCCTTCTAGTGACGAGATTCGCTACGGG
GTGGTAGCACTGAAGCAGGCTAGCGTGTTCTCATTCGGCCTTGGAGCCCAGGCCGCCTCCAGGGCAGAGCTTCAG
CACATAGCTACCGATGACAACTTGGTGTTTACTGTCCCGGAATTCCGTAGCTTTGGGGACCTCCAGGAGAAATTA
CTGCCGTACATTGTTGGCGTGGCCCAAAGGCACATTGTCTTGAAACCGCCAACCATTGTCACACAAGTCATTGAA
GTCAACAAGAGAGACATAGTCTTCCTGGTGGATGGCTCATCTGCACTGGGACTGGCCAACTTCAATGCCATCCGA
GACTTCATTGCTAAAGTCATCCAGAGGCTGGAAATCGGACAGGATCTTATCCAGGTGGCAGTGGCCCAGTATGCA
GACACTGTGAGGCCTGAATTTTATTTCAATACCCATCCAACAAAAAGGGAAGTCATAACCGCTGTGCGGAAAATG
AAGCCCCTGGACGGCTCGGCCCTGTACACGGGCTCTGCTCTAGACTTTGTTCGTAACAACCTATTCACGAGTTCA
GCCGGCTACCGGGCTGCCGAGGGGATTCCTAAGCTTTTGGTGCTGATCACAGGTGGTAAGTCCCTAGATGAAATC
AGCCAGCCTGCCCAGGAGCTGAAGAGAAGCAGCATAATGGCCTTTGCCATTGGGAACAAGGGTGCCGATCAGGCT
GAGCTGGAAGAGATCGCTTTCGACTCCTCCCTGGTGTTCATCCCAGCTGAGTTCCGAGCCGCCCCATTGCAAGGC
ATGCTGCCTGGCTTGCTGGCACCTCTCAGGACCCTCTCTGGAACCCCTGAAGTTCACTCAAACAAAAGAGATATC
ATCTTTCTTTTGGATGGATCAGCCAACGTTGGAAAAACCAATTTCCCTTATGTGCGCGACTTTGTAATGAACCTA
GTTAACAGCCTTGATATTGGAAATGACAATATTCGTGTTGGTTTAGTGCAATTTAGTGACACTCCTGTAACGGAG
TTCTCTTTAAACACATACCAGACCAAGTCAGATATCCTTGGTCATCTGAGGCAGCTGCAGCTCCAGGGAGGTTCG
GGCCTGAACACAGGCTCAGCCCTAAGCTATGTCTATGCCAACCACTTCACGGAAGCTGGCGGCAGCAGGATCCGT
GAACACGTGCCGCAGCTCCTGCTTCTGCTCACAGCTGGGCAGTCTGAGGACTCCTATTTGCAAGCTGCCAACGCC
TTGACACGCGCGGGCATCCTGACTTTTTGTGTGGGAGCTAGCCAGGCGAATAAGGCAGAGCTTGAGCAGATTGCT
TTTAACCCAAGCCTGGTGTATCTCATGGATGATTTCAGCTCCCTGCCAGCTTTGCCTCAGCAGCTGATTCAGCCC
CTAACCACATATGTTAGTGGAGGTGTGGAGGAAGTACCACTCGCTCAGCCAGAGAGCAAGCGAGACATTCTGTTC
CTCTTTGACGGCTCAGCCAATCTTGTGGGCCAGTTCCCTGTTGTCCGTGACTTTCTCTACAAGATTATCGATGAG
CTCAATGTGAAGCCAGAGGGGACCCGAATTGCGGTGGCTCAGTACAGCGATGATGTCAAGGTGGAGTCCCGTTTT
GATGAGCACCAGAGTAAGCCTGAGATCCTGAATCTTGTGAAGAGAATGAAGATCAAGACGGGCAAAGCCCTCAAC
CTGGGCTACGCGCTGGACTATGCACAGAGGTACATTTTTGTGAAGTCTGCTGGCAGCCGGATCGAGGATGGAGTG
CTTCAGTTCCTGGTGCTGCTGGTCGCAGGAAGGTCATCTGACCGTGTGGATGGGCCAGCAAGTAACCTGAAGCAG
AGTGGGGTTGTGCCTTTCATCTTCCAAGCCAAGAACGCAGACCCTGCTGAGTTAGAGCAGATCGTGCTGTCTCCA
GCGTTTATCCTGGCTGCAGAGTCGCTTCCCAAGATTGGAGATCTTCATCCACAGATAGTGAATCTCTTAAAATCA
GTGCACAACGGAGCACCAGCACCAGTTTCAGGTGAAAAGGACGTGGTGTTTCTGCTTGATGGCTCTGAGGGCGTC
AGGAGCGGCTTCCCTCTGTTGAAAGAGTTTGTCCAGAGAGTGGTGGAAAGCCTGGATGTGGGCCAGGACCGGGTC
CGCGTGGCCGTGGTGCAGTACAGCGACCGGACCAGGCCCGAGTTCTACCTGAATTCATACATGAACAAGCAGGAC
GTCGTCAACGCTGTCCGCCAGCTGACCCTGCTGGGAGGGCCGACCCCCAACACCGGGGCCGCCCTGGAGTTTGTC

FIGURE 212B

CTGAGGAACATCCTGGTCAGCTCTGCGGGAAGCAGGATAACAGAAGGTGTGCCCCAGCTGCTGATCGTCCTCACG
GCCGACAGGTCTGGGGATGATGTGCGGAACCCCTCCGTGGTCGTGAAGAGGGGTGGGGCTGTGCCCATTGGCATT
GGCATCGGGAACGCTGACATCACAGAGATGCAGACCATCTCCTTCATCCCGGACTTTGCCGTGGCCATTCCCACC
TTTCGCCAGCTGGGGACCGTCCAACAGGTCATCTCTGAGAGGGTGACCCAGCTCACCCGCGAGGAGCTGAGCAGG
CTGCAGCCGGTGTTGCAGCCTCTACCGAGCCCAGGTGTTGGTGGCAAGAGGGACGTGGTCTTTCTCATCGATGGG
TCCCAAAGTGCCGGGCCTGAGTTCCAGTACGTTCGCACCCTCATAGAGAGGCTGGTTGACTACCTGGACGTGGGC
TTTGACACCACCCGGGTGGCTGTCATCCAGTTCAGCGATGACCCCAAGGCGGAGTTCCTGCTGAACGCCCATTCC
AGCAAGGATGAAGTGCAGAACGCGGTGCAGCGGCTGAGGCCCAAGGGAGGGCGGCAGATCAACGTGGGCAATGCC
CTGGAGTACGTGTCCAGGAACATCTTCAAGAGGCCCCTGGGGAGCCGCATTGAAGAGGGCGTCCCACAGTTCCTG
GTCCTCATCTCGTCTGGAAAGTCTGACGATGAGGTGGTCGTCCCGGCGGTGGAGCTCAAGCAGTTTGGCGTGGCC
CCTTTCACGATCGCCAGGAACGCAGACCAGGAGGAGCTGGTGAAGATCTCGCTGAGCCCCGAATATGTGTTCTCG
GTGAGCACCTTCCGGGAGCTGCCCAGCCTGGAGCAGAAACTGCTGACGCCCATCACGACCCTGACCTCAGAGCAG
ATCCAGAAGCTCTTAGCCAGCACTCGCTATCCACCTCCAGTGCGAGAGTTCAGAGAGCTTCCCAACATAGAAGAA
AGAATCATGAACTCGTTTGGACCCTCCGCAGCCACTCCTGCACCTCCAGGGGTGGACACCCCTCCTCCTTCACGG
CCAGAGAAGAAGAAAGCAGACATTGTGTTCCTGTTGGATGGTTCCATCAACTTCAGGAGGGACAGTTTCCAGGAA
GTGCTTCGTTTTGTGTCTGAAATAGTGGACACAGTTTATGAAGATGGCGACTCCATCCAAGTGGGGCTTGTCCAG
TACAACTCTGACCCCACTGACGAATTCTTCCTGAAGGACTTCTCTACCAAGAGGCAGATTATTGACGCCATCAAC
AAAGTGGTCTACAAAGGGGGAAGACACGCCAACACTAAGGTGGGCCTTGAGCACCTGCGGGTAAACCACTTTGTG
CCTGAGGCAGGCAGCCGCCTGGACCAGCGGGTCCCTCAGATTGCCTTTGTGATCACGGGAGGAAAGTCGGTGGAA
GATGCACAGGATGTGAGCCTGGCCCTCACCCAGAGGGGGGTCAAAGTGTTTGCTGTTGGAGTGAGGAATATCGAC
TCGGAGGAGGTTGGAAAGATAGCGTCCAACAGCGCCACAGCGTTCCGCGTGGGCAACGTCCAGGAGCTGTCCGAA
CTGAGCGAGCAAGTTTTGGAAACTTTGCATGATGCGATGCATGAAACCCTTTGCCCTGGTGTAACTGATGCTGCC
AAAGCTTGTAATCTGGATGTGATTCTGGGGTTTGATGGTTCTAGAGACCAGAATGTTTTTGTGGCCCAGAAGGGC
TTCGAGTCCAAGGTGGACGCCATCTTGAACAGAATCAGCCAGATGCACAGGGTCAGCTGCAGCGGTGGCCGCTCG
CCCACCGTGCGTGTGTCAGTGGTGGCCAACACGCCCTCGGGCCCGGTGGAGGCCTTTGACTTTGACGAGTACCAG
CCAGAGATGCTCGAGAAGTTCCGGAACATGCGCAGCCAGCACCCCTACGTCCTCACGGAGGACACCCTGAAGGTC
TACCTGAACAAGTTCAGACAGTCCTCGCCGGACAGCGTGAAGGTGGTCATTCATTTTACTGATGGAGCAGACGGA
GATCTGGCTGATTTACACAGAGCATCTGAGAACCTCCGCCAAGAAGGAGTCCGTGCCTTGATCCTGGTGGGCCTT
GAACGAGTGGTCAACTTGGAGCGGCTAATGCATCTGGAGTTTGGGCGAGGGTTTATGTATGACAGGCCCCTGAGG
CTTAACTTGCTGGACTTGGATTATGAACTAGCGGAGCAGCTTGACAACATTGCCGAGAAAGCTTGCTGTGGGGTT
CCCTGCAAGTGCTCTGGGCAGAGGGGAGACCGCGGGCCCATCGGCAGCATCGGGCCAAAGGGTATTCCTGGAGAA
GACGGCTACCGAGGCTATCCTGGTGATGAGGGTGGACCCGGTGAGCGTGGTCCGCCTGGTGTGAACGGCACTCAA
GGTTTCCAGGGCTGCCCGGGCCAGAGAGGAGTAAAGGGCTCTCGGGGATTCCCAGGAGAGAAGGGCGAAGTAGGA
GAAATTGGACTGGATGGTCTGGATGGTGAAGATGGAGACAAAGGATTGCCTGGTTCTTCTGGAGAGAAAGGGAAT
CCTGGAAGAAGGGGTGATAAAGGACCTCGAGGAGAGAAAGGAGAAAGAGGAGATGTTGGGATTCGAGGGGACCCG
GGTAACCCAGGACAAGACAGCCAGGAGAGAGGACCCAAAGGAGAAACCGGTGACCTCGGCCCCATGGGTGTCCCA
GGGAGAGATGGAGTACCTGGAGGACCTGGAGAAACTGGGAAGAATGGTGGCTTTGGCCGAAGGGGACCCCCCGGA
GCTAAGGGCAACAAGGGCGGTCCTGGCCAGCCGGGCTTTGAGGGAGAGCAGGGGACCAGAGGTGCACAGGGCCCA
GCTGGTCCTGCTGGTCCTCCAGGGCTGATAGGAGAACAAGGCATTTCTGGACCTAGGGGAAGCGGAGGTGCCCGT
GGCGCTCCTGGAGAACGAGGCAGAACCGGTCCACTGGGAAGAAAGGGTGAGCCCGGAGAGCCAGGACCAAAAGGA
GGAATCGGGAACCCGGGCCCTCGTGGGGAGACGGGAGATGACGGGAGAGACGGAGTTGGCAGTGAAGGACGCAGA
GGCAAAAAAGGAGAAAGAGGATTTCCTGGATACCCAGGACCAAAGGGTAACCCAGGTGAACCTGGGCTAAATGGA
ACAACAGGACCCAAAGGCATCAGAGGCCGAAGGGGAAATTCGGGACCTCCAGGGATAGTTGGACAGAAGGGGAGA
CCTGGCTACCCAGGACCAGCTGGTCCAAGGGGCAACAGGGGCGACTCCATCGATCAATGTGCCCTCATCCAAAGC
ATCAAAGATAAATGCCCTTGCTGTTACGGGCCCCTGGAGTGCCCCGTCTTCCCAACAGAACTAGCCTTTGCTTTA
GACACCTCTGAGGGAGTCAACCAAGACACTTTCGGCCGGATGCGAGATGTGGTCTTGAGTATTGTGAATGTCCTG
ACCATTGCTGAGAGCAACTGCCCGACGGGGGCCCGGGTGGCTGTGGTCACCTACAACAACGAGGTGACCACGGAG
ATCCGGTTTGCTGACTCCAAGAGGAAGTCGGTCCTCCTGGACAAGATTAAGAACCTTCAGGTGGCTCTGACATCC

FIGURE 212C

AAACAGCAGAGTCTGGAGACTGCCATGTCGTTTGTGGCCAGGAACACATTTAAGCGTGTGAGGAACGGATTCCTA
ATGAGGAAAGTGGCTGTTTTCTTCAGCAACACACCCACAAGAGCATCCCCACAGCTCAGAGAGGCTGTGCTCAAA
CTCTCAGATGCGGGGATCACCCCCTTGTTCCTTACAAGGCAGGAAGACCGGCAGCTCATCAACGCTTTGCAGATC
AATAACACAGCAGTGGGGCATGCGCTTGTCCTGCCTGCAGGGAGAGACCTCACAGACTTCCTGGAGAATGTCCTC
ACGTGTCATGTTTGCTTGGACATCTGCAACATCGACCCATCCTGTGGATTTGGCAGTTGGAGGCCTTCCTTCAGG
GACAGGAGAGCGGCAGGGAGTGATGTGGACATCGACATGGCTTTCATCTTAGACAGCGCTGAGACCACCACCCTG
TTCCAGTTCAATGAGATGAAGAAGTACATAGCGTACCTGGTCAGACAACTGGACATGAGCCCAGATCCCAAGGCC
TCCCAGCACTTCGCCAGAGTGGCAGTTGTGCAGCACGCGCCCTCTGAGTCCGTGGACAATGCCAGCATGCCACCT
GTGAAGGTGGAATTCTCCCTGACTGACTATGGCTCCAAGGAGAAGCTGGTGGACTTCCTCAGCAGGGGAATGACA
CAGTTGCAGGGAACCAGGGCCTTAGGCAGTGCCATTGAATACACCATAGAGAATGTCTTTGAAAGTGCCCCAAAC
CCACGGGACCTGAAAATTGTGGTCCTGATGCTGACGGGCGAGGTGCCGGAGCAGCAGCTGGAGGAGGCCCAGAGA
GTCATCCTGCAGGCCAAATGCAAGGGCTACTTCTTCGTGGTCCTGGGCATTGGCAGGAAGGTGAACATCAAGGAG
GTATACACCTTCGCCAGTGAGCCAAACGACGTCTTCTTCAAATTAGTGGACAAGTCCACCGAGCTCAACGAGGAG
CCTTTGATGCGCTTCGGGAGGCTGTTGCCGTCCTTCGTCAGCAGTGAAAATGCTTTTTACTTGTCCCCAGATATC
AGGAAACAGTGTGATTGGTTCCAAGGGGACCAACCCACAAAGAACCTTGTGAAGTTTGGTCACAAACAAGTAAAT
GTTCCGAATAACGTTACTTCAAGTCCTACATCCAACCCAGTGACGACAACGAAGCCGGTGACTACGACGAAGCCG
GTGACCACCACAACAAAGCCTGTAACCACCACAACAAAGCCTGTGACTATTATAAATCAGCCATCTGTGAAGCCA
GCCGCTGCAAAGCCGGCCCCTGCGAAACCTGTGGCTGCCAAGCCTGTGGCCACAAAGACGGCCACTGTTAGACCC
CCAGTGGCGGTGAAGCCAGCAACAGCAGCGAAGCCTGTAGCAGCAAAGCCAGCAGCTGTAAGACCCCCCGCTGCT
GCTGCAAAACCAGTGGCGACCAAGCCTGAGGTCCCTAGGCCACAGGCAGCCAAACCAGCTGCCACCAAGCCAGCC
ACCACTAAGCCCGTGGTTAAGATGCTCCGTGAAGTCCAGGTGTTTGAGATAACAGAGAACAGCGCCAAACTCCAC
TGGGAGAGGCCTGAGCCCCCCGGTCCTTATTTTTATGACCTCACCGTCACCTCAGCCCATGATCAGTCCCTGGTT
CTGAAGCAGAACCTCACGGTCACGGACCGCGTCATTGGAGGCCTGCTCGCTGGGCAGACATACCATGTGGCTGTG
GTCTGCTACCTGAGGTCTCAGGTCAGAGCCACCTACCACGGAAGTTTCAGTACAAAGAAATCTCAGCCCCCACCT
CCACAGCCAGCAAGGTCAGCTTCTAGTTCAACCATCAATCTAATGGTGAGCACAGAACCATTGGCTCTCACTGAA
ACAGATATATGCAAGTTGCCGAAAGACGAAGGAACTTGCAGGGATTTCATATTAAAATGGTACTATGATCCAAAC
ACCAAAAGCTGTGCAAGATTCTGGTATGGAGGTTGTGGTGGAAACGAAAACAAATTTGGATCACAGAAAGAATGT
GAAAAGGTTTGCGCTCCTGTGCTCGCCAAACCCGGAGTCATCAGTGTGATGGGAACCTAAGCGTGGGTGGCCAAC
ATCATATACCTCTTGAAGAAGAAGGAGTCAGCCATCGCCAACTTGTCTCTGTAGAAGCTCCGGGTGTAGATTCCC
TTGCACTGTATCATTTCATGCTTTGATTTACACTCGAACTCGGGAGGGAACATCCTGCTGCATGACCTATCAGTA
TGGTGCTAATGTGTCTGTGGACCCTCGCTCTCTGTCTCCAGCAGTTCTCTCGAATACTTTGAATGTTGTGTAACA
GTTAGCCACTGCTGGTGTTTATGTGAACATTCCTATCAATCCAAATTCCCTCTGGAGTTTCATGTTATGCCTGTT
GCAGGCAAATGTAAAGTCTAGAAAATAATGCAAATGTCACGGCTACTCTATATACTTTTGCTTGGTTCATTTTTT
TTCCCTTTTAGTTAAGCATGACTTTAGATGGGAAGCCTGTGTATCGTGGAGAAACAAGAGACCAACTTTTTCATT
CCCTGCCCCCAATTTCCCAGACTAGATTTCAAGCTAATTTTCTTTTTCTGAAGCCTCTAACAAATGATCTAGTTC
AGAAGGAAGCAAAATCCCTTAATCTATGTGCACCGTTGGGACCAATGCCTTAATTAAAGAATTTAAAAAAGTTGT
AATAGAGAATATTTTTGGCATTCCTCTCAATGTTGTGTGTTTTTTTTTTTTGTGTGCTGGAGGGAGGGGATTTAA
TTTTAATTTTAAAATGTTTAGGAAATTTATACAAAGAAACTTTTTAATAAAGTATATTGAAAGTTTAAAAAAAAA
AAAAAAA

FIGURE 213

MRKHRHLPLVAVFCLFLSGFPTTHAQQQQADVKNGAAADIIFLVDSSWTIGEEHFQLVREFLYDVVKSLAVGEND
FHFALVQFNGNPHTEFLLNTYRTKQEVLSHISNMSYIGGTNQTGKGLEYIMQSHLTKAAGSRAGDGVPQVIVVLT
DGHSKDGLALPSAELKSADVNVFAIGVEDADEGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVHSSVSPER
AGDTETLKDITAQDSADIIFLIDGSNNTGSVNFAVILDFLVNLLEKLPIGTQQIRVGVVQFSDEPRTMFSLDTYS
TKAQVLGAVKALGFAGGELANIGLALDFVVENHFTRAGGSRVEEGVPQVLVLISAGPSSDEIRYGVVALKQASVF
SFGLGAQAASRAELQHIATDDNLVFTVPEFRSFGDLQEKLLPYIVGVAQRHIVLKPPTIVTQVIEVNKRDIVFLV
DGSSALGLANFNAIRDFIAKVIQRLEIGQDLIQVAVAQYADTVRPEFYFNTHPTKREVITAVRKMKPLDGSALYT
GSALDFVRNNLFTSSAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSSIMAFAIGNKGADQAELEEIAFDSS
LVFIPAEFRAAPLQGMLPGLLAPLRTLSGTPEVHSNKRDIIFLLDGSANVGKTNFPYVRDFVMNLVNSLDIGNDN
IRVGLVQFSDTPVTEFSLNTYQTKSDILGHLRQLQLQGGSGLNTGSALSYVYANHFTEAGGSRIREHVPQLLLLL
TAGQSEDSYLQAANALTRAGILTFCVGASQANKAELEQIAFNPSLVYLMDDFSSLPALPQQLIQPLTTYVSGGVE
EVPLAQPESKRDILFLFDGSANLVGQFPVVRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDEHQSKPEIL
NLVKRMKIKTGKALNLGYALDYAQRYIFVKSAGSRIEDGVLQFLVLLVAGRSSDRVDGPASNLKQSGVVPFIFQA
KNADPAELEQIVLSPAFILAAESLPKIGDLHPQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEGVRSGFPLLKEF
VQRVVESLDVGQDRVRVAVVQYSDRTRPEFYLNSYMNKQDVVNAVRQLTLLGGPTPNTGAALEFVLRNILVSSAG
SRITEGVPQLLIVLTADRSGDDVRNPSVVVKRGGAVPIGIGIGNADITEMQTISFIPDFAVAIPTFRQLGTVQQV
ISERVTQLTREELSRLQPVLQPLPSPGVGGKRDVVFLIDGSQSAGPEFQYVRTLIERLVDYLDVGFDTTRVAVIQ
FSDDPKAEFLLNAHSSKDEVQNAVQRLRPKGGRQINVGNALEYVSRNIFKRPLGSRIEEGVPQFLVLISSGKSDD
EVVVPAVELKQFGVAPFTIARNADQEELVKISLSPEYVFSVSTFRELPSLEQKLLTPITTLTSEQIQKLLASTRY
PPPVREFRELPNIEERIMNSFGPSAATPAPPGVDTPPPSRPEKKKADIVFLLDGSINFRRDSFQEVLRFVSEIVD
TVYEDGDSIQVGLVQYNSDPTDEFFLKDFSTKRQIIDAINKVVYKGGRHANTKVGLEHLRVNHFVPEAGSRLDQR
VPQIAFVITGGKSVEDAQDVSLALTQRGVKVFAVGVRNIDSEEVGKIASNSATAFRVGNVQELSELSEQVLETLH
DAMHETLCPGVTDAAKACNLDVILGFDGSRDQNVFVAQKGFESKVDAILNRISQMHRVSCSGGRSPTVRVSVVAN
TPSGPVEAFDFDEYQPEMLEKFRNMRSQHPYVLTEDTLKVYLNKFRQSSPDSVKVVIHFTDGADGDLADLHRASE
NLRQEGVRALILVGLERVVNLERLMHLEFGRGFMYDRPLRLNLLDLDYELAEQLDNIAEKACCGVPCKCSGQRGD
RGPIGSIGPKGIPGEDGYRGYPGDEGGPGERGPPGVNGTQGFQGCPGQRGVKGSRGFPGEKGEVGEIGLDGLDGE
DGDKGLPGSSGEKGNPGRRGDKGPRGEKGERGDVGIRGDPGNPGQDSQER

FIGURE 214

GTTGGTGAGCATC**ATG**GCAACCGTTACAGCCACAACCAAAGTCCCGGAGATCCGTGATGTAACAAGGATTGAGCG
AATCGGTGCCCACTCCCACATCCGGGGACTGGGGCTGGACGATGCCTTGGAGCCTCGGCAGGCTTCGCAAGGCAT
GGTGGGTCAGCTGGCGGCACGGCGGGCGGCTGGCGTGGTGCTGGAGATGATCCGGGAAGGGAAGATTGCCGGTCG
GGCAGTCCTTATTGCTGGCCAGCCGGGCACGGGGAAGACGGCCATCGCCATGGGCATGGCGCAGGCCCTGGGCCC
TGACACGCCATTCACAGCCATCGCCGGCAGTGAAATCTTCTCCCTGGAGATGAGCAAGACCGAGGCGCTGACGCA
GGCCTTCCGGCGGTCCATCGGCGTTCGCATCAAGGAGGAGACGGAGATCATCGAAGGGGAGGTGGTGGAGATCCA
GATTGATCGACCAGCAACAGGGACGGGCTCCAAGGTGGGCAAACTGACCCTCAAGACCACAGAGATGGAGACCAT
CTACGACCTGGGCACCAAGATGATTGAGTCCCTGACCAAGGACAAGGTCCAGGCCGGGGACGTGATCACCATCGA
CAAGGCGACGGGCAAGATCTCCAAGCTGGGCCGCTCCTTCACACGCGCCCGCGACTACGACGCTATGGGCTCCCA
GACCAAGTTCGTGCAGTGCCCAGATGGGGAGCTCCAGAAACGCAAGGAGGTGGTGCACACCGTGTCCCTGCACGA
GATCGACGTCATCAACTCTCGCACCCAGGGCTTCCTGGCGCTCTTCTCAGGTGACACAGGGGAGATCAAGTCAGA
AGTCCGTGAGCAGATCAATGCCAAGGTGGCTGAGTGGCGCGAGGAGGGCAAGGCGGAGATCATCCCTGGAGTGCT
GTTCATCGACGAGGTCCACATGCTGGACATCGAGAGCTTCTCCTTCCTCAACCGGGCCCTGGAGAGTGACATGGC
GCCTGTCCTGATCATGGCCACCAACCGTGGCATCACGCGAATCCGGGGCACCAGCTACCAGAGCCCTCACGGCAT
CCCCATAGACCTGCTGGACCGGCTGCTTATCGTCTCCACCACCCCCTACAGCGAGAAAGACACGAAGCAGATCCT
CCGCATCCGGTGCGAGGAAGAAGATGTGGAGATGAGTGAGGACGCCTACACGGTGCTGACCCGCATCGGGCTGGA
GACGTCACTGCGCTACGCCATCCAGCTCATCACAGCTGCCAGCTTGGTGTGCCGGAAACGCAAGGGTACAGAAGT
GCAGGTGGATGACATCAAGCGGGTCTACTCACTCTTCCTGGACGAGTCCCGCTCCACGCAGTACATGAAGGAGTA
CCAGGACGCCTTCCTCTTCAACGAACTCAAAGGCGAGACCATGGACACCTCC**TGA**GTTGGATGTCATCCCCCGAC
CCCACCCTGTTTTCCACCAGAGTTCTGACACTGTGACTCTGTATAAAATGGTTGGGAAGCTGC

FIGURE 215

MATVTATTKVPEIRDVTRIERIGAHSHIRGLGLDDALEPRQASQGMVGQLAARRAAGVVLEMIREGKIAGRAVLI
AGQPGTGKTAIAMGMAQALGPDTPFTAIAGSEIFSLEMSKTEALTQAFRRSIGVRIKEETEIIEGEVVEIQIDRP
ATGTGSKVGKLTLKTTEMETIYDLGTKMIESLTKDKVQAGDVITIDKATGKISKLGRSFTRARDYDAMGSQTKFV
QCPDGELQKRKEVVHTVSLHEIDVINSRTQGFLALFSGDTGEIKSEVREQINAKVAEWREEGKAEIIPGVLFIDE
VHMLDIESFSFLNRALESDMAPVLIMATNRGITRIRGTSYQSPHGIPIDLLDRLLIVSTTPYSEKDTKQILRIRC
EEEDVEMSEDAYTVLTRIGLETSLRYAIQLITAASLVCRKRKGTEVQVDDIKRVYSLFLDESRSTQYMKEYQDAF
LFNELKGETMDTS

FIGURE 216

GAGCAGCGCGGCCTGACGGGACCAAGGCGGCGGGAGTCTGCGGTCGTTCCCTCGGCTGTGGACCGGGCGGCACGC
ACGCGGTGCAGGGTAAC**ATG**GCGGATGCGGAAGTAATTATTTTGCCAAAGAAACATAAGAAGAAAAAGGAGCGGA
AGTCATTGCCAGAAGAAGATGTAGCCGAAATACAACACGCTGAAGAATTTCTTATCAAACCTGAATCCAAAGTTG
CTAAGTTGGACACGTCTCAGTGGCCCCTTTTGCTAAAGAATTTTGATAAGCTGAATGTAAGGACAACACACTATA
CACCTCTTGCATGTGGTTCAAATCCTCTGAAGAGAGAGATTGGGGACTATATCAGGACAGGTTTCATTAATCTTG
ACAAGCCCTCTAACCCCTCTTCCCATGAGGTGGTAGCCTGGATTCGACGGATACTTCGGGTGGAGAAGACAGGGC
ACAGTGGTACTCTGGATCCCAAGGTGACTGGTTGTTTAATCGTGTGCATAGAACGAGCCACTCGCTTGGTGAAGT
CACAACAGAGTGCAGGCAAAGAGTATGTGGGGATTGTCCGGCTGCACAATGCTATTGAAGGGGGGACCCAGCTTT
CTAGGGCCCTAGAAACTCTGACAGGTGCCTTATTCCAGCGACCCCCACTTATTGCTGCAGTAAAGAGGCAGCTCC
GAGTGAGGACCATCTACGAGAGCAAAATGATTGAATACGATCCTGAAAGAAGATTAGGAATCTTTTGGGTGAGTT
GTGAGGCTGGCACCTACATTCGGACATTATGTGTGCACCTTGGTTTGTTATTGGGAGTTGGTGGTCAGATGCAGG
AGCTTCGGAGGGTTCGTTCTGGAGTCATGAGTGAAAAGGACCACATGGTGACAATGCATGATGTGCTTGATGCTC
AGTGGCTGTATGATAACCACAAGGATGAGAGTTACCTGCGGCGAGTTGTTTACCCTTTGGAAAAGCTGTTGACAT
CTCATAAACGGCTGGTTATGAAAGACAGTGCAGTAAATGCCATCTGCTATGGGGCCAAGATTATGCTTCCAGGTG
TTCTTCGATATGAGGACGGCATTGAGGTCAATCAGGAGATTGTGGTTATCACCACCAAAGGAGAAGCAATCTGCA
TGGCTATTGCATTAATGACCACAGCGGTCATCTCTACCTGCGACCATGGTATAGTAGCCAAGATCAAGAGAGTGA
TCATGGAGAGAGACACTTACCCTCGGAAGTGGGGTTTAGGTCCAAAGGCAAGTCAGAAGAAGCTGATGATCAAGC
AGGGCCTTCTGGACAAGCATGGGAAGCCCACAGACAGCACACCTGCCACCTGGAAGCAGGAGTATGTTGACTACA
GTGAGTCTGCCAAAAAAGAGGTGGTTGCTGAAGTGGTAAAAGCCCCGCAGGTAGTTGCCGAAGCAGCAAAAACTG
CGAAGCGGAAGCGAGAGAGTGAGAGTGAAAGTGACGAGACTCCTCCAGCAGCTCCTCAGTTGATCAAGAAGGAAA
AGAAGAAGAGTAAGAAGGACAAGAAGGCCAAAGCTGGTCTGGAGAGCGGGGCCGAGCCTGGAGATGGGGACAGTG
ATACCACCAAGAAGAAGAAGAAGAAGAAAGCAAAAGAGGTAGAATTGGTTTCTGAG**TAG**TGAAGGCCACTTG
AAGCTGGAGGAGAAACTAAAGCCTTATTGAGAAAACATGTTATAGATCCTTTTGTTGCTGAGAGAGTGGAACATA
GGTCCTAGACAGGGTGAAGAGTTCTGGCACATTTTAGCTGCTACTTTGAGACCTCGGTGATGTTACCTGGTGTGG
TCATCCCATCTTGTCCTGTTTTAAGGATATGGGTGGTGAAAGATGAAAGAGGCAGAGTTTATCCCAATGACTTCT
CTGTTTGAGTTGGGAAGCCTCACCTTCAGACCCAGTAACTGTCCGCAGCTGTCTGCTAGTGGTTGTCTTAACATC
GTAGTCCTAGTTTGCATTTTTTAAATCCCCTCTGTTTAAAAGGTTTGTAAAACAAAAACAAAAAACTAAGTCTGC
TCAGTGAAATGCTGTAGAACCCTAAATAAGTGGTAGAAGAGTGTCACTGAATTTTGTCTCTGAATTCAGTATAAC
TGAGTTTTGTCCATGCTGGTGTCTGGGTTATAGGCCTGATGGGCCTGGTAGTTTTCCATCTTGTTCTGGCCTAGA
GGTCAGTCCTTTGCACTTCCTCAAAGCTTGTGTACAGTGCTCACCTAAATCCATCTGACTACTTGTTCCTGTGCC
CTCTTGTTTTAGGCCTCGTTTACTTTTAAAAAATGAAATTGTTCATTGCTGGGAGAAGAATGTTGTAATTTTTAC
TTATTAAAGTCAACTTGTTAAGTTTTTTATGTATTCCTGTTGGGTTTTCTTGTTGATCTCATGCTAGCAGAGCAA
AAATTGTAAAATATTTTGATTAAAAATCTAGGGACCTTTATGTCCTATTTGGAATTCGATATCAA

FIGURE 217

MADAEVIILPKKHKKKKERKSLPEEDVAEIQHAEEFLIKPESKVAKLDTSQWPLLLKNFDKLNVRTTHYTPLACG
SNPLKREIGDYIRTGFINLDKPSNPSSHEVVAWIRRILRVEKTGHSGTLDPKVTGCLIVCIERATRLVKSQQSAG
KEYVGIVRLHNAIEGGTQLSRALETLTGALFQRPPLIAAVKRQLRVRTIYESKMIEYDPERRLGIFWVSCEAGTY
IRTLCVHLGLLLGVGGQMQELRRVRSGVMSEKDHMVTMHDVLDAQWLYDNHKDESYLRRVVYPLEKLLTSHKRLV
MKDSAVNAICYGAKIMLPGVLRYEDGIEVNQEIVVITTKGEAICMAIALMTTAVISTCDHGIVAKIKRVIMERDT
YPRKWGLGPKASQKKLMIKQGLLDKHGKPTDSTPATWKQEYVDYSESAKKEVVAEVVKAPQVVAEAAKTAKRKRE
SESESDETPPAAPQLIKKEKKKSKKDKKAKAGLESGAEPGDGDSDTTKKKKKKKAKEVELVSE

FIGURE 218

TCTGGGCGCGCGCGACGTCAGTTTGAGTTCTGTGTTCTCCCCGCCCGTGTCCCGCCCGACCCGCGCCCGCG**ATG**C
TGGCGCTGCGCTGCGGCTCCCGCTGGCTCGGCCTGCTCTCCGTCCCGCGCTCCGTGCCGCTGCGCCTCCCCGCGG
CCCGCGCCTGCAGCAAGGGCTCCGGCGACCCGTCCTCTTCCTCCTCCTCCGGGAACCCGCTCGTGTACCTGGACG
TGGACGCCAACGGGAAGCCGCTCGGCCGCGTGGTGCTGGAGCTGAAGGCAGATGTCGTCCCAAAGACAGCTGAGA
ACTTCAGAGCCCTGTGCACTGGTGAGAAGGGCTTCGGCTACAAAGGCTCCACCTTCCACAGGGTGATCCCTTCCT
TCATGTGCCAGGCGGGCGACTTCACCAACCACAATGGCACAGGCGGGAAGTCCATCTACGGAAGCCGCTTTCCTG
ACGAGAACTTTACACTGAAGCACGTGGGGCCAGGTGTCCTGTCCATGGCTAATGCTGGTCCTAACACCAACGGCT
CCCAGTTCTTCATCTGCACCATAAAGACAGACTGGTTGGATGGCAAGCATGTTGTGTTCGGTCACGTCAAAGAGG
GCATGGACGTCGTGAAGAAAATAGAATCTTTCGGCTCTAAGAGTGGGAGGACATCCAAGAAGATTGTCATCACAG
ACTGTGGCCAGTTGAGC**TAA**TCTGTGGCCAGGGTGCTGGCATGGTGGCAGCTGCAAATGTCCATGCACCCAGGTG
GCCGCGTTGGGCTGTCAGCCAAGGTGCCTGAAACGATACGTGTGCCCACTCCACTGTCACAGTGTGCCTGAGGAA
GGCTGCTAGGGATGTTAGACCTCGGCCAGGACCCACCACATTGCTTCCTAATACCCACCCTTCCTCACGACCTCA
TTTCTGGGCATCTTTGTGGACATGATGTCACCCACCCCTTGTCAAGCATTGCCTGTGATTGCCCAGCCCAGATTC
ATCTGTGCCTTGGACATGGTGATGGTGATGGGTTGCCATCCAAGTGAAAGTCTTTTCCTTGACCAAGGGGGACAG
TCAGTTTTGCAAAAGGACTCTAATACCTGTTTAATATTGTCTTCCTAATTGGGATAATTTAATTAACAAGATTGA
CTAGAAGTGAAACTGCAACACTAACTTCCCCGTGCTGTGGTGTGACCTGAGTTGGTGACACAGGCCACAGACCCC
AGAGCTTGGCTTTTGAAACACAACTCAGGGCTTTTGTGAAGGTTCCCCCGCTGAGATCTTTCCTCCTGGTTACTG
TGAAGCCTGTTGGTTTGCTGCTGTCGTTTTTGAGGAGGGCCCATGGGGGTAGGAGCAGTTGAACCTGGGAACAAA
CCTCACTTGAGCTGTGCCTAGACAATGTGAATTCCTGTGTTGCTAACAGAAGTGGCCTGTAAGCTCCTGTGCTCC
GGAGGGAAGCATTTCCTGGTAGGCTTTGATTTTTCTGTGTGTTAAAGAAATTCAATCTACTCATGATGTGTTATG
CATAAAACATTTCTGGAACATGGATTTGTGTTCACCTTAAATGTGAAAATAAATCCTATTTTCTATGGAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 219

MLALRCGSRWLGLLSVPRSVPLRLPAARACSKGSGDPSSSSSSGNPLVYLDVDANGKPLGRVVLELKADVVPKTA
ENFRALCTGEKGFGYKGSTFHRVIPSFMCQAGDFTNHNGTGGKSIYGSRFPDENFTLKHVGPGVLSMANAGPNTN
GSQFFICTIKTDWLDGKHVVFGHVKEGMDVVKKIESFGSKSGRTSKKIVITDCGQLS

FIGURE 220

TCTGGGCGCGCGCGACGTCAGTTTGAGTTCTGTGTTCTCCCCGCCCGTGTCCCGCCCGACCCGCGCCCGCG**ATG**C
TGGCGCTGCGCTGCGGCTCCCGCTGGCTCGGCCTGCTCTCCGTCCCGCGCTCCGTGCCGCTGCGCCTCCCCGCGG
CCCGCGCCTGCAGCAAGGGCTCCGGCGACCCGTCCTCTTCCTCCTCCTCCGGGAACCCGCTCGTGTACCTGGACG
TGGACGCCAACGGGAAGCCGCTCGGCCGCGTGGTGCTGGAGCTGAAGGCAGATGTCGTCCCAAAGACAGCTGAGA
ACTTCAGAGCCCTGTGCACTGGTGAGAAGGGCTTCGGCTACAAAGGCTCCACCTTCCACAGGGTGATCCCTTCCT
TCATGTGCCAGGCGGGCGACTTCACCAACCACAATGGCACAGGCGGGAAGTCCATCTACGGAAGCCGCTTTCCTG
ACGAGAACTTTACACTGAAGCACGTGGGGCCAGGTGTCCTGTCCATGGCTAATGCTGGTCCTAACACCAACGGCT
CCCAGTTCTTCATCTGCACCATAAAGACAGACTGGTTGGATGGCAAGCATGTTGTGTTCGGTCACGTCAAAGAGG
GCATGGACGTCGTGAAGAAAATAGAATCTTTCGGCTCTAAGAGTGGGAGGACATCCAAGAAGATTGTCATCACAG
ACTGTGGCCAGTTGAGC**TAA**TCTGTGGCCAGGGTGCTGGCATGGTGGCAGCTGCAAATGTCCATGCACCCAGGTG
GCCGCGTTGGGCTGTCAGCCAAGGTGCCTGAAACGATACGTGTGCCCACTCCACTGTCACAGTGTGCCTGAGGAA
GGCTGCTAGGGATGTTAGACCTCGGCCAGGACCCACCACATTGCTTCCTAATACCCACCCTTCCTCACGACCTCA
TTTCTGGGCATCTTTGTGGACATGATGTCACCCACCCCTTGTCAAGCATTGCCTGTGATTGCCCAGCCCAGATTC
ATCTGTGCCTTGGACATGGTGATGGTGATGGGTTGCCATCCAAGTGAAAGTCTTTTCCTTGACCAAGGGGGACAG
TCAGTTTTGCAAAAGGACTCTAATACCTGTTTAATATTGTCTTCCTAATTGGGATAATTTAATTAACAAGATTGA
CTAGAAGTGAAACTGCAACACTAACTTCCCCGTGCTGTGGTGTGACCTGAGTTGGTGACACAGGCCACAGACCCC
AGAGCTTGGCTTTTGAAACACAACTCAGGGCTTTTGTGAAGGTTCCCCCGCTGAGATCTTTCCTCCTGGTTACTG
TGAAGCCTGTTGGTTTGCTGCTGTCGTTTTTGAGGAGGGCCCATGGGGGTAGGAGCAGTTGAACCTGGGAACAAA
CCTCACTTGAGCTGTGCCTAGACAATGTGAATTCCTGTGTTGCTAACAGAAGTGGCCTGTAAGCTCCTGTGCTCC
GGAGGGAAGCATTTCCTGGTAGGCTTTGATTTTTCTGTGTGTTAAAGAAATTCAATCTACTCATGATGTGTTATG
CATAAAACATTTCTGGAACATGGATTTGTGTTCACCTTAAATGTGAAAATAAATCCTATTTTCTATGGAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 221

MLALRCGSRWLGLLSVPRSVPLRLPAARACSKGSGDPSSSSSSGNPLVYLDVDANGKPLGRVVLELKADVVPKTA
ENFRALCTGEKGFGYKGSTFHRVIPSFMCQAGDFTNHNGTGGKSIYGSRFPDENFTLKHVGPGVLSMANAGPNTN
GSQFFICTIKTDWLDGKHVVFGHVKEGMDVVKKIESFGSKSGRTSKKIVITDCGQLS

FIGURE 222

TGCCGCCGTCCCGCCCGCCAGCGCCCCAGCGAGGAAGCAGCGCGCAGCCCGCGGCCCAGCGCACCCGCAGCAGCG
CCCGCAGCTCGTCCGCGCC**ATG**TTCCAGGCGGCCGAGCGCCCCCAGGAGTGGGCCATGGAGGGCCCCCGCGACGG
GCTGAAGAAGGAGCGGCTACTGGACGACCGCCACGACAGCGGCCTGGACTCCATGAAAGACGAGGAGTACGAGCA
GATGGTCAAGGAGCTGCAGGAGATCCGCCTCGAGCCGCAGGAGGTGCCGCGCGGCTCGGAGCCCTGGAAGCAGCA
GCTCACCGAGGACGGGGACTCGTTCCTGCACTTGGCCATCATCCATGAAGAAAAGGCACTGACCATGGAAGTGAT
CCGCCAGGTGAAGGGAGACCTGGCTTTCCTCAACTTCCAGAACAACCTGCAGCAGACTCCACTCCACTTGGCTGT
GATCACCAACCAGCCAGAAATTGCTGAGGCACTTCTGGGAGCTGGCTGTGATCCTGAGCTCCGAGACTTTCGAGG
AAATACCCCCCTACACCTTGCCTGTGAGCAGGGCTGCCTGGCCAGCGTGGGAGTCCTGACTCAGTCCTGCACCAC
CCCGCACCTCCACTCCATCCTGAAGGCTACCAACTACAATGGCCACACGTGTCTACACTTAGCCTCTATCCATGG
CTACCTGGGCATCGTGGAGCTTTTGGTGTCCTTGGGTGCTGATGTCAATGCTCAGGAGCCCTGTAATGGCCGGAC
TGCCCTTCACCTCGCAGTGGACCTGCAAAATCCTGACCTGGTGTCACTCCTGTTGAAGTGTGGGGCTGATGTCAA
CAGAGTTACCTACCAGGGCTATTCTCCCTACCAGCTCACCTGGGGCCGCCCAAGCACCCGGATACAGCAGCAGCT
GGGCCAGCTGACACTAGAAAACCTTCAGATGCTGCCAGAGAGTGAGGATGAGGAGAGCTATGACACAGAGTCAGA
GTTCACGGAGTTCACAGAGGACGAGCTGCCCTATGATGACTGTGTGTTTGGAGGCCAGCGTCTGACGTTA**TGA**GT
GCAAAGGGGCTGAAAGAACATGGACTTGTATATTTGTACAAAAAAAAAGTTTTATTTTTCTAAAAAAAGAAAAAA
GAAGAAAAAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTAGCCCAAAACGTCTTATTGTGGTAGGA
TCAGCCCTCATTTTGTTGCTTTTGTGAACTTTTTGTAGGGGACGAGAAAGATCATTGAAATTCTGAGAAAACTTC
TTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCAAAAATTTCATGGAAGGACCACATTTTATATTTA
TTGTGCTTCGAGTGACTGACCCCAGTGGTATCCTGTGACATGTAACAGCCAGGAGTGTTAAGCGTTCAGTGATGT
GGGGTGAAAAGTTACTACCTGTCAAGGTTTGTGTTACCCTCCTGTAAATGGTGTACATAATGTATTGTTGGTAAT
TATTTTGGTACTTTTATGATGTATATTTATTAAAGAGATTTTTACAAATG

FIGURE 223

MFQAAERPQEWAMEGPRDGLKKERLLDDRHDSGLDSMKDEEYEQMVKELQEIRLEPQEVPRGSEPWKQQLTEDGD
SFLHLAIIHEEKALTMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHL
ACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVELLVSLGADVNAQEPCNGRTALHLAV
DLQNPDLVSLLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTESEFTEFTE
DELPYDDCVFGGQRLTL

FIGURE 224

CGGCGGAGCTGGTCCCGTTGTGCTGCGGCGCCGCGCGGCCTGCAGTCCCGGGCCCGCGCCCCGCGCCGCCCGCCC
GCCCGCC**ATG**GAGCCCGGCCCCGACGGCCCCGCCGCCTCCGGCCCCGCCGCCATCCGCGAGGGCTGGTTCCGCGA
GACCTGCAGCCTGTGGCCCGGCCAGGCCCTGTCGCTGCAGGTGGAGCAGCTGCTCCACCACCGGCGCTCGCGCTA
CCAGGACATCCTCGTCTTCCGCAGTAAGACCTATGGCAACGTGCTGGTGTTGGACGGTGTCATCCAGTGCACGGA
GAGAGACGAGTTCTCCTACCAGGAGATGATCGCCAACCTGCCTCTCTGCAGCCACCCCAACCCGCGAAAGGTGCT
GATCATCGGGGGCGGAGATGGAGGTGTCCTGCGGGAGGTGGTGAAGCACCCCTCCGTGGAGTCCGTGGTCCAGTG
TGAGATCGACGAGGATGTCATCCAAGTCTCCAAGAAGTTCCTGCCAGGCATGGCCATTGGCTACTCTAGCTCGAA
GGTGACCCTACATGTGGGTGACGGTTTTGAGTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGA
CTCCTCAGACCCCATGGGCCCCGCCGAAAGTCTCTTCAAGGAGTCCTATTACCAGCTCATGAAGACAGCCCTCAA
GGAAGATGGTGTCCTCTGCTGCCAGGGCGAGTGCGAGTGGCTGCACCTGGACCTCATCAAGGAGATGCGGCAGTT
CTGCCAGTCCCTGTTCCCCGTGGTGGCCTATGCCTACTGCACCATCCCCACCTACCCCAGCGGCCAGATCGGCTT
CATGCTGTGCAGCAAGAACCCGAGCACGAACTTCCAGGAGCCGGTGCAGCCGCTGACACAGCAGCAGGTGGCGCA
GATGCAGCTGAAGTACTACAACTCCGACGTGCACCGCGCCGCCTTTGTGCTGCCCGAGTTTGCCCGCAAGGCCCT
GAATGATGTGAGC**TGA**GCCCAGGCGCCACCACTGATGCCACCCAGGACCTCGGACCTTGGAGCCTGCGGGGTGCC
TCGGCCCCTCCAGCCCCGGGCCGGACCTCCTGCTGGCTCTCGCCCACCAACCAAGTGTTACAAGCCCCAGAATGC
TGCCCGGCCTGCCCTGCTGGGCGGACTGTCTGTGTGTCTGTCTCTCTGGCGTTCCACCTCCAAGCCTATACCAGC
TGTGTACAGCGCCATCTCTCTGCCTTCTGTTGCCCCCG

FIGURE 225

MEPGPDGPAASGPAAIREGWFRETCSLWPGQALSLQVEQLLHHRRSRYQDILVFRSKTYGNVLVLDGVIQCTERD
EFSYQEMIANLPLCSHPNPRKVLIIGGGDGGVLREVVKHPSVESVVQCEIDEDVIQVSKKFLPGMAIGYSSSKVT
LHVGDGFEFMKQNQDAFDVIITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECEWLHLDLIKEMRQFCQ
SLFPVVAYAYCTIPTYPSGQIGFMLCSKNPSTNFQEPVQPLTQQQVAQMQLKYYNSDVHRAAFVLPEFARKALND
VS

FIGURE 226

ACTCGTGCGTGAGGCGAGAGGAGCCGGAGACGAGACCAGAGGCCGAACTCGGGTTCTGACAAG**ATG**GCCGGGCTG
CCCCGCAGGATCATCAAGGAAACCCAGCGTTTGCTGGCAGAACCAGTTCCTGGCATCAAAGCCGAACCAGATGAG
AGCAACGCCCGTTATTTTCATGTGGTCATTGCTGGCCCTCAGGATTCCCCCTTTGAGGGAGGGACTTTTAAACTT
GAACTATTCCTTCCAGAAGAATACCCAATGGCAGCCCCTAAAGTACGTTTCATGACCAAAATTTATCATCCTAAT
GTAGACAAGTTGGGAAGAATATGTTTAGATATTTTGAAAGATAAGTGGTCCCCAGCACTGCAGATCCGCACAGTT
CTGCTATCGATCCAGGCCTTGTTAAGTGCTCCCAATCCAGATGATCCATTAGCAAATGATGTAGCGGAGCAGTGG
AAGACCAACGAAGCCCAAGCCATAGAAACAGCTAGAGCATGGACTAGGCTATATGCCATGAATAATATT**TAA**ATT
GATACGATCATCAAGTGTGCATCACTTCTCCTGTTCTGCCAAGACTTCCTCCTCTTTGTTTGCATTTAATGGACA
CAGTCTTAGAAACATTACAGAATAAAAAAGCCCAGACATCTTCAGTCCTTTGGTGATTAAATGCACATTAGCAAA
TCTATGTCTTGTCCTGATTCACTGTCATAAAGCATGAGCAGAGGCTAGAAGTATCATCTGGATTGTTGTGAAACG
TTTAAAAGCAGTGGCCCCTCCCTGCTTTTATTCATTTCCCCCATCCTGGTTTAAGTATAAAGCACTGTGAATGAA
GGTAGTTGTCAGGTTAGCTGCAGGGGTGTGGGTGTTTTTATTTTATTTTATTTTATTTTATTTTTGAGGGGGGAG
GTAGTTTAATTTTATGGGCTCCTTTCCCCCTTTTTTGGTGATCTAATTGCATTGGTTAAAAGCAGCTAACCAGGT
CTTTAGAATATGCTCTAGCCAAGTCTAACTTTATTTAGACGCTGTAGATGGACAAGCTTGATTGTTGGAACCAAA
ATGGGAACATTAAACAAACATCACAGCCCTCACTAATAACATTGCTGTCAAGTGTAGATTCCCCCCTTCAAAAAA
AGCTTGTGACCATTTTGTATGGCTTGTCTGGAAACTTCTGTAAATCTTATGTTTTAGTAAAATATTTTTTGTTAT
TCT

FIGURE 227

MAGLPRRIIKETQRLLAEPVPGIKAEPDESNARYFHVVIAGPQDSPFEGGTFKLELFLPEEYPMAAPKVRFMTKI
YHPNVDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETARAWTRLYAMN
NI

FIGURE 228

CTAGTTTCTAAGGATC**ATG**TCTGCGAGCCAGGATTCCCGATCCAGAGACAATGGCCCCGATGGGATGGAGCCCGA
AGGCGTCATCGAGAGTAACTGGAATGAGATTGTTGACAGCTTTGATGACATGAACCTCTCGGAGTCCCTTCTCCG
TGGCATCTACGCCTATGGTTTTGAGAAGCCCTCTGCCATCCAGCAGCGAGCCATTCTACCTTGTATCAAGGGTTA
TGATGTGATTGCTCAAGCCCAATCTGGGACTGGGAAAACGGCCACATTTGCCATATCGATTCTGCAGCAGATTGA
ATTAGATCTAAAAGCCACCCAGGCCTTGGTCCTAGCACCCACTCGAGAATTGGCTCAGCAGATACAGAAGGTGGT
CATGGCACTAGGAGACTACATGGGCGCCTCCTGTCACGCCTGTATCGGGGGCACCAACGTGCGTGCTGAGGTGCA
GAAACTGCAGATGGAAGCTCCCCACATCATCGTGGGTACCCCTGGCCGTGTGTTTGATATGCTTAACCGGAGATA
CCTGTCCCCCAAATACATCAAGATGTTTGTACTGGATGAAGCTGACGAAATGTTAAGCCGTGGATTCAAGGACCA
GATCTATGACATATTCCAAAAGCTCAACAGCAACACCCAGGTAGTTTTGCTGTCAGCCACAATGCCTTCTGATGT
GCTTGAGGTGACCAAGAAGTTCATGAGGGACCCCATTCGGATTCTTGTCAAGAAGGAAGAGTTGACCCTGGAGGG
TATCCGCCAGTTCTACATCAACGTGGAACGAGAGGAGTGGAAGCTGGACACACTATGTGACTTGTATGAAACCCT
GACCATCACCCAGGCAGTCATCTTCATCAACACCCGGAGGAAGGTGGACTGGCTCACCGAGAAGATGCATGCTCG
AGATTTCACTGTATCCGCCATGCATGGAGATATGGACCAAAAGGAACGAGACGTGATTATGAGGGAGTTTCGTTC
TGGCTCTAGCAGAGTTTTGATTACCACTGACCTGCTGGCCAGAGGCATTGATGTGCAGCAGGTTTCTTTAGTCAT
CAACTATGACCTTCCCACCAACAGGGAAAACTATATCCACAGAATCGGTCGAGGTGGACGGTTTGGCCGTAAAGG
TGTGGCTATTAACATGGTGACAGAAGAAGACAAGAGGACTCTTCGAGACATTGAGACCTTCTACAACACCTCCAT
TGAGGAAATGCCCCTCAATGTTGCTGACCTCATC**TGA**GGGGCTGTCCTGCCACCCAGCCCCAGCCAGGGCTCAAT
CTCTGGGGGCTGAGGAGCAGCAGGAGGGGGGAGGGAAGGGAGCCAAGGGATGGACATCTTGTCATTTTTTTTCTT
TGAATAAATGTCACTTTTTGAGGCAAAAGAAGG

FIGURE 229

MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSESLLRGIYAYGFEKPSAIQQRAILPCIKGYDVIAQ
AQSGTGKTATFAISILQQIELDLKATQALVLAPTRELAQQIQKVVMALGDYMGASCHACIGGTNVRAEVQKLQME
APHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDEADEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLEVTK
KFMRDPIRILVKKEELTLEGIRQFYINVEREEWKLDTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFTVS
AMHGDMDQKERDVIMREFRSGSSRVLITTDLLARGIDVQQVSLVINYDLPTNRENYIHRIGRGGRFGRKGVAINM
VTEEDKRTLRDIETFYNTSIEEMPLNVADLI

FIGURE 230

GCACG**ATG**AGCTCAATCGGCACTGGGTATGACCTGTCAGCCTCTACATTCTCTCCTGACGGAAGAGTTTTTCAAG
TTGAATATGCTATGAAGGCTGTGGAAAATAGTAGTACAGCTATTGGAATCAGATGCAAAGATGGTGTTGTCTTTG
GGGTAGAAAAATTAGTCCTTTCTAAACTTTATGAAGAAGGTTCCAACAAAAGACTTTTTAATGTTGATCGGCATG
TTGGAATGGCAGTAGCAGGTTTGTTGGCAGATGCTCGTTCTTTAGCAGACATAGCAAGAGAAGAAGCTTCCAACT
TCAGATCTAACTTTGGCTACAACATTCCACTAAAACATCTTGCAGACAGAGTGGCCATGTATGTGCATGCATATA
CACTCTACAGTGCTGTTAGACCTTTTGGCTGCAGTTTCATGTTAGGGTCTTACAGTGTGAATGACGGTGCGCAAC
TCTACATGATTGACCCATCAGGTGTTTCATACGGTTATTGGGGCTGTGCCATCGGCAAAGCCAGGCAAGCTGCAA
AGACGGAAATAGAGAAGCTTCAGATGAAAGAAATGACCTGCCGTGATATCGTTAAAGAAGTTGCAAAAATAATTT
ACATAGTACATGACGAAGTTAAGGATAAAGCTTTTGAACTAGAACTCAGCTGGGTTGGTGAATTAACTAATGGAA
GACATGAAATTGTTCCAAAAGATATAAGAGAAGAAGCAGAGAAATATGCTAAGGAATCTCTGAAGGAAGAAGATG
AATCAGATGATGATAATATG**TAA**CATTTACTCCAGCATCTATTGTATTTTAAATTTCTACTCCAGTCCAATGTAA
CTATTTAGCCCTG

FIGURE 231

MSSIGTGYDLSASTFSPDGRVFQVEYAMKAVENSSTAIGIRCKDGVVFGVEKLVLSKLYEEGSNKRLFNVDRHVG
MAVAGLLADARSLADIAREEASNFRSNFGYNIPLKHLADRVAMYVHAYTLYSAVRPFGCSFMLGSYSVNDGAQLY
MIDPSGVSYGYWGCAIGKARQAAKTEIEKLQMKEMTCRDIVKEVAKIIYIVHDEVKDKAFELELSWVGELTNGRH
EIVPKDIREEAEKYAKESLKEEDESDDDNM

FIGURE 232

ATTCTGAGCCGAGCCCGGTGCCAAGCGCAGCTAGCTCAGCAGGCGGCAGCGGCGGCCTGAGCTTCAGGGCAGCCA
GCTCCTCCCGGTCTCGCCTTCCTCGCGGTCAGC**ATG**AAAGCCTTCAGTCCCGTGAGGTCCGTTAGGAAAAACAGC
CTGTCGGACCACAGCCTGGGCATCTCCCGGAGCAAAACCCCTGTGGACGACCCGATGAGCCTGCTATACAACATG
AACGACTGCTACTCCAAGCTCAAGGAGCTGGTGCCCAGCATCCCCCAGAACAAGAAGGTGAGCAAGATGGAAATC
CTGCAGCACCTCATCGACTACATCTTGGACCTGCAGATCGCCCTGGACTCGCATCCCACTATTGTCAGCCTGCAT
CACCAGAGACCCGGGCAGAACCAGCGCTCCAGGACGCCGCTGACCACCCTCAACACGGATATCAGCATCCTGTCC
TTGCAGGCTTCTGAATTCCCTTCTGAGTTAATGTCAAATGACAGCAAAGCACTGTGTGGC**TGA**ATAAGCGGTGTT
CATGATTTCTTTTATTCTTTGCACAACAACAACAACAACAAATTCACGGAATCTTTTAAGTGCTGAACTTATTTT
TCAACCATTTCACAAGGAGGACAAGTTGAATGGACCTTTT

FIGURE 233

MKAFSPVRSVRKNSLSDHSLGISRSKTPVDDPMSLLYNMNDCYSKLKELVPSIPQNKKVSKMEILQHLIDYILDL
QIALDSHPTIVSLHHQRPGQNQRSRTPLTTLNTDISILSLQASEFPSELMSNDSKALCG

FIGURE 234A

ATTGCAACACATGCAGCTGCCTGGAGAGAGGGAGCCGGTGTCCTACGTCAGAGCCGCCGCCGCCGCGAGCCGCCG
CCGGGGAGGAGCAGCCGCTGCCGCCCAGGACTGGGCCCTTAGGGAGGAGGAGGCGAGAAG**ATG**GCGGACGACCCC
AGTGCTGCCGACAGGAACGTGGAGATCTGGAAGATCAAGAAGCTCATTAAGAGCTTGGAGGCGGCCCGCGGCAAT
GGCACCAGCATGATATCATTGATCATTCCTCCCAAAGACCAGATTTCACGAGTGGCAAAAATGTTAGCGGATGAG
TTTGGAACTGCATCTAACATTAAGTCACGAGTAAACCGCCTTTCAGTCCTGGGAGCCATTACATCTGTACAACAA
AGACTCAAACTTTATAACAAAGTACCTCCAAATGGTCTGGTTGTATACTGTGGAACAATTGTAACAGAAGAAGGA
AAGGAAAAGAAAGTCAACATTGACTTTGAACCTTTCAAACCAATTAATACGTCATTGTATTTGTGTGACAACAAA
TTCCATACAGAGGCTCTTACAGCACTACTTTCAGATGATAGCAAGTTTGGATTCATTGTAATAGATGGTAGTGGT
GCACTTTTTGGCACACTCCAAGGAAACACAAGAGAAGTCCTGCACAAATTCACTGTGGATCTCCCAAAGAAACAC
GGTAGAGGAGGTCAGTCAGCCTTGCGTTTTGCCCGTTTAAGAATGGAAAAGCGACATAACTATGTTCGGAAAGTA
GCAGAGACTGCTGTGCAGCTGTTTATTTCTGGGGACAAAGTGAATGTGGCTGGTCTAGTTTTAGCTGGATCCGCT
GACTTTAAAACTGAACTAAGTCAATCTGATATGTTTGATCAGAGGTTACAATCAAAAGTTTTAAAATTAGTTGAT
ATATCCTATGGTGGTGAAAATGGATTCAACCAAGCTATTGAGTTATCTACTGAAGTCCTCTCCAACGTGAAATTC
ATTCAAGAGAAGAAATTAATAGGACGATACTTTGATGAAATCAGCCAGGACACGGGCAAGTACTGTTTTGGCGTT
GAAGATACACTAAAGGCTTTGGAAATGGGAGCTGTAGAAATTCTAATAGTCTATGAAAATCTGGATATAATGAGA
TATGTTCTTCATTGCCAAGGCACAGAAGAGGAGAAAATTCTCTATCTAACTCCAGAGCAAGAAAAGGATAAATCT
CATTTCACAGACAAAGAGACCGGACAGGAACATGAGCTTATCGAGAGCATGCCCCTGTTGGAATGGTTTGCTAAC
AACTATAAAAAATTTGGAGCTACGTTGGAAATTGTCACAGATAAATCACAAGAAGGGTCTCAGTTTGTGAAAGGA
TTTGGTGGAATTGGAGGTATCTTGCGGTACCGAGTAGATTTCCAGGGAATGGAATACCAAGGAGGAGACGATGAA
TTTTTTGACCTTGATGACTAC**TAG**GTAGTCGACATGGGTCCGGCAAAACGTGCCTCACCCTCCAGCATCCAACCC
AAGGAGCATACCCATGGTGGAATCCAAACAGATCCCTGCCTTACAATTGGAACATTTCCAGAACTTAATCCATGA
GCATTGGATATTGAAAAGAAAACCGAAACAAAACCAGACCCAGCCCTACACTTTGGTTTGTCATGGTGTCAGCGC
AGCAGCCTACAACTAAGTTCCTAAACGCCACTTTGGACTAATTTAAAAAAGAATCCCAGTTTTTACTTTTACTGG
ATGGTGAAATTGGTTGCTCTTGTATTTTATGAAAAAAAATGATTTTTTTAACCTTCATACATAGAAGCAAAAATA
CTTTAACTGCTGTAAACCTTCAAAAGTTAATAGAAGTGAGATCATACTGGTTTGTTTCTTATTTTGATTGGAGAA
AAATTAAATTGCTGCATTTCGCAGTGACCCATTTACATGGCATTCTCAGCTTAGACTGCGTAAGAAGAAATATAT
GTGGTGAAATGTTGGAACCATTTCTCTCTTGGTCTCTGTTTAATGTTGAAAGGGTGAGCTAATAGGAGGCACTTT
CAACTTCACTCCCTCACGCTACCCCGTCCCCCTCCAGACTGGCAGTTTCAAGGATGCAAATTGCATTGCAAAATC
AAACTGACTCATGAAGCATTTGGGCCAGTGCACTGTTTACTTCCATCTGTTTGCAGACACATTTGTGCCCGGCGT
TTGGGAGCCCTTTGTATCAATGTTCTGACAAGGGTCCCTATAACCTTAACCTACTCGAAACCGGTTTGGGATGGA
TATGATGGGGCTTCTGTGCTATTGCTGGGATTGGGAGAAATAAAACATGCAATTTAAGTGGAAGCGAAGAAATTT
AAAGAGGATTTTATTTTGCTTGGGTCAATCCTTGTTAAAAGGGAGGTGGATGTGTTTCCTTGTGTTGGATGGCAT
GAGATTATGTGAATGTTTTGATTTATTAAAATGAACTGCAAGGTTTTTCACAGGAACGACAGACATGTATGACTG
CATGTAATTATAAACTCCTGACCTCCTGGTGGGGTTGGAGCATCTGTTTCAAATGTGGGACTTACAAGCACTTCT
CACATGAGAAATTAGGGGCGGGTGGGAAGGGATGGGACACAGCTTCTGGCACCATGGATTTAAGACCATGTTGGA
TCCAAAAGTTGGCCTGAAACCCTGAAGCTGATGCTTCACAGCTGGGCTGTAAGTCAGACTTGAACCCAGCTGATA
TGCAAGGTCATGGCGTGCCAGGGTGGTGACAGTTGAACAAAGTGTATAGTACGTGCCCAGTGGTAGCGATGGAAA
AAAGTATACCAAATGGACTTTGAAGGACCAAAGGTTTTAAAAGTCAATTGGTATCACCTCCACACTGACTAGGGT
AGTGGGGTGCATTTGGTTTTCAAATTGGGTACTTTTAACACTTTAGTGCCTGACTGCTGTTCTTTACTGACTTGA
TTCAGTCACTCGTAGCTTTATTGGTCTGAACCAGCTCCTTGTTCCCAGGTTACAGACCTGCCTATCGTTCCAATA
ATCCTGTTTCACTTGAATGAAGGGAGTATGTCTTAAATGTAAAGTTTCTGGTTCTCACACTGTACTCTGAGGTCC
AAATACTGTCTGTCAATGTGTAACCTGATGTCTCAACCCCCTGTGAGAAGAGTCCATTATTTGGTGTTCACCAAC
GTGGGAGACTTCACCGGAACAGGCTTTTTTGCTTTGGGCTCTGCTATTTGTTTGCAGAACACCCAAGAGCGAGCA
AACACGCTCTCTTCACAGCAGTACCTTAGGGTTTTGCCATTGTAAATGGGTCTGATGTGATATGACAAGACCAGA
GAAATTGGATGTAAATTTACATTTTTGAATATGCTTGTTGTTTCACATGATACATTTAGGGTATGCAGCTCCTTT
TGTAGTTTTTATTTTTACTATTTAAGTTTGGAAATGATGCCAAATTTTTGTATTTCTTTAATCAATGTGTTCTCT
TCGGTGATATATATTGCATTATATATTGATGTGTGTATCAATATATATTGATATGTATTACACTTACACATACAA
ACACATATAAGAGGGGGTGAAAACCGTAGCCTTTGCATTCTCTATAGCCTCTGCAGAGAGATACTAAGCAGCAAA

FIGURE 234B

ATCTTGGTGTTGTGATGTACAGAAATGGAGAAGAGTATTAAACCATATTTAAG

FIGURE 235

MADDPSAADRNVEIWKIKKLIKSLEAARGNGTSMISLIIPPKDQISRVAKMLADEFGTASNIKSRVNRLSVLGAI
TSVQQRLKLYNKVPPNGLVVYCGTIVTEEGKEKKVNIDFEPFKPINTSLYLCDNKFHTEALTALLSDDSKFGFIV
IDGSGALFGTLQGNTREVLHKFTVDLPKKHGRGGQSALRFARLRMEKRHNYVRKVAETAVQLFISGDKVNVAGLV
LAGSADFKTELSQSDMFDQRLQSKVLKLVDISYGGENGFNQAIELSTEVLSNVKFIQEKKLIGRYFDEISQDTGK
YCFGVEDTLKALEMGAVEILIVYENLDIMRYVLHCQGTEEEKILYLTPEQEKDKSHFTDKETGQEHELIESMPLL
EWFANNYKKFGATLEIVTDKSQEGSQFVKGFGGIGGILRYRVDFQGMEYQGGDDEFFDLDDY

FIGURE 236

TGCTGCGAACCACGTGGGTCCCGGGCGCGTTTCGGGTGCTGGCGGCTGCAGCCGGAGTTCAAACCTAAGCAGCTG
GAAGGAACC**ATG**GCCAACTGTGAGCGTACCTTCATTGCGATCAAACCAGATGGGGTCCAGCGGGGTCTTGTGGGA
GAGATTATCAAGCGTTTTGAGCAGAAAGGATTCCGCCTTGTTGGTCTGAAATTCATGCAAGCTTCCGAAGATCTT
CTCAAGGAACACTACGTTGACCTGAAGGACCGTCCATTCTTTGCCGGCCTGGTGAAATACATGCACTCAGGGCCG
GTAGTTGCCATGGTCTGGGAGGGGCTGAATGTGGTGAAGACGGGCCGAGTCATGCTCGGGGAGACCAACCCTGCA
GACTCCAAGCCTGGGACCATCCGTGGAGACTTCTGCATACAAGTTGGCAGGAACATTATACATGGCAGTGATTCT
GTGGAGAGTGCAGAGAAGGAGATCGGCTTGTGGTTTCACCCTGAGGAACTGGTAGATTACACGAGCTGTGCTCAG
AACTGGATCTATGAA**TGA**CAGGAGGGCAGACCACATTGCTTTTCACATCCATTTCCCCTCCTTCCCATGGGCAGA
GGACCAGGCTGTAGGAAATCTAGTTATTTACAGGAACTTCATCATAATTTGGAGGGAAGCTCTTGGAGCTGTGAG
TTCTCCCTGTACAGTGTTACCATCCCCGACCATCTGATTAAAATGCTTCCTCCCAGC

FIGURE 237

MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPFFAGLVKYMHSGPVVA
MVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWI
YE

FIGURE 238

CCGCCATTTTGTGAGAAGCAAGGTGGCCTCCACGTTTCCTGAGCGTCTTCTTCGCTTTTGCCTCGACCGCCCCTT
GACCACAGAC**ATG**TCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGAGGAGG
CGGCGGCCGCGGCGGCCTCCACGACTTCCGTTCTCCGCCGCCCGGCATGGGCCTCAATCAGAATCGCGGCCCCAT
GGGTCCTGGCCCGGGCCAGAGCGGCCCTAAGCCTCCGATCCCGCCACCGCCTCCACACCAACAGCAGCAACAGCC
ACCACCGCAGCAGCCACCGCCGCAGCAGCCGCCACCGCATCAGCCGCCGCCGCATCCACAGCCGCATCAGCAGCA
GCAGCCGCCGCCACCGCCGCAGGACTCTTCCAAGCCCGTCGTTGCTCAGGGACCCGGCCCCGCTCCCGGAGTAGG
CAGCGCACCACCAGCCTCCAGCTCGGCCCCGCCCGCCACTCCACCAACCTCGGGGGCCCCGCCAGGGTCCGGGCC
AGGCCCGACTCCGACCCCGCCGCCTGCAGTCACCTCGGCCCCTCCCGGGGCGCCGCCACCCACCCCGCCAAGCAG
CGGGGTCCCTACCACACCTCCTCAGGCCGGAGGCCCGCCGCCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCAGG
GCCTAAGCAGGGCCCAGGTCCGGGTGGTCCCAAAGGCGGCAAAATGCCTGGCGGGCCGAAGCCAGGTGGCGGCCC
GGGCCTAAGTACGCCTGGCGGCCACCCCAAGCCGCCGCATCGAGGCGGCGGGGAGCCCCGCGGGGGCCGCCAGCA
CCACCCGCCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCCGGCGGGCCCGGCGGCCGCAGCGAGGAGAAGAT
CTCGGACTCGGAGGGGTTTAAAGCCAATTTGTCTCTCTTGAGGAGGCCTGGAGAGAAAACTTACACACAGCGATG
TCGGTTGTTTGTTGGGAATCTACCTGCTGATATCACGGAGGATGAATTCAAAAGACTATTTGCTAAATATGGAGA
ACCAGGAGAAGTTTTTATCAACAAAGGCAAAGGATTCGGATTTATTAAGCTTGAATCTAGAGCTTTGGCTGAAAT
TGCCAAAGCCGAACTGGATGATACACCCATGAGAGGTAGACAGCTTCGAGTTCGCTTTGCCACACATGCTGCTGC
CCTTTCTGTTCGTAATCTTTCACCTTATGTTTCCAATGAACTGTTGGAAGAAGCCTTTAGCCAATTTGGTCCTAT
TGAAAGGGCTGTTGTAATAGTGGATGATCGTGGAAGATCTACAGGGAAAGGCATTGTTGAATTTGCTTCTAAGCC
AGCAGCAAGAAAGGCATTTGAACGATGCAGTGAAGGTGTTTTCTTACTGACGACAACTCCTCGTCCAGTCATTGT
GGAACCACTTGAACAACTAGATGATGAAGATGGTCTTCCTGAAAAACTTGCCCAGAAGAATCCAATGTATCAAAA
GGAGAGAGAAACCCCTCCTCGTTTTGCCCAGCATGGCACGTTTGAGTACGAATATTCTCAGCGATGGAAGTCTTT
GGATGAAATGGAAAAACAGCAAAGGGAACAAGTTGAAAAAAACATGAAAGATGCAAAAGACAAATTGGAAAGTGA
AATGGAAGATGCCTATCATGAACATCAGGCAAATCTTTTGCGCCAAGATCTGATGAGACGACAGGAAGAATTAAG
ACGCATGGAAGAACTTCACAATCAAGAAATGCAGAAACGTAAAGAAATGCAATTGAGGCAAGAGGAGGAACGACG
TAGAAGAGAGGAAGAGATGATGATTCGTCAACGTGAGATGGAAGAACAAATGAGGCGCCAAAGAGAGGAAAGTTA
CAGCCGAATGGGCTACATGGATCCACGGGAAAGAGACATGCGAATGGGTGGCGGAGGAGCAATGAACATGGGAGA
TCCCTATGGTTCAGGAGGCCAGAAATTTCCACCTCTAGGAGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGG
CGTTCCACCAGCAACCATGAGTGGTTCCATGATGGGAAGTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGC
GGGGCCTGTGGGTGGACAGGGTCCTAGAGGAATGGGGCCTGGAACTCCAGCAGGATATGGTAGAGGGAGAGAAGA
GTACGAAGGCCCAAACAAAAAACCCCGATTT**TAG**ATGTGATATTTAGGCTTTCATTCCAGTTTGTTTTGTTTTTT
TGTTTAGATACCAATCTTTTAAATTCTTGCATTTTAGTAAGAAAGCTATCTTTTTATGGATGTTAGCAGTTTATT
GACCTAATATTTGTAAATGGTCTGTTTGGGCAGGTAAAATTATGTAATGCAGTGTTTGGAACAGGAGAATTTTTT
TTTCCTTTTTATTTCTTTATTTTTTCTTTTTTACTGTATAATGTCCCTCAAGTTTATGGCAGTGTACCTTGTGCC
ACTGAATTTCCAAAGTGTACCAATTTTTTTTTTTTTACTGTGCTTCAAATAAATAGAAAAATAGTTATAATATTG
GATCTTCAACTTTGCCATTCATGCTTCTATGCATATTAGGCTACGTATTCCACATTGAAAGCATGAGAGTGTCTA
GGCCTTTGAATGGCATATGCCATTTCTGGGAAATGCATCTGGAGGCTAAGTATTGCTTTCTACAAATAATTGCCC
CCTTTGTTTTAAAAAGAAGAAATGCATATTGAAGTAGTTTGATGATTTGTTTGGCATATAGGAAGCACGCTGGTG
CTAAGTATTTTTTAAATGGTTATGTAAGCAAAGCTGAACTGTAAATCTTCAGGAATATGTATTAAGATTGTGGAA
TGGGTGTAAGACAATTGGTAGGGGGTGAAAGTGGGTTTGATTAAATGGATCTTTTATGGCCCTATGATCTATCCT
TTACTTGAAAGCTTTTGAAAAGTGGAAAGGTCATTTTGTTGCATTTCCCCATTTCTTGTTTTTAAAAGACCAACA
AATCTCAAGCCCTATAAATGGCTTGTATTGAACTTTTACATTTGAATTAAAGATGTTAAACATGAAAAAAA

FIGURE 239

MSRDRFRSRGGGGGGFHRRGGGGGRGGLHDFRSPPPGMGLNQNRGPMGPGPGQSGPKPPIPPPPPHQQQQQPPPQ
QPPPQQPPPHQPPPHPQPHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAPPASSSAPPATPPTSGAPPGSGPGPT
PTPPPAVTSAPPGAPPPTPPSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPGGPKGGKMPGGPKPGGGPGLS
TPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQGPPPGGPGGRSEEKISDSEGFKANLSLLRRPGEKTYTQRCRLF
VGNLPADITEDEFKRLFAKYGEPGEVFINKGKGFGFIKLESRALAEIAKAELDDTPMRGRQLRVRFATHAAALSV
RNLSPYVSNELLEEAFSQFGPIERAVVIVDDRGRSTGKGIVEFASKPAARKAFERCSEGVFLLTTTPRPVIVEPL
EQLDDEDGLPEKLAQKNPMYQKERETPPRFAQHGTFEYEYSQRWKSLDEMEKQQREQVEKNMKDAKDKLESEMED
AYHEHQANLLRQDLMRRQEELRRMEELHNQEMQKRKEMQLRQEEERRRREEEMMIRQREMEEQMRRQREESYSRM
GYMDPRERDMRMGGGGAMNMGDPYGSGGQKFPPLGGGGGIGYEANPGVPPATMSGSMMGSDMRTERFGQGGAGPV
GGQGPRGMGPGTPAGYGRGREEYEGPNKKPRF

FIGURE 240

GCCCGTCCCGCCGCCCGCCCGCCAGCC**ATG**AGCTCCACGCAGTTCAACAAGGGCCCCTCGTACGGGCTGTCGGCC
GAGGTCAAGAACCGGCTCCTGTCCAAATATGACCCCCAGAAGGAGGCAGAGCTCCGCACCTGGATCGAGGGACTC
ACCGGCCTCTCCATCGGCCCCGACTTCCAGAAGGGCCTGAAGGATGGAACTATCTTATGCACACTCATGAACAAG
CTACAGCCGGGCTCCGTCCCCAAGATCAACCGCTCCATGCAGAACTGGCACCAGCTAGAAAACCTGTCCAACTTC
ATCAAGGCCATGGTCAGCTACGGCATGAACCCTGTGGACCTGTTCGAGGCCAACGACCTGTTTGAGAGTGGGAAC
ATGACGCAGGTGCAGGTGTCTCTTCTCGCCCTGGCGGGGAAGGCCAAGACTAAGGGGCTGCAGAGCGGGGTGGAC
ATTGGCGTCAAGTACTCGGAGAAGCAGGAGCGGAATTTCGACGATGCCACCATGAAGGCTGGCCAGTGCGTCATC
GGGCTGCAGATGGGCACCAACAAATGCGCCAGCCAGTCGGGCATGACTGCCTACGGCACGAGAAGGCATCTCTAT
GACCCCAAGAACCATATCCTGCCCCCCATGGACCACTCGACCATCAGCCTCCAGATGGGCACGAACAAGTGCGCC
AGCCAGGTGGGCATGACGGCTCCCGGGACCCGGCGGCACATCTATGATACCAAGCTGGGAACCGACAAGTGTGAC
AACTCCTCCATGTCCCTGCAGATGGGCTACACGCAGGGCGCCAACCAGAGCGGCCAGGTCTTCGGCCTGGGCCGG
CAGATATATGACCCCAAGTACTGCCCGCAAGGCACAGTGGCCGATGGGGCTCCCTCGGGCACCGGCGACTGCCCG
GACCCGGGGGAGGTCCCTGAATATCCCCCTTACTACCAGGAGGAGGCCGGCTAC**TGA**GGCTCCCAGCACGCTCTC
TCCCCACATCGTCTTCCCATCTGGGTTTTTGGGTTTTTCTGTGTTTTCATCTTTTTTTTTTTTTTTCTTGACCCG
TTCAGTGCTGCCAGTCAACCAAGGGTCTGTGAGTGTCAGCGTGGGATCAGGCAGCAGAGCTTTTTTCCCCTTTGC
CTTGATCCTTCGCAAGGCTGAGCCACTGGGCTGTGGGGGAAGGGGTCAAGGCCATATCCCAATACGTGTAGGGCG
AGGGTCCCTGCTGGCACATTCAGGCTGTGCTGGGAAGAAGAGACCTGGGCTTGGAAGGAACCGGTCCCCGACGGT
TTCTGGTTGCCTCGCCTCTTCCCCCTTTTGTCAGCTGAGCAGTTTGTGGTTTCTATGCCCGCAAGTTTCAGGAAG
TATTCACAAAAGAAAAATACATTTTTTCCCCCAGGGGTGGGGCAAGGACAGTGGAGAGAGTGCTAGGAAATGAGT
CCCCTGGGAAAGGGGACCGGGCCGTGATGTTAAATATCTCCGGCTCCCAAGTGACTGGATTTGCCTAGGACCTTC
AGATCAACAGACTTCAGACCCTCAGACCTGCCCCGGGGCCAGGTGGAGAAAGTGAGGGCCGTACAAGGAAGTGAA
ATTCTGAGTTGTTGGGGCTAAGCCTGACCCCCTCTCCATGCTCCCCGCCCCAACTCACTCTGGCCTCAGTAGATT
TTTTTTCAGTTGTGGTTGTTGCCCAGGCTGGAGTGCAGTGGCGCCATCTTGGCTCACTGCACCTCCACCTTCCG
GGCTCAAGCGATTCTCCAGCCTCAGCCTCCTGAGTAGCTAGGACTGCAGGTGCTCCACCACGCCCGGCTAATTTT
TGTATTTTTAGTAGAGATGGGGTTTCCCCATGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAGGTGTGATCCG
CCCGCCTCCGCCTCCCCAAGCGCTGAGATTACAGGTGTGAGCCACCGTGCCCAGGCCCTCAGTAGGTTTTAAGGA
GTCCCCAGCCCTCCTCCCTTCTGGGCCCGACCAGCTTATACTGCTCCATCTTCCCCGGCCACATGCCCCGCCAAG
TACTGCACAGGGACCCCCCACCCAGGGGCCCTGCTCCGTGAGATAATGTGAAATACGACTGTGGACCAAACGCAA
TAAAACCTTTGTTTGTAGGAAG

FIGURE 241

MSSTQFNKGPSYGLSAEVKNRLLSKYDPQKEAELRTWIEGLTGLSIGPDFQKGLKDGTILCTLMNKLQPGSVPKI
NRSMQNWHQLENLSNFIKAMVSYGMNPVDLFEANDLFESGNMTQVQVSLLALAGKAKTKGLQSGVDIGVKYSEKQ
ERNFDDATMKAGQCVIGLQMGTNKCASQSGMTAYGTRRHLYDPKNHILPPMDHSTISLQMGTNKCASQVGMTAPG
TRRHIYDTKLGTDKCDNSSMSLQMGYTQGANQSGQVFGLGRQIYDPKYCPQGTVADGAPSGTGDCPDPGEVPEYP
PYYQEEAGY

FIGURE 242

CTGAAG**ATG**GCGGCTGCTGTAGGACGGTTGCTCCGAGCGTCGGTTGCCCGACATGTGAGTGCCATTCCTTGGGGC
ATTTCTGCCACTGCAGCCCTCAGGCCTGCTGCATGTGGAAGAACGAGCTTGACAAATTTATTGTGTTCTGGTTCC
AGTCAAGCAAAATTATTCAGCACCAGTTCCTCATGCCATGCACCTGCTGTCACCCAGCATGCACCCTATTTTAAG
GGTACAGCCGTTGTCAATGGAGAGTTCAAAGACCTAAGCCTTGATGACTTTAAGGGGAAATATTTGGTGCTTTTC
TTCTATCCTTTGGATTTCACCTTTGTGTGTCCTACAGAAATTGTTGCTTTTAGTGACAAAGCTAACGAATTTCAC
GATGTGAACTGTGAAGTTGTCGCAGTCTCAGTGGATTCCCACTTTAGCCATCTTGCCTGGATAAATACACCAAGA
AAGAATGGTGGTTTGGGCCACATGAACATCGCACTCTTGTCAGACTTAACTAAGCAGATTTCCCGAGACTACGGT
GTGCTGTTAGAAGGTTCTGGTCTTGCACTAAGAGGTCTCTTCATAATTGACCCCAATGGAGTCATCAAGCATTTG
AGCGTCAACGATCTCCCAGTGGGCCGAAGCGTGGAAGAAACCCTCCGCTTGGTGAAGGCGTTCCAGTATGTAGAA
ACACATGGAGAAGTCTGCCCAGCGAACTGGACACCGGATTCTCCTACGATCAAGCCAAGTCCAGCTGCTTCCAAA
GAGTACTTTCAGAAGGTAAATCAG**TAG**ATCACCCATGTGTATCTGCACCTTCTCAACTGAGAGAAGAACCACAGT
TGAAACCTGCTTTTATCATTTTCAAGATGGTTATTTGTAGAAGGCAAGGAACCAATTATGCTTGTATTCATAAGT
ATTACTCTAAATGTTTTGTTTTTGTAATTCTGGCTAGGACCTTTTAAACATGGTTAGTTGCTAGTACAGGAATCG
TTTATTGGTAACATCTTGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTT
AGATCATGTCTCAATGGAAACACTCTTCTTTCTTAGCCTTACTTGAATCTTGCCTATAATAAAGTAGAGCAACAC
ACATTGAAAGCTTCTGATCAACGGTCCTGAAATTTTCATCTTGAATGTCTTTGTATTAAACTGAATTTTCTTTTA
AGCTAACAAAGATCATAATTTTCAATGATTAGCCGTGTAACTCCTGCAATGAATGTTTATGTGATTGAAGCAAAT
GTGAATCGTATTATTTTAAAAAGTGGCAGAGTGACTTAACTGATCATGCATGATCCCTCATCCCTGAAATTGAGT
TTATGTAGTCATTTTACTTATTTTATTCATTAGCTAACTTTGTCTATGTATATTTCTAGATATTGATTAGTGTAA
TCGATTATAAAGGATATTTATCAAATCCAGGGATTGCATTTTGAAATTATAATTATTTTCTTTGCTGAAGTATTC
ATTGTAAAACATACAAATAACATATTTAAACAAAAAAAAAAA

FIGURE 243

MAAAVGRLLRASVARHVSAIPWGISATAALRPAACGRTSLTNLLCSGSSQAKLFSTSSSCHAPAVTQHAPYFKGT
AVVNGEFKDLSLDDFKGKYLVLFFYPLDFTFVCPTEIVAFSDKANEFHDVNCEVVAVSVDSHFSHLAWINTPRKN
GGLGHMNIALLSDLTKQISRDYGVLLEGSGLALRGLFIIDPNGVIKHLSVNDLPVGRSVEETLRLVKAFQYVETH
GEVCPANWTPDSPTIKPSPAASKEYFQKVNQ

FIGURE 244

TGGCCGGAATTCCGGGGAGGGAGAAGCCCCTTTGGCCTGCCTTACGGAAGCCTGCGAGGGAGGGTGGTGTCCACT
GCCCAGTTCCGTGTCCCG**ATG**CCCAGCGCCACGCAGCGCAAGAGTCAGGAGAAGCCGCGGGAGATCATGGACGCG
GCGGAAGATTATGCTAAAGAGAGATATGGAATATCTTCAATGATACAATCACAAGAAAAACCAGATCGAGTTTTG
GTTCGGGTTAGAGACTTGACAATACAAAAAGCTGATGAAGTTGTTTGGGTACGTGCAAGAGTTCATACAAGCAGA
GCTAAAGGGAAACAGTGCTTCTTAGTCCTACGTCAGCAGCAGTTTAATGTCCAGGCTCTTGTGGCGGTGGGAGAC
CATGCAAGCAAGCAGATGGTTAAATTTGCTGCCAACATCAACAAAGAGAGCATTGTGGATGTAGAAGGTGTTGTG
AGAAAAGTGAATCAGAAAATTGGAAGCTGTACACAGCAAGACGTTGAGTTACATGTTCAGAAGATTTATGTGATC
AGTTTGGCTGAACCCCGTCTGCCCCTGCAGCTGGATGATGCTGTTCGGCCTGAGCAAGAAGGAGAAGAGGAAGGA
AGAGCTACTGTTAACCAGGATACAAGATTAGACAACAGAGTCATTGATCTTAGGACATCAACTAGTCAGGCAGTC
TTCCGTCTCCAGTCTGGCATCTGCCATCTCTTCCGAGAAACTTTAATTAACAAAGGTTTTGTGGAAATCCAAACT
CCTAAAATTATTTCAGCTGCCAGTGAAGGAGGAGCCAATGTTTTTACTGTGTCATATTTTAAAAATAATGCATAC
CTGGCTCAGTCCCCACAGCTATATAAGCAAATGTGCATTTGTGCTGATTTTGAGAAGGTTTTCTCTATTGGACCA
GTATTCAGAGCGGAAGACTCTAATACCCATAGACATCTAACTGAGTTTGTTGGTTTGGACATTGAAATGGCTTTT
AATTACCATTACCACGAAGTTATGGAAGAAATTGCTGACACCATGGTACAAATATTCAAAGGACTTCAAGAAAGG
TTTCAGACTGAAATTCAAACAGTGAATAAACAGTTCCCATGTGAGCCATTCAAATTTTTGGAGCCAACTCTAAGA
CTAGAATATTGTGAAGCATTGGCTATGCTTAGGGAAGCTGGAGTCGAAATGGGAGATGAAGACGATCTGAGCACA
CCAAATGAAAAGCTGTTGGGTCATTTGGTAAAGGAAAAGTATGATACAGATTTTTATATTCTTGATAAATATCCA
TTGGCTGTAAGACCTTTCTATACCATGCCTGACCCAAGAAATCCCAAACAGTCCAAGTCTTACGATATGTTCATG
AGAGGAGAAGAAATATTGTCAGGAGCTCAAAGAATACATGATCCTCAACTGCTAACAGAGAGAGCTTTACATCAT
GGAAATGATTTGGAGAAAATTAAGGCTTACATTGATTCCTTCCGCTTTGGAGCCCCTCCTCATGCTGGTGGAGGC
ATTGGATTGGAACGAGTTACTATGCTGTTTCTGGGATTGCATAATGTTCGTCAGACCTCCATGTTCCCTCGTGAT
CCCAAACGACTCACTCCT**TAA**ATTCACACTTTGCCACTTAACTCCAGTGTGGATGACAGAGCGAGACCCTGCCTC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAGCCACACTT
ATTCTTTTCAGTAACCTGCTAGTGCACAGGCTGTACTTTAGGTACTTAAAATATGCACTAGAATAAATTTGCAAG
GCCCTAAAATATCACTGTTATTTTTGGAGTAATTCAGTATAGGTTCGTTTAAAAGAGATTTTTATAACTTCAGAC
ATGCATCAGTAGGAAATAACTTGAGAAATTCATATGGTTATGTTACAAATTCATATTCTGTTACTACAGTAAACG
TTAAGAGTTTTAAACAGTTAAGATTGTACAATTTTTCTTCTTTTCTATATTACAAGGGCCCCAGTGTTAATGTCT
TAGATTTTCAGTATTTGAACTTATTTTTTTAAATTCTGTCATTGAGATAAGAATAATTCAGGTAGCATCTGAAAT
TTTAATGAATGTATAATTGGCATATCATGGAAAATTAACCAGAAAGTATCAGTTCTTAAAAGTTATGCCTAGAAA
TTATGTAAAGCTAAACTACTGGTTAGAAAGTATTCAGTGTAATATTGTATTAATTTGTTAAATTCTAAACTTGAA
TTTCAATAAAATTTTAAAGCT

FIGURE 245

MPSATQRKSQEKPREIMDAAEDYAKERYGISSMIQSQEKPDRVLVRVRDLTIQKADEVVWVRARVHTSRAKGKQC
FLVLRQQQFNVQALVAVGDHASKQMVKFAANINKESIVDVEGVVRKVNQKIGSCTQQDVELHVQKIYVISLAEPR
LPLQLDDAVRPEQEGEEEGRATVNQDTRLDNRVIDLRTSTSQAVFRLQSGICHLFRETLINKGFVEIQTPKIISA
ASEGGANVFTVSYFKNNAYLAQSPQLYKQMCICADFEKVFSIGPVFRAEDSNTHRHLTEFVGLDIEMAFNYHYHE
VMEEIADTMVQIFKGLQERFQTEIQTVNKQFPCEPFKFLEPTLRLEYCEALAMLREAGVEMGDEDDLSTPNEKLL
GHLVKEKYDTDFYILDKYPLAVRPFYTMPDPRNPKQSKSYDMFMRGEEILSGAQRIHDPQLLTERALHHGNDLEK
IKAYIDSFRFGAPPHAGGGIGLERVTMLFLGLHNVRQTSMFPRDPKRLTP

FIGURE 246

ACTTGGCCTTACACTCCGCTCGGCTCACC**ATG**TGTCACTCTCGCAGCTGCCACCCGACCATGACCATCCTGCAGG
CCCCGACCCCGGCCCCCTCCACCATCCCGGGACCCCGGCGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTC
TCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGGGTCT
CTCTACCCTCGAGTGGTGAGTATCGCCGAAGTGGGCATTCGCGGTGTGCGCTGCCCTGGAGTCACTGGGGAACGA
CCCGACTCCAGAGCCTCGACCTGACCTGTCTCCTGTTTTGTCTCCCCTTAGTCCGGCGCCAGCTGCCAGTCGAGG
AACCGAACCCAGCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGG
GTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCC
TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGG
CCGCCTTC**TAA**CTGTGACTCCCCGCACTCCCCAAAAAGAATCCGAAAAACCACAAAGAAACACCAGGCGTACCTG
GTGCGCGAGAGCGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACACTACAGCGGAGACGCCACCC
GGTGCTTGAGGCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCGAGGCACAGCCCAGCTGGGCTAGGC
CGGTGGGAAGGAGAGCGTCGTTAATTTATTTCTTATTGCTCCTAATTAATATTTATATGTATTTATGTACGTCCT
CCTAGGTGATGGAGATGTGTACGTAATATTTATTTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGCTGTAAA
TGCAGGTCTCTTGGTATTTATTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGCAAAGTAGGA
GAAGAAATGGGGAGGACTCGGGTGGGGGAGGACGTCCCGGCTGGGATGAAGTCTGGTGGTGGGTCGTAAGTTTAG
GAGGTGACTGCATCCTCCAGCATCTCAACTCCGTCTGTCTACTGTGTGAGACTTCGGCGGACCATTAGGAATGAG
ATCCGTGAGATCCTTCCATCTTCTTGAAGTCGCCTTTAGGGTGGCTGCGAGGTAGAGGGTTGGGGGTTGGTGGGC
TGTCACGGAGCGACTGTCGAGATCGCCTAGTATGTTCTGTGAACACAAATAAAATTGATTTACTGTCTGC

FIGURE 247

MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVSLPSSGEYRR
SGHSRCALPWSHWGTTRLQSLDLTCLLFCLPLVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPED
APNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF

FIGURE 248A

GCGCGACCGTCCCGGGGGTGGGGCCGGGCGCAGCGGCGAGAGGAGGCGAAGGTGGCTGCGGTAGCAGCAGCGCGG
CAGCCTCGGACCCAGCCCGGAGCGCAGGGCGGCCGCTGCAGGTCCCCGCTCCCCTCCCCGTGCGTCCGCCC**ATG**G
CCGCCGCCGGGCAGCTGTGCTTGCTCTACCTGTCGGCGGGGCTCCTGTCCCGGCTCGGCGCAGCCTTCAACTTGG
ACACTCGGGAGGACAACGTGATCCGGAAATATGGAGACCCCGGGAGCCTCTTCGGCTTCTCGCTGGCCATGCACT
GGCAACTGCAGCCCGAGGACAAGCGGCTGTTGCTCGTGGGGGCCCCGCGCGGAGAAGCGCTTCCACTGCAGAGAG
CCAACAGAACGGGAGGGCTGTACAGCTGCGACATCACCGCCCGGGGGCCATGCACGCGGATCGAGTTTGATAACG
ATGCTGACCCCACGTCAGAAAGCAAGGAAGATCAGTGGATGGGGGTCACCGTCCAGAGCCAAGGTCCAGGGGGCA
AGGTCGTGACATGTGCTCACCGATATGAAAAAAGGCAGCATGTTAATACGAAGCAGGAATCCCGAGACATCTTTG
GGCGGTGTTATGTCCTGAGTCAGAATCTCAGGATTGAAGACGATATGGATGGGGGAGATTGGAGCTTTTGTGATG
GGCGATTGAGAGGCCATGAGAAATTTGGCTCTTGCCAGCAAGGTGTAGCAGCTACTTTTACTAAAGACTTTCATT
ACATTGTATTTGGAGCCCCGGGTACTTATAACTGGAAAGGGATTGTTCGTGTAGAGCAAAAGAATAACACTTTTT
TTGACATGAACATCTTTGAAGATGGGCCTTATGAAGTTGGTGGAGAGACTGAGCATGATGAAAGTCTCGTTCCTG
TTCCTGCTAACAGTTACTTAGGTTTTTCTTTGGACTCAGGGAAAGGTATTGTTTCTAAAGATGAGATCACTTTTG
TATCTGGTGCTCCCAGAGCCAATCACAGTGGAGCCGTGGTTTTGCTGAAGAGAGACATGAAGTCTGCACATCTCC
TCCCTGAGCACATATTCGATGGAGAAGGTCTGGCCTCTTCATTTGGCTATGATGTGGCGGTGGTGGACCTCAACA
AGGATGGGTGGCAAGATATAGTTATTGGAGCCCCACAGTATTTTGATAGAGATGGAGAAGTTGGAGGTGCAGTGT
ATGTCTACATGAACCAGCAAGGCAGATGGAATAATGTGAAGCCAATTCGTCTTAATGGAACCAAAGATTCTATGT
TTGGCATTGCAGTAAAAAATATTGGAGATATTAATCAAGATGGCTACCCAGATATTGCAGTTGGAGCTCCGTATG
ATGACTTGGGAAAGGTTTTTATCTATCATGGATCTGCAAATGGAATAAATACCAAACCAACACAGGTTCTCAAGG
GTATATCACCTTATTTTGGATATTCAATTGCTGGAAACATGGACCTTGATCGAAATTCCTACCCTGATGTTGCTG
TTGGTTCCCTCTCAGATTCAGTAACTATTTTCAGATCCCGGCCTGTGATTAATATTCAGAAAACCATCACAGTAA
CTCCTAACAGAATTGACCTCCGCCAGAAAACAGCGTGTGGGGCGCCTAGTGGGATATGCCTCCAGGTTAAATCCT
GTTTTGAATATACTGCTAACCCCGCTGGTTATAATCCTTCAATATCAATTGTGGGCACACTTGAAGCTGAAAAAG
AAAGAAGAAAATCTGGGCTATCCTCAAGAGTTCAGTTTCGAAACCAAGGTTCTGAGCCCAAATATACTCAAGAAC
TAACTCTGAAGAGGCAGAAACAGAAAGTGTGCATGGAGGAAACCCTGTGGCTACAGGATAATATCAGAGATAAAC
TGCGTCCCATTCCCATAACTGCCTCAGTGGAGATCCAAGAGCCAAGCTCTCGTAGGCGAGTGAATTCACTTCCAG
AAGTTCTTCCAATTCTGAATTCAGATGAACCCAAGACAGCTCATATTGATGTTCACTTCTTAAAAGAGGGATGTG
GAGACGACAATGTATGTAACAGCAACCTTAAACTAGAATATAAATTTTGCACCCGAGAAGGAAATCAAGACAAAT
TTTCTTATTTACCAATTCAAAAAGGTGTACCAGAACTAGTTCTAAAAGATCAGAAGGATATTGCTTTAGAAATAA
CAGTGACAAACAGCCCTTCCAACCCAAGGAATCCCACAAAAGATGGCGATGACGCCCATGAGGCTAAACTGATTG
CAACGTTTCCAGACACTTTAACCTATTCTGCATATAGAGAACTGAGGGCTTTCCCTGAGAAACAGTTGAGTTGTG
TTGCCAACCAGAATGGCTCGCAAGCTGACTGTGAGCTCGGAAATCCTTTTAAAAGAAATTCAAATGTCACTTTTT
ATTTGGTTTTAAGTACAACTGAAGTCACCTTTGACACCCCATATCTGGATATTAATCTGAAGTTAGAAACAACAA
GCAATCAAGATAATTTGGCTCCAATTACAGCTAAAGCAAAAGTGGTTATTGAACTGCTTTTATCGGTCTCGGGAG
TTGCTAAACCTTCCCAGGTGTATTTTGGAGGTACAGTTGTTGGCGAGCAAGCTATGAAATCTGAAGATGAAGTGG
GAAGTTTAATAGAGTATGAATTCAGGGTAATAAACTTAGGTAAACCTCTTACAAACCTCGGCACAGCAACCTTGA
ACATTCAGTGGCCAAAAGAAATTAGCAATGGGAAATGGTTGCTTTATTTGGTGAAAGTAGAATCCAAAGGATTGG
AAAAGGTAACTTGTGAGCCACAAAAGGAGATAAACTCCCTGAACCTAACGGAGTCTCACAACTCAAGAAAGAAAC
GGGAAATTACTGAAAAACAGATAGATGATAACAGAAAATTTTCTTTATTTGCTGAAAGAAAATACCAGACTCTTA
ACTGTAGCGTGAACGTGAACTGTGTGAACATCAGATGCCCGCTGCGGGGGCTGGACAGCAAGGCGTCTCTTATTT
TGCGCTCGAGGTTATGGAACAGCACATTTCTAGAGGAATATTCCAAACTGAACTACTTGGACATTCTCATGCGAG
CCTTCATTGATGTGACTGCTGCTGCCGAAAATATCAGGCTGCCAAATGCAGGCACTCAGGTTCGAGTGACTGTGT
TTCCCTCAAAGACTGTAGCTCAGTATTCGGGAGTACCTTGGTGGATCATCCTAGTGGCTATTCTCGCTGGGATCT
TGATGCTTGCTTTATTAGTGTTTATACTATGGAAGTGTGGTTTCTTCAAGAGAAATAAGAAAGATCATTATGATG
CCACATATCACAAGGCTGAGATCCATGCTCAGCCATCTGATAAAGAGAGGCTTACTTCTGATGCA**TAG**TATTGAT
CTACTTCTGTAATTGTGTGGATTCTTTAAACGCTCTAGGTACGATGACAGTGTTCCCCGATACCATGCTGTAAGG
ATCCGGAAAGAAGAGCGAGAGATCAAAGATGAAAAGTATATTGATAACCTTGAAAAAAAACAGTGGATCACAAAG
TGGAACAGAAATGAAAGCTACTCATAGCGGGGGCCTAAAAAAAAAAAAAGCTTCACAGTACCCAAACTGCTTTTTC

FIGURE 248B

CAACTCAGAAATTCAATTTGGATTTAAAAGCCTGCTCAATCCCTGAGGACTGATTTCAGAGTGACTACACACAGT
ACGAACCTACAGTTTTAACTGTGGATATTGTTACGTAGCCTAAGGCTCCTGTTTTGCACAGCCAAATTTAAAACT
GTTGGAATGGATTTTTCTTTAACTGCCGTAATTTAACTTTCTGGGTTGCCTTTGTTTTTGGCGTGGCTGACTTAC
ATCATGTGTTGGGGAAGGGCCTGCCCAGTTGCACTCAGGTGACATCCTCCAGATAGTGTAGCTGAGGAGGCACCT
ACACTCACCTGCACTAACAGAGTGGCCGTCCTAACCTCGGGCCTGCTGCGCAGACGTCCATCACGTTAGCTGTCC
CACATCACAAGACTATGCCATTGGGGTAGTTGTGTTTCAACGGAAAGTGCTGTCTTAAACTAAATGTGCAATAGA
AGGTGATGTTGCCATCCTACCGTCTTTTCCTGTTTCCTAGCTGTGTGAATACCTGCTCACGTCAAATGCATACAA
GTTTCATTCTCCCTTTCACTAAAAACACACAGGTGCAACAGACTTGAATGCTAGTTATACTTATTTGTATATGGT
ATTTATTTTTTCTTTTCTTTACAAACCATTTTGTTATTGACTAACAGGCCAAAGAGTCTCCAGTTTACCCTTCAG
GTTGGTTTAATCAATCAGAATTAGAATTAGAGCATGGGAGGGTCATCACTATGACCTAAATTATTTACTGCAAAA
AGAAAATCTTTATAAATGTACCAGAGAGAGTTGTTTTAATAACTTATCTATAAACTATAACCTCTCCTTCATGAC
AGCCTCCACCCCACAACCCAAAAGGTTTAAGAAATAGAATTATAACTGTAAAGATGTTTATTTCAGGCATTGGAT
ATTTTTTACTTTAGAAGCCTGCATAATGTTTCTGGATTTACATACTGTAACATTCAGGAATTCTTGGAGAAGATG
GGTTTATTCACTGAACTCTAGTGCGGTTTACTCACTGCTGCAAATACTGTATATTCAGGACTTGAAAGAAATGGT
GAATGCCTATGGAACTAGTGGATCCAAACTGATCCAGTATAAGACTACTGAATCTGCTACCAAAACAGTTAATCA
GTGAGTCGAGTGTTCTATTTTTTGTTTTGTTTCCTCCCCTATCTGTATTCCCAAAAATTACTTTGGGGCTAATTT
AACAAGAACTTTAAATTGTGTTTTAATTGTAAAAATGGCAGGGGGTGGAATTATTACTCTATACATTCAACAGAG
ACTGAATAGATATGAAAGCTGATTTTTTTTAATTACCATGCTTCACAATGTTAAGTTATATGGGGAGCAACAGCA
AACAGGTGCTAATTTGTTTTGGATATAGTATAAGCAGTGTCTGTGTTTTGAAAGAATAGAACACAGTTTGTAGTG
CCACTGTTGTTTTGGGGGGGGCTTTTTTTCTTTTTCCGGAAAATCCTTAAACCTTAAGATACTAAGGACGTTGTT
TTGGTTGTACTTGGAATTCTTAGTCACAAAATATATTTTGTTTACAAAAATTTCTGTAAAACAGGTTATAACAGT
GTTTAAAGTCTCAGTTTCTTGCTTGGGGAACTTGTGTCCCTAATGTGTTAGATTGCTAGATTGCTAAGGAGCTGA
TACTTGACAGTTTTTTAGACCTGTGTTACTAAAAAAAAGATGAATGTCGGAAAAGGGTGTTGGGAGGGTGGTCAA
CAAAGAAACAAAGATGTTATGGTGTTTAGACTTATGGTTGTTAAAAATGTCATCTCAAGTCAAGTCACTGGTCTG
TTTGCATTTGATACATTTTTGTACTAACTAGCATTGTAAAATTATTTCATGATTAGAAATTACCTGTGGATATTT
GTATAAAAGTGTGAAATAAATTTTTTATAAAAGTGTTCATTGTTTCGTAACACAGCATTGTATATGTGAAGCAAA
CTCTAAAATTATAAATGACAACCTGAATTATCTATTTCATCAAAAAAAAAAAAAAAAAAAA

FIGURE 249

MAAAGQLCLLYLSAGLLSRLGAAFNLDTREDNVIRKYGDPGSLFGFSLAMHWQLQPEDKRLLLVGAPRGEALPLQ
RANRTGGLYSCDITARGPCTRIEFDNDADPTSESKEDQWMGVTVQSQGPGGKVVTCAHRYEKRQHVNTKQESRDI
FGRCYVLSQNLRIEDDMDGGDWSFCDGRLRGHEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNT
FFDMNIFEDGPYEVGGETEHDESLVPVPANSYLGFSLDSGKGIVSKDEITFVSGAPRANHSGAVVLLKRDMKSAH
LLPEHIFDGEGLASSFGYDVAVVDLNKDGWQDIVIGAPQYFDRDGEVGGAVYVYMNQQGRWNNVKPIRLNGTKDS
MFGIAVKNIGDINQDGYPDIAVGAPYDDLGKVFIYHGSANGINTKPTQVLKGISPYFGYSIAGNMDLDRNSYPDV
AVGSLSDSVTIFRSRPVINIQKTITVTPNRIDLRQKTACGAPSGICLQVKSCFEYTANPAGYNPSISIVGTLEAE
KERRKSGLSSRVQFRNQGSEPKYTQELTLKRQKQKVCMEETLWLQDNIRDKLRPIPITASVEIQEPSSRRRVNSL
PEVLPILNSDEPKTAHIDVHFLKEGCGDDNVCNSNLKLEYKFCTREGNQDKFSYLPIQKGVPELVLKDQKDIALE
ITVTNSPSNPRNPTKDGDDAHEAKLIATFPDTLTYSAYRELRAFPEKQLSCVANQNGSQADCELGNPFKRNSNVT
FYLVLSTTEVTFDTPYLDINLKLETTSNQDNLAPITAKAKVVIELLLSVSGVAKPSQVYFGGTVVGEQAMKSEDE
VGSLIEYEFRVINLGKPLTNLGTATLNIQWPKEISNGKWLLYLVKVESKGLEKVTCEPQKEINSLNLTESHNSRK
KREITEKQIDDNRKFSLFAERKYQTLNCSVNVNCVNIRCPLRGLDSKASLILRSRLWNSTFLEEYSKLNYLDILM
RAFIDVTAAAENIRLPNAGTQVRVTVFPSKTVAQYSGVPWWIILVAILAGILMLALLVFILWKCGFFKRNKKDHY
DATYHKAEIHAQPSDKERLTSDA

FIGURE 250

GGAAACTCCCGCAGACTTCTCTGTAGATCGCTGAGCGATACTTTCGGCAGCACCTCCTTGATTCTCAGTTTTGCT
GGAGGCCGCAACCAGGCCCGCGCCGCCACC**ATG**TTTCGAAATCAGTATGACAATGATGTCACTGTTTGGAGCCCC
CAGGGCAGGATTCATCAAATTGAATATGCAATGGAAGCTGTTAAACAAGGTTCAGCCACAGTTGGTCTGAAATCA
AAAACTCATGCAGTTTTGGTTGCATTGAAAAGGGCGCAATCAGAGCTTGCAGCTCATCAGAAAAAAATTCTCCAT
GTTGACAACCACATTGGTATCTCAATTGCGGGGCTTACTGCTGATGCTAGACTGTTATGTAATTTTATGCGTCAG
GAGTGTTTGGATTCCAGATTTGTATTCGATAGACCACTGCCTGTGTCTCGTCTTGTATCTCTAATTGGAAGCAAG
ACCCAGATACCAACACAACGATATGGCCGGAGACCATATGGTGTTGGTCTCCTTATTGCTGGTTATGATGATATG
GGCCCTCACATTTTCCAAACCTGTCCATCTGCTAACTATTTTGACTGCAGAGCCATGTCCATTGGAGCCCGTTCC
CAATCAGCTCGTACTTACTTGGAGAGACATATGTCTGAATTTATGGAGTGTAATTTAAATGAACTAGTTAAACAT
GGTCTGCGTGCCTTAAGAGAGACGCTTCCTGCAGAACAGGACCTGACTACAAAGAATGTTTCCATTGGAATTGTT
GGTAAAGACTTGGAGTTTACAATCTATGATGATGATGATGTGTCTCCATTCCTGGAAGGTCTTGAAGAAAGACCA
CAGAGAAAGGCACAGCCTGCTCAACCTGCTGATGAACCTGCAGAAAAGGCTGATGAACCAATGGAACAT**TAA**GTG
ATAAGCCAGTCTATATATGTATTATCAAATATGTAAGAATACAGGCACCACATACTGATGACAATAATCTATACT
TTGAACCAAAAGTTGCAGAGTGGTGGAATGCTATGCTATGTTTTAGGAATCAGTCCAGATGTGAGTTTTTTCCAA
GCAACCTCACTGAAACCTATATAATGGAATACATTTTTCTTTGAAAGGGTCTGTATAATCATTTTCTAGAAGTAT
GGGTATCTATACTAATGTTTTTTATATAAGAACATAGGTGTCTTTGTGGTTTTAAAGACAACTGTGAAATAAAAT
TGTTTCACCGCCTGGTAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 251

MFRNQYDNDVTVWSPQGRIHQIEYAMEAVKQGSATVGLKSKTHAVLVALKRAQSELAAHQKKILHVDNHIGISIA
GLTADARLLCNFMRQECLDSRFVFDRPLPVSRLVSLIGSKTQIPTQRYGRRPYGVGLLIAGYDDMGPHIFQTCPS
ANYFDCRAMSIGARSQSARTYLERHMSEFMECNLNELVKHGLRALRETLPAEQDLTTKNVSIGIVGKDLEFTIYD
DDDVSPFLEGLEERPQRKAQPAQPADEPAEKADEPMEH

FIGURE 252

GGGGTGACGCAGGCGCAGCGCGGGCTGCGCGCGCTACTGCCCATCCCCGGTTGTCCCACTTTTGTTCGCCTCTCT
TCGGTCCTCTACTCAAGAGCTCCGTCTCCGTCTCGCCCTCCTCGAAGTCCTCGTCGCGCGCCCGCGACCCAGGTC
GCCCTGAAATCTAGCCCGTCCGAGCGCGAGTCCAACGGCCGCGGCCGCACCAAGGCCCCCTCAGACCGTGCCATG
GGTGACAGTGATGACGAGTACGATCGAAGGCGCAGGGACAAGTTCAGAAGAGAGCGCAGCGACTACGACCGTTCC
CGCGAGAGAGATGAAAGACGTCGAGGGGACGATTGGAATGACAGAGAGTGGGACCGTGGCCGTGAGCGCCGTAGT
CGGGGTGAATATCGGGACTATGACCGGAATCGGCGAGAGCGCTTCTCGCCACCTCGCCACGAACTCAGCCCGCCA
CAGAAGCGCATGAGGAGAGACTGGGATGAGCACAGCTCTGACCCATACCACAGTGGCTATGAGATGCCCTATGCT
GGGGGGGGGTGGGGGCCCAACTTATGGCCCCCCTCAGCCCTGGGGCCACCCTGACGTCCACATCATGCAGCACCA
TGTCCTGCCTATCCAGGCCAGGCTGGGCAGCATTGCAGAGATTGACCTGGGTGTGCCGCCGCCCGTGATGAAGAC
CTTCAAGGAGTTTCTCCTCTCCCTGGATGACTCGGTGGATGAGACGGAGGCCGTCAAGCGCTATAATGACTACAA
GCTGGATTTCCGGAGGCAACAGATGCAGGATTTCTTCCTGGCGCACAAAGATGAGGAGTGGTTTCGGTCTAAGTA
CCACCCAGATGAGGTGGGGAAGCGTCGGCAGGAGGCCCGGGGGGCCCTGCAAAACCGACTGAGGGTCTTCCTGTC
CCTCATGGAGACTGGCTGGTTTGATAACCTTCTCCTGGACATAGACAAAGCTGATGCCATTGTCAAGATGCTGGA
TGCAGCCGTGATTAAGATGGAAGGAGGCACGGAGAATGATCTCCGCATCCTGGAGCAGGAGGAGGAGGAGGAGCA
GGCAGGAAAGCCTGGGGAGCCCAGCAAGAAAGAAGAAGGACGGGCTGGAGCAGGCCTAGGGGACGGGGAGCGCAA
AACCAACGACAAGGATGAGAAGAAGGAAGACGGCAAGCAGGCTGAGAATGACAGTTCTAATGATGACAAAACAAA
GAAGTCGGAGGGTGATGGGGACAAGGAAGAGAAGAAAGAAGACTCCGAGAAGGAAGCCAAAAAGAGTAGCAAGAA
GCGGAACCGGAAGCACAGTGGTGACGACAGCTTTGACGAGGGCAGCGTGTCAGAGTCTGAGTCGGAGTCAGAGAG
CGGCCAGGCTGAGGAGGAGAAGGAGGAGGCCGAAGCGCTCAAGGAGAAGGAGAAGCCCAAGGAAGAAGAATGGGA
GAAGCCCAAGGACGCCGCGGGGCTGGAGTGCAAGCCGCGGCCGCTGCATAAGACCTGCTCCCTCTTCATGCGCAA
CATCGCGCCCAACATCTCCCGGGCCGAGATCATCTCCCTTTGTAAAAGGTACCCAGGCTTTATGCGGGTGGCGCT
CTCAGAGCCCCAGCCAGAGAGGAGGTTTTTCCGTCGTGGCTGGGTGACCTTCGACCGCAGTGTTAACATTAAAGA
GATCTGTTGGAACCTGCAGAACATCCGTCTCCGGAGTGTGAGCTGAGCCCTGGTGTGAACTGGGACCTGACCCGG
CGCGTTCGCAACATCAACGGCATCACCCAGCACAAGCAGATTGTGCGCAACGACATCAAGCTGGCGGCCAAGCTG
ATCCACACGCTGGATGACAGGACACAGCTTTGGGCCTCAGAACCAGGGACGCCTCCCCTGCCCACGAGCCTGCCC
TCGCAAAACCCGATCTTGAAGAATATCACCGACTACCTGATCGAGGAAGTAAGCGCCGAGGAGGAGGAGCTGCTG
GGGAGCAGCGGGGGCGCTCCTCCTGAGGAGCCTCCTAAGGAAGGGAACCCGGCAGAGATCAACGTGGAGCGGGAT
GAGAAGTTGATTAAGGTCTTGGACAAGCTCCTCCTTTACCTGCGCATCGTGCATTCCTTGGATTATTACAACACC
TGTGAGTACCCCAACGAGGACGAGATGCCCAATCGCTGTGGGATCATCCACGTTCGGGGGCCCATGCCACCCAAC
CGCATCAGTCACGGGGAAGTGCTGGAGTGGCAGAAGACTTTTGAGGAGAAGCTCACGCCGTTGCTGAGTGTGCGG
GAGTCACTCTCAGAGGAAGAGGCCCAGAAGATGGGGCGCAAAGACCCAGAGCAGGAAGTGGAGAAGTTCGTCACC
TCCAACACGCAGGAACTGGGCAAGGATAAGTGGCTGTGTCCTCTCAGTGGCAAGAAATTCAAGGGTCCTGAGTTT
GCGCGCAAACATATCTTCAACAAGCATGCAGAGAAAATTGAGGAAGTGAGAAAGGAAGTCGCGTTTTTTAACAAC
TTCCTCACTGATGCTAAGCGCCCAGCTCTGCCTGAGATCAAGCCAGCCCAGCCACCTGGCCCCGCCCAGATACTC
CCCCCAGGTTTGACCCCAGGACTCCCCTACCCACACCAGACTCCCCAGGGCCTGATGCCCTATGGTCAGCCCCGG
CCCCCGATCTTGGGCTATGGAGCTGGTGCTGTCCGCCCTGCAGTCCCCACAGGAGGCCCTCCATACCCCCATGCC
CCGTATGGTGCTGGTCGAGGGAACTATGATGCCTTCCGAGGCCAGGGAGGCTATCCTGGGAAACCTCGCAACAGG
ATGGTTCGTGGAGACCCAAGGGCCATTGTGGAATATCGGGACCTGGATGCCCCAGACGATGTTGATTTCTTTTGA
GCCGTCCCCCGTTCCTCAGTCCTGTATCATCCATACTTGTACTACCTTGTCCTATGAAGCTCTGAGAATTTTTTG
TACGATCAGCCTTACTGCTAATAAAAGCACTTCCACAGGGAAAAAAAAAAAAAAAAAA

FIGURE 253

CCGCAGAACTTGGGGAGCCGCCGCCGCCATCCGCCGCCGCAGCCAGCTTCCGCCGCCGCAGGACCGGCCCCTGCC
CCAGCCTCCGCAGCCGCGGCGCGTCCACGCCCGCCCGCGCCCAGGGCGAGTCGGGGTCGCCGCCTGCACGCTTCT
CAGTGTTCCCCGCGCCCCGCATGTAACCCGGCCAGGCCCCCGCAACGGTGTCCCCTGCAGCTCCAGCCCCGGGCT
GCACCCCCCCGCCCCGACACCAGCTCTCCAGCCTGCTCGTCCAGG**ATG**GCCGCGGCCAAGGCCGAGATGCAGCTG
ATGTCCCCGCTGCAGATCTCTGACCCGTTCGGATCCTTTCCTCACTCGCCCACCATGGACAACTACCCTAAGCTG
GAGGAGATGATGCTGCTGAGCAACGGGGCTCCCCAGTTCCTCGGCGCCGCCGGGGCCCCAGAGGGCAGCGGCAGC
AACAGCAGCAGCAGCAGCAGCGGGGGCGGTGGAGGCGGCGGGGGCGGCAGCAACAGCAGCAGCAGCAGCACC
TTCAACCCTCAGGCGGACACGGGCGAGCAGCCCTACGAGCACCTGACCGCAGAGTCTTTTCCTGACATCTCTCTG
AACAACGAGAAGGTGCTGGTGGAGACCAGTTACCCCAGCCAAACCACTCGACTGCCCCCCATCACCTATACTGGC
CGCTTTTCCCTGGAGCCTGCACCCAACAGTGGCAACACCTTGTGGCCCGAGCCCCTCTTCAGCTTGGTCAGTGGC
CTAGTGAGCATGACCAACCCACCGGCCTCCTCGTCCTCAGCACCATCTCCAGCGGCCTCCTCCGCCTCCGCCTCC
CAGAGCCCACCCCTGAGCTGCGCAGTGCCATCCAACGACAGCAGTCCCATTTACTCAGCGGCACCCACCTTCCCC
ACGCCGAACACTGACATTTTCCCTGAGCCACAAAGCCAGGCCTTCCCGGGCTCGGCAGGGACAGCGCTCCAGTAC
CCGCCTCCTGCCTACCCTGCCGCCAAGGGTGGCTTCCAGGTTCCCATGATCCCCGACTACCTGTTTCCACAGCAG
CAGGGGGATCTGGGCCTGGGCACCCCAGACCAGAAGCCCTTCCAGGGCCTGGAGAGCCGCACCCAGCAGCCTTCG
CTAACCCCTCTGTCTACTATTAAGGCCTTTGCCACTCAGTCGGGCTCCCAGGACCTGAAGGCCCTCAATACCAGC
TACCAGTCCCAGCTCATCAAACCCAGCCGCATGCGCAAGTATCCCAACCGGCCCAGCAAGACGCCCCCCCACGAA
CGCCCTTACGCTTGCCCAGTGGAGTCCTGTGATCGCCGCTTCTCCCGCTCCGACGAGCTCACCCGCCACATCCGC
ATCCACACAGGCCAGAAGCCCTTCCAGTGCCGCATCTGCATGCGCAACTTCAGCCGCAGCGACCACCTCACCACC
CACATCCGCACCCACACAGGCGAAAAGCCCTTCGCCTGCGACATCTGTGGAAGAAAGTTTGCCAGGAGCGATGAA
CGCAAGAGGCATACCAAGATCCACTTGCGGCAGAAGGACAAGAAAGCAGACAAAAGTGTTGTGGCCTCTTCGGCC
ACCTCCTCTCTCTCTTCCTACCCGTCCCCGGTTGCTACCTCTTACCCGTCCCCGGTTACTACCTCTTATCCATCC
CCGGCCACCACCTCATACCCATCCCCTGTGCCCACCTCCTTCTCCTCTCCCGGCTCCTCGACCTACCCATCCCCT
GTGCACAGTGGCTTCCCCTCCCCGTCGGTGGCCACCACGTACTCCTCTGTTCCCCCTGCTTTCCCGGCCCAGGTC
AGCAGCTTCCCTTCCTCAGCTGTCACCAACTCCTTCAGCGCCTCCACAGGGCTTTCGGACATGACAGCAACCTTT
TCTCCCAGGACAATTGAAATTTGC**TAA**AGGGAAAGGGGAAAGAAAGGGAAAAGGGAGAAAAAGAAACACAAGAGA
CTTAAAGGACAGGAGGAGGAGATGGCCATAGGAGAGGAGGGTTCCTCTTAGGTCAGATGGAGGTTCTCAGAGCCA
AGTCCTCCCTCTCTACTGGAGTGGAAGGTCTATTGGCCAACAATCCTTTCTGCCCACTTCCCCTTCCCCAATTAC
TATTCCCTTTGACTTCAGCTGCCTGAAACAGCCATGTCCAAGTTCTTCACCTCTATCCAAAGAACTTGATTTGCA
TGGATTTTGGATAAATCATTTCAGTATCATCTCCATCATATGCCTGACCCCTTGCTCCCTTCAATGCTAGAAAAT
CGAGTTGGCAAAATGGGGTTTGGGCCCCTCAGAGCCCTGCCCTGCACCCTTGTACAGTGTCTGTGCCATGGATTT
CGTTTTTCTTGGGGTACTCTTGATGTGAAGATAATTTGCATATTCTATTGTATTATTTGGAGTTAGGTCCTCACT
TGGGGGAAAAAAAAAAAAAAAAGCCAAGCAAACCAATGGTGATCCTCTATTTTGTGATGATGCTGTGACAATAAG
TTTGAACCTTTTTTTTTGAAACAGCAGTCCCAGTATTCTCAGAGCATGTGTCAGAGTGTTGTTCCGTTAACCTTT
TTGTAAATACTGCTTGACCGTACTCTCACATGTGGCAAAATATGGTTTGGTTTTTCTTTTTTTTTTTTGAAAGTG
TTTTTTCTTCGTCCTTTTGGTTTAAAAAGTTTCACGTCTTGGTGCCTTTTGTGTGATGCCCCTTGCTGATGGCTT
GACATGTGCAATTGTGAGGGACATGCTCACCTCTAGCCTTAAGGGGGGCAGGGAGTGATGATTTGGGGGAGGCTT
TGGGAGCAAAATAAGGAAGAGGGCTGAGCTGAGCTTCGGTTCTCCAGAATGTAAGAAAACAAAATCTAAAACAAA
ATCTGAACTCTCAAAAGTCTATTTTTTTAACTGAAAATGTAAATTTATAAATATATTCAGGAGTTGGAATGTTGT
AGTTACCTACTGAGTAGGCGGCGATTTTTGTATGTTATGAACATGCAGTTCATTATTTTGTGGTTCTATTTTACT
TTGTACTTGTGTTTGCTTAAACAAAGTGACTGTTTGGCTTATAAACACATTGAATGCGCTTTATTGCCCATGGGA
TATGTGGTGTATATCCTTCCAAAAAATTAAAACGAAAATAAAGTAGCTGCGATTGGG

FIGURE 254

MAAAKAEMQLMSPLQISDPFGSFPHSPTMDNYPKLEEMMLLSNGAPQFLGAAGAPEGSGSNSSSSSSGGGGGGGG
GSNSSSSSSTFNPQADTGEQPYEHLTAESFPDISLNNEKVLVETSYPSQTTRLPPITYTGRFSLEPAPNSGNTLW
PEPLFSLVSGLVSMTNPPASSSSAPSPAASSASASQSPPLSCAVPSNDSSPIYSAAPTFPTPNTDIFPEPQSQAF
PGSAGTALQYPPPAYPAAKGGFQVPMIPDYLFPQQQGDLGLGTPDQKPFQGLESRTQQPSLTPLSTIKAFATQSG
SQDLKALNTSYQSQLIKPSRMRKYPNRPSKTPPHERPYACPVESCDRRFSRSDELTRHIRIHTGQKPFQCRICMR
NFSRSDHLTTHIRTHTGEKPFACDICGRKFARSDERKRHTKIHLRQKDKKADKSVVASSATSSLSSYPSPVATSY
PSPVTTSYPSPATTSYPSPVPTSFSSPGSSTYPSPVHSGFPSPSVATTYSSVPPAFPAQVSSFPSSAVTNSFSAS
TGLSDMTATFSPRTIEIC

FIGURE 255

CTTCCCCTTCTCTGCCCTGCTCCAGGCACCAGGCTCTTTCCCCTTCAGTGTCTCAGAGGAGGGGACGGCAGCACC
ATGGACCCCCGCTTGTCCACTGTCCGCCAGACCTGCTGCTGCTTCAATGTCCGCATCGCAACCACCGCCCTGGCC
ATCTACCATGTGATCATGAGCGTCTTGTTGTTCATCGAGCACTCAGTAGAGGTGGCCCATGGCAAGGCGTCCTGC
AAGCTCTCCCAGATGGGCTACCTCAGGATCGCTGACCTGATCTCCAGCTTCCTGCTCATCACCATGCTCTTCATC
ATCAGCCTGAGCCTACTGATCGGCGTAGTCAAGAACCGGGAGAAGTACCTGCTGCCCTTCCTGTCCCTGCAAATC
ATGGACTATCTCCTGTGCCTGCTCACCCTGCTGGGCTCCTACATTGAGCTGCCCGCCTACCTCAAGTTGGCCTCC
CGGAGCCGTGCTAGCTCCTCCAAGTTCCCCCTGATGACGCTGCAGCTGCTGGACTTCTGCCTGAGCATCCTGACC
CTCTGCAGCTCCTACATGGAAGTGCCCACCTATCTCAACTTCAAGTCCATGAACCACATGAATTACCTCCCCAGC
CAGGAGGATATGCCTCATAACCAGTTCATCAAGATGATGATCATCTTTTCCATCGCCTTCATCACTGTCCTTATC
TTCAAGGTCTACATGTTCAAGTGCGTGTGGCGGTGCTACAGATTGATCAAGTGCATGAACTCGGTGGAGGAGAAG
AGAAACTCCAAGATGCTCCAGAAGGTGGTCCTGCCGTCCTACGAGGAAGCCCTGTCTTTGCCATCGAAGACCCCA
GAGGGGGGCCCAGCACCACCCCCATACTCAGAGGTG**TGA**CCCTCGCCAGGCCCCAGCCCCAGTGCTGGGAGGGGT
GGAGCTGCCTCATAATCTGCTTTTTTGCTTTGGTGGCCCCTGTGGCCTGGGTGGGCCCTCCCGCCCCTCCCTGGC
AGGACAATCTGCTTGTGTCTCCCTCGCTGGCCTGCTCCTCCTGCAGGGCCTGTGAGCTGCTCACAACTGGGTCAA
CGCTTTAGGCTGAGTCACTCCTCGGGTCTCTCCATAATTCAGCCCAACAATGCTTGGTTTATTTCAATCAGCTCT
GACACTTGTTTAGACGATTGGCCATTCTAAAGTTGGTGAGTTTGTCAAGCAACTATCGACTTGATCAGTTCAGCC
AAGCAACTGACAAATCAAAAACCCACTTGTCAGTTCAGTAAAATAATTTGGTCAAACAACAGTCTATTGCATTGA
TTTATAAATAGTTGTCAGTTCACATAGCAATTTAATCAAGTAATCATTAATTAGTTACCCCCTATATATAAATAT
ATGTAATCAATTTCTTCAAATAGCTTGCTTACATGATAATCAATTAGCCAACCATGAGTCATTTAGAATAGTGAT
AAATAGAATACACAGAATAGTGATGAAATTCAATTTAAAAAATCACGTTAGCCTCCAAACCATTTAATTCAAATG
AACCCATCAACTGGATGCCAACTCTGGCGAATGTAGGACCTCTGAGTGGCTGTATAATTGTTAATTCAAATGAAA
TTCATTTAAACAGTTGACAAACTGTCATTCAACAATTAGCTCCAGGAAATAACAGTTATTTCATCATAAAACAGT
CCCTTCAAACACACAATTGTTCTGCTGAAGAGTTGTCATCAACAATCCAATGCTCACCTATTCAGTTGCTCTGTG
GTCAGTGTGGCTGCATAGCAGTGGATTCCATGAAAGGAGTCATTTTAGTGATGAGCTGCCAGTCCATTCCCAGGC
CAGGCTGTCGCTGGCCATCCATTCAGTCGATTCAGTCATAGGCGAATCTGTTCTGCCCGAGGCTTGTGGTCAAGC
AAAAATTCAGCCCTGAAATCAGGCACATCTGTTCGTTGGACTAAACCCACAGGTTAGTTCAGTCAAAGCAGGCAA
CCCCCTTGTGGGCACTGACCCTGCCACTGGGGTCATGGCGGTTGTGGCAGCTGGGGAGGTTTGGCCCCAACAGCC
CTCCTGTGCCTGCTTCCCTGTGTGTCGGGGTCCTCCAGGGAGCTGACCCAGAGGTGGAGGCCACGGAGGCAGGGT
CTCTGGGGACTGTCGGGGGGTACAGAGGGAGAAGGCTCTGCAAGAGCTCCCTGGCAATACCCCCTTGTGTAATTG
CTTTGTGTGCGACAGGGAGGAAGTTTCAATAAAGCAACAACAAGCTTCAAGGAATTC

FIGURE 256

MDPRLSTVRQTCCCFNVRIATTALAIYHVIMSVLLFIEHSVEVAHGKASCKLSQMGYLRIADLISSFLLITMLFI
ISLSLLIGVVKNREKYLLPFLSLQIMDYLLCLLTLLGSYIELPAYLKLASRSRASSSKFPLMTLQLLDFCLSILT
LCSSYMEVPTYLNFKSMNHMNYLPSQEDMPHNQFIKMMIIFSIAFITVLIFKVYMFKCVWRCYRLIKCMNSVEEK
RNSKMLQKVVLPSYEEALSLPSKTPEGGPAPPPYSEV

FIGURE 257

CACGAGGGAGCGCTAACGTCTTTCTGTCTCCCCGCGGTGGTG**ATG**ACGGTGAAAACTGAGGCTGCTAAGGGCACC
CTCACTTACTCCAGGATGAGGGGCATGGTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAAC
GACTTTATTCAGAAGATTGCCAATAACTCCTATGCATGCAAACACCCTGAAGTTCAGTCCATCTTGAAGATCTCC
CAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCTCAGCAAATCAACCTTGGC
CCGTCGTCCAATCCTCATGCTAAACCATCTGACTTTCACTTCTTGAAAGTGATCGGAAAGGGCAGTTTTGGAAAG
GTTCTTCTAGCAAGACACAAGGCAGAAGAAGTGTTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAA
AAGAAAGAGGAGAAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCTTTCCTGGTGGGC
CTTCACTTCTCTTTCCAGACTGCTGACAAATTGTACTTTGTCCTAGACTACATTAATGGTGGAGAGTTGTTCTAC
CATCTCCAGAGGGAACGCTGCTTCCTGGAACCACGGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTGGGC
TACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAACCAGAGAATATTTTGCTAGATTCACAGGGACACATT
GTCCTTACTGATTTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAACATCCACCTTCTGTGGCACGCCG
GAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGGTGGTGCCTGGGAGCTGTC
TTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGAAACACAGCTGAAATGTACGACAACATTCTGAAC
AAGCCTCTCCAGCTGAAACCAAATATTACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGG
ACAAAGCGGCTCGGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAACTGGGAT
GATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCAACGAGCTACGGCACTTTGAC
CCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTC
AAGGAAGCTGCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCACGGACTCTTTCCTC**TGA**ACCCTGTTAGGG
CTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGGTGGAGCCGCCAGCTGACAGGA
CATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGCAATCTTATTGCACACTGTTCGCTGGAATTTTTTGAA
GAGCACATTCTCCTCAGTGAGCTCATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAAC
GAGCGTTAGAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACCTGTTCTAAAAAAGGTCTCCTG
CAGATCTGTCTGGGCTGTGATGACGAATATTATGAAATGTGCCTTTTCTGAAGAGATTGTGTTAGCTCCAAAGCT
TTTCCTATCGCAGTGTTTCAGTTCTTTATTTTCCCTTGTGGATATGCTGTGTGAACCGTCGTGTGAGTGTGGTAT
GCCTGATCACAGATGGATTTTGTTATAAGCATCAATGTGACACTTGCAGGACACTACAACGTGGGACATTGTTTG
TTTCTTCCATATTTGGAAGATAAATTTATGTGTAGACTTTTTTGTAAGATACGGTTAATAACTAAAATTTATTGA
AATGGTCTTGCAATGACTCGTATTCAGATGCCTAAAGAAAGCATTGCTGCTACAAATATTTCTATTTTTAGAAAG
GGTTTTTATGGACCAATGCCCCAGTTGTCAGTCAGAGCCGTTGGTGTTTTTCATTGTTTAAAATGTCACCTGTAA
AATGGGCATTATTTATGTTTTTTTTTTTGCATTCCTGATAATTGTATGTATTGTATAAAGAACGTCTGTACATTG
GGTTATAACACTAGTATATTTAAACTTACAGGCTTATTTGTAATGTAAACCACCATTTTAATGTACTGTAATTAA
CATGGTTATAATACGTACAATCCTTCCCTCATCCCATCACACAACTTTTTTTGTGTGTGATAAACTGATTTTGGT
TTGCAATAAAACCTTGAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 258

MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNSYACKHPEVQSILKISQPQEPELMNANPSP
PPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAEEVFYAVKVLQKKAILKKKEEKHIMSERNVL
LKNVKHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKP
ENILLDSQGHIVLTDFGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPN
VSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPTDSFL

FIGURE 259

GGCCTGTTCTCGAGTCCGCGCTTTTCGTCACCGCC**ATG**TCGGGAGGTGGTGTGATTCGTGGCCCCGCAGGGAACA
ACGATTGCCGCATCTACGTGGGTAACTTACCTCCAGACATCCGAACCAAGGACATTGAGGACGTGTTCTACAAAT
ACGGCGCTATCCGCGACATCGACCTCAAGAATCGCCGCGGGGGACCGCCCTTCGCCTTCGTTGAGTTCGAGGACC
CGCGAGACGCGGAAGACGCGGTGTATGGTCGCGACGGCTATGATTACGATGGGTACCGTCTGCGGGTGGAGTTTC
CTCGAAGCGGCCGTGGAACAGGCCGAGGCGGCGGCGGGGGTGGAGGTGGCGGAGCTCCCCGAGGTCGCTATGGCC
CCCCATCCAGGCGGTCTGAAAACAGAGTGGTTGTCTCTGGACTGCCTCCAAGTGGAAGTTGGCAGGATTTAAAGG
ATCACATGCGTGAAGCAGGTGATGTATGTTATGCTGATGTTTACCGAGATGGCACTGGTGTCGTGGAGTTTGTAC
GGAAAGAAGATATGACCTATGCAGTTCGAAAACTGGATAACACTAAGTTTAGATCTCATGAGGGAGAAACTGCCT
ACATCCGGGTTAAAGTTGATGGGCCCAGAAGTCCAAGTTATGGAAGATCTCGATCTCGAAGCCGTAGTCGTAGCA
GAAGCCGTAGCAGAAGCAACAGCAGGAGTCGCAGTTACTCCCCAAGGAGAAGCAGAGGATCACCACGCTATTCTC
CCCGTCATAGCAGATCTCGCTCTCGTACA**TAA**GATGATTGGTGACACTTTTTGTAGAACCCATGTTGTATACAGT
TTTCCTTTATTCAGTACAATCTTTTCATTTTTTAATTCAAACTGTTTTGTTCAGAATGGGCTAAAGTGTTGAATT
GCATTCTTGTAATATCCCCTTGCTCCTAACATCTACATTCCCTTCGTGTCTTTGATAAATTGTATTTTAAGTGAT
GTCATAGACAGGATTGTTTAAATTTAGTTAACTCCATACTCTTCAGACTGTGATATTGTGTAAATGTCTATCTGC
CCTGGTTTGTGTGAACTGGGATGTTGGGGGTGTTTGTGGTTATCTTACCTGGGGAAGTTCTTATGTTTATCTTGC
TTTTCATGTGTCTTTCTGTAGACATATCTGAAGAGATGGATTAAGAATGCTTTGGATTAAGGATTGTGGAGCACA
TTTCAATCATTTTAGGATTGTCAAAAGGAGGATTGAGGAGGATCAGATCAATAATGGAGGCAATGGTATGACTCC
AAGTGCTATTGTCACAGATGAAATTGGCAGTATTGACCTTATACTAAAAGGCAGGGGTTAAAAATGATTATATAC
ATTTTCCTTAAAACACTTGCAAACATTTTATTCAGTTGTCTTTAGCTACAATTGCTTTGCTTTTTAAACCTTGGC
AATTGTGGCAAAATTATATTGCCCATTTTGTAGCAACTTATTTTGCTCCCTTCCCCCCATTTTTGTTTTAATAGG
GACTAATGTGGGAAGAACTGGCTAATTTGTCACAGTGCTTAGTTACAACTGTTAATGTGTGACCTGCTGTTGGTG
TACATGTGGGTACAGGGTGTTTTTAAATCCAACAAGATAGAGTATAATATCAATACTGCTAAATCTGCATGTCCT
CTGTGTGACTGATAGAGCGTTGCTATTTCATTTTTTTAAGACAAAATGAAAGCAAAATATAGAGTTCCAATGTAT
TGGTGTAGATAATCTAGTTGGGAATACTTTTAAGTCTCACCTTCCCCTTTAAACTAATATTCATAATTGGTTCAT
ATGTTTAAAAGACTTTAATTTACAAATTAAATTGCAAATGGGAGCATTAGATTTAGTTTTAGACTTAGGTGGGTA
GCAATGCCAGTAAACTTAAATTACGTAACTTCTTGCAACCACGAAACCTGTAATACGCTGTACAGTAACAAGTGT
TGGCATTATCAGTTGAACTGTAAATACAAAATGCTTCTTCCAATTAGTCTCTATGATGATTAAGTTTCTAAAATT
TATCTGAACACCATTCAGAAACTTGTTTTGGGGAATTTGATAGTTATTGATGTGCATCTGTTAAACTGATGACAG
ACATAACTCATCATTCCCCAGAAACCTTTTTTGATTACAGTATCTAACATTTTGCCTCCTCTTTTTTGGTTTTGC
TGGTTATAAAGGTTTGGATTGGAGAGGGCTCACTGGATCCCAATCCTTGGAGCTGGATCATTGGATTCAAATCAT
AATGTGGATAGGATAGGGAGGATGAATTACCAGGATTCATGGAGCGGGATCAGATTACCAGGAACATAGGAGTGG
ATTCCTGCCCCAACCAAACCGCATTCGTGTGGATTTTTTTATTCAACTTAATTGGCTATTCCAAAGATTTTTTTT
TTCCTATTTTTGACGATTGGAGCCCTTAAGATGCACGATGGAATTGTGTTTTGCGTTTTTTTGGTAAAAGGAGCAA
AGCGAGGACCTGGAGATAAACGCTGGAGCAATCTCCTTGGAAGGATTCAGCACGAGTAGATGGTAAACATTTAAA
GGGGAAAGGGGGGGTTTGTTTAAAATAGTAAATCAGTAAGTCACTTCTAAATTTAAAGAAAACAAAATTGGAGTT
GAAGAATAAGTAGGTTTCCAATTGGCTATTGCCGTTTTCTTTGAAAAAATAAACATTTTTTAAAAAACAAAAAAA
AAAAAAAA

FIGURE 260

MSGGGVIRGPAGNNDCRIYVGNLPPDIRTKDIEDVFYKYGAIRDIDLKNRRGGPPFAFVEFEDPRDAEDAVYGRD
GYDYDGYRLRVEFPRSGRGTGRGGGGGGGGGAPRGRYGPPSRRSENRVVVSGLPPSGSWQDLKDHMREAGDVCYA
DVYRDGTGVVEFVRKEDMTYAVRKLDNTKFRSHEGETAYIRVKVDGPRSPSYGRSRSRSRSRSRSRSRSNSRSRS
YSPRRSRGSPRYSPRHSRSRSRT

FIGURE 261

AGATAACAAGAGTAATCCACAGACTTAAAAC**ATG**AGCTCAGATGCCAGCCAAGGCGTGATTACCACTCCTCCTCC
TCCCAGCATGCCTCACAAAGAGAGATATTTTGACCGCATCAATGAAAATGACCCAGAATACATTAGGGAGAGGAA
CATGTCTCCTGATCTACGACAAGACTTCAACATGATGGAGCAGAGGAAACGAGTTACTCAGATCCTGCAAAGTCC
TGCCTTTCGGGAAGACTTGGAATGCCTTATTCAAGAACAGATGAAGAAAGGCCACAACCCAACTGGATTACTAGC
ATTACAGCAGATTGCAGATTACATCATGGCCAATTCTTTCTCGGGTTTTTCTTCACCTCCTCTCAGTCTTGGCAT
GGTCACACCTATCAATGACCTTCCTGGTGCAGATACATCCTCATATGTGAAGGGAGAAAAACTTACTCGCTGTAA
ACTTGCCAGCCTGTACAGACTTGTAGACTTGTTTGGATGGGCACACCTGGCAAATACCTATATCTCAGTAAGAAT
AAGTAAGGAGCAAGACCACATTATAATAATTCCCAGAGGCCTATCTTTTTCTGAAGCTACAGCCTCCAATTTGGT
GAAAGTCAATATAATAGGAGAAGTGGTTGACCAGGGAAGTACCAATTTGAAAATTGACCATACAGGATTCAGTCC
CCATGCTGCAATCTATTCAACACGTCCTGATGTTAAGTGTGTCATACACATCCATACCCTTGCAACAGCAGCTGT
ATCCTCCATGAAATGTGGGATCCTTCCAATTTCTCAAGAGTCTCTTCTTCTGGGAGATGTTGCCTATTATGACTA
CCAAGGGTCACTTGAAGAACAGGAGGAGAGAATTCAACTGCAGAAGGTTCTGGGACCAAGTTGTAAGGTGCTGGT
ACTCAGGAATCATGGTGTGGTTGCACTTGGAGAAACATTAGAGGAGGCTTTTCATTATATTTTTAATGTGCAACT
AGCCTGTGAGATTCAGGTGCAGGCCCTAGCAGGTGCAGGTGGAGTAGACAATCTCCATGTACTGGACTTTCAGAA
GTATAAAGCTTTCACTTACACTGTAGCAGCGTCTGGTGGAGGAGGTGTGAATATGGGTTCCCATCAAAAATGGAA
GGTTGGCGAAATTGAGTTTGAAGGGCTTATGAGGACTCTGGACAACTTGGGGTATAGAACAGGCTATGCTTACAG
GCATCCTCTCATTCGAGAGAAGCCTAGGCACAAGAGTGATGTGGAAATCCCAGCAACTGTGACTGCTTTTTCCTT
TGAAGACGATACAGTGCCACTCTCTCCTCTCAAATACATGGCACAGAGGCAACAGCGTGAAAAAACAAGATGGCT
GAACTCACCAAATACTTACATGAAAGTGAATGTGCCTGAGGAGTCTCGGAACGGAGAAACCAGTCCCCGAACCAA
AATCACGTGGATGAAAGCAGAAGACTCATCTAAAGTTAGTGGTGGAACACCTATCAAAATTGAAGATCCAAATCA
GTTTGTTCCTTTAAACACAAACCCGAATGAGGTACTAGAAAAGAGAAATAAGATTCGGGAACAAAATCGATATGA
CTTGAAAACAGCAGGACCACAATCTCAGTTGCTTGCTGGAATTGTTGTGGATAAGCCACCTTCTACTATGCAATT
TGAAGATGATGATCATGGCCCACCAGCTCCTCCTAACCCATTTAGTCATCTCACAGAAGGAGAACTTGAAGAGTA
TAAGAGGACAATCGAACGTAAACAACAAGGCCTAGAAGATGCTGAGCAGGAATTACTCTCAGATGACGCTTCATC
TGTTTCACAAATTCAGTCTCAAACTCAGTCACCGCAAAATGTCCCTGAAAAATTAGAAGAAAACCATGAGCTGTT
TTCCAAGAGCTTCATCTCCATGGAAGTGCCTGTCATGGTAGTAAATGGCAAGGATGATATGCATGATGTTGAAGA
TGAGCTTGCTAAGCGAGTGAGTAGGTTAAGCACAAGTACAACCATAGAAAACATCGAGATTACTATTAAGTCTCC
AGAGAAAATCGAAGAAGTCCTGTCACCTGAAGGCTCCCCTTCAAAATCGCCATCCAAGAAAAAGAAGAAATTCCG
CACTCCTTCTTTTCTGAAAAAGAACAAAAAAAAAGGAGAAAGTTGAGGCC**TAA**ATAAAGTCTTTTTATAATTATTA
TTATAACAATGTGACATTGCACATCTAAATACCACATTTAAGTTGATCATTAATATGCAATGGTAGATCAGATTG
GGGGATGTAGCAAACTGGACTTTAAGAACTGGAAAGAGGTTTTACAAAAGAAAAACTTTCAGATTCATCTCTCAT
TTTATATGTCCAGAAATGGCTTTGAATTTTAAGCAATTACTAGTTTTAATTAGCTCTGCCCTCATGAAGTATTAT
TATAATTCACCATAAACAGCTATCTGTCTGAATTACTTCAGGCCTTCTCCATAATATCTGTTAGAAAGAAATTGC
CAGTGAGCAAGTGAGAATTTTTATTTCTCAATACCTGCTTCACTTGATAATCATATTATAATTTTTTATCATGAT
TATTGACTATATTTTTGGAGTCCCATTGTTTCAGTGGGCATTAACAGAATGCTTTAAAAACTTCTAAGACAAGAA
TCTATAGCATTAGTATACACTGGCACATAATTTTTTAAAAAGTTTTAAGAAAAGATTCATTTGGAATTTTATTCA
CAGTATAAAATTTCCTCACCTGAAGTAACTTTGTTTGCCAAAAAAGTTGTTTTAATAAACTATAATTTTTGAAAA
CTTCCTTTTTTATTAGTTTAGAAAGCCCCTTATTTTTCAACAAAGGGGATTTTGTACACATAACATGGGTTATTT
AGTTTAACTCTGGC

FIGURE 262

MSSDASQGVITTPPPPSMPHKERYFDRINENDPEYIRERNMSPDLRQDFNMMEQRKRVTQILQSPAFREDLECLI
QEQMKKGHNPTGLLALQQIADYIMANSFSGFSSPPLSLGMVTPINDLPGADTSSYVKGEKLTRCKLASLYRLVDL
FGWAHLANTYISVRISKEQDHIIIIPRGLSFSEATASNLVKVNIIGEVVDQGSTNLKIDHTGFSPHAAIYSTRPD
VKCVIHIHTLATAAVSSMKCGILPISQESLLLGDVAYYDYQGSLEEQEERIQLQKVLGPSCKVLVLRNHGVVALG
ETLEEAFHYIFNVQLACEIQVQALAGAGGVDNLHVLDFQKYKAFTYTVAASGGGGVNMGSHQKWKVGEIEFEGLM
RTLDNLGYRTGYAYRHPLIREKPRHKSDVEIPATVTAFSFEDDTVPLSPLKYMAQRQQREKTRWLNSPNTYMKVN
VPEESRNGETSPRTKITWMKAEDSSKVSGGTPIKIEDPNQFVPLNTNPNEVLEKRNKIREQNRYDLKTAGPQSQL
LAGIVVDKPPSTMQFEDDDHGPPAPPNPFSHLTEGELEEYKRTIERKQQGLEDAEQELLSDDASSVSQIQSQTQS
PQNVPEKLEENHELFSKSFISMEVPVMVVNGKDDMHDVEDELAKRVSRLSTSTTIENIEITIKSPEKIEEVLSPE
GSPSKSPSKKKKKFRTPSFLKKNKKKEKVEA

FIGURE 263

ATATAACCGCGTGGCCCGCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
A**ATG**TCTGCTTTGGCTGCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCATTTCTGGAAGGAAACTGGCCCAGCAGATCAAGCAGGAAGTGCGGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCCTCAACAAAACCAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAACTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATACAATTCTTGCAGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAACTGCCAAACCCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAAGCTGGGTATATCAC
TCCAGTTCCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATTGCTGCAAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGCTGAAGTCTAAAGAGCTTGGGGTAGCCACTAAT**TAA**CTACTGTGTCTTCT
GTGTCACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTTAATTTATTC
TACTGAAATGGTTTAAAATGATGCCTTGTATTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGGTCCTGTGATCTAGCCAGGAGCAGCCATTAACCTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTCGCCTT
TTCTAGGATTGCATTTCCCAAGTGCTATTGCAATAACAGTTGATACTCATTTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAACCAAAGGAAAAGTGTTGCTAGAGAAAATTGGGGAAAAGGTGAAAAAGAAAAAATGGTAGTAATT
GAGCAGAAAAAAATTAATTTATATATGTATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCCTTCAGTAAGTTCTCCCCATTTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAAACCTATTTTTGAAAAACAAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTTTAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

FIGURE 264

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVRQEVEEWVASGNKRPHLSVILVGENPAS
HSYVLNKTRAAAVVGINSETIMKPASISEEELLNLINKLNNDDNVDGLLVQLPLPEHIDERRICNAVSPDKDVDG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQKAGYIT
PVPGGVGPMTVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

FIGURE 265

GGGGGAGTGAAAGCGAAAGCCCGGGCGACTAGCCGGGAGACCAGAGATCTAGCGACTGAAGCAGC**ATG**GCCAAGC
CGTGTGGGGTGCGCCTGAGCGGGGAAGCCCGCAAACAGGTGGAGGTCTTCAGGCAGAATCTTTTCCAGGAGGCTG
AGGAATTCCTCTACAGATTCTTGCCACAGAAAATCATATACCTGAATCAGCTCTTGCAAGAGGACTCCCTCAATG
TGGCTGACTTGACTTCCCTCCGGGCCCCACTGGACATCCCCATCCCAGACCCTCCACCCAAGGATGATGAGATGG
AAACAGATAAGCAGGAGAAGAAAGAAGTCCCTAAGTGTGGATTTCTCCCTGGGAATGAGAAAGTCCTGTCCCTGC
TTGCCCTGGTTAAGCCAGAAGTCTGGACTCTCAAAGAGAAATGCATTCTGGTGATTACATGGATCCAACACCTGA
TCCCCAAGATTGAAGATGGAAATGATTTTGGGGTAGCAATCCAGGAGAAGGTGCTGGAGAGGGTGAATGCCGTCA
AGACCAAAGTGGAAGCTTTCCAGACAACCATTTCCAAGTACTTCTCAGAACGTGGGGATGCTGTGGCCAAGGCCT
CCAAGGAGACTCATGTAATGGATTACCGGGCCTTGGTGCATGAGCGAGATGAGGCAGCCTATGGGGAGCTCAGGG
CCATGGTGCTGGACCTGAGGGCCTTCTATGCTGAGCTTTATCATATCATCAGCAGCAACCTGGAGAAAATTGTCA
CCCCAAAGGGTGAAGAAAAGCCATCTATGTAC**TGA**ACCCGGGACTAGAAGGAAAATAAATGATCTATATGTTGTG
TGG

FIGURE 266

MAKPCGVRLSGEARKQVEVFRQNLFQEAEEFLYRFLPQKIIYLNQLLQEDSLNVADLTSLRAPLDIPIPDPPPKD
DEMETDKQEKKEVPKCGFLPGNEKVLSLLALVKPEVWTLKEKCILVITWIQHLIPKIEDGNDFGVAIQEKVLERV
NAVKTKVEAFQTTISKYFSERGDAVAKASKETHVMDYRALVHERDEAAYGELRAMVLDLRAFYAELYHIISSNLE
KIVTPKGEEKPSMY

FIGURE 267

AGTCAAG**ATG**GAGGAGTACGCGCGAGAGCCTTGCCCATGGCGAATTGTGGATGACTGTGGTGGGGCCTTTACGAT
GGGTACCATTGGTGGTGGTATCTTTCAAGCAATCAAAGGTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACT
ACGAGGGAGTTTGACAGCTATTAAAACCAGGGCTCCACAGTTAGGAGGTAGCTTTGCAGTTTGGGGAGGGCTGTT
TTCCATGATTGACTGTAGTATGGTTCAAGTCAGAGGAAAGGAAGATCCCTGGAACTCCATCACAAGTGGTGCCTT
AACGGGAGCCATACTGGCAGCAAGAAATGGACCAGTGGCCATGGTTGGGTCAGCCGCAATGGGTGGCATTCTCCT
AGCTTTAATTGAAGGAGCTGGTATCTTGTTGACAAGATTTGCCTCTGCACAGTTTCCCAATGGTCCTCAGTTTGC
AGAAGACCCCTCCCAGTTGCCTTCAACTCAGTTACCTTCCTCACCTTTTGGAGACTATCGACAATATCAG**TAG**GA
CTTCTTTCCTAGGATTTCTTTAACAGAACGAGTTGTGGTTCGAGAAGGATTTCAGAAGATCAAGTTACAGTCTGT
TTTTAAAACCATAGGTGGGACAGCTATGGCCAATAGGCTATAAAGAGACATTTAGCACTTTTTTCTATTTAAAGG
AACAAGCGGGGAAGGGTGCTAAAAGATAATACGTTTATTTATTCACACTTGAATTGCATTTGTGATCAAAATAAA
TGTTTAAATCGCTAAAGGAAAATACAGTAAGTGCTTGAAAGATGAAGGACCAAAAGGCCAAAAAACAGTGAAATA
TGATCATCATCTCTTGCGGACTTCTCTGCCTGGTTTTGTGTGTTCTGTTATTCAAACAATAAAAAGCTGGTGGAA
CTTACTCTTTCTTTTAAGATAAGTTGTAGACTTCGATGTTTCATGCTCATGTACTTCAAATAATGCATGTTTTAT
AGTTAGTCCCTCATCACTTGAAGTGACTTCTGAGAATTATGCAGAGTCAACATGGATCATTTCACAGTGAGATGC
TTTATGGATTGAAGGATATGGTAAAATGTTTATAGTTTACTTTGAAAGTAAAATATACTATGTCTTGGTTTTGAG
GATATTGGATACAAAACTCTCTTCCTTTAGGGCTACTGAGTCTTGATTCCTGATCATCAGAAATTTCACCAGAAA
CAACTTGCTTCCAATATACCCAATTCTATATGAAGAATTCATGGAGAGTGTACTGGCACTGGAAGAGTTTAGTGT
TTCTTGTATGCTTGAAAATAAAGTATGTACTGTTTTGAATGTGTTCCAAGTCCTCTGCATAAACGATGTATTTTG
GGGTCTGGTTGGGCCTGGAAAATGGATGAGCACTTCAGAACAGGTCATTTTCCTGATATTGGAAGTGACATGTGG
CCCTATAGGAGGCATGATGTTAGTTAATTACACATTTGCCTACATCTGTGGGAAATGGAGAACAAAGCCATGTGG
GTACTGTAAACACACGTTTATCTTTTGGCCCAATGCCATACATATGGTAGGCATTTAATTACTGATTGTGTTTGG
ATAATTTGGGAATTTTCGACTGTGGTAAAATATACATAAAATAATACTTATTAAAAAAAAAAAAAAAAAA

FIGURE 268

MEEYAREPCPWRIVDDCGGAFTMGTIGGGIFQAIKGFRNSPVGVNHRLRGSLTAIKTRAPQLGGSFAVWGGLFSM
IDCSMVQVRGKEDPWNSITSGALTGAILAARNGPVAMVGSAAMGGILLALIEGAGILLTRFASAQFPNGPQFAED
PSQLPSTQLPSSPFGDYRQYQ

FIGURE 269

AGAGGCTTCCCTGGCTGGTGCCTGAGCCCGGCGTCCCTCGCCCCCCGCCCTCCCCGCATCCCTCTCCTCCCTCGC
GCCTGGCCCTGTGGCTCTTCCTCCCTCCCTCCTTCCCCCCCCCCCCCACCCCTCGCCCGCTGCCTCCCTCGGCCCA
GCCAGCTGTGCCGGCGTTTGTTGGCTGCCCTGCGCCCGGCCCTCCAGCCAGCCTTCTGCCGGCCCCGCCGCG**ATG**

GAGGTGCCCCAGCCGGAGCCCGCGCCAGGCTCGGCTCTCAGTCCAGCAGGCGTGTGCGGTGGCGCCCAGCGTCCG
GGCCACCTCCCGGGCCTCCTGCTGGGATCTCATGGCCTCCTGGGGTCCCCGGTGCGGGCGGCCGCTTCCTCGCCG
GTCACCACCCTCACCCAGACCATGCACGACCTCGCCGGGCTCGGCAGCCGCAGCCGCCTGACGCACCTATCCCTG
TCTCGACGGGCATCCGAATCCTCCCTGTCGTCTGAATCCTCCGAATCTTCTGATGCAGGTCTCTGCATGGATTCC
CCCAGCCCTATGGACCCCCACATGGCGGAGCAGACGTTTGAACAGGCCATCCAGGCAGCCAGCCGGATCATTCGA
AACGAGCAGTTTGCCATCAGACGCTTCCAGTCTATGCCGGTGAGGCTGCTGGGCCACAGCCCCGTGCTTCGGAAC
ATCACCAACTCCCAGGCGCCCGACGGCCGGAGGAAGAGCGAGGCGGGCAGTGGAGCTGCCAGCAGCTCTGGGGAA
GACAAGGAGAATGTGCGCTTCTGGAAGGCCGGGGTGGGAGCTCTCCGGGAAGAGGAGGGGGCATGCTGGGGTGGT
TCCCTGGCATGTGAGGACCCTCCTCTCCCATCTTGGCTGCAGGATGGATTTGTCTTCAAGATGCCATGGAAGCCC
ACACATCCCAGCTCCACCCATGCTCTGGCAGAGTGGGCCAGCCGCAGGGAAGCCTTTGCCCAGAGACCCAGCTCG
GCCCCCGACCTGATGTGTCTCAGTCCTGACCGGAAGATGGAAGTGGAGGAGCTCAGCCCCCTGGCCCTAGGTCGC
TTCTCTCTGACCCCTGCAGAGGGGGATACTGAGGAAGATGATGGATTTGTGGACATCCTAGAGAGTGACTTAAAG
GATGATGATGCAGTTCCCCCAGGCATGGAGAGTCTCATTAGTGCCCCACTGGTCAAGACCTTGGAAAAGGAAGAG
GAAAAGGACCTCGTCATGTACAGCAAGTGCCAGCGGCTCTTCCGCTCTCCGTCCATGCCCTGCAGCGTGATCCGG
CCCATCCTCAAGAGGCTGGAGCGGCCCCAGGACAGGGACACGCCCGTGCAGAATAAGCGGAGGCGGAGCGTGACC
CCTCCTGAGGAGCAGCAGGAGGCTGAGGAACCTAAAGCCCGCGTCCTCCGCTCAAAATCACTGTGTCACGATGAG
ATCGAGAACCTCCTGGACAGTGACCACCGAGAGCTGATTGGAGATTACTCTAAGGCCTTCCTCCTACAGACAGTA
GACGGAAAGCACCAAGACCTCAAGTACATCTCACCAGAAACGATGGTGGCCCTATTGACGGGCAAGTTCAGCAAC
ATCGTGGATAAGTTTGTGATTGTAGACTGCAGATACCCCTATGAATATGAAGGCGGGCACATCAAGACTGCGGTG
AACTTGCCCCTGGAACGCGACGCCGAGAGCTTCCTACTGAAGAGCCCCATCGCGCCCTGTAGCCTGGACAAGAGA
GTCATCCTCATTTTCCACTGTGAATTCTCATCTGAGCGTGGGCCCCGCATGTGCCGTTTCATCAGGGAACGAGAC
CGTGCTGTCAACGACTACCCCAGCCTCTACTACCCTGAGATGTATATCCTGAAAGGCGGCTACAAGGAGTTCTTC
CCTCAGCACCCGAACTTCTGTGAACCCCAGGACTACCGGCCCATGAACCACGAGGCCTTCAAGGATGAGCTAAAG
ACCTTCCGCCTCAAGACTCGCAGCTGGGCTGGGGAGCGGAGCCGGCGGGAGCTCTGTAGCCGGCTGCAGGACCAG
TGAGGGGCCTGCGCCAGTCCTGCTACCTCCCTTGCCTTTCGAGGCCTGAAGCCAGCTGCCCTATGGGCCTGCCGG
GCTGAGGGCCTGCTGGAGGCCTCAGGTGCTGTCCATGGGAAAGATGGTGTGGTGTCCTGCCTGTCTGCCCCAGCC
CAGATTCCCCTGTGTCATCCCATCATTTTCCATATCCTGGTGCCCCCCACCCCTGGAAGAGCCCAGTCTGTTGAG
TTAGTTAAGTTGGGTTAATACCAGCTTAAAGGCAGTATTTTGTGTCCTCCAGGAGCTTCTTGTTTCCTTGTTAGG
GTTAACCCTTCATCTTCCTGTGTCCTGAAACGCTCCTTTGTGTGTGTGTCAGCTGAGGCTGGGGAGAGCCGTGGT
CCCTGAGGATGGGTCAGAGCTAAACTCCTTCCTGGCCTGAGAGTCAGCTCTCTGCCCTGTGTACTTCCCGGGCCA
GGGCTGCCCCTAATCTCTGTAGGAACCGTGGTATGTCTGCCATGTTGCCCCTTTCTCTTTTCCCCTTTCCTGTCC
CACCATACGAGCACCTCCAGCCTGAACAGAAGCTCTTACTCTTTCCTATTTCAGTGTTACCTGTGTGCTTGGTCT
GTTTGACTTTACGCCCATCTCAGGACACTTCCGTAGACTGTTTAGGTTCCCCTGTCAAATATCAGTTACCCACTC
GGTCCCAGTTTTGTTGCCCCAGAAAGGGATGTTATTATCCTTGGGGGCTCCCAGGGCAAGGGTTAAGGCCTGAAT
CATGAGCCTGCTGGAAGCCCAGCCCCTACTGCTGTGAACCCTGGGGCCTGACTGCTCAGAACTTGCTGCTGTCTT
GTTGCGGATGGATGGAAGGTTGGATGGATGGGTGGATGGCCGTGGATGGCCGTGGATGCGCAGTGCCTTGCATAC
CCAAACCAGGTGGGAGCGTTTTGTTGAGCATGACACCTGCAGCAGGAATATATGTGTGCCTATTTGTGTGGACAA
AAATATTTACACTTAGGGTTTGGAGCTATTCAAGAGGAAATGTCACAGAAGCAGCTAAACCAAGGACTGAGCACC
CTCTGGATTCTGAATCTCAAGATGGGGGCAGGGCTGTGCTTGAAGGCCCTGCTGAGTCATCTGTTAGGGCCTTGG
TTCAATAAAGCACTGAGCAAGTTGAGAAAAAAAAAAAAAAAAAA

FIGURE 270

MEVPQPEPAPGSALSPAGVCGGAQRPGHLPGLLLGSHGLLGSPVRAAASSPVTTLTQTMHDLAGLGSRSRLTHLS
LSRRASESSLSSESSESSDAGLCMDSPSPMDPHMAEQTFEQAIQAASRIIRNEQFAIRRFQSMPVRLLGHSPVLR
NITNSQAPDGRRKSEAGSGAASSSGEDKENVRFWKAGVGALREEEGACWGGSLACEDPPLPSWLQDGFVFKMPWK
PTHPSSTHALAEWASRREAFAQRPSSAPDLMCLSPDRKMEVEELSPLALGRFSLTPAEGDTEEDDGFVDILESDL
KDDDAVPPGMESLISAPLVKTLEKEEEKDLVMYSKCQRLFRSPSMPCSVIRPILKRLERPQDRDTPVQNKRRRSV
TPPEEQQEAEEPKARVLRSKSLCHDEIENLLDSDHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFS
NIVDKFVIVDCRYPYEYEGGHIKTAVNLPLERDAESFLLKSPIAPCSLDKRVILIFHCEFSSERGPRMCRFIRER
DRAVNDYPSLYYPEMYILKGGYKEFFPQHPNFCEPQDYRPMNHEAFKDELKTFRLKTRSWAGERSRRELCSRLQD
Q

FIGURE 271

GAATTCCGCTAGACTAAGTTGGTC**ATG**ATGCAGAAGCTACTCAAATGCAGTCGGCTTGTCCTGGCTCTTGCCCTC
ATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCAGAGAGCCAGGTACCAATGGGTGCGCTGCAATCCA
GACAGTAATTCTGCAAACTGCCTTGAAGAAAAAGGACCAATGTTCGAACTACTTCCAGGTGAATCCAACAAGATC
CCCCGTCTGAGGACTGACCTTTTTCCAAAGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGAC
TACTCTGGATCAGGCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGGAA
CAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCCATGACAACCTTAGGTCTCTTGACAGGAATCTGCCCTCA
GACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTATGTTA**TAA**AAGAGGATTTTCCCACCTTGACAC
CAGGCAATGTAGTTAGCATATTTTATGTACCATGGTTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATT
TTTAAACATCTGAAAAAGAAGCTTAAGTTTTATCATCCTTTTTTTTCTCATGAATTCTTAAAGGATTATGCTTTA
ATGCTGTTATCTATCTTATTGTTCTTGAAAATACCTGCATTTTTTGGTATCATGTTCAACCAACATCATTATGAA
ATTAATTAGATTCCCATGGCCATAAAATGGCTTTAAAGAATATATATATATTTTTAAAGTAGCTTGAGAAGCAAA
TTGGCAGGTAATATTTCATACCTAAATTAAGACTCTGACTTGGATTGTGAATTATAATGATATGCCCCTTTTCTT
ATAAAAACAAAAAAAAAAATAATGAAACACAGTGAATTTGTAGAGTGGGGGTATTTGACATATTTTACAGGGTGGA
GTGTACTATATACTATTACCTTTGAATGTGTTTGCAGAGCTAGTGGATGTGTTTGTCTACAAGTATGATTGCTGT
TACATAACACCCCAAATTAACTCCCAAATTAAAACACAGTTGTGCTGTCAATACCTCATACTGCTTTACCTTTTT
TTCCTGGATATCTGTGTATTTTCAAATGTTACTATATATTAAAGCAGAAATATAACC

FIGURE 272

MMQKLLKCSRLVLALALILVLESSVQGYPTQRARYQWVRCNPDSNSANCLEEKGPMFELLPGESNKIPRLRTDLF
PKTRIQDLNRIFPLSEDYSGSGFGSGSGSGSGSGSGFLTEMEQDYQLVDESDAFHDNLRSLDRNLPSDSQDLGQH
GLEEDFML

FIGURE 273

CCGGTCCTGAGACACGCTGTGTGGCTGAAAAGTGAAGGCAAGAGCTCATTTGGCCTCTGTGCTCCCCTCCGCAAG
GGATCGTTTCTCCAGAAGAGCTGGATATTCTTTCGCCCAGTT**ATG**GCAGACAAGTTAACGAGAATTGCTATTGTC
AACCATGACAAATGTAAACCTAAGAAATGTCGACAGGAATGCAAAAAGAGTTGTCCTGTAGTTCGAATGGGAAAA
TTATGCATAGAGGTTACACCCCAGAGCAAAATAGCATGGATTTCCGAAACTCTTTGTATTGGTTGTGGTATCTGT
ATTAAGAAATGCCCCTTTGGCGCCTTATCAATTGTCAATCTACCAAGCAACTTGGAAAAAGAAACCACACATCGA
TATTGTGCCAATGCCTTCAAACTTCACAGGTTGCCTATCCCTCGTCCAGGTGAAGTTTTGGGATTAGTTGGAACT
AATGGTATTGGAAAGTCAGCTGCTTTAAAAATTTTAGCAGGAAAACAAAAGCCAAACCTTGGAAAGTACGATGAT
CCTCCTGACTGGCAGGAGATTTTGACTTATTTCCGTGGATCTGAATTACAAAATTACTTTACAAAGATTCTAGAA
GATGACCTAAAAGCCATCATCAAACCTCAATATGTAGCCAGATTCCTAAGGCTGGCAAAGGGGACAGTGGGATCT
ATTTTGGACCGAAAAGATGAAACAAAGACACAGGCAATTGTATGTCAGCAGCTTGATTTAACCCACCTAAAAGAA
CGAAATGTTGAAGATCTTTCAGGAGGAGAGTTGCAGAGATTTGCTTGTGCTGTCGTTTGCATACAGAAAGCTGAT
ATTTTCATGTTTGATGAGCCTTCTAGTTACCTAGATGTCAAGCAGCGTTTAAAGGCTGCTATTACTATACGATCT
CTAATAAATCCAGATAGATATATCATTGTGGTGGAACATGATCTAAGTGTATTAGACTATCTCTCCGACTTCATC
TGCTGTTTATATGGTGTACCAAGCGCCTATGGAGTTGTCACTATGCCTTTTAGTGTAAGAGAAGGCATAAACATT
TTTTTGGATGGCTATGTTCCAACAGAAAACTTGAGATTCAGAGATGCATCACTTGTTTTTAAAGTGGCTGAGACA
GCAAATGAAGAAGAAGTTAAAAAGATGTGTATGTATAAATATCCAGGAATGAAGAAAAAAATGGGAGAATTTGAG
CTAGCAATTGTAGCTGGAGAGTTTACAGATTCTGAAATTATGGTGATGCTGGGGGAAAATGGAACGGGTAAAACG
ACATTTATCAGAATGCTTGCTGGAAGACTTAAACCTGATGAAGGAGGAGAAGTACCAGTTCTAAATGTCAGTTAT
AAGCCACAGAAAATTAGTCCCAAATCAACTGGAAGTGTTCGCCAGTTACTACATGAAAAGATAAGAGATGCTTAT
ACTCACCCACAATTTGTGACCGATGTAATGAAGCCTCTGCAAATTGAAAACATCATTGATCAAGAGGTGCAGACA
TTATCTGGTGGTGAACTACAGCGAGTACGTTTACGCCTTTGCTTGGGCAAACCTGCTGATGTCTATTTAATTGAT
GAACCATCTGCATATTTGGATTCTGAGCAAAGACTGATGGCAGCTCGAGTTGTCAAACGTTTCATACTCCATGCA
AAAAAGACAGCCTTTGTTGTGGAACATGACTTCATCATGGCCACCTATCTAGCGGATCGCGTCATCGTTTTTGAT
GGTGTTCCATCTAAGAACACAGTTGCAAACAGTCCTCAAACCCTTTTGGCTGGCATGAATAAATTTTTGTCTCAG
CTTGAAATTACATTCAGAAGAGATCCAAACAACTATAGGCCACGAATAAACAAACTTAATTCAATTAAGGATGTA
GAACAAAAGAAGAGTGGAAACTACTTTTTCTTGGATGAT**TAG**ACTGACTCTGAGAATATTGATAAGCCATTTATT
AAAAGGAGTATTTACTAGAATTTTTTGTCATATAAAACTTGAATCAGGATTTTATGCCCCACATACTCTGGAACT
TGAAGTATAATATACTTAATATAACATAAAAAGCCAGTTGGGTTCTAAATTGTAGTTGAAACACAGAAAATGCCA
CTTTTCTGTTCCTGAAGAGGCTCTTTTGTGCATAATATTCTAAAATGAAGACATTTCAAGCTATACAAATTACTT
CCAAGTTTTCATGATGTATGGGAAGATTTTCAGTAGGTGTATTATATTCACGGTACCAAATGCTGACCAGTGTTG
CTCCATTTTTTAAATCTTGAAAAGGGTTTCTGTACTTACCTGGTTTGCCAAGTATGCCAGTGTAATGAAACTGCC
CTTATTTTAAAAGCCAGTCAAAGATTCCACTGATTGACATTTGATAAATAAACATCAGGATTATGTTTATTGTTT
GTTTTCAGTCTTTGCACTATATTACCAGTATATGGTTTCCGAGGAAGATTATCTACTGCAAAACACCACTGTTGG
AAAAATAGGTATTTTTAAATTGTTTTTAATCCTTTTTTGGTGCTTTTAAACATGTTTAAGCAAAAACCAATTCAG
TCCATTCCCCGCAAAAAACCCCTAACTTTACTCTGAACTTTTTTTGTTTTTGCATTCCATGAGGTTCTGTATTCA
GTCATTCTCTAGGTAATGTCATTTTTGTACACATATATTTATATAATCACTGATTGAGATTTAGGAAAAAGCATT
TCTAAAGAATATTTGCTTCCCTTAGAACTACAGACTCGAAATCTTTAAAGATGGTGCCTAAGCATCTATGTATTT
TTTTTAAGTTCCACAGATTTTTCTGTTGGGCAGGCCAAGGATTATAAACCACTTCCCTAAAGGCAACATTAATGC
AAAAGTCCCCAGATGGCAATACAAAGTATCCCCTGGTACCACATATATTCATTTGTGAGTTTGGATATAGAGCAC
ATTATCTAAACCATTTTGTAGTTCCAAAAACCCATCTAAATTTCTTGAGTTCCTGAATTTTGAACAGGATTACCT
GGAGCCTGGAGCCACTTTAAGTTGTACTTCTGACTAAACTGGAATTATGAGTGAGGAAGAGTGTTTACTAAATAA
ATGACTGGGGCAAGCAAAATTGAGGAGGAAATTAGAAACTGTTTGACAAACTTTAAGAGCTACTTGAAATAACAG
AAGTCTTGATTAATATGCAAATAATGGCTAGAAAGTATGGTTTAACTGGACCCTATTATGCCTTTTAAAAATAAT
TTCAGTAACCCATAAATACATGTTGTAAAAAATTCAAATATACAGAATGGAATAAAAAAATGATCTCCCTTTATT
ACCCTCCCAAAGGTTACCAGCGTTTGAATTTAATAATGTATATTCTTTCATGCTTTTTTCTGTGCACTTACCTAA
GTGTGAATATGTAAAGGGTTTGTTTTGTATACAAATGGGATTATACTAAAATAAGTAATGCCTATTTTTAAGGAT
AGGTTAAATTTGTGAATGATCATTTCAAATATATTGAATAAAATAAGCAAAAGCTATTGTTATTTACTGATCCTG
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MADKLTRIAIVNHDKCKPKKCRQECKKSCPVVRMGKLCIEVTPQSKIAWISETLCIGCGICIKKCPFGALSIVNL
PSNLEKETTHRYCANAFKLHRLPIPRPGEVLGLVGTNGIGKSAALKILAGKQKPNLGKYDDPPDWQEILTYFRGS
ELQNYFTKILEDDLKAIIKPQYVARFLRLAKGTVGSILDRKDETKTQAIVCQQLDLTHLKERNVEDLSGGELQRF
ACAVVCIQKADIFMFDEPSSYLDVKQRLKAAITIRSLINPDRYIIVVEHDLSVLDYLSDFICCLYGVPSAYGVVT
MPFSVREGINIFLDGYVPTENLRFRDASLVFKVAETANEEEVKKMCMYKYPGMKKKMGEFELAIVAGEFTDSEIM
VMLGENGTGKTTFIRMLAGRLKPDEGGEVPVLNVSYKPQKISPKSTGSVRQLLHEKIRDAYTHPQFVTDVMKPLQ
IENIIDQEVQTLSGGELQRVRLRLCLGKPADVYLIDEPSAYLDSEQRLMAARVVKRFILHAKKTAFVVEHDFIMA
TYLADRVIVFDGVPSKNTVANSPQTLLAGMNKFLSQLEITFRRDPNNYRPRINKLNSIKDVEQKKSGNYFFLDD

FIGURE 275

CCGGAGGAGTCCGAGAGGAAGCGGAGGCGCGAGCTGGAGGCGGCGGCTCCCGTCGGCCTCCGGCAGGACTGAGCG
CTGGGAGGCCGGAAGGCGGGCGCGCACGGCGGAGAGGCGGGCGGGAGGCCGGAGCATATTAATGAAAAGTGCCAT
AAACTGAAAAACCAAAC**ATG**AGGGTAGCAGGTGCTGCAAAGTTGGTGGTAGCTGTGGCAGTGTTTTTACTGACAT
TTTATGTTATTTCTCAAGTATTTGAAATAAAAATGGATGCAAGTTTAGGAAATCTATTTGCAAGATCAGCATTGG
ACACAGCTGCACGTTCTACAAAGCCTCCCAGATATAAGTGTGGGATCTCAAAAGCTTGCCCTGAGAAGCATTTTG
CTTTTAAAATGGCAAGTGGAGCAGCCAACGTGGTGGGACCCAAAATCTGCCTGGAAGATAATGTTTTAATGAGTG
GTGTTAAGAATAATGTTGGAAGAGGGATCAATGTTGCCTTGGCAAATGGAAAAACAGGAGAAGTATTAGACACTA
AATATTTTGACATGTGGGGAGGAGATGTGGCACCATTTATTGAGTTTCTGAAGGCCATACAAGATGGAACAATAG
TTTTAATGGGAACATACGATGATGGAGCAACCAAACTCAATGATGAGGCACGGCGGCTCATTGCTGATTTGGGGA
GCACATCTATTACTAATCTTGGTTTTAGAGACAACTGGGTCTTCTGTGGTGGGAAGGGCATTAAGACAAAAAGCC
CTTTTGAACAGCACATAAAGAACAATAAGGATACAAACAAATATGAAGGATGGCCTGAAGTTGTAGAAATGGAAG
GATGCATCCCCCAGAAGCAAGAC**TAA**TGGAAATGTGGAGAGAATTGAAGAAAGCGCACTTTCACTCTTAATGGGA
GAGCTATAAATGGCAGAGCTATGTGTAAATATTTTAAGAGCATGCAGCCATCTTGGTGTGTGCATGAGTATTGTC
TCTTTTGATATCAGGATTATTTATTGCTAACGTAAATAGATAGCATTGTAAATAATCATCACAATGATCAAATCA
CTGAACCATGTCTCCGCACATTTCCCTAAAAGTACAATGTTTAGACTGCTATGGTAATACATATTTTAAATTCTA
AAAGCATACACAATGTGTAACTGAATGGTTTGTGAAAAATATATTGATATATATACTAGTTGCTATGAAAATATC
ATGGAATAATAGGGATTTTAGGGTGGATACTTTATTTTCTTTTATGTTTCTATATGTTGCGTTGTGATGACATTA
TCTTTTAAATTAAAAAGAGATTTGGCTAGTTGTGTGTGTAATGTTACTTTACAGTCCGACTCTCCTGATGTACCT
CTTTTCATGATCTTTTTCTTTCCTTCCCAAGAAACTGAGGAATGTTTAATATGAAAACATACATCGGATATGTGA
AAAGCACAACAAAATTCTTAATGTACACAGTAAAAAAGTAAATATATAAATGTAGATGGCATTTAGGACCACAGC
TTGCTGGATTTGTGTTAGCTATGGGAATAACTTGATTTTGTATAAGCTATTTAGAGTGAGGCTGGAGGTGGCAGC
TTCACAGAACTGGAGAACCAGGCCAAGTCCCCTCCCCAACCTAATTAGGTCATTCAGGACAGCTAAGTCAGTATA
TTTAGAGCAATACTAGCATACGTTTTTCTTAATTGTTATCAGCATTGACCAAGTGGTTTGGAAGGAGGCATGCTT
TAATATCACAATAATTTTGATTTGTAAACCAAGAAATTAATCCTGTGTTTATCTAACTTCATAATAGCAATTATT
GCCCGAAGCTATAGTGGCATATTTACAAAAGTTCTTATTACTGGGCGGACTGATAACATTTAAAAAATAATTGTG
TTTGACCCCAAATGACTTTATACCCAATTCTACATAAAAATATAGAAGATCTATCTTTTTTTGTTACCTTCAGAT
GTTCACTAAATAACTCAGTTTTTAAGCAGAAGTTTTCAGGGCATTAAATATATGTTGTGTATGAAGTATCTCAAA
CTGGAACATAAATTTAGTGATCAAACTGCCATTCACAGTGTAAGGCAGCACTTAAATTTCGAACCTAAAGTTTAG
ATGCATTGTATAAAAAAACCTAAAAGCAGTATCTGTTATTTAGCTGTAAACCAAGTTGGAAGCTATTCGGATAAT
TTCTTAAATATTGATGAACTTTGGAGTACTGTTTCTTCCTTCAAACTGAATGTAATTAATTCATGAATAAATGCA
CCTTATATGTTTAAACAATCTTTGTATACTTTTGGGATTTTTGGTGCTTATATGCTAAATCACATTCAGCATGTG
TATTTTGACATTTAAAATACTTCCCTCAATTCTGTAAATTAAAAGAATAGTTATTTTACAGTTCCAGGGATTGTG
AAATAAATGTTGCAGTTTTTTAAAATAATGAAAATAAATACTCTTGGTTTTGCTTTGTGAAAAAAAAAAAAAAAA

FIGURE 276

MRVAGAAKLVVAVAVFLLTFYVISQVFEIKMDASLGNLFARSALDTAARSTKPPRYKCGISKACPEKHFAFKMAS
GAANVVGPKICLEDNVLMSGVKNNVGRGINVALANGKTGEVLDTKYFDMWGGDVAPFIEFLKAIQDGTIVLMGTY
DDGATKLNDEARRLIADLGSTSITNLGFRDNWVFCGGKGIKTKSPFEQHIKNNKDTNKYEGWPEVVEMEGCIPQK
QD

FIGURE 277

TACTGACTTTCAGCACCAACTTGTGGTCCCAGGTAAGTTTCCACGCTGGTACTTTAGCCCTGGGCTCGAACCTGC
GGACACGCTGTGGCTGCAACTCCCCGCCCGCCAGACCTCAGTACGCAGCGCGGCTGGTGAGAAACATAATGCACT
CTGACTTCCACGCGTGGAATGGGGAGATGGACTGCACGGCGGGCGGACCTGCTCGGGCTGATGGACGGCAGGTGG
ACTGATGTGCGCAGGGACTGGCGGCAGCGCGGTCAGAGCCAGTCAGCCAAAGCCAGGCCAGCACAATAGACTGTC
CCGGTTCCCGCCAGGAGGCGGCCGAGCACCAACTGTACGGTACTGCGCCTGCGCCGCGACCGCCAACGCGCCCAG
TCTACGCTTGCGCGGCGCAACAGGGCCGACTGCAGCTGGAAG**ATG**GCGGCGTCCGTGGTCTGTCGGGCCGCTACC
GCCGGGGCACAAGTGCTATTGCGCGCCCGCCGCTCGCCGGCCCTGCTGCGGACGCCAGCCTTGCGGAGTACGGCA
ACCTTCGCTCAGGCGCTCCAGTTCGTGCCGGAGACGCAGGTTAGCCTGCTGGACAACGGCCTGCGTGTGGCCTCC
GAGCAGTCCTCTCAGCCCACTTGCACGGTGGGAGTGTGGATTGATGTTGGCAGCCGTTTTGAGACTGAGAAGAAT
AATGGGGCAGGCTACTTTTTGGAGCATCTGGCTTTCAAGGGAACAAAGAATCGGCCTGGCAGTGCCCTGGAGAAG
GAGGTGGAGAGCATGGGGGCCCATCTTAATGCCTACAGCACCCGGGAGCACACAGCTTACTACATCAAGGCGCTG
TCCAAGGATCTGCCGAAAGCTGTGGAGCTCCTGGGTGACATTGTGCAGAACTGTAGTCTGGAAGACTCACAGATT
GAGAAGGAACGTGATGTGATCCTGCGGGAGATGCAGGAGAATGATGCATCTATGCGAGATGTGGTCTTTAACTAC
CTGCATGCCACAGCATTCCAGGGCACACCTCTAGCCCAGGCTGTGGAGGGGCCCAGTGAGAATGTCAGGAAGCTG
TCTCGTGCAGACTTGACCGAGTACCTCAGCACACATTACAAGGCCCCTCGAATGGTGCTGGCAGCAGCTGGAGGA
GTGGAGCACCAGCAACTGTTAGACCTCGCCCAGAAGCACCTCGGTGGCATCCCATGGACATATGCAGAGGACGCT
GTGCCCACTCTTACTCCATGCCGCTTCACTGGCAGTGAGATCCGCCACCGTGATGATGCTCTACCTTTTGCCCAC
GTGGCCATTGCAGTAGAGGGTCCTGGCTGGGCCAGCCCGGACAGTGTGGCCTTGCAAGTGGCCAATGCCATCATC
GGCCACTATGACTGCACTTATGGTGGTGGCGTGCACCTGTCCAGCCCACTGGCTTCAGGTGCTGTGGCCAACAAG
CTATGCCAGAGTTTCCAGACCTTCAGCATCTGCTATGCAGAGACGGGCTTGCTGGGTGCACACTTTGTCTGTGAC
CGAATGAAAATCGATGACATGATGTTCGTCCTGCAAGGGCAGTGGATGCGCCTGTGTACCAGTGCCACGGAGAGT
GAGGTGGCCCGGGGCAAAAACATCCTCAGAAATGCCCTGGTATCTCATCTAGATGGCACTACTCCTGTGTGTGAG
GACATCGGACGCAGCCTCCTGACCTATGGCCGCCGCATCCCCCTGGCTGAATGGGAAAGCCGGATTGCGGAGGTG
GATGCCAGTGTGGTACGTGAGATCTGCTCCAAGTACATCTATGACCAGTGCCCAGCAGTGGCTGGATATGGCCCC
ATTGAGCAGCTCCCAGACTACAACCGGATCCGTAGCGGCATGTTCTGGCTGCGCTTC**TAG**GCGGGAAGCCTATGT
AAGCAAGAGGGCAGGGCCGGGGTTTGTGGTCCCCCCCCCACCACAAACACAGCACTTCGGCTCCTCTAACCTGTG
CCACAGGTGACCACCAATAAAATCCTCTGCTGAGA

FIGURE 278

MAASVVCRAATAGAQVLLRARRSPALLRTPALRSTATFAQALQFVPETQVSLLDNGLRVASEQSSQPTCTVGVWI
DVGSRFETEKNNGAGYFLEHLAFKGTKNRPGSALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLGDI
VQNCSLEDSQIEKERDVILREMQENDASMRDVVFNYLHATAFQGTPLAQAVEGPSENVRKLSRADLTEYLSTHYK
APRMVLAAAGGVEHQQLLDLAQKHLGGIPWTYAEDAVPTLTPCRFTGSEIRHRDDALPFAHVAIAVEGPGWASPD
SVALQVANAIIGHYDCTYGGGVHLSSPLASGAVANKLCQSFQTFSICYAETGLLGAHFVCDRMKIDDMMFVLQGQ
WMRLCTSATESEVARGKNILRNALVSHLDGTTPVCEDIGRSLLTYGRRIPLAEWESRIAEVDASVVREICSKYIY
DQCPAVAGYGPIEQLPDYNRIRSGMFWLRF

FIGURE 279

GGCACACACGAGGAGGAGGGTTGAGCTGCTGCCGCCGCCGCCTCTGTCGTCGTCGCGAGTGTGGAGTCGGGACTG
GAGCTGCTGCCGCGGCGACGCCGGGGATCTTTGTCGCTAGCTCCCGGCCCTTCTGCCCCGCCGCCTTCCCTCAGT
CAGCGTTGCCCACTCCTCTCCGGCCGGGCGCCCCTGCCTCCATTTCTCGCTCTCTGTCCACCACACACACGGCCC
CCCCGATCATGGATCCGGGCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGGAGCAGCAGCGGCAGCAGCA
GCAGCGACTCGGCGCCTGACTGCTGGGACCAGGCGGACATGGAAGCCCCCGGGCCGGGCCCTTGCGGCGGCGGCG
GCTTCCCTGGCGGCGGCGGCCGAGGCCCAGCGGGAGAACCTCAGCGCGGCCTTCAGCCGGCAACTCAACGTCAAC
GCCAAGCCCTTCGTGCCCAACGTCCACGCCGCCGAGTTCGTGCCGTCCTTCCTGCGGGGCCCGGCAGCGCCGCCA
CCCCCAGCTGGCGGCGCCGCCAATAACCACGGAGCCGGCAGCGGCGCGGGAGGCCGTGCGGCACCTGTGGAATCC
TCTCAAGAGGAACAGTCATTGTGTGAAGGTTCAAATTCAGCTGTTAGC**ATG**GAACTTTCAGAACCTATTGTAGAA
AATGGAGAGACAGAAATGTCTCCAGAAGAATCATGGGAGCACAAAGAAGAAATAAGTGAAGCAGAGCCAGGGGGT
GGTTCCTTGGGAGATGGAAGGCCGCCAGAGGAAAGTGCCCATGAAATGATGGAGGAGGAAGAGGAAATCCCAAAA
CCTAAGTCTGTGGTTGCACCGCCAGGTGCTCCTAAGAAAGAGCATGTAAATGTAGTATTCATTGGGCACGTAGAT
GCTGGCAAGTCAACCATTGGAGGACAAATAATGTATTTGACTGGAATGGTTGACAAAAGGACGCTTGAAAAGTAT
GAAAGAGAAGCTAAAGAGAAAAACAGAGAAACTTGGTACTTGTCTTGGGCCTTAGACACAAATCAGGAAGAACGA
GACAAGGGTAAAACAGTAGAAGTGGGTCGTGCCTATTTTGAAACCGAAAAGAAGCATTTCACAATTCTAGATGCC
CCTGGCCACAAGAGTTTTGTCCCAAATATGATTGGTGGTGCCTCTCAAGCTGATTTGGCTGTGCTGGTAATCTCA
GCCAGGAAAGGAGAGTTTGAAACTGGATTTGAAAAAGGAGGACAGACAAGAGAACATGCAATGTTGGCAAAGACA
GCAGGTGTAAAACACCTAATTGTGCTAATTAATAAGATGGATGATCCAACAGTAAATTGGAGCAATGAGAGATAT
GAAGAATGTAAGGAGAAACTAGTGCCATTTTTGAAAAAAGTTGGCTTCAATCCCAAAAAGGACATTCACTTTATG
CCCTGCTCAGGACTTACTGGAGCAAATCTCAAAGAGCAGTCGGATTTCTGTCCTTGGTACATTGGATTACCGTTT
ATTCCATATCTGGATAATTTGCCGAACTTCAATAGATCAGTTGATGGACCAATCAGGCTGCCAATTGTGGATAAG
TACAAGGATATGGGCACTGTGGTCCTGGGAAAGCTGGAATCAGGATCTATTTGTAAAGGCCAGCAGCTTGTGATG
ATGCCAAACAAGCACAACGTGGAAGTTCTTGGAATACTTTCCGATGATGTAGAGACTGATACCGTAGCCCCAGGT
GAAAACCTCAAAATCAGACTGAAAGGAATTGAAGAAGAGGAGATTCTTCCAGGGTTTATACTTTGTGATCCTAAT
AATCTTTGTCATTCTGGACGCACATTTGATGCCCAGATAGTGATTATAGAGCACAAATCCATCATCTGCCCAGGC
TATAATGCGGTGCTGCATATTCATACCTGTATTGAGGAGGTGGAAATAACAGCCTTAATCTGCTTGGTAGACAAA
AAATCAGGAGAAAAAAGTAAGACCCGACCCCGTTTTGTGAAACAAGATCAAGTATGCATTGCTCGCTTAAGGACA
GCAGGAACCATCTGCCTTGAGACCTTTAAAGACTTCCCTCAGATGGGTCGTTTCACCTTAAGAGATGAGGGTAAG
ACCATTGCAATTGGAAAAGTTCTGAAACTGGTTCCAGAGAAAGAC**TAA**GCATTTTCTTGATGACCCTGCACAATA
CTGTGAGGAAAATTGACTGCAGAAGCCTACTTCACACCGCCTTCTCTTATTTTCTGCCCATTGATAAACCTCTCC
CCATATTTTGCAAAGAGGAAATTCACAGCAAAAGTCCACATTATGTCAGCTTTCTCATATTGAGAGCTCTGCTAT
GCCACTGTTGAATTTTTCCCAAGATTCCTGTCCCTAGCCCTCACTTCAAACTCTGCTTCCTTGGACAGATTTGGC
AATAGCTTTGTAAGTGATGTGGACATAATTGCCTACAATAATGAAAACCTACAGGAATTTTTTTATTTTTCATTT
TCCCCTTAGGCATATTTAGTATTTTTCCCCCAGGCCAGATCATTCGTGAGTGTGCGAGTGTGTGTGCACATGTTA
CAAAGGCAACTACCATGTTAATAAAATATTCAATTTG

FIGURE 280

MELSEPIVENGETEMSPEESWEHKEEISEAEPGGGSLGDGRPPEESAHEMMEEEEEIPKPKSVVAPPGAPKKEHV
NVVFIGHVDAGKSTIGGQIMYLTGMVDKRTLEKYEREAKEKNRETWYLSWALDTNQEERDKGKTVEVGRAYFETE
KKHFTILDAPGHKSFVPNMIGGASQADLAVLVISARKGEFETGFEKGGQTREHAMLAKTAGVKHLIVLINKMDDP
TVNWSNERYEECKEKLVPFLKKVGFNPKKDIHFMPCSGLTGANLKEQSDFCPWYIGLPFIPYLDNLPNFNRSVDG
PIRLPIVDKYKDMGTVVLGKLESGSICKGQQLVMMPNKHNVEVLGILSDDVETDTVAPGENLKIRLKGIEEEEIL
PGFILCDPNNLCHSGRTFDAQIVIIEHKSIICPGYNAVLHIHTCIEEVEITALICLVDKKSGEKSKTRPRFVKQD
QVCIARLRTAGTICLETFKDFPQMGRFTLRDEGKTIAIGKVLKLVPEKD

FIGURE 281

GCGGCGCTCGCGCCAAGGGACGTGTTTCTGCGCTCGCGTGGTC**ATG**GAGGCGCTGCCGCTGCTAGCCGCGACAAC
TCCGGACCACGGCCGCCACCGAAGGCTGCTTCTGCTGCCGCTACTGCTGTTCCTGCTGCCGGCTGGAGCTGTGCA
GGGCTGGGAGACAGAGGAGAGGCCCCGGACTCGCGAAGAGGAGTGCCACTTCTACGCGGGTGGACAAGTGTACCC
GGGAGAGGCATCCCGGGTATCGGTCGCCGACCACTCCCTGCACCTAAGCAAAGCGAAGATTTCCAAGCCAGCGCC
CTACTGGGAAGGAACAGCTGTGATCGATGGAGAATTTAAGGAGCTGAAGTTAACTGATTATCGTGGGAAATACTT
GGTTTTCTTCTTCTACCCACTTGATTTCACATTTGTGTGTCCAACTGAAATTATCGCTTTTGGCGACAGACTTGA
AGAATTCAGATCTATAAATACTGAAGTGGTAGCATGCTCTGTTGATTCACAGTTTACCCATTTGGCCTGGATTAA
TACCCCTCGAAGACAAGGAGGACTTGGGCCAATAAGGATTCCACTTCTTTCAGATTTGACCCATCAGATCTCAAA
GGACTATGGTGTATACCTAGAGGACTCAGGCCACACTCTTAGAGGTCTCTTCATTATTGATGACAAAGGAATCCT
AAGACAAATTACTCTGAATGATCTTCCTGTGGGTAGATCAGTGGATGAGACACTACGTTTGGTTCAAGCATTCCA
GTACACTGACAAACACGGAGAAGTCTGCCCTGCTGGCTGGAAACCTGGTAGTGAAACAATAATCCCAGATCCAGC
TGGAAAGCTGAAGTATTTCGATAAACTGAAT**TGA**GAAATACTTCTTCAAGTTATGATGCTTGAAAGTTCTCAATA
AAGTTCACGGTTTCATTACCA

FIGURE 282

MEALPLLAATTPDHGRHRRLLLLPLLLFLLPAGAVQGWETEERPRTREEECHFYAGGQVYPGEASRVSVADHSLH
LSKAKISKPAPYWEGTAVIDGEFKELKLTDYRGKYLVFFFYPLDFTFVCPTEIIAFGDRLEEFRSINTEVVACSV
DSQFTHLAWINTPRRQGGLGPIRIPLLSDLTHQISKDYGVYLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSV
DETLRLVQAFQYTDKHGEVCPAGWKPGSETIIPDPAGKLKYFDKLN

FIGURE 283

GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAATATGGACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAAACTGTT
CCTGGACTTCTTGGAGGAGTTTCAGAGCAGCGATGGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCTTACCTGTGTCGGGCCTTGAAAACATTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTCGAGAGCTCACCTCATCCAG
AATTGGTTTGCTCACTCGCATCAGTGGGCAGGTGGTGCGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCCGCAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAAACTAATTCCCGTGTCAGTGGTGTTGATGGATATGAGACAGAAGG
CATTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTTGCCTGCTGTGTTGCGCC
AACCAACCCAAGGTTTGGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAAGAACCAAATGAC
TGTGAAAGAATGGGAGAAAGTGTTTGAGATGAGTCAAGATAAAAATCTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAAACGGGGTGTCCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGCTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTCATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTGTGTTGTATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATAAATTTGTCAGCTCCCATCATGTCCCGATT
CGATCTCTTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCGACAGCTTGAGAGCATGATTCGTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAAATAAAAAAAGAATCATAGAGAAAGTTATTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCCTAACTACTTGCTCGAAGATTGAGATAGTGAAAGTAACTGACCAGA
GCTGAGGAACTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTTTCTGG
AAGTGATGCTTCCAGGATTTGTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTCACATTCATCACAGGT
TTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCAGTGAAGTTGGAACCAAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTCATGTGTAAGAAAAGGCCCATTACTTTTAAGGTATGTGCTGTCCTATT
GAGCAAATAACTTTTTTTCAATTGCCAGCTACTGCTTTTATTCATCAAAATAAAATAACTTGTTCTG

FIGURE 284

MDLAAAAEPGAGSQHLEVRDEVAEKCQKLFLDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLLDTNKSRFVDFQKVRIQETQAELPRGSIPRSLE
VILRAEAVESAQAGDKCDFTGTLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPRFGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSPRAVYTSGKASSAAGLTAAVVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAGVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGSGVTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLLNKSIIRVETPDVNLDQEEEIQME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRLGFSEYCRISNLIVLHLRKVEEEEDESALKRSELVN
WYLKEIESEIDSEEELINKKRIIEKVIHRLTHYDHVLIELTQAGLKGSTEGSESYEEDPYLVVNPNYLLED

FIGURE 285

GCCCCCACCATCAAGGGGAAGAAAGTGCTCTTCGGATTCCGGTTCGCCCTGGCCTCCCGCAGCCGCCGCGGGACC
GGCCCCCAGCACACCCCCGGGGCGCCGGGCGCGGGGCAGCCGCCCGGACGCGCGCGGGCCTCAGGCGCCGCCGGG
ACCCCAGCCCCCCAAACTTTGGCAAGTTGCGGGCGCCGAGCGCACCCGGAGGCGCGGGGCGCGGCCGCAGGCGGA
GCCGCCCCCTGACGCCGGGCCGCCCCCTCCCGGCCCCGGCCGCCCCGCCGGCTCCGCGGAAAGTTTGCGGCCGCC
CCTGCGCCGCACCCGGGGCCTGGGTGAGACTGCGGCGGCGGCAGGGCGCGGACGGCCATATTTGCCGGCGCGGCC
CGAGCCGCCGACAACAAAAAGTGCGCGGGCGCTCGGCGGGCGCTCGGACGGGCGCGGGGCTGCAGCGCTACCGCC
CGGCCTCGCCGCCGCCGCCGCCCTCGCGGCCTGGCCCCGCCGCGCCCGGCGCGCCCGCCGCCCGGGGGG**ATG**

TCTTACAAACCGAACTTGGCCGCGCACATGCCCGCCGCCGCCCTCAACGCCGCTGGGAGTGTCCACTCGCCTTCC
ACCAGCATGGCAACGTCTTCACAGTACCGCCAGCTGCTCAGTGACTACGGGCCACCGTCCCTAGGCTACACCCAG
GGAACTGGGAACAGCCAGGTGCCCCAAAGCAAATACGCGGAGCTGCTGGCCATCATTGAAGAGCTGGGGAAGGAG
ATCAGACCCACGTACGCAGGGAGCAAGAGTGCCATGGAGAGGCTGAAGCGCGGCATCATTCACGCTAGAGGACTG
GTTCGGGAGTGCTTGGCAGAAACGGAACGGAATGCCAGATCC**TAG**CTGCCTTGTTGGTTTTGAAGGATTTCCATC
TTTTTACAAGATGAGAAGTTACAGTTCATCTCCCCTGTTCAGATGAAACCCTTGTTTTCAAAATGGTTACAGTTT
CGTTTTTCCTCCCATGGTTCACTTGGCTCTGAACCTACAGTCTCAAAGATTGAGAAAAGATTTTGCAGTTAATTA
GGATTTGCATTTTAAGTAGTTAGGAACTGCCCAGGTTTTTTTTGTTTTTTAAGCATTGATTTAAAAGATGCACGG
AAAGTTATCTTACAGCAAACTGTAGTTTGCCTCCAAGACACCATTGTCTCCCTTTAATCTTCTCTTTTGTATACA
TTTGTTACCCATGGTGTTCTTTGTTCCTTTTCATAAGCTAATACCACTGTAGGGATTTTGTTTTGAACGCATATT
GACAGCACGCTTTACTTAGTAGCCGGTTCCCATTTGCCATACAATGTAGGTTCTGCTTAATGTAACTTCTTTTTT
GCTTAAGCATTTGCATGACTATTAGTGCTTCAAAGTCAATTTTTAAAAATGCACAAGTTATAAATACAGAAGAAA
GAGCAACCCACCAAACCTAACAAGGACCCCCGAACACTTTCATACTAAGACTGTAAGTAGATCTCAGTTCTGCGT
TTATTGTAAGTTGATAAAAACATCTGGAAGAAAATGACTAAAACTGTTTGCATCTTTGTATGTATTTATTACTTG
ATGTAATAAAGCTTATTTTCATTAACAATTTGTATTAAAAAAAAAAAAAAA

FIGURE 286

MSYKPNLAAHMPAAALNAAGSVHSPSTSMATSSQYRQLLSDYGPPSLGYTQGTGNSQVPQSKYAELLAIIEELGK
EIRPTYAGSKSAMERLKRGIIHARGLVRECLAETERNARS

FIGURE 287A

GCGGGGAAGCAGCAGCGGCCAGGATGAATCCCAGGTGCTCTGGAGCTGGATGGTGAAGGTCGGCACTCTTCACCC
TCCCGAGCCCTGCCCGTCTCGGCCCCATGCCCCCACCAGTCAGCCCCGGGCCACAGGCAGTGAGCAGGCACCTGG
GAGCCGAGGCCCTGTGACCAGGCCAAGGAGACGGGCGCTCCAGGGTCCCAGCCACCTGTCCCCCCCC**ATG**GAGCTG
AGGCCCTGGTTGCTATGGGTGGTAGCAGCAACAGGAACCTTGGTCCTGCTAGCAGCTGATGCTCAGGGCCAGAAG
GTCTTCACCAACACGTGGGCTGTGCGCATCCCTGGAGGCCCAGCGGTGGCCAACAGTGTGGCACGGAAGCATGGG
TTCCTCAACCTGGGCCAGATCTTCGGGGACTATTACCACTTCTGGCATCGAGGAGTGACGAAGCGGTCCCTGTCG
CCTCACCGCCCGCGGCACAGCCGGCTGCAGAGGGAGCCTCAAGTACAGTGGCTGGAACAGCAGGTGGCAAAGCGA
CGGACTAAACGGGACGTGTACCAGGAGCCCACAGACCCCAAGTTTCCTCAGCAGTGGTACCTGTCTGGTGTCACT
CAGCGGGACCTGAATGTGAAGGCGGCCTGGGCGCAGGGCTACACAGGGCACGGCATTGTGGTCTCCATTCTGGAC
GATGGCATCGAGAAGAACCACCCGGACTTGGCAGGCAATTATGATCCTGGGGCCAGTTTTGATGTCAATGACCAG
GACCCTGACCCCCAGCCTCGGTACACACAGATGAATGACAACAGGCACGGCACACGGTGTGCGGGGGAAGTGGCT
GCGGTGGCCAACAACGGTGTCTGTGGTGTAGGTGTGGCCTACAACGCCCGCATTGGAGGGGTGCGCATGCTGGAT
GGCGAGGTGACAGATGCAGTGGAGGCACGCTCGCTGGGCCTGAACCCCAACCACATCCACATCTACAGTGCCAGC
TGGGGCCCCGAGGATGACGGCAAGACAGTGGATGGGCCAGCCCGCCTCGCCGAGGAGGCCTTCTTCCGTGGGGTT
AGCCAGGGCCGAGGGGGGCTGGGCTCCATCTTTGTCTGGGCCTCGGGGAACGGGGGCCGGGAACATGACAGCTGC
AACTGCGACGGCTACACCAACAGTATCTACACGCTGTCCATCAGCAGCGCCACGCAGTTTGGCAACGTGCCGTGG
TACAGCGAGGCCTGCTCGTCCACACTGGCCACGACCTACAGCAGTGGCAACCAGAATGAGAAGCAGATCGTGACG
ACTGACTTGCGGCAGAAGTGCACGGAGTCTCACACGGGCACCTCAGCCTCTGCCCCCTTAGCAGCCGGCATCATT
GCTCTCACCCTGGAGGCCAATAAGAACCTCACATGGCGGGACATGCAACACCTGGTGGTACAGACCTCGAAGCCA
GCCCACCTCAATGCCAACGACTGGGCCACCAATGGTGTGGGCCGGAAAGTGAGCCACTCATATGGCTACGGGCTT
TTGGACGCAGGCGCCATGGTGGCCCTGGCCCAGAATTGGACCACAGTGGCCCCCCAGCGGAAGTGCATCATCGAC
ATCCTCACCGAGCCCAAAGACATCGGGAAACGGCTCGAGGTGCGGAAGACCGTGACCGCGTGCCTGGGCGAGCCC
AACCACATCACTCGGCTGGAGCACGCTCAGGCGCGGCTCACCCTGTCCTATAATCGCCGTGGCGACCTGGCCATC
CACCTGGTCAGCCCCATGGGCACCCGCTCCACCCTGCTGGCAGCCAGGCCACATGACTACTCCGCAGATGGGTTT
AATGACTGGGCCTTCATGACAACTCATTCCTGGGATGAGGATCCCTCTGGCGAGTGGGTCCTAGAGATTGAAAAC
ACCAGCGAAGCCAACAACTATGGGACGCTGACCAAGTTCACCCTCGTACTCTATGGCACCGCCCCTGAGGGGCTG
CCCGTACCTCCAGAAAGCAGTGGCTGCAAGACCCTCACGTCCAGTCAGGCCTGTGTGGTGTGCGAGGAAGGCTTC
TCCCTGCACCAGAAGAGCTGTGTCCAGCACTGCCCTCCAGGGTTCGCCCCCCAAGTCCTCGATACGCACTATAGC
ACCGAGAATGACGTGGAGACCATCCGGGCCAGCGTCTGCGCCCCCTGCCACGCCTCATGTGCCACATGCCAGGGG
CCGGCCCTGACAGACTGCCTCAGCTGCCCCAGCCACGCCTCCTTGGACCCTGTGGAGCAGACTTGCTCCCGGCAA
AGCCAGAGCAGCCGAGAGTCCCCGCCACAGCAGCAGCCACCTCGGCTGCCCCCGGAGGTGGAGGCGGGGCAACGG
CTGCGGGCAGGGCTGCTGCCCTCACACCTGCCTGAGGTGGTGGCCGGCCTCAGCTGCGCCTTCATCGTGCTGGTC
TTCGTCACTGTCTTCCTGGTCCTGCAGCTGCGCTCTGGCTTTAGTTTTCGGGGGGTGAAGGTGTACACCATGGAC
CGTGGCCTCATCTCCTACAAGGGGCTGCCCCCTGAAGCCTGGCAGGAGGAGTGCCCGTCTGACTCAGAAGAGGAC
GAGGGCCGGGGCGAGAGGACCGCCTTTATCAAAGACCAGAGCGCCCTC**TGA**TGAGCCCACTGCCCACCCCCTCAA
GCCAATCCCCTCCTTGGGCACTTTTTAATTCACCAAAGTATTTTTTTATCTTGGGACTGGGTTTGGACCCCAGCT
GGGAGGCAAGAGGGGTGGAGACTGCTTCCCATCCTACCCTCGGGCCCACCTGGCCACCTGAGGTGGGCCCAGGAC
CAGCTGGGGCGTGGGGAGGGCCGTACCCCACCCTCAGCACCCCTTCCATGTGGAGAAAGGAGTGAAACCTTTAGG
GCAGCTTGCCCCGGCCCCGGCCCCAGCCAGAGTTCCTGCGGAGTGAAGAGGGGCAGCCCTTGCTTGTTGGGATTC
CTGACCCAGGCCGCAGCTCTTGCCCTTCCCTGTCCCTCTAAAGCAATAATGGTCCCATCCAGGCAGTCGGGGGCT
GGCCTAGGAGATATCTGAGGGAGGAGGCCACCTCTCCAAGGGCTTCTGCACCCTCCACCCTGTCCCCCAGCTCTG
GTGAGTCTTGGCGGCAGCAGCCATCATAGGAAGGGACCAAGGCAAGGCAGGTGCCTCCAGGTGTGCACGTGGCAT
GTGGCCTGTGGCCTGTGTCCCATGACCCACCCCTGTGCTCCGTGCCTCCACCACCACTGGCCACCAGGCTGGCGC
AGCCAAGGCCGAAGCTCTGGCTGAACCCTGTGCTGGTGTCCTGACCACCCTCCCCTCTCTTGCACCCGCCTCTCC
CGTCAGGGCCCAAGTCCCTGTTTTCTGAGCCCGGGCTGCCTGGGCTGTTGGCACTCACAGACCTGGAGCCCCTGG
GTGGGTGGTGGGGAGGGGCGCTGGCCCAGCCGGCCTCTCTGGCCTCCCACCCGATGCTGCTTTCCCCTGTGGGGA
TCTCAGGGGCTGTTTGAGGATATATTTTCACTTTGTGATTATTTCACTTTAGATGCTGATGATTTGTTTTTGTAT
TTTTAATGGGGGTAGCAGCTGGACTACCCACGTTCTCACACCCACCGTCCGCCCTGCTCCTCCCTGGCTGCCCTG

FIGURE 287B

GCCCTGAGGTGTGGGGGCTGCAGCATGTTGCTGAGGAGTGAGGAATAGTTGAGCCCCAAGTCCTGAAGAGGCGGG
CCAGCCAGGCGGGCTCAAGGAAAGGGGGTCCCAGTGGGAGGGGCAGGCTGACATCTGTGTTTCAAGTGGGGCTCG
CCATGCCGGGGGTTCATAGGTCACTGGCTCTCCAAGTGCCAGAGGTGGGCAGGTGGTGGCACTGAGCCCCCCCAA
CACTGTGCCCTGGTGGAGAAAGCACTGACCTGTCATGCCCCCCTCAAACCTCCTCTTCTGACGTGCCTTTTGCAC
CCCTCCCATTAGGACAATCAGTCCCCTCCCATCTGGGAGTCCCCTTTTCTTTTCTACCCTAGCCATTCCTGGTAC
CCAGCCATCTGCCCAGGGGTGCCCCCTCCTCTCCCATCCCCCTGCCCTCGTGGCCAGCCCGGCTGGTTTTGTAAG
ATGCTGGGTTGGTGCACAGTGATTTTTTTCTTGTAATTTAAACAGGCCCAGCATTGCTGGTTCTATTTAATGGAC
ATGAGATAATGTTAGAGGTTTTAAAGTGATTAAACGTGCAGACTATGCAAACCAG

FIGURE 288

MELRPWLLWVVAATGTLVLLAADAQGQKVFTNTWAVRIPGGPAVANSVARKHGFLNLGQIFGDYYHFWHRGVTKR
SLSPHRPRHSRLQREPQVQWLEQQVAKRRTKRDVYQEPTDPKFPQQWYLSGVTQRDLNVKAAWAQGYTGHGIVVS
ILDDGIEKNHPDLAGNYDPGASFDVNDQDPDPQPRYTQMNDNRHGTRCAGEVAAVANNGVCGVGVAYNARIGGVR
MLDGEVTDAVEARSLGLNPNHIHIYSASWGPEDDGKTVDGPARLAEEAFFRGVSQGRGGLGSIFVWASGNGGREH
DSCNCDGYTNSIYTLSISSATQFGNVPWYSEACSSTLATTYSSGNQNEKQIVTTDLRQKCTESHTGTSASAPLAA
GIIALTLEANKNLTWRDMQHLVVQTSKPAHLNANDWATNGVGRKVSHSYGYGLLDAGAMVALAQNWTTVAPQRKC
IIDILTEPKDIGKRLEVRKTVTACLGEPNHITRLEHAQARLTLSYNRRGDLAIHLVSPMGTRSTLLAARPHDYSA
DGFNDWAFMTTHSWDEDPSGEWVLEIENTSEANNYGTLTKFTLVLYGTAPEGLPVPPESSGCKTLTSSQACVVCE
EGFSLHQKSCVQHCPPGFAPQVLDTHYSTENDVETIRASVCAPCHASCATCQGPALTDCLSCPSHASLDPVEQTC
SRQSQSSRESPPQQQPPRLPPEVEAGQRLRAGLLPSHLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFSFRGVKVY
TMDRGLISYKGLPPEAWQEECPSDSEEDEGRGERTAFIKDQSAL

FIGURE 289

CTGGTCCCGAGCACGAGCTGTGAGGGGATTCACTTGTGTGCGGAACTCCTCGGAACC**ATG**GCGTCCCTTTCCCTT
GCACCTGTTAACATCTTTAAGGCAGGAGCTGATGAAGAGAGAGCAGAGACAGCTCGTCTGACTTCTTTTATTGGT
GCCATCGCCATTGGAGACTTGGTAAAGAGCACCTTGGGACCCAAAGGCATGGACAAAATTCTTCTAAGCAGTGGA
CGAGATGCCTCTCTTATGGTAACCAATGATGGTGCCACTATTCTAAAAAACATTGGTGTTGACAATCCAGCAGCT
AAAGTTTTAGTTGATATGTCAAGGGTTCAAGATGATGAAGTTGGTGATGGCACTACCTCTGTTACCGTTTTAGCA
GCAGAATTATTAAGGGAAGCAGAATCTTTAATTGCAAAAAAGATTCATCCACAGACCATCATAGCGGGTTGGAGA
GAAGCCACGAAGGCTGCAAGAGAGGCGCTGTTGAGTTCTGCAGTTGATCATGGTTCCGATGAAGTTAAATTCCGT
CAAGATTTAATGAATATTGCGGGCACAACATTATCCTCAAAACTTCTTACTCATCACAAAGACCACTTTACAAAG
TTAGCTGTAGAAGCAGTTCTCAGACTGAAAGGCTCTGGCAACCTGGAGGCAATTCATATTATCAAGAAGCTAGGA
GGAAGTTTGGCAGATTCCTATTTAGATGAAGGCTTCCTGTTGGATAAAAAAATTGGAGTAAATCAACCAAAACGA
ATTGAAAATGCTAAAATTCTTATTGCAAATACTGGTATGGATACAGACAAAATAAAGATATTTGGTTCCCGGGTA
AGAGTTGACTCTACAGCAAAGGTTGCAGAAATAGAACATGCGGAAAAGGAAAAAATGAAGGAGAAAGTTGAACGT
ATTCTTAAGCATGGAATAAATTGCTTTATTAACAGGCAATTAATTTATAATTATCCTGAACAGCTCTTTGGTGCT
GCTGGTGTCATGGCTATTGAGCATGCAGATTTTGCAGGTGTGGAACGCCTAGCTCTTGTCACAGGTGGTGAAATT
GCCTCTACCTTTGATCACCCAGAACTGGTGAAGCTTGGAAGTTGCAAACTTATCGAGGAAGTCATGATTGGAGAA
GACAAACTCATTCACTTTTCTGGGGTTGCCCTTGGTGAGGCTTGTACCATTGTTTTGCGTGGTGCCACTCAACAA
ATTTTAGATGAAGCAGAAAGATCATTGCATGATGCTCTTTGTGTTCTTGCGCAAACTGTAAAGGACTCTAGAACA
GTTTATGGAGGAGGCTGTTCTGAGATGTTGATGGCTCATGCTGTGACACAGCTTGCCAATAGAACACCAGGCAAA
GAAGCTGTTGCAATGGAGTCTTATGCTAAAGCACTGAGAATGTTGCCAACCATCATAGCTGACAATGCAGGCTAT
GACAGTGCAGACCTGGTGGCACAGCTCAGGGCTGCTCACAGTGAAGGCAATACCACTGCTGGATTGGATATGAGG
GAAGGCACCATTGGAGATATGGCTATCCTGGGTATAACAGAAAGTTTTCAAGTGAAGCGACAGGTTCTTCTGAGT
GCAGCTGAAGCAGCAGAGGTGATTCTGCGTGTGGACAACATCATCAAAGCGGCACCCAGGAAACGTGTCCCTGAT
CACCACCCCTGT**TAA**GCATTCCCACGTGCTGTCGATCTTTGGACCAGTTTCTAGCAAAGTTGTGTTTGAAAGATA
CTCTATTAAAGAAGACTGTGGAATCTGTTTATCGGTGCCCATTATATCCTTAAGTTTGGATATTTAGCTGACCTT
CGCTTTAACATAGGTCTAATTTATTTGCCGTGTCATTTTCCATACAAATCAGTTGATTTAAAGGAGTTCATTTCG
CATACTGGGCATTAAAATAAAAATTTGAACAATGAAAGGAAAAAAAGGAGAAAAAAAAAA

FIGURE 290

MASLSLAPVNIFKAGADEERAETARLTSFIGAIAIGDLVKSTLGPKGMDKILLSSGRDASLMVTNDGATILKNIG
VDNPAAKVLVDMSRVQDDEVGDGTTSVTVLAAELLREAESLIAKKIHPQTIIAGWREATKAAREALLSSAVDHGS
DEVKFRQDLMNIAGTTLSSKLLTHHKDHFTKLAVEAVLRLKGSGNLEAIHIIKKLGGSLADSYLDEGFLLDKKIG
VNQPKRIENAKILIANTGMDTDKIKIFGSRVRVDSTAKVAEIEHAEKEKMKEKVERILKHGINCFINRQLIYNYP
EQLFGAAGVMAIEHADFAGVERLALVTGGEIASTFDHPELVKLGSCKLIEEVMIGEDKLIHFSGVALGEACTIVL
RGATQQILDEAERSLHDALCVLAQTVKDSRTVYGGGCSEMLMAHAVTQLANRTPGKEAVAMESYAKALRMLPTII
ADNAGYDSADLVAQLRAAHSEGNTTAGLDMREGTIGDMAILGITESFQVKRQVLLSAAEAAEVILRVDNIIKAAP
RKRVPDHHPC

FIGURE 291

GCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTTCTCGCAGGCTCTATTCCGTTCGCTGGTTCGCCACCT
CAGGGGAACG**ATG**GCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGACGTGGTTTCTGCCGACAAAATTGA
AGATGTCCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGTGAAGCTAAGAAACTATT
GGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTCCAGGAAGCAGCTAGTCT
TTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTTCTATGGGAAATCACTTCTGGA
GTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGGAAGGTGTGCATGTGGAAGAGGAAGAAGGAGAAAA
AACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAAGAGTTGAGAGAACAGGT
TTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAAACAGAAGACAAGTCTTTGGCAAAGCCTGAAACTGATAA
AGAACAGGACAGTGAAATGGAGAAGGGTGGAAGAGAAGATATGGATATAAGTAAATCTGCAGAGGAGCCACAGGA
AAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGAGCAGCACCAGAAGGACC
GAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAAGAAAAATCAGTTTCTGG
AACTGATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTCAGGAGAAGCAGGGAGAGGTAATTGTGAGCATAGAGGA
GAAGCCAAAAGAAGTTTCAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACTGCAGTGGAGGTAGAAGC
AGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAGAAGGTAGTTACCTCTGA
AAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCTGAAGAGTCACCAGAGGT
GCAAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAGCCTGGGCAGGAGGCTCC
AGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCTATTGAACCACAGACTTC
TATAGAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTCAGGGCAAAGCTGGTTCCTAGTCA
GGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACCAAGGTAGCCCAGGGAGC
TACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAGAGAGAAGAACAGATGAA
AGAGGGTGAAGAAACTGAAGGCTCGGAAGAGGATGATAAAGAAAATGATAAGACTGAAGAAATGCCAAATGATTC
AGTCCTTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAGCTTGCCTGGGATATGCT
GGATTTAGCAAAGATCATTTTTAAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCTGCCCAGGCACATCTTAA
ACTCGGAGAAGTTAGTGTTGAATCTGAAAACTATGTGCAAGCTGTGGAGGAGTTCCAGTCCTGCCTTAACCTGCA
GGAACAGTACCTGGAAGCCCACGACCGTCTGCTTGCAGAGACCCACTACCAGCTGGGCTTGGCTTATGGGTACAA
CTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAACAGAATGGCTGTACTAAA
CGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGAATACAAGAAAGAAATTGAGGAACTAAAGGAACTGCTACCCGA
AATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCTGAACTGGCTCTGAAAGCTAC
TCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTCTCCATGATTGCCAGTAGAAA
GCCAACAGACGGTGCTTCCTCATCAAATTGTGTGACTGATATTTCCCACCTTGTCAGAAAGAAGAGGAAACCAGA
GGAAGAGAGTCCCCGGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTGAACGGAGGCAGTGGGGATGC
TGTCCCGAGTGGAAATGAAGTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAGCTGAAACGCGGAGCAGCAGT
GGAGGGGACACTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGT**TAA**GAGGGGGCACAGCCTCCTCCCAAGGG
AAAGTGTTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTTGTATAACTTCAATAAAGATTGTAAG
CAAAAAAAAAA

FIGURE 292

MAMESTATAAVAADVVSADKIEDVPAPSTSADKVESLDVDSEAKKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGVLGNALEGVHVEEEEGEKTEDESLVENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPDAEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTLEKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVQTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVGDQTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDSVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQAHLKLGEVSVESENYVQAVEEFQSCLNLQEQYLEAHDRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSIEVIENRMAVLNEQVKEAEGSSEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLVE
SSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVPS
GNEVSENMEEEAENQLKRGAAVEGTLEAGATVESTAC

FIGURE 293

AAGCG**ATG**GCTGGGCCCGCGTGGATCTCCAAGGTCTCTCGGCTGCTGGGGGCATTCCACAACCCAAAACAGGTGA
CCAGAGGTTTTACTGGTGGTGTTCAGACAGTAACTTTAATTCCAGGAGATGGTATTGGCCCAGAAATTTCAGCTG
CAGTTATGAAGATTTTTGATGCTGCCAAAGCACCTATTCAGTGGGAGGAGCGGAACGTCACTGCCATTCAAGGAC
CTGGAGGAAAGTGGATGATCCCTTCAGAGGCTAAAGAGTCCATGGATAAGAACAAGATGGGCTTGAAAGGCCCTT
TGAAGACCCCAATAGCAGCCGGTCACCCATCTATGAATTTACTGCTGCGCAAAACATTTGACCTTTACGCGAATG
TCCGACCATGTGTCTCTATCGAAGGCTATAAAACCCCTTACACCGATGTAAATATTGTGACCATTCGAGAGAACA
CAGAAGGAGAATACAGTGGAATTGAGCATGTGATTGTTGATGGAGTCGTGCAGAGTATCAAGCTCATCACCGAGG
GGGCGAGCAAGCGCATTGCTGAGTTTGCCTTTGAGTATGCCCGGAACAACCACCGGAGCAACGTCACGGCGGTGC
ACAAAGCCAACATCATGCGGATGTCAGATGGGCTTTTTCTACAAAAATGCAGGGAAGTTGCAGAAAGCTGTAAAG
ATATTAAATTTAATGAGATGTACCTTGATACAGTATGTTTGAATATGGTACAAGATCCTTCCCAATTTGATGTTC
TTGTTATGCCAAATTTGTATGGAGACATCCTTAGTGACTTGTGTGCAGGATTGATCGGAGGTCTCGGTGTGACAC
CAAGTGGCAACATTGGAGCCAATGGGGTTGCAATTTTTGAGTCGGTTCATGGGACGGCTCCAGACATTGCAGGCA
AGGACATGGCGAATCCCACAGCCCTCCTGCTCAGTGCCGTGATGATGCTGCGCCACATGGGACTTTTTGACCATG
CTGCAAGAATTGAGGCTGCGTGTTTTGCTACAATTAAGGACGGAAAGAGCTTGACAAAAGATTTGGGAGGCAATG
CAAAATGCTCAGACTTCACAGAGGAAATCTGTCGCCGAGTAAAAGATTTAGAT**TAA**CACTTCTACAACTGGCATT
TACATCAGTCACTCTAAATGGACACCACATGAACCTCTGTTTAGAATACCTACGTATGTATGCATTGGTTTGCTT
GTTTCTTGACAGTACATTTTTAGATCTGGCCTTTTCTTAACAAAATCTGTGCAAAAGATGCAGGTGGATGTCCCT
AGGTCTGTTTTCAAAGAACTTTTTCCAAGTGCTTGTTTTATTTATTAAGTGTCTACCTGGTAAATGTTTTTTTTG
TAAACTCTGAGTGGACTGTATCATTTGCTATTCTAAACCATTTTACACTTAAGTTAAAATAGTTTCTCTTCAGCT
GTAAATAACAGGATACAGAATTAACAAGAGAAAATGTCTAACTTTTTAAGAAAAACCTTATTTTCTTCGGTTTTT
GAAAAACATAATGGAAATAAAACAGGATATTGACATAATAGCACAAAATGACACTCTTCTAAAACTAAATGGGCA
CAAGAGAATTTTCCTGGGAAAGTTCACATCAAAAAGAGTGAATGTGGTATATTTCTAAATGATATGGAAAATAGA
GACAGATTTGTCCTTTACAGAAATTACTGAGTGTGAATAAAAACTTCAGATCCAAGAAATATATAATGAGAGATA
TAATTTTTGTTAATAAGACAAAGGTAATATATTGGATACAAAGACACAAATGTATTGTGTGTTCAATTATTTTGT
TGTCTTGAGATTTAATATTCTTTCCAAGAGCTTTTAATGAAGCAGAGAGCTAGTACTTCATTTTCACTGGATACA
TTTTCAGCATCATGAGTTGTCACAGCCTCTGAGCCCCTGATCTGAAGCCAGAAGGGCTGAGTGTATTGTAAACTT
ATTCTTGCATGTTGCTGTCTGGGAATGGACCACACTACAGCAGGTAGTTCTGGGGGCGATACTGCCGAAAGGCCC
GAACACATGTATTTTGGCTGCAATTGAGGAACTTGGGATGCTATTAATTTTGTATTTCAGCAACTGCCCCTTCTC
CTATCCCAAAGCACCAATTACTGCCCTCTGCCTCAGCAGTACCAGTATAAGATGACATTCCAAAGACTGGAGGCA
ACTCAGCCTGAGTTAATTCACAAAATTATGCCATGCTGGGGCTTGAGCTTGAGCTTGGGCTTAGGCTTGGGCTCA
GCTTTTGACCCTCAGGCATCTCCTTTTCCTTCCTGTCTTCCTCTCCCTTCTCCTCTGCTGCAGCATGATTTTCTT
AATCTTCAGACACTCACTATTTTCATGAACAGTTACCCTCTGTCCCCACAACCAAAGACAACTCATGGCCTCCTT
TGGCCCTTGTGTAACATTGCAAACCTGTGGCTTTGCAAAATGTACCCAGGTCACAAGGGGATTTTTTTTTTTTTA
GCAATGATATCCCTGTCTGGGTCACTTTTTAAGCTTGTAACCGCCCCCCCAGACTTATAATCTTAAATGTATTTT
CCTTTGTTTAAGCTGCTGCTTCCTCTGTTTCATTGGATTGTGCCAGTTATCAGTGGCTCTTGGGTTCAAAGTAAT
AAA

FIGURE 294

MAGPAWISKVSRLLGAFHNPKQVTRGFTGGVQTVTLIPGDGIGPEISAAVMKIFDAAKAPIQWEERNVTAIQGPG
GKWMIPSEAKESMDKNKMGLKGPLKTPIAAGHPSMNLLLRKTFDLYANVRPCVSIEGYKTPYTDVNIVTIRENTE
GEYSGIEHVIVDGVVQSIKLITEGASKRIAEFAFEYARNNHRSNVTAVHKANIMRMSDGLFLQKCREVAESCKDI
KFNEMYLDTVCLNMVQDPSQFDVLVMPNLYGDILSDLCAGLIGGLGVTPSGNIGANGVAIFESVHGTAPDIAGKD
MANPTALLLSAVMMLRHMGLFDHAARIEAACFATIKDGKSLTKDLGGNAKCSDFTEEICRRVKDLD

FIGURE 295

GCGCGCCTTCTCCAGTCCGCGGTGCC**ATG**GCCCCCGCCCGTCTGTTCGCGCTGCTGCTGCTCTTCGTAGGCGGAG
TCGCCGAGTCGATCCGAGAGACTGAGGTCATCGACCCCCAGGACCTCCTAGAAGGCCGATACTTCTCCGGAGCCC
TACCAGACGATGAGGATGTAGTGGGGCCCGGGCAGGAATCTGATGACTTTGAGCTGTCTGGCTCTGGAGATCTGG
ATGACTTGGAAGACTCCATGATCGGCCCTGAAGTTGTCCATCCCTTGGTGCCTCTAGATAACCATATCCCTGAGA
GGGCAGGGTCTGGGAGCCAAGTCCCCACCGAACCCAAGAAACTAGAGGAGAATGAGGTTATCCCCAAGAGAATCT
CACCCGTTGAAGAGAGTGAGGATGTGTCCAACAAGGTGTCAATGTCCAGCACTGTGCAGGGCAGCAACATCTTTG
AGAGAACGGAGGTCCTGGCAGCTCTGATTGTGGGTGGCATCGTGGGCATCCTCTTTGCCGTCTTCCTGATCCTAC
TGCTCATGTACCGTATGAAGAAGAAGGATGAAGGCAGCTATGACCTGGGCAAGAAACCCATCTACAAGAAAGCCC
CCACCAATGAGTTCTACGCG**TGA**AGCTTGCTTGTGGGCACTGGCTTGGACTTTAGCGGGGAGGGAAGCCAGGGGA
TTTTGAAGGGTGGACATTAGGGTAGGGTGAGGTCAACCTAATACTGACTTGTCAGTATCTCCAGCTCTGATTACC
TTTGAAGTGTTCAGAAGAGACATTGTCTTCTACTGTTCTGCCAGGTTCTTCTTGAGCTTTGGGCCTCAGTTGCCC
TGGCAGAAAAATGGATTCAACTTGGCCTTTCTGAAGGCAAGACTGGGATTGGATCACTTCTTAAACTTCCAGTTA
AGAATCTAGGTCCGCCCTCAAGCCCATACTGACCATGCCTCATCCAGAGCTCCTCTGAAGCCAGGGGGCTAACGG
ATGTTGTGTGGAGTCCTGGCTGGAGGTCCTCCCCCAGTGGCCTTCCTCCCTTCCTTTCACAGCCGGTCTCTCTGC
CAGGAAATGGGGGAAGGAACTAGAACCACCTGCACCTTGAGATGTTTCTGTAAATGGGTACTTGTGATCACACTA
CGGGAATCTCTGTGGTATATACCTGGGGCCATTCTAGGCTCTTTCAAGTGACTTTTGGAAATCAACCTTTTTTAT
TTGGGGGGGAGGATGGGGAAAAGAGCTGAGAGTTTATGCTGAAATGGATTTATAGAATATTTGTAAATCTATTTT
TAGTGTTTGTTCGTTTTTTTAACTGTTCATTCCTTTGTGCAGAGTGTATATCTCTGCCTGGGCAAGAGTGTGGAG
GTGCCGAGGTGTCTTCATTCTCTCGCACATTTCCACAGCACCTGCTAAGTTTGTATTTAATGGTTTTTGTTTTTG
TTTTTGTTTGTTTCTTGAAAATGAGAGAAGAGCCGGAGAGATGATTTTTATTAATTTTTTTTTTTTTTTTTTTT
TACTATTTATAGCTTTAGATAGGGCCTCCCTTCCCCTCTTCTTTCTTTGTTCTCTTTCATTAAACCCCTTCCCCA
GTTTTTTTTTTATACTTTAAACCCCGCTCCTCATGGCCTTGGCCCTTTCTGAAGCTGCTTCCTCTTATAAAATAG
CTTTTGCCGAAACATAGTTTTTTTTTAGCAGATCCCAAAATATAATGAAGGGGATGGTGGGATATTTGTGTCTGT
GTTCTTATAATATATTATTATTCTTCCTTGGTTCTAGAAAAATAGATAAATATATTTTTTTCAGGAAATAGTGTG
GTGTTTCCAGTTTGATGTTGCTGGGTGGTTGAGTGAGTGAATTTTCATGTGGCTGGGTGGGTTTTTGCCTTTTTC
TCTTGCCCTGTTCCTGGTGCCTTCTGATGGGGCTGGAATAGTTGAGGTGGATGGTTCTACCCTTTCTGCCTTCTG
TTTGGGACCCAGCTGGTGTTCTTTGGTTTGCTTTCTTCAGGCTCTAGGGCTGTGCTATCCAATACAGTAACCACA
TGCGGCTGTTTAAAGTTAAGCCAATTAAAATCACATAAGATTAAAAATTCCTTCCTCAGTTGCACTAACCACGTT
TCTAGAGGCGTCACTGTATGTAGTTCATGGCTACTGTACTGACAGCGAGAGCATGTCCATCTGTTGGACAGCACT
ATTCTAGAGAACTAAACTGGCTTAACGAGTCACAGCCTCAGCTGTGCTGGGACGACCCTTGTCTCCCTGGGTAGG
GGGGGGGGAATGGGGGAGGGCTGATGAGGCCCCAGCTGGGGCCTGTTGTCTGGGACCCTCCCTCTCCTGAGAGGG
GAGGCCTGGTGGCTTAGCCTGGGCAGGTCGTGTCTCCTCCTGACCCCAGTGGCTGCGGTGAGGGGAACCACCCTC
CCTTGCTGCACCAGTGGCCATTAGCTCCCGTCACCACTGCAACCCAGGGTCCCAGCTGGCTGGGTCCTCTTCTGC
CCCCAGTGCCCTTCCCCTTGGGCTGTGTTGGAGTGAGCACCTCCTCTGTAGGCACCTCTCACACTGTTGTCTGTT
ACTGATTTTTTTTGATAAAAAGATAATAAAACCTGGTACTTTCTAAAAAAAAAAAAAAAAAAA

FIGURE 296

MAPARLFALLLLFVGGVAESIRETEVIDPQDLLEGRYFSGALPDDEDVVGPGQESDDFELSGSGDLDDLEDSMIG
PEVVHPLVPLDNHIPERAGSGSQVPTEPKKLEENEVIPKRISPVEESEDVSNKVSMSSTVQGSNIFERTEVLAAL
IVGGIVGILFAVFLILLLMYRMKKKDEGSYDLGKKPIYKKAPTNEFYA

FIGURE 297

CACTGCGCTTGCGCGGGTTGAGGGCGGTGGCTCAGTCTCCTGGAAAGGACCGTCCACCCCTCCGCGCTGGCGGTG
TGGACGCGGAACTCAGCGGAGAAACGCGATTGAGAAATGGAAAAGAAAATGAAATAAATCAGCAGTTATGAGGCA
GAGCCTAAGAGAACT**ATG**GCAACATCAGGTGACTGTCCCAGAAGTGAATCGCAGGGAGAAGAGCCTGCTGAGTGC
AGTGAGGCGGGTCTCCTGCAGGAGGGAGTACAGCCAGAGGAGTTTGTGGCCATCGCGGACTACGCTGCCACCGAT
GAGACCCAGCTCAGTTTTTTGAGAGGAGAAAAAATTCTTATCCTGAGACAAACCACTGCAGATTGGTGGTGGGGT
GAGCGTGCGGGCTGCTGTGGGTACATTCCGGCAAACCATGTGGGGAAGCACGTGGATGAGTACGACCCCGAGGAC
ACGTGGCAGGATGAAGAGTACTTCGGCAGCTATGGAACTCTGAAACTCCACTTGGAGATGTTGGCAGACCAGCCA
CGAACAACTAAATACCACAGTGTCATCCTGCAGAATAAAGAATCCCTGACGGATAAAGTCATCCTGGACGTGGGC
TGTGGGACTGGGATCATCAGTCTCTTCTGTGCACACTATGCGCGGCCTAGAGCGGTGTACGCGGTGGAGGCCAGT
GAGATGGCACAGCACACGGGGCAGCTGGTCCTGCAGAACGGCTTTGCTGACATCATCACCGTGTACCAGCAGAAG
GTGGAGGATGTGGTGCTGCCCGAGAAGGTGGACGTGCTGGTGTCTGAGTGGATGGGGACCTGCCTGCTGTTTGAG
TTCATGATCGAGTCCATCCTGTATGCCCGGGATGCCTGGCTGAAGGAGGACGGGGTCATTTGGCCCACCATGGCT
GCGTTGCACCTTGTGCCCTGCAGTGCTGATAGGATTATCGTAGCCAAGGTGCTCTTCTGGGACAACGCGTACGAG
TTCAACCTCAGCGCTCTGAAATCTTTAGCAGTTAAGGAGTTTTTTTCAAAGCCCAAGTATAACCACATTTTGAAA
CCAGAAGACTGTCTCTCTGAACCGTGCACTATATTGCAGTTGGACATGAGAACCGTGCAAATTTCTGATCTAGAG
ACCCTGAGGGGCGAGCTGCGCTTCGACATCAGGAAGGCGGGGACCCTGCACGGCTTCACGGCCTGGTTTAGCGTC
CACTTCCAGAGCCTGCAGGAGGGGCAGCCGCCGCAGGTGCTCAGCACGGGGCCCTTCCACCCCACCACACACTGG
AAGCAGACGCTGTTCATGATGGACGACCCAGTCCCTGTCCATACAGGAGACGTGGTCACGGGTTCAGTTGTGTTG
CAGAGAAACCCAGTGTGGAGAAGGCACATGTCTGTGGCTCTGAGCTGGGCTGTCACTTCCAGACAAGACCCCACA
TCTCAAAAAGTTGGAGAAAAAGTCTTCCCCATCTGGAGA**TGA**CAGTTGATGCTTTATTTGGAAAGCAGTGTGCAT
ATCTTGAGGGGTGATGAACACAAGCAAACCAAGTTGCACCTGGCTTCTGCACACTCCTGCGAAAGTCGGTGAACA
TTCACTCCACATTGACCCCTCCCTAGCCTGGCAGGTGACGTCAGGGTCCTTCACAGACAAACACGCTTGGGCTCG
GCAGGAGCTGCCGTGGCCACCCCCGCTGCCCAGTGTCTGCCCTCTAGAAGTAGGCTGTGTTTCCAGGTGTTCACC
CGTGGTGCCCACAGTGCCGACCCGTGGCTGGGTCGGAGCTCCATGTTCCTAAGCTAGGTCTAGGTCTACACTCCT
AGGACGCACGCATATCAGCCCGTGTACCCTGTGACAGTGACTGTCCCCACCTCCTGTGTTAGTGGTGCCCTTACT
GCCGTCGCTCATCCACTCGTGTGGGACGTAGGATTGCACAGGGCTGTGCCAGTGGCGTGTAGGGAACACTGCCCT
GGCTCAGCGTGCGAGCTAAGGTGGCGATGTATGCGATGGGACTCTGCATGGGATAGTACAGTTGTGTAGACGTCT
TCCAAATAAATTATGTGTTGGTGCCATCGCACATGCTCAATAAATATTTTAAATGAGTGAAAAAAAAA

FIGURE 298

MATSGDCPRSESQGEEPAECSEAGLLQEGVQPEEFVAIADYAATDETQLSFLRGEKILILRQTTADWWWGERAGC
CGYIPANHVGKHVDEYDPEDTWQDEEYFGSYGTLKLHLEMLADQPRTTKYHSVILQNKESLTDKVILDVGCGTGI
ISLFCAHYARPRAVYAVEASEMAQHTGQLVLQNGFADIITVYQQKVEDVVLPEKVDVLVSEWMGTCLLFEFMIES
ILYARDAWLKEDGVIWPTMAALHLVPCSADRIIVAKVLFWDNAYEFNLSALKSLAVKEFFSKPKYNHILKPEDCL
SEPCTILQLDMRTVQISDLETLRGELRFDIRKAGTLHGFTAWFSVHFQSLQEGQPPQVLSTGPFHPTTHWKQTLF
MMDDPVPVHTGDVVTGSVVLQRNPVWRRHMSVALSWAVTSRQDPTSQKVGEKVFPIWR

FIGURE 299

AATTCCGCGGAATCATCGGAATCCTTCACC**ATG**GCATCCAGCCCGGCCCAGCGTCGGCGAGGCAATGATCCTCTC
ACCTCCAGCCCTGGCCGAAGCTCCCGGCGTACTGATGCCCTCACCTCCAGCCCTGGCCGTGACCTTCCACCATTT
GAGGATGAGTCCGAGGGGCTCCTAGGCACAGAGGGGCCCCTGGAGGAAGAAGAGGATGGAGAGGAGCTCATTGGA
GATGGCATGGAAAGGGACTACCGCGCCATCCCAGAGCTGGACGCCTATGAGGCCGAGGGACTGGCTCTGGATGAT
GAGGACGTAGAGGAGCTGACGGCCAGTCGAAGGGAGGCAGCAGACGGGCCATGCGGCACGGTGACCGGGAGCTGG
CCGGGGCTGGGCGCATGCGCCGTGGGCTCCTGTATGACAGCGATGAGGAGGACGAGGAGCGCCCTGCCCGCAAGC
GCCGCCAGTGGAGCCGGCACGGAGGACGGCGAGGAGGACGAGCAGATGATTGAGAGCATCGAGAACCTGGAGGAT
CTCAAAGGCCACTCTGTGCGCGAGTGGGTGAGCATGGCGGGCCCCCGGCTGGAGATCCACCACCGCTTCAAGAAC
TTCCTGCGCACTCACGTCGACAGCCACGGCCACAACGTCTTCAAGGAGCGCATCAGCGACATGTGCAAAGAGAAC
CGTGAGAGCCTGGTGGTGAACTATGAGGACTTGGCAGCCAGGGAGCACGTGCTGGCCTACTTCCTGCCTGAGGCA
CCGGCGGAGCTGCTGCAGATCTTTGATGAGGCTGCCCTGGAGGTGGTACTGGCCATGTACCCCAAGTACGACCGC
ATCACCAACCACATCCATGTCCGCATCTCCCACCTGCCTCTGGTGGAGGAGCTGCGCTCGCTGAGGCAGCTGCAT
CTGAACCAGCTGATCCGCACCAGTGGGGTGGTGACCAGCTGCACTGGCGTCCTGCCCCAGCTCAGCATGGTCAAG
TACAACTGCAACAAGTGCAATTTCGTCCTGGGTCCTTTCTGCCAGTCCCAGAACCAGGAGGTGAAACCAGGCTCC
TGTCCTGAGTGCCAGTCGGCCGGCCCCTTTGAGGTCAACATGGAGGAGACCATCTATCAGAACTACCAGCGTATC
CGAATCCAGGAGAGTCCAGGCAAAGTGGCGGCTCGGCGGCTGCCCCGCTCCAAGGACGCCATTCTCCTCGCAGAT
CTGGTGGACAGCTGCAACGCAGGAGACGAGATAGAGCTGACTGGCATCTATCACAACAACTATGATGGCTCCCTC
AACACTGCCAATGGCTTCCCTGTCTTTGCCACTGTCATCCTAGCCAACCACGTGGCCAAGAAGGACAACAAGGTT
GCTGTAGGGGAACTGACCGATGAAGATGTGAAGATGATCACTAGCCTCTCCAAGGATCAGCAGATCGGAGAGAAG
ATCTTTGCCAGCATTGCTCCTTCCATCTATGGTCATGAAGACATCAAGAGAGGCCCTGCTCTGGCCCTGTTCGGA
GGGGAGCCCAAAAACCCAGGTGGCAAGCACAAGGTACGTGGTGATATCAACGTGCTCTTGTGCGGAGACCCTGGC
ACAGCGAAGTCGCAGTTTCTCAAGTATATTGAGAAAGTGTCCAGCCGAGCCATCTTCACCACTGGCCAGGGGGCG
TCGGCTGTGGCCGTCACGGCGTATGTCCAGCGGCACCCTGTCAGCAGGGAGTGGACCTTGGAGGCTGGGGCCCTG
GTTCTGGCTGACCGAGGAGTGTGTCTCATTGATGAATTTGACAAGATGAATGACCAGGACAGAACCAGCATCCAT
GAGGCCATGGAGCAACAGAGCATCTCCATCTCGAAGGCTGGCATCGTCACCTCCCTGCAGGCTCGCTGCACGGTC
ATTGCTGCCGCCAACCCCATAGGAGGGCGCTACGACCCCTCGCTGACTTTCTCTGAGAACGTGGACCTCACAGAG
CCCATCATCTCACGCTTTGACATCCTGTGTGTGGTGAGGGACACCGTGGACCCAGTCCAGGACGAGATGCTGGCC
CGCTTCGTGGTGGGCAGCCACGTCAGACACCACCCCAGCAACAAGGAGGAGGAGGGGCTGGCCAATGGCAGCGCT
GCTGAGCCCGCCATGCCCAACACGTATGGCGTGGAGCCCCTGCCCCAGGAGGTCCTGAAGAAGTACATCATCTAC
GCCAAGGAGAGGGTCCACCCGAAGCTCAACCAGATGGACCAGGACAAGGTGGCCAAGATGTACAGTGACCTGAGG
AAAGAATCTATGGCGACAGGCAGCATCCCCATTACGGTGCGGCACATCGAGTCCATGAGTCATGGCGGAGGCCCA
CGCGCGCATCCATCTGCGGGACTATGTGATCGAAGACGACGTCAACATGGCCATCCGCGTGATGCTGGAGAGCTT
CATAGACACACAGAAGTTCAGCGTCATCGCAGCATGCGCAAGACTTTTGCCCGCTACCTTTCATTCCGGCGTGAC
AACAATGAGCTGTTGCTCTTCATACTGAAGCAGTTAGTGGCAGAGCAGGTGACATATCAGCGCAACCGCTTTGGG
GCCCAGCAGGACACTATTGAGGTCCCTGAGAAGGACTTGGTGGATAAGGCTCGTCAGATCAACATCCACAACCTC
TCTGCATTTTATGACAGTGAGCTCTTCAGGATGAACAAGTTCAGCCACGACCTGAAAAGGAAAATGATCCTGCAG
CAGTTC**TGA**GGCCCTATGCCATCCATAAGGATTCCTTGGGATTCTGGTTTGGGGTGGTCAGTGCCCTCTGTGCTT
TATGGACACAAAACCAGAGCACTTGATGAACTCGGGGTACTAGGGTCAGGGCTTATAGCAGGATGTCTGGCTGCA
CCTGGCATGACTGTTTGTTTCTCCAAGCCTGCTTTGTGCTTCTCACCTTTGGGTGGGATGCCTTGCCAGTGTGTC
TTACTTGGTTGCTGAACATCTTGCCACCTCCGAGTGCTTTGTCTCCACTCAGTACCTTGGATCAGAGCTGCTGAG
TTCAGGATGCCTGCGTGTGGTTTAGGTGTTAGCCTTCTTACATGGATGTCAGGAGAGCTGCTGCCCTCTTGGCGT
GAGTTGCGTATTCAGGCTGCTTTTGCTCGCTTTGGCCAGAGAGCTGGTTGAAGATGTTTGTAATCGTTTTCAGTC
TCCTGCAGGTTTCTGTGCCCCTGTGGTGGAAGAGGCACGACAGTGCCAGCGCAGCGTTCTGGGCTCCTCAGTCGC
AGGGGTGGGATGTGAGTCATGCGGATTATCCACTCGCCACAGTTATCAGCTGCCATTGCTCCCTGTCTGTTTCCC
CACTCTCTTATTTGTGCATTCGGTTTGGTTTCTGTAGTTTTAATTTTTAATAAAGTTGAATAAAATATAAAAAAA
AAAA

FIGURE 300

MASSPAQRRRGNDPLTSSPGRSSRRTDALTSSPGRDLPPFEDESEGLLGTEGPLEEEEDGEELIGDGMERDYRAI
PELDAYEAEGLALDDEDVEELTASRREAADGPCGTVTGSWPGLGACAVGSCMTAMRRTRSALPASAASGAGTEDG
EEDEQMIESIENLEDLKGHSVREWVSMAGPRLEIHHRFKNFLRTHVDSHGHNVFKERISDMCKENRESLVVNYED
LAAREHVLAYFLPEAPAELLQIFDEAALEVVLAMYPKYDRITNHIHVRISHLPLVEELRSLRQLHLNQLIRTSGV
VTSCTGVLPQLSMVKYNCNKCNFVLGPFCQSQNQEVKPGSCPECQSAGPFEVNMEETIYQNYQRIRIQESPGKVA
ARRLPRSKDAILLADLVDSCNAGDEIELTGIYHNNYDGSLNTANGFPVFATVILANHVAKKDNKVAVGELTDEDV
KMITSLSKDQQIGEKIFASIAPSIYGHEDIKRGPALALFGGEPKNPGGKHKVRGDINVLLCGDPGTAKSQFLKYI
EKVSSRAIFTTGQGASAVAVTAYVQRHPVSREWTLEAGALVLADRGVCLIDEFDKMNDQDRTSIHEAMEQQSISI
SKAGIVTSLQARCTVIAAANPIGGRYDPSLTFSENVDLTEPIISRFDILCVVRDTVDPVQDEMLARFVVGSHVRH
HPSNKEEEGLANGSAAEPAMPNTYGVEPLPQEVLKKYIIYAKERVHPKLNQMDQDKVAKMYSDLRKESMATGSIP
ITVRHIESMSHGGGPRAHPSAGLCDRRRRQHGHPRDAGELHRHTEVQRHRSMRKTFARYLSFRRDNNELLLFILK
QLVAEQVTYQRNRFGAQQDTIEVPEKDLVDKARQINIHNLSAFYDSELFRMNKFSHDLKRKMILQQF

FIGURE 301

GAGCTGCGAAAGGGCGGGAAAGGCAGTTGGAGAAGAGGTAAGCGGTTACTCACTCCATGGCTGCAGCAAGGAGAG
GCGGCGGCGGCCTCGGCTGAAGAAAGAAGGTGGGAGCGGAGAGCGCAGGCGTGAAATCTTCCCAAGGCTGCAGAC
ACCGACGGATTTGCTTTGGGAGCCAGAGTAGCTGCCGCCACCAGAGTCCGGAGCC**ATG**AGCGGGTTTAATTTTGG
AGGCACTGGGGCCCCTACAGGCGGGTTCACGTTTGGCACTGCAAAGACGGCAACAACCACACCTGCTACAGGGTT
TTCTTTCTCCACCTCTGGCACTGGAGGGTTTAATTTTGGGGCTCCCTTCCAACCAGCCACAAGTACCCCTTCCAC
CGGCCTGTTCTCACTTGCCACCCAGACTCCGGCCACACAGACGACAGGCTTCACTTTTGGAACAGCGACTCTTGC
TTCGGGGGGAACTGGATTTTCTTTGGGGATCGGTGCTTCAAAGCTCAACTTGAGCAACACAGCTGCCACCCCAGC
CATGGCAAACCCCAGCGGCTTTGGGCTGGGCAGCAGCAACCTCACTAATGCCATATCGAGCACCGTCACCTCCAG
CCAGGGCACAGCACCCACCGGCTTTGTGTTTGGCCCCTCCACCACCTCTGTGGCTCCAGCTACCACATCTGGAGG
CTTCTCATTCACTGGTGGAAGCACGGCCCAACCCTCCGGTTTCAACATTGGCTCAGCAGGGAATTCAGCCCAGCC
CACGGCACCTGCCACGTTGCCCTTCACTCCGGCCACGCCAGCAGCCACCACAGCAGGTGCCACACAGCCAGCTGC
TCCCACACCCACAGCCACCATCACCAGTACTGGGCCCAGCCTCTTTGCGTCAATAGCAACTGCTCCAACCTCATC
TGCCACCACTGGACTCTCCCTCTGTACCCCTGTGACCACAGCGGGCGCCCCCACTGCTGGGACACAGGGCTTCAG
CTTAAAGGCACCTGGAGCAGCTTCCGGCACCTCCACAACAACATCCACCGCTGCCACCGCCACCGCCACCACCAC
CACCAGCAGCAGCACCACCGGCTTTGCCTTGAATTTAAAACCACTGGCGCCAGCCGGGATCCCCAGCAATACAGC
AGCTGCCGTGACCGCTCCACCTGGCCCTGGCGCAGCTGCAGGGGCGGCTGCCAGCTCCGCCATGACCTACGCGCA
GCTGGAGAGCCTGATCAACAAATGGAGCCTGGAGCTAGAGGACCAGGAGCGGCACTTCCTCCAGCAGGCCACCCA
GGTCAACGCCTGGGACCGCACGCTGATCGAGAATGGAGAAAAGATCACCAGCCTGCACCGCGAGGTGGAGAAGGT
GAAGCTGGACCAGAAGAGGCTGGACCAGGAGCTCGACTTCATCCTGTCCCAGCAGAAGGAGCTGGAAGACCTGCT
GAGCCCACTGGAGGAGTTGGTCAAGGAGCAGAGCGGGACCATCTACCTGCAGCACGCGGATGAGGAGCGTGAGAA
AACCTACAAGCTGGCTGAGAACATCGACGCACAGCTCAAGCGCATGGCCCAGGATCTCAAGGACATCATCGAGCA
CCTGAACACGTCCGGGGCCCCCGCCGACACCAGTGACCCACTGCAGCAGATCTGCAAGATCCTCAATGCGCACAT
GGACTCACTGCAGTGGATCGACCAGAACTCGGCCCTGCTGCAGAGGAAGGTGGAGGAGGTGACCAAGGTGTGCGA
GGGCCGGCGCAAGGAGCAGGAGCGCAGCTTCCGGATCACCTTTGAC**TGA**GCGACAGCAGCCCTGGGGCCCGCAGG
TCCCTAGGGAGTTCATGAGGGGAATGCGCCCTGTTGTCTGTAGTTTGGGGTTGTGGCAAGATACTTGTTTGTTTG
TTTCTTTCTTTCACATGACTGCCCTTGACATGATCGCTGTGTGCTTTGCGTTTTTCCATTTAGGAGGGTATTCTG
GGCCTTCTGCCCAGGCAGCAGCCTCATGGGTGTGGCTTCTGTGGCTTTCATTTGAGTATCTTTGGCCCCTTTTCA
CCTACTGCGACCACCCACCTCATCCTGGCTCAGCCTGGTGATGGAGAAGTGCTGATGGTCTTGGTCCCAGCCAGG
GTCGTGGGGGCAGCCACTCTCTCCAAAGCATAGTCATGGGTGTCATGAAAAAATACCAAATGTAAGAGAACCTCC
AAGTCAGGGCGCAGTGGCTCACCCCTGTAATCTCAGCACTTTGGGTGGCCAAGGCGGGCAGATGACTTGAGGTCA
GGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGTCAGGTGTGGT
GGACGCCTGTGATCTCAATCTCAGCTACTCGGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGTGTTGCA
GTGAACCAAGATCACACCACTGCACTCCAGCCTAGGCAACAGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAG
AAACTCCCAGGAGACAGCAGCCTAGTTTTCGAGTGTGAGCTTGTGCTTGTGAAAGCTAACCATGCTAACCACCAA
GGCAAAGCAGCACAGTGTGAATAGAACAGAGCGGGATCAAGAATTTCACAGAAGACAGGTCAGCTGAGGGGCCTG
CACACACAGGGTGTTGAGGAACCACAGATGGGCGCCGAGAGGCCTGCCTTTTGCCTGGCCCAGGCTCACCCCCAC
CTTGGGCCTCACCTCCTCTAGGAAGCCTTCCCAGCTACCCGAAGCTCAGGTGGCCTTCTTGCAGGTCCCCGTAGC
ACCCTGAGCCTGTACCTTGGGTGGCACTTGTTATGCTATCCTGTGCTAGCCGTTTGTGCCTCGTCTCGCTGTTAG
ATTGTGAGTTCCCATGGGCAGAGACCCACTGTCGTTCCCCGTGTGTCCCCAGCCCGGTCCCTGTCACATTTGTTA
AATGAAAGAACAATGAAGCCCAGTGTAACGTCAGTCCACAGAAATAGCCACAGCTTCCAGTGGTGGCCGTAGACT
TGGCTCGGAACTTAGTGGCACCAGAGTAACTCTAGTCAGTTACAGTAAAATCCACTGTGTGTGGAAGGCAGAAGC
TAGCGGTTGTATCCCAAGCATCTTTTGTATTTGTCTTTATACTTTGCTGAATTCTCTGAAATACCTATTACTGTA
TGTGGCTTTTCTAAATAAATGTATTGTGAAACTAAAAAAAAAAAAAAAAA

FIGURE 302

MSGFNFGGTGAPTGGFTFGTAKTATTTPATGFSFSTSGTGGFNFGAPFQPATSTPSTGLFSLATQTPATQTTGFT
FGTATLASGGTGFSLGIGASKLNLSNTAATPAMANPSGFGLGSSNLTNAISSTVTSSQGTAPTGFVFGPSTTSVA
PATTSGGFSFTGGSTAQPSGFNIGSAGNSAQPTAPATLPFTPATPAATTAGATQPAAPTPTATITSTGPSLFASI
ATAPTSSATTGLSLCTPVTTAGAPTAGTQGFSLKAPGAASGTSTTTSTAATATATTTTSSSTTGFALNLKPLAPA
GIPSNTAAAVTAPPGPGAAAGAAASSAMTYAQLESLINKWSLELEDQERHFLQQATQVNAWDRTLIENGEKITSL
HREVEKVKLDQKRLDQELDFILSQQKELEDLLSPLEELVKEQSGTIYLQHADEEREKTYKLAENIDAQLKRMAQD
LKDIIEHLNTSGAPADTSDPLQQICKILNAHMDSLQWIDQNSALLQRKVEEVTKVCEGRRKEQERSFRITFD

FIGURE 303

CGCAGGGACCGTGCTCCGCCGTCTCCGCCGCATCTTCCACCCTCGCCGCCGCCGCAGCTCCCCGCGCTCGTGCCA
CCGCCGCCGCGTCCACCCTCAGCGCCACCGCC**ATG**CGGGAGATCGTGCACCTGCAGGCCGGCCAGTGCGGCAACC
AGATCGGGGCCAAGTTTTGGGAGGTTATCAGTGACGAACATGGCATCGACCCCACAGGCACATACCATGGGGACA
GTGACCTGCAACTGGAGAGGATCAACGTGTACTACAACGAGGCCACAGGAGGAAATTATGTCCCCAGAGCGGTGC
TGGTGGACCTGGAACCCGGCACCATGGACTCTGTCCGTTCTGGCCCCTTCGGTCAGATCTTTCGGCCGGACAACT
TCGTGTTTGGCCAATCCGGAGCCGGCAACAACTGGGCAAAGGGGCACTACACGGAGGGCGCAGAGCTGGTGGACG
CTGTCCTGGACGTAGTCCGGAAGGAGGCCGAGAGCTGCGACTGCCTTCAGGGCTTCCAGCTGACCCACTCGCTGG
GGGGTGGCACGGGGTCCGGAATGGGCACGCTGCTCATCAGTAAGATCCGCGAGGAGTTCCCAGACCGCATCATGA
ACACCTTCAGCGTGGTGCCCTCGCCCAAAGTGTCAGACACGGTGGTGGAGCCCTACAACGCCACGCTGTCTGTGC
ACCAGCTGGTGGAGAATACGGATGAGACCTACTGCATCGACAACGAGGCACTCTACGACATCTGTTTCCGCACCC
TCAAGCTGACCACCCCCACCTACGGGGACCTCAACCACCTGGTGTCGGCCACCATGAGCGGGGTCACCACCTGCC
TGCGCTTCCCGGGCCAGCTGAACGCCGACCTGCGCAAGCTGGCCGTCAACATGGTTCCCTTTCCTCGCCTGCACT
TCTTCATGCCCGGCTTCGCACCCCTGACCAGCCGGGGCAGCCAGCAGTACCGGGCCCTGACGGTGCCCGAGCTCA
CCCAGCAGATGTTCGATGCCAAGAACATGATGGCGGCGTGCGACCCGCGCCACGGCCGCTACCTGACCGTGGCCG
CCGTGTTCCGGGGCCGCATGTCCATGAAGGAGGTGGACGAGCAGATGCTGAGCGTGCAGAGCAAGAACAGCAGCT
ACTTCGTGGAGTGGATCCCCAACAACGTGAAGACGGCCGTGTGCGACATCCCGCCCCGCGGCCTGAAGATGGCCG
CGACCTTCATCGGCAACAGCACGGCCATCCAGGAGCTGTTCAAGCGCATCTCCGAGCAGTTCACGGCCATGTTCC
GGCGCAAGGCCTTCTTGCACTGGTACACGGGCGAGGGCATGGACGAGATGGAGTTCACCGAGGCCGAGAGCAACA
TGAATGACCTGGTATCTGAGTACCAGCAGTACCAGGACGCCACGGCCGAGGAGGGCGAGTTCGAGGAGGAGGCGG
AGGAGGAGGTGGCC**TAG**GCTGCTCCCATCGCTTCCCACCTGTCCCCTCGAGGCTTCTGACCTTTGATCCGCTAGG
CCCCCCATCTCTGAACCCTAGAGCCCCGCTTTCCCTCCAAGGCTGACTCCCCGCTGACCCTAACAATACCTTTGG
AGCTCGCTTTACCTCTGGCTACTTCATCTCCGACCCTGGCTCCCCTTTGAGCCCTAATTTATCTTTAACCCCCTT
GAGCTCTTCCAACCTTGACATTCCCAGGAGGAGCCCCGCTTCACCCCTTCTGACTCTGGAAACCGCACCTTTAAC
TTTGCAGACCTTCCTTCACCCCTGACTTCTGCTTCACCTTTGACCTCTGCCCCCCATGAATCCCATTTTACCTCT
AGACCTATAAGTTCTGGTTTATGTTTGACCCCTCCCTCTGAGCTGCACTTCACCGCTGACCTTGCCTCACCTTTA
ACCCCCCACCTGAGCCCCAGCTCCTACCTCTGACCCCAACTTCTCTTTGATCTCTGAATCCCCTCTGACTCCAAC
TTCTCTTTCACCCTCTATGAGTCCCATTTTACTTCTACACCTGCAAGTCCTGGTTTATATTGGACCCCTCCCTCC
GAGCTGCAGTTCACCTTTGACCTTGCCTCACCTTTCACCCCCCACCCCCCACAGCGTCAGCTCCTACCTCTGACC
CCAGCTTCTCTCTGATTCCCACAGGCCCCATGCATCCTCCCTGCCTCACTCCCCTCAGCCCCTGCCGACCTTAGC
TTATCTGGGAGAGAAACAAGGCCTGGTGCCTGTGAGGAAGAGAGGTCACCCCTACCCTCCCTCCCCGCTTCCCTG
CCTCACCCTCAATAAATAAATTAATTGTTGTCATGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 304

MREIVHLQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLERINVYYNEATGGNYVPRAVLVDLEPGTMDS
VRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDAVLDVVRKEAESCDCLQGFQLTHSLGGGTGSGMGTL
LISKIREEFPDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDL
NHLVSATMSGVTTCLRFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMM
AACDPRHGRYLTVAAVFRGRMSMKEVDEQMLSVQSKNSSYFVEWIPNNVKTAVCDIPPRGLKMAATFIGNSTAIQ
ELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQDATAEEGEFEEEAEEEVA

FIGURE 305

CGGCCGCGTCCTCAAGCCGGCACCTGAGCGGCGGAGACGGCTGTAGCACAAGGATCTGCATCTCCA**ATG**GATACT
GAGGGGTTTGGTGAGCTCCTTCAGCAAGCTGAACAGCTTGCTGCTGAGACTGAGGGCATCTCAGAGCTTCCCCAT
GTGGAACGGAACTTACAGGAGATCCAGCAGGCGGGAGAGCGCCTGCGTTCCCGTACCCTAACACGCACGTCCCAG
GAGACGGCAGATGTCAAGGCGTCAGTTCTCCTCGGGTCTCGGGGACTTGACATATCCCACATCTCCCAGCGATTG
GAGAGTCTGAGTGCAGCCACCACCTTTGAGCCTCTTGAGCCTGTGAAGGACACTGACATTCAGGGCTTCCTGAAG
AATGAGAAGGACAATGCCCTGCTGTCTGCCATCGAAGAGTCCCGGAAGAGGACCTTCGGCATGGCTGAGGAGTAC
CATCGGGAGTCAATGTTGGTTGAGTGGGAGCAAGTGAAACAGCGAATTCTGCACACACTGCTGGCATCAGGAGAA
GACGCCCTTGACTTTACTCAAGAAAGCGAGCCAAGCTACATCAGTGATGTGGGACCCCCTGGTCGAAGCTCTCTG
GATAACATCGAGATGGCCTATGCGCGGCAAATTTATATCTATAATGAGAAAATTGTAAATGGACACCTGCAGCCT
AACCTGGTGGACCTTTGTGCTTCCGTCGCAGAGCTGGATGATAAGAGCATTTCCGACATGTGGACCATGGTAAAA
CAAATGACAGACGTGTTGTTGACACCGGCAACGGATGCCCTGAAGAACCGCAGCAGCGTGGAAGTGCGCATGGAG
TTTGTCAGGCAGGCCTTGGCGTACCTTGAGCAGAGTTATAAGAATTACACCCTTGTGACTGTCTTTGGAAATTTG
CATCAGGCCCAGCTGGGCGGGGTGCCTGGGACTTACCAATTGGTTCGAAGTTTCCTGAACATTAAACTGCCAGCT
CCCTTGCCTGGACTACAGGATGGAGAGGTGGAAGGCCATCCTGTGTGGGCGCTAATTTACTACTGCATGCGCTGT
GGAGACCTGCTTGCCGCTTCACAGGTAGTTAATCGAGCCCAGCACCAGCTGGGAGAGTTTAAAACCTGGTTCCAG
GAGTACATGAACAGCAAGGACAGAAGATTGTCCCCAGCTACGGAAAACAAGCTCCGGCTGCATTACCGTAGGGCC
CTCAGGAACAATACAGATCCCTACAAGCGGGCCGTGTACTGTATCATTGGCAGATGTGACGTCACCGACAACCAG
AGTGAAGTGGCGGACAAAACTGAGGATTACCTGTGGCTGAAGTTGAACCAAGTGTGTTTTGACGACGATGGCACC
AGCTCCCCACAAGACAGGCTCACTCTCTCACAGTTCCAGAAGCAGTTGTTGGAAGACTATGGCGAGTCCCACTTT
ACGGTGAACCAGCAACCCTTCCTCTACTTCCAAGTCCTGTTCCTGACAGCGCAGTTTGAAGCAGCAGTTGCCTTT
CTTTTCCGCATGGAGCGGCTGCGCTGCCATGCTGTCCATGTAGCACTGGTGCTGTTTGAGCTGAAGCTGCTTTTA
AAGTCCTCTGGACAGAGTGCTCAGCTCCTCAGCCACGAGCCTGGTGACCCTCCTTGCTTGCGGCGGCTGAACTTC
GTGCGGCTCCTCATGCTGTACACCCGGAAGTTTGAGTCCACGGACCCAAGGGAGGCCCTCCAGTACTTCTATTTC
CTCAGGGATGAGAAAGATAGTCAAGGAGAAAACATGTTTCTGCGCTGTGTGAGTGAGCTTGTGATTGAAAGCCGA
GAGTTCGATATGATTCTTGGGAAACTAGAGAATGACGGAAGTAGAAAGCCTGGAGTCATAGATAAGTTTACTAGT
GACACAAAGCCTATTATCAACAAAGTTGCTTCTGTGGCAGAAAATAAAGGACTGTTTGAAGAGGCAGCAAAGCTG
TATGACCTTGCCAAGAATGCTGACAAGGTACTGGAGCTGATGAACAAACTGCTGAGCCCTGTCGTCCCCCAGATC
AGTGCCCCGCAATCCAACAAGGAGAGGCTGAAGAACATGGCACTCTCCATTGCCGAACGGTATAGGGCTCAAGGA
ATAAGCGCAAATAAATTTGTGGACTCCACGTTCTATCTTCTTTTGGACTTGATCACCTTTTTTGACGAGTATCAT
AGTGGTCATATTGATAGAGCTTTTGATATCATTGAGCGCTTGAAGCTGGTGCCCCTGAATCAGGAAAGTGTGGAA
GAGAGAGTGGCTGCTTTCAGAAATTTCAGTGATGAAATCAGGCACAACCTCTCAGAAGTGCTTCTTGCCACCATG
AACATCTTGTTCACACAGTTTAAGAGGCTCAAGGGGACAAGTCCATCCTCGTCATCCAGGCCCCAGCGAGTCATC
GAGGACCGCGACTCTCAACTCCGAAGTCAAGCCCGCACTCTGATTACCTTTGCTGGAATGATACCATACCGAACG
TCTGGGGACACCAATGCGAGGCTGGTGCAGATGGAGGTCCTCATGAAT**TAA**GTGCCATGCTTTGTGGGAGTCTGG
GTCGGCACACTGTCAGTACATCAGGCACATGGGCCCACTAGGCTGGGGTTTCTGGTTTTGTTTCTGTTGTGTTTT
GTTTTGGTTTCTGTATTATGTATTTTTGTCAACGCCAATAAATTTCTTTGATTTGT

FIGURE 306

MDTEGFGELLQQAEQLAAETEGISELPHVERNLQEIQQAGERLRSRTLTRTSQETADVKASVLLGSRGLDISHIS
QRLESLSAATTFEPLEPVKDTDIQGFLKNEKDNALLSAIEESRKRTFGMAEEYHRESMLVEWEQVKQRILHTLLA
SGEDALDFTQESEPSYISDVGPPGRSSLDNIEMAYARQIYIYNEKIVNGHLQPNLVDLCASVAELDDKSISDMWT
MVKQMTDVLLTPATDALKNRSSVEVRMEFVRQALAYLEQSYKNYTLVTVFGNLHQAQLGGVPGTYQLVRSFLNIK
LPAPLPGLQDGEVEGHPVWALIYYCMRCGDLLAASQVVNRAQHQLGEFKTWFQEYMNSKDRRLSPATENKLRLHY
RRALRNNTDPYKRAVYCIIGRCDVTDNQSEVADKTEDYLWLKLNQVCFDDDGTSSPQDRLTLSQFQKQLLEDYGE
SHFTVNQQPFLYFQVLFLTAQFEAAVAFLFRMERLRCHAVHVALVLFELKLLLKSSGQSAQLLSHEPGDPPCLRR
LNFVRLLMLYTRKFESTDPREALQYFYFLRDEKDSQGENMFLRCVSELVIESREFDMILGKLENDGSRKPGVIDK
FTSDTKPIINKVASVAENKGLFEEAAKLYDLAKNADKVLELMNKLLSPVVPQISAPQSNKERLKNMALSIAERYR
AQGISANKFVDSTFYLLLDLITFFDEYHSGHIDRAFDIIERLKLVPLNQESVEERVAAFRNFSDEIRHNLSEVLL
ATMNILFTQFKRLKGTSPSSSSRPQRVIEDRDSQLRSQARTLITFAGMIPYRTSGDTNARLVQMEVLMN

FIGURE 307

CCCCAGCGAGGCTCCGGGAGCCCTTGCCTGCGGGGGTCCGGGGACTCGAGCCGGCCTCCGCCCCCCGGACGCACA
GCCAGCGTGGTCCCCGCGTGCAACGCGAGCGCCGGGGAGTGGCTCCTGCTTTGCCCCTCGTGGGGGCCGAGCCAA
GACCAGTCTGCAAACTCCATCCCGCCGGCTGGAAGAAGTCGCGGAGCCGGCACCAAACCCGCAGCGTCTTCCCGC
GCGGATCCCGGGACTTAAAAAGCCGGGGCCACCCCGGCCCAGGACGGG**ATG**CGGGTCGGTCCGGTGCGCTCTGCC
ATGAGCGGCGCCTCGCAGCCCCGCGGCCCGGCCCTGCTCTTCCCAGCCACCCGAGGCGTCCCGGCCAAACGCCTG
CTGGACGCCGACGACGCGGCGGCTGTGGCGGCCAAGTGCCCGCGCCTCTCCGAGTGCTCCAGCCCCCCGGACTAC
CTCAGCCCCCCCGGCTCGCCCTGCAGCCCGCAGCCCCCGCCTGCCGCTCCGGGGGCCGGCGGAGGCTCCGGGAGC
GCGCCGGGGCCCAGCCGCATCGCCGACTACCTGCTGCTGCCCCTAGCCGAGCGCGAGCATGTGTCCCGGGCGCTG
TGCATCCACACTGGACGCGAGCTGCGCTGCAAGGTGTTTCCCATTAAACACTACCAGGACAAAATCAGGCCTTAC
ATCCAGCTGCCATCGCACAGCAACATTACTGGCATTGTGGAAGTGATCCTTGGGGAAACCAAGGCCTATGTCTTC
TTTGAGAAGGACTTTGGGGACATGCACTCCTATGTGCGAAGCCGGAAGAGGCTGCGGGAAGAGGAAGCCGCCCGG
CTCTTCAAGCAGATTGTCTCCGCCGTCGCCCACTGCCACCAGTCAGCCATCGTGCTGGGGGACCTGAAGCTTAGG
AAGTTCGTCTTCTCCACGGAGGAGAGAACCCAGCTTAGACTAGAAAGTCTAGAAGACACACACATAATGAAGGGG
GAAGATGATGCTTTGTCAGACAAACATGGCTGCCCAGCCTACGTGAGCCCTGAGATCCTCAACACCACTGGGACC
TACTCCGGAAAGGCTGCGGACGTTTGGAGCCTGGGGGTGATGCTCTACACCCTTCTGGTTGGACGATACCCCTTC
CATGACTCAGACCCCAGTGCCCTTTTCTCCAAAATTCGGCGTGGACAGTTCTGCATTCCTGAGCACATTTCCCCC
AAAGCCAGGTGCCTCATTCGCAGCCTCTTGAGACGGGAGCCCTCCGAGAGACTCACTGCCCCCGAGATCCTACTG
CACCCCTGGTTTGAGTCCGTCTTGGAACCCGGGTACATCGACTCAGAAATAGGAACTTCAGACCAGATTGTTCCA
GAGTACCAGGAGGACAGTGACATTAGTTCCTTCTTCTGC**TAA**TCCCCAAAACCTCAGAAACCTCATAATTCTTAA
CACCTGGCATTTCCATTTCTAAAGATGGACAGGCCCTTTGGCATGGTACCAACCAGATAATGACTGCATCAGGAT
GAAAGCTGCTGAACTCGGCATGGCGCCTCCTCTTCTCTGTTGGGATGAGTGACTTTATTGATTTGAGCAGCATAT
GCTGTGATTGGCTGCCCTGCAAATTTGTTTCCCTTAAGGAACCCTCACCAACTATCTCTGCTGGATTTGGGAGTT
CCGCATCTTTTGTGGAGGGCAGAGTATGGACATCTTACACCCGGTGGTCAAGTGTGTAATAAACTTGAGCATTCG
AATGGGAGAAAAAGCAAATCGCACAATGACATATTTTGAGTAATAACCGTATTTTTCACAGGGTGACAAATTGGG
CCAATAAATCTGCCATCTTTGAACTCATCTTTGGTGGCTAGACTGCTACGGCAGCTTCTCTGATGGGAAAGTTCC
TTTTTTGGCTTAACACTCACCCTTTCTTCACACTCACATTTACCAATGACTCTGCTCCGTTTTTGGAGCAGACTG
TTTTAAGTTGCTCAGGAGCCTGATGGAACCATGAACCGAGACTCTTCTCTGTTTCCTGCCAAGACCTCATCTGCA
CTAATGCCTTCTCCCTGACCTTGACACTTCCCCCTTTAGCTATAAAAGCACTTACCAGCCGAACGTGGAACAGTA
TCACAAAAGATTCCATCTCCCAACGATTTCAGAACTCTGAGCTCAGAGAGACTCCAGATTTTAAAAAATAATTTG
AGTGCTTGGAAACTATTAGCTTTTTAAGTTCCTTCCAAATATGTTAGTACCTACCCTTTACTTTTTCCCCAAGAC
CATCTCAGGGTGGAGCATTCTGTCTAAGAGAAGAAAGATAAGGAGGCTCCCACCCACCTCTCCCAAGAGCAGACA
TTAAACATCTTTGTGCTTTGAAGAGAGTGAATTTTGGATAGTCTTGTGATTCTCAGACTAACTTCCAGAATTATA
CTTTAACCCCTCCCAGATATGGTCCGCCTTTGGCATTGTGTGTACATCTGCAGTTTTGCATGGTGGGTTGTTAAT
ATTTCAAATGTGTGGTTTATGAATACGTCTGTATAATCGGCTTCTGGAGTGAAACAGCAAACCCCAAATCTTCAA
AGTTGGAAGGAACTTTAAAAATCATCCGGTCCAATCTCTTTCCTCTTTCTGCCACCTCCCAAGGCAGAAATCCCC
TCTTCAGCTTCTTTTGTAGGTGGGAATCCAGCCTCTGTTAGATATGTCCAGAGATGGAAACTCACTCCCCTACAA
AAGATGGAGCTTAATGGAGAAATTGCAACTTTCATTAAAAAACAAATTCAGATGAAATATCAGTAACTGTCTTGG
ACAGTGCTGAAATCAGGTGGTTAAACGGGTAAACAAAATATACTGTATTTTGAGAAATGGCACAAAAACAGGCAG
TCATCTTTAAGGGCTATGCCTAGGCAAACTACTAACATGCATTGTGAGAATGCCGTGTATACCTCACGTACTGTG
TACTTTGTACATATATTTTACCTTTTATACCTATGTTCGATTTTGTTTTGTTTTGTTCTGGCTTTGAGGCTTGTT
TTGTTGTCTGTGTCTGTCTGAATAACCTGCGTGTCTAAAACCACGTGAAATGTGAATGATTATTGGCAATATTAC
CTTGACAGAATCATGGGACTTTGAGAAGAGGGAGGACAGAGGCCTCTGTCGCACTAACGCTCTCGTGGTTGCTCG
ACTGTTGTATCTGTGATACATTATCCGACTAAGGACTCTGGGCTGGCAGGGCCTTCTGCCGGGAAAGCTAGAAAC
ACTAGGTTCTTCCTGTACATACGTGTATATATGTGAACAGTGAGATGGCCGTTTCTGACTTGTAGAGAAATTTTA
ATAAACCTGGTTTCGTA

FIGURE 308

MRVGPVRSAMSGASQPRGPALLFPATRGVPAKRLLDADDAAAVAAKCPRLSECSSPPDYLSPPGSPCSPQPPPAA
PGAGGGSGSAPGPSRIADYLLLPLAEREHVSRALCIHTGRELRCKVFPIKHYQDKIRPYIQLPSHSNITGIVEVI
LGETKAYVFFEKDFGDMHSYVRSRKRLREEEAARLFKQIVSAVAHCHQSAIVLGDLKLRKFVFSTEERTQLRLES
LEDTHIMKGEDDALSDKHGCPAYVSPEILNTTGTYSGKAADVWSLGVMLYTLLVGRYPFHDSDPSALFSKIRRGQ
FCIPEHISPKARCLIRSLLRREPSERLTAPEILLHPWFESVLEPGYIDSEIGTSDQIVPEYQEDSDISSFFC

FIGURE 309

GGCACGAGGGAGAACTAGTCTCGATTTTTTTTTTTTTTTTTTCTTTGTTTTGTTTTTCCTGTATAAAAAAGGAC
CCCAAATATAAAGGTAGGGAAAGGGACAAGAGGGAACATACCCCTTAGTGTAGAGAAATGGGAAGGAGAAGGAGA
AGCCTCAAAAGGAGAGGTGGGAGGGGAATGTCATTAAGGCAGCAAAGTAATCTCTGTAGAAAGATGGAGGAGGAC
CCTCCATAGCCTCAGAGATAAAGGCAAAGATTGCCCTCTCAGTGTCCAGAAGGGAAATGGCAGCTTTTCTTCCTT
CCATGGCAGCCACTCCATTGCTCACTCCGGATTACCTTCATCCTTATGTAGATAAGAGTGCTGCAGAGCTCGAAA
GGCAGAGATTCGCTTGTGTGGGTTAAAAGTCAGCATTTCCAGCAGCAGCTGTGCTCCCGACTCCTCCATCTCAGG
TACCACCGACTGCACTGGGCGGGGCCCTCTGGGGGGAAAGGCTCCACGGGGCAGGGATACATCTCGAGGCCAGTC
ATCCTCTGGAGGCAGCCCAATCAGGTCAAAGATTTTGCCCAACTGGTCGGCTTCAGAGTTTCCACAGAAGAGAGG
CTTTCGACGAAACATCTCTGCAAAGATACAGCCAACACTCCAC**ATG**TCCACAGGTGTTGCATATGTGGACTGCAG
AAGAACTTCGGGAGCTCGGTACCAGAGTGTAACAACCACGGGTGTAAGTGCCATCTGG**TAG**CTGTAGATTCTGGC
CAGGCCAAAGTCAGCCAGCTTGACTGTTCCACCACTTGTCACCAGAATGTTCTCTGGCTTCAGATCTCGGTGAAC
GATGCAATTGGCATGAAGGAAATCTAGGCCTCTTAGAAACTGGCGCATCAGATCCTTGATCGTTTCGGCTGGCAA
GCCTGGTGGGGGTGCCTTGTCCAGATATGTCCTTAGGTCCTGGTCTACATGCTCAAACACCAGGGTTACCTTGAT
CTCCCGGTCAGTTCGGGATGTGGCACAGACGTCCATCAGCCGGACAACATTGGGATGCTCAAAAGCCTCCAGTCG
CCTCAGTAAAGCCACCTCACGAACTGTGCTGATGGGAAGGCCTCCTCCACCTCCTCCTCCATTGGGGACTCTCAC
ACTCTTGAGGGCCACAAAGTGGCCACTGTGGGGATCACGGGCCTTGTACACTGTCCCATAGGCACCGACACCAAT
TTCAGCCACTGGCTCATATCGAGAGGTAGCCATTCTCAGATCAAGGGAGACCCTCACGCCAGCCCGGGGTGCTGT
GGGGGCGGCCCGTTATCGGGGCCCCGGAGCCGGTTCCTACGGCCCCATACACCCGAGCTCGGTCCGGAGCAG

FIGURE 310

MSTGVAYVDCRRTSGARYQSVTTTGVSAIW

FIGURE 311

CGCGATTCTCAGGGATTGATCCGCCTCTTCAGGTAAGTTATCTTCCGGCCCCGTACCACTGTGCCACAGGCGCAG
CCCGCTTCCTCAGGTGCCCTATCCCGCGCAGAAGACCACGGCTTCACAGAGTGTTATTTAAGGGCGTGGCCAGCG
GAACATCCCGCCCCATTCTGTGACGCACGGGGTGGCGCGCGTGGGACCCGAGGGGTGGGGCTGGGTTTAGTAGGA
GACCTGGGGCAAGGCCCCCTGTGGACGACCATCTGCCAGCTTCTCTCGTTCCGTCGATTGGGAGGAGCGGTGGCG
ACCTCGGCCTTCAGTGTTTCCGACGGAGTGA**ATG**GCGGCGGCGGCTGGGATGCTGCTGCTGGGCTTGCTGCAGGC
GGGTGGGTCGGTGCTGGGCCAGGCGATGGAGAAGGTGACAGGCGGCAACCTCTTGTCCATGCTGCTGATCGCCTG
CGCCTTCACCCTCAGCCTGGTCTACCTGATCCGTCTGGCCGCCGGCCACCTGGTCCAGCTGCCCGCAGGGGTGAA
AAGTCCTCCATACATTTTCTCCCCAATTCCATTCCTTGGGCATGCCATAGCATTTGGGAAAAGTCCAATTGAATT
TCTAGAAAATGCATATGAGAAGTATGGACCTGTATTTAGTTTTACCATGGTAGGCAAGACATTTACTTACCTTCT
GGGGAGTGATGCTGCTGCACTGCTTTTTAATAGTAAAAATGAAGACCTGAATGCAGAAGATGTCTACAGTCGCCT
GACAACACCTGTGTTTGGGAAGGGAGTTGCATACGATGTGCCTAATCCAGTTTTCTTGGAGCAGAAGAAAATGTT
AAAAAGTGGCCTTAACATAGCCCACTTTAAACAGCATGTTTCTATAATTGAAAAAGAAACAAAGGAATACTTTGA
GAGTTGGGGAGAAAGTGGAGAAAAAAATGTGTTTGAAGCTCTTTCTGAGCTCATAATTTTAACAGCTAGCCATTG
TTTGCATGGAAAGGAAATCAGAAGTCAACTCAATGAAAAGGTAGCACAGCTGTATGCAGATTTGGATGGAGGTTT
CAGCCATGCAGCCTGGCTCTTACCAGGTTGGCTGCCTTTGCCTAGTTTCAGACGCAGGGACAGAGCTCATCGGGA
AATCAAGGATATTTTCTATAAGGCAATCCAGAAACGCAGACAGTCTCAAGAAAAAATTGATGACATTCTCCAAAC
TTTACTAGATGCTACATACAAGGATGGGCGTCCTTTGACTGATGATGAAGTAGCAGGGATGCTTATTGGATTACT
CTTGGCAGGGCAGCATACATCCTCAACTACTAGTGCTTGGATGGGCTTCTTTTTGGCCAGAGACAAAACACTTCA
AAAAAAATGTTATTTAGAACAGAAAACAGTCTGTGGAGAGAATCTGCCTCCTTTAACTTATGACCAGCTCAAGGA
TCTAAATTTACTTGATCGCTGTATAAAAGAAACATTAAGACTTAGACCTCCTATAATGATCATGATGAGAATGGC
CAGAACTCCTCAGACTGTGGCAGGGTATACCATTCCTCCAGGACATCAGGTGTGTGTTTCTCCCACTGTCAATCA
AAGACTTAAAGACTCATGGGTAGAACGCCTGGACTTTAATCCTGATCGCTACTTACAGGATAACCCAGCATCAGG
GGAAAAGTTTGCCTATGTGCCATTTGGAGCTGGGCGTCATCGTTGTATTGGGGAAAATTTTGCCTATGTTCAAAT
TAAGACAATTTGGTCCACTATGCTTCGTTTATATGAATTTGATCTCATTGATGGATACTTTCCCACTGTGAATTA
TACAACTATGATTCACACCCCTGAGAACCCAGTTATCCGTTACAAACGAAGATCAAAA**TGA**AAAAGGTTGCAAGG
AACGAATATATGTGATTATCACTGTAAGCCACAAAGGCATTCGAAGAGAATGAAGTGTACAAAACAACTCTTGTA
GTTTACTGTTTTTTTAAGTGTGTAATTCTAAAAGCCAGTTTATGATTTAGGATTTTGTTAACTGAATGGTTCTAT
CAAATATAATAGCATTTGACACATTTTCTAATAGTTATGATACTTATACATGTGCTTTCAGGAAGTTCCTTGGTG
AAACAATTGTTGAGGGGGGATCTAGGTAATTGGCAGATTCTAAATAATATAATTTCCAGATAGTAATTTTAAGAG
TACTCATCGCTCTTGCCAAATAAGTTCAGGGTATTCAAATCTTGGACTAGTCCTGCAAGGTATAAAGAATAAAAA
TCCCAGTGAGATACTTGGAAACCACAGTTTATTATTATTTATCTGGGCAATTATTGTGTGTGTGAGGATGGAAGG
GTAGGGAATAATCGAACATCTAAAGCCTTGAATAAGAGAATACTAATTGTTTTGGTATGATGATACTCAGAAATG
GAGATATTATAGGAAAAAGAAATCCTTTGGAATTTTAACTAAAATCACTGCATATGGGAAATTAAGAGATCCAGG
ACCATATTTGATAAGAGTTCCTAAAAATAATGTAATTATTAATGCTAAAGACTGCTCATGTATCTTGATCTAATT
ACTAAATAAATTACATATTTATTTACCTGATAAATATGTATCTAGTTCTACAAGGTCACATTTATGTGGAAGTCC
AAAGTCAAGTCCTTAGGGGATAATTTTGTTTTGGGCTCAGTTGTTCCCTGCTTCCTTTTTTTTTTTTTTTTTTT
TTGAGATGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGTGCGATCTCAGCTCACTGCATCCTCTGCCTC
CCGGGTTCAAGCAATTCTCTGCCTCAGCCTCCCAAGTAGTTGGGATTACAGGCACCTGCCACCATGCCTGGCTAA
TTTTTTGTATTTTTAGTAGAGACGGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACTCCTGAGCCTCGTGAG
TCCACCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCACCTGGCCTTCCCTGCTTCCTCT
CTAGAATCCAATTAGGGATGTTTGTTACTACTCATATTGATTAAAACAGTTAACAAACTTTTTTCTTTTTAAAAT
GTGAGATCAGTGAACTCTGGTTTTAAGATAATCTGAAACAAGGTCCTTGGGAGTAATAAAATTGGTCACATTCTG
TAAAGCACATTCTGTTTAGGAATCAACTTATCTCAAATTGTAACTCGGGGCCTAACTATATGAGATGGCTGAAAA
AATACCACATCGTCTGTTTTCACTAGGTGATGCCAAAATATTTTGCTTTATGTATATTACAGTTCTTTTTAAAAC
ACTGGAAGACTCATGTTAAACTCTAATTGTGAAGGCAGAATCTCTGCTAATTTTTCAGATTAAAATTCTCTTTGA
AAAAAT

FIGURE 312

MAAAAGMLLLGLLQAGGSVLGQAMEKVTGGNLLSMLLIACAFTLSLVYLIRLAAGHLVQLPAGVKSPPYIFSPIP
FLGHAIAFGKSPIEFLENAYEKYGPVFSFTMVGKTFTYLLGSDAAALLFNSKNEDLNAEDVYSRLTTPVFGKGVA
YDVPNPVFLEQKKMLKSGLNIAHFKQHVSIIEKETKEYFESWGESGEKNVFEALSELIILTASHCLHGKEIRSQL
NEKVAQLYADLDGGFSHAAWLLPGWLPLPSFRRRDRAHREIKDIFYKAIQKRRQSQEKIDDILQTLLDATYKDGR
PLTDDEVAGMLIGLLLAGQHTSSTTSAWMGFFLARDKTLQKKCYLEQKTVCGENLPPLTYDQLKDLNLLDRCIKE
TLRLRPPIMIMMRMARTPQTVAGYTIPPGHQVCVSPTVNQRLKDSWVERLDFNPDRYLQDNPASGEKFAYVPFGA
GRHRCIGENFAYVQIKTIWSTMLRLYEFDLIDGYFPTVNYTTMIHTPENPVIRYKRRSK

FIGURE 313

ACCGCCGACGCAGACCCCTCTCTGCACGCCAGCCCGCCCGCACCCACC**ATG**GCCACAGTTCAGCAGCTGGAAGGA
AGATGGCGCCTGGTGGACAGCAAAGGCTTTGATGAATACATGAAGGAGCTAGGAGTGGGAATAGCTTTGCGAAAA
ATGGGCGCAATGGCCAAGCCAGATTGTATCATCACTTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACT
TTGAAAACAACACAGTTTTCTTGTACCCTGGGAGAGAAGTTTGAAGAAACCACAGCTGATGGCAGAAAAACTCAG
ACTGTCTGCAACTTTACAGATGGTGCATTGGTTCAGCATCAGGAGTGGGATGGGAAGGAAAGCACAATAACAAGA
AAATTGAAAGATGGGAAATTAGTGGTGGAGTGTGTCATGAACAATGTCACCTGTACTCGGATCTATGAAAAAGTA
GAA**TAA**AAATTCCATCATCACTTTGGACAGGAGTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAATCT
CCATACTGTTTCTTTCTTTTTTTTTTCATTACTGTGTTCAATTATCTTTATCATAAACATTTTACATGCAGCTAT
TTCAAAGTGTGTTGGATTAATTAGGATCATCCCTTTGGTTAATAAATAAATGTGTTTGTGCT

FIGURE 314

MATVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTQFSCTLGEKFEE
TTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLVVECVMNNVTCTRIYEKVE

FIGURE 315

TGGCCGAAGCAGGGGGACAGCAAGGGACGCTCAGGCGGGGACC**ATG**GCGGACGGCGGCTCGGAGCGGGCTGACGG
GCGCATCGTCAAGATGGAGGTGGACTACAGCGCCACGGTGGATCAGCGCCTACCCGAGTGTGCGAAGCTAGCCAA
GGAAGGAAGACTTCAAGAAGTCATTGAAACCCTTCTCTCTCTGGAAAAGCAGACTCGTACTGCTTCCGATATGGT
ATCGACATCCCGTATCTTAGTTGCAGTAGTGAAGATGTGCTATGAGGCTAAAGAATGGGATTTACTTAATGAAAA
TATTATGCTTTTGTCCAAAAGGCGGAGTCAGTTAAAACAAGCTGTTGCCAAAATGGTTCAACAGTGCTGTACTTA
TGTTGAGGAAATCACAGACCTTCCTATCAAACTTCGATTAATTGATACTCTACGAATGGTTACCGAAGGCAAGAT
TTATGTTGAAATTGAGCGTGCGCGACTGACTAAAACATTAGCAACTATAAAAGAACAAAATGGTGATGTGAAAGA
GGCAGCCTCCATTTTACAGGAGTTACAGGTGGAAACCTACGGGTCAATGGAAAAGAAAGAGCGAGTGGAATTTAT
TTTGGAGCAAATGAGGCTCTGCCTAGCTGTGAAGGATTACATTCGAACACAAATCATCAGCAAGAAAATTAACAC
CAAATTTTTCCAGGAAGAAAATACAGAGAAATTAAAGTTGAAGTACTATAATTTAATGATTCAGCTGGATCAACA
TGAGGGATCCTATTTGTCTATTTGTAAGCACTACAGAGCAATATATGATACTCCCTGTATACAGGCAGAAAGTGA
AAAATGGCAGCAGGCTCTGAAGAGTGTTGTACTCTATGTTATCCTGGCTCCTTTTGACAATGAACAGTCAGATTT
GGTTCACCGAATAAGTGGTGACAAGAAGTTAGAAGAAATTCCCAAATACAAGGATCTTTTAAAGCTTTTTACCAC
AATGGAGTTGATGCGTTGGTCCACACTTGTTGAGGACTATGGAATGGAATTAAGAAAAGGTTCCCTTGAGAGTCC
TGCAACGGATGTTTTTGGTTCTACAGAGGAAGGTGAAAAAAGGTGGAAAGACTTGAAGAACAGAGTTGTTGAACA
TAATATTAGAATAATGGCCAAGTATTATACTCGGATAACAATGAAAAGGATGGCACAGCTTCTGGATCTATCTGT
TGATGAGTCCGAAGCCTTTCTCTCAAATCTAGTAGTTAACAAGACCATCTTTGCTAAAGTAGACAGATTAGCAGG
AATTATCAACTTCCAGAGACCCAAGGATCCAAATAATTTATTAAATGACTGGTCTCAGAAACTGAACTCATTAAT
GTCTCTGGTTAACAAAACTACGCATCTCATAGCCAAAGAGGAGATGATACATAATCTACAA**TAA**GGGTCTTAGTG
CTTTAGAAAAAAGTTAAAATTGGAAGTCATTAAAAAAAGACTGTTATAATGGTGTATATGTTGGGGTTTTTTTTC
TAAGCTTCTTTGTCTTAAATTTTAAAATAGTGAATATGTTTGAGACTCCCTTTGACCTTTCAGTTCCCCAAGTTC
ATTGTTAACTTTGCATTTGCAATTGGTGCAAAAATACAGATTTCTGTCGTCTGAATACACAAAAAGTTGTGTCAT
AACTTACCCAGATATGTTTTTCTATCATTTGAAACCTTTTTAGCTACTGTTTGTTTTCATTCAACTAACAAACAT
ATTCCAATAATAAAAGCAGTATATACATATTTCCTTTCTACAGTTACCTCTGATTCTCAACATTTTGTGGGGTAG
TGATTTGGCAAGTGTTTTTTAAATAAAACAAATCTCATTGTAAAGTTATCAGTCATTTAGTAGAATAGAAAAGCA
ACATAGAGCATACAAGAACATTTGGGATAGAGTTGTGATTTGTGAAGAATTTGTACTTTGATATTGTGGCGGAAA
GTCTAGACTGAGTGTGTATGCTGGTAAACTGTAGACTTTTTTTTTTTTTTTTGAGTCCGGCTGGTTCCAATCACA
GTAGCTTGATTGCTTTCAGCCCTCATCCTCTCACTTGATCAGTTGTTCAACAGAATCAGCTGACATAATTGACAC
AGTTTATTGGGTGTTAAGTCCGCTCTATAGGGATAGTGACTACTTTTTTTTTTTTTTTTTTTTTGCTCTTCTTC
CTCTCCCCTTTCTTTATATGGGTTTAAATTTAACATAAAGTTGTTTTTATAAGGCTTATTTGTGGCTTTAACTTG
TAAGTCTGATTACATCATTATTGTTCCAAATTCATTATCTCTGTAGGAACTTTTAGTTCCATTATATGAACACTG
GATAACCTAATTTTTTTTAATGCTTTAAAAAAATGGCAAAAAGACGTCAGGCCACCCTCATAGTAAGTGGTGTAG
TATTAAAATATTTTCACGGAATTAAAAGTAGCTTGCTGTCAAAGAAACACCTGAGATGAATTGGTGTGAACGAAT
TTTGCAAGTTTAATTTGATTTATTTCAGAGAAAATAGAAAAAACAATGTTAGAAGGTTATTTAAAATGATACTTA
AATAAAGAAAGTGTGAGGTCTACTTTAAAAAAATTCAAATGAAGAGAAAAAGAAAAACAGCATTCTAGAAATGGC
ATTTCTCCTAATTAATTTTCCACTTAATGGAAGATTATCAATTGTCCTATTTTATGATCCCAGGACTGAAGACAG
TTGTGGGATATCTGTCATATTTATCCTGTGAGTCATTGTGAATAATGACATACAGTACTGAAGTAATCTGATTTT
ATTCTTTGGAAATTCAATGCATTGGTCACACTAATAACATCAACATCTGCTATCACTTATCTTTTTAAAACTAAC
CAAAAAAGGCTGGGATTACAGGCATGAGCCACTGCACCCAACTCCTCTTTCGTCTTTCTTTAACACACACTAGGC
TCTTTGTGTATTATGATTCAGTGCTATTTGTAACTGTGTCCCAGTGACCAAATTGCACTCGACTCGATCAGCTGT
TCATCCATTTCGTGTTTTTTCCTGTCAAACATTAATCCAGCAAATATATGAGGTATTTACCAATTTATTTTCTTA
GTATTACAAAATAATTCATTAGCATAAAGTACAATAGTGAAATATTTGAGTTGTTCGGAACCTCAATTAATCCTG
TTTTACATTTCAGACCTAAAGCTGGCAATCAGGAGAAGAAGCACTTTGTTTTAAATGTGGAGAAGATAACACTTG
ATTCCATTTCATTGTCATTAGTGTATTAACCAGCAGGAGAGGTGATGAGCCATTTTTCAAATGAAATACCTTTTA
TTTCCATATAATTTTTTTATTTTAGAGTTCAATAGCTGTTTCTATGATTATCCTCAATTTCCATATGTTACTGAA
TCTGAAAAACATCTTTAAAATTCAAACAGTTCCATTTTCTCTCTTGTAAGTGTTAAATGTGATAAAAGTACATAT
TTTAAATTGTTTTCAGCTCTTGGATATAGCAGCAATAAAAACACTAATTTGTGGGTATTTAAGAAAACCTGGAGA
ATAAACTCATACTTTAAAAGATC

FIGURE 316

MADGGSERADGRIVKMEVDYSATVDQRLPECAKLAKEGRLQEVIETLLSLEKQTRTASDMVSTSRILVAVVKMCY
EAKEWDLLNENIMLLSKRRSQLKQAVAKMVQQCCTYVEEITDLPIKLRLIDTLRMVTEGKIYVEIERARLTKTLA
TIKEQNGDVKEAASILQELQVETYGSMEKKERVEFILEQMRLCLAVKDYIRTQIISKKINTKFFQEENTEKLKLK
YYNLMIQLDQHEGSYLSICKHYRAIYDTPCIQAESEKWQQALKSVVLYVILAPFDNEQSDLVHRISGDKKLEEIP
KYKDLLKLFTTMELMRWSTLVEDYGMELRKGSLESPATDVFGSTEEGEKRWKDLKNRVVEHNIRIMAKYYTRITM
KRMAQLLDLSVDESEAFLSNLVVNKTIFAKVDRLAGIINFQRPKDPNNLLNDWSQKLNSLMSLVNKTTHLIAKEE
MIHNLQ

FIGURE 317

CTGCTCGCGGCCGCCACCGCCGGGCCCCGGCCGTCCCTGGCTCCCCTCCTGCCTCGAGAAGGGCAGGGCTTCTCA
GAGGCTTGGCGGGAAAAAAGAACGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTCGGGGCTTTATCTAA
CTCGCTGTAGTAATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAGCCGGGCGAGCA
GAGCTGCGCTGCGGGCGTCCTGGGAAGGGAGATCCGGAGCGAATAGGGGGCTTCGCCTCTGGCCCAGCCCTCCCG
CTTGATCCCCCAGGCCAGCGGTCCGCAACCCTTGCCGCATCCACGAAACTTTGCCCATAGCAGCGGGCGGGCACT
TTGCACTGGAACTTACAACACCCGAGCAAGGACGCGACTCTCCCGACGCGGGGAGGCTATTCTGCCCATTTGGGG
ACACTTCCCCGCCGCTGCCAGGACCCGCTTCTCTGAAAGGCTCTCCTTGCAGCTGCTTAGACGCTGGATTTTTTT
CGGGTAGTGGAAAACCAGCAGCCTCCCGCGACG**ATG**CCCCTCAACGTTAGCTTCACCAACAGGAACTATGACCTC
GACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGAGGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAG
CTGCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATTCGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGC
CGCCGCTCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTTCTCCCTTCGGGGAGACAACGACGGCGGT
GGCGGGAGCTTCTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTGGGAGGAGACATGGTGAACCAGAGT
TTCATCTGCGACCCGGACGACGAGACCTTCATCAAAAACATCATCATCCAGGACTGTATGTGGAGCGGCTTCTCG
GCCGCCGCCAAGCTCGTCTCAGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAGCGGCAGCCCGAACCCC
GCCCGCGGCCACAGCGTCTGCTCCACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCTCAGAGTGCATC
GACCCCTCGGTGGTCTTCCCCTACCCTCTCAACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACTCCAGC
GCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTG
CTCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTGAGGAGGAACAAGAAGATGAGGAAGAAATCGATGTT
GTTTCTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGTCTGGATCACCTTCTGCTGGAGGCCACAGCAAA
CCTCCTCACAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACATCAGCACAACTACGCAGCGCCTCCCTCC
ACTCGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGTCCTGAGACAGATCAGCAACAAC
CGAAAATGCACCAGCCCCAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCGC
CAGAGGAGGAACGAGCTAAAACGGAGCTTTTTTGCCCTGCGTGACCAGATCCCGGAGTTGGAAAACAATGAAAAG
GCCCCCAAGGTAGTTATCCTTAAAAAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAGCAAAAGCTCATT
TCTGAAGAGGACTTGTTGCGGAAACGACGAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACTCTTGTGCG
TAAGGAAAAGTAAGGAAAACGATTCCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAACTTGTTTCAAATGC
ATGATCAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTTAGCCATAATGTAAACTGCCTCAA
ATTGGACTTTGGGCATAAAAGAACTTTTTTATGCTTACCATCTTTTTTTTTTCTTTAACAGATTTGTATTTAAGA
ATTGTTTTTAAAAAATTTTAA

FIGURE 318

MPLNVSFTNRNYDLDYDSVQPYFYCDEEENFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRRSGLCSPSYV
AVTPFSLRGDNDGGGGSFSTADQLEMVTELLGGDMVNQSFICDPDDETFIKNIIIQDCMWSGFSAAAKLVSEKLA
SYQAARKDSGSPNPARGHSVCSTSSLYLQDLSAAASECIDPSVVFPYPLNDSSSPKSCASQDSSAFSPSSDSLLS
STESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEEIDVVSVEKRQAPGKRSESGSPSAGGHSKPPHSPLVLKRC
HVSTHQHNYAAPPSTRKDYPAAKRVKLDSVRVLRQISNNRKCTSPRSSDTEENVKRRTHNVLERQRRNELKRSFF
ALRDQIPELENNEKAPKVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLRNSCA

FIGURE 319A

ACTCTGGAGTGGGAGTGGGAGCGAGCGCTTCTGCGACTCCAGTTGTGAGAGCCGCAAGGGCATGGGAATTGACGC
CACTCACCGACCCCCAGTCTCAATCTCAACGCTGTGAGGAAACCTCGACTTTGCCAGGTCCCCAAGGGCAGCGGG
GCTCGGCGAGCGAGGCACCCTTCTCCGTCCCCATCCCAATCCAAGCGCTCCTGGCACTGACGACGCCAAGAGACT
CGAGTGGGAGTTAAAGCTTCCAGTGAGGGCAGCAGGTGTCCAGGCCGGGCCTGCGGGTTCCTGTTGACGTCTTGC
CCTAGGCAAAGGTCCCAGTTCCTTCTCGGAGCCGGCTGTCCCGCGCCACTGGAAACCGCACCTCCCCGCAGC**ATG**

GGCACCAGCCTCAGCCCGAACGACCCTTGGCCGCTAAACCCGCTGTCCATCCAGCAGACCACGCTCCTGCTACTC
CTGTCGGTGCTGGCCACTGTGCATGTGGGCCAGCGGCTGCTGAGGCAACGGAGGCGGCAGCTCCGGTCCGCGCCC
CCGGGCCCGTTTGCGTGGCCACTGATCGGAAACGCGGCGGCGGTGGGCCAGGCGGCTCACCTCTCGTTCGCTCGC
CTGGCGCGGCGCTACGGCGACGTTTTCCAGATCCGCCTGGGCAGCTGCCCCATAGTGGTGCTGAATGGCGAGCGC
GCCATCCACCAGGCCCTGGTGCAGCAGGGCTCGGCCTTCGCCGACCGGCCGGCCTTCGCCTCCTTCCGTGTGGTG
TCCGGCGGCCGCAGCATGGCTTTCGGCCACTACTCGGAGCACTGGAAGGTGCAGCGGCGCGCAGCCCACAGCATG
ATGCGCAACTTCTTCACGCGCCAGCCGCGCAGCCGCCAAGTCCTCGAGGGCCACGTGCTGAGCGAGGCGCGCGAG
CTGGTGGCGCTGCTGGTGCGCGGCAGCGCGGACGGCGCCTTCCTCGACCCGAGGCCGCTGACCGTCGTGGCCGTG
GCCAACGTCATGAGTGCCGTGTGTTTCGGCTGCCGCTACAGCCACGACGACCCCGAGTTCCGTGAGCTGCTCAGC
CACAACGAAGAGTTCGGGCGCACGGTGGGCGCGGGCAGCCTGGTGGACGTGATGCCCTGGCTGCAGTACTTCCCC
AACCCGGTGCGCACCGTTTTCCGCGAATTCGAGCAGCTCAACCGCAACTTCAGCAACTTCATCCTGGACAAGTTC
TTGAGGCACTGCGAAAGCCTTCGGCCCGGGGCCGCCCCCCGCGACATGATGGACGCCTTTATCCTCTCTGCGGAA
AAGAAGGCGGCCGGGGACTCGCACGGTGGTGGCGCGCGGCTGGATTTGGAGAACGTACCGGCCACTATCACTGAC
ATCTTCGGCGCCAGCCAGGACACCCTGTCCACCGCGCTGCAGTGGCTGCTCCTCCTCTTCACCAGGTATCCTGAT
GTGCAGACTCGAGTGCAGGCAGAATTGGATCAGGTCGTGGGGAGGGACCGTCTGCCTTGTATGGGTGACCAGCCC
AACCTGCCCTATGTCCTGGCCTTCCTTTATGAAGCCATGCGCTTCTCCAGCTTTGTGCCTGTCACTATTCCTCAT
GCCACCACTGCCAACACCTCTGTCTTGGGCTACCACATTCCCAAGGACACTGTGGTTTTTGTCAACCAGTGGTCT
GTGAATCATGACCCAGTGAAGTGGCCTAACCCGGAGAACTTTGATCCAGCTCGATTCTTGGACAAGGATGGCCTC
ATCAACAAGGACCTGACCAGCAGAGTGATGATTTTTTCAGTGGGCAAAAGGCGGTGCATTGGCGAAGAACTTTCT
AAGATGCAGCTTTTTCTCTTCATCTCCATCCTGGCTCACCAGTGCGATTTCAGGGCCAACCCAAATGAGCCTGCG
AAAATGAATTTCAGTTATGGTCTAACCATTAAACCCAAGTCATTTAAAGTCAATGTCACTCTCAGAGAGTCCATG
GAGCTCCTTGATAGTGCTGTCCAAAATTTACAAGCCAAGGAAACTTGCCAA**TAA**GAAGCAAGAGGCAAGCTGAAA
TTTTAGAAATATTCACATCTTCGGAGATGAGGAGTAAAATTCAGTTTTTTTCCAGTTCCTCTTTTGTGCTGCTTC
TCAATTAGCGTTTAAGGTGAGCATAAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCAT
GAGTAGTGGGCTATGCAGGAGCTTCTGGGAGATTTTTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATTATA
TACATACTGCATCTTGGTTATTTCTGAAGGTAGCATTCTTTGGAGTTAAAATGCACATATAGACACATACACCCA
AACACTTACACCAAACTACTGAATGAAGAAGTATTTTGGTAACCAGGCCATTTTTGGTGGGAATCCAAGATTGGT
CTCCCATATGCAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAAGAGACAGAGACAAG
TAATTTCAGTGTAAAGTGTGTGATTGAAGGTGATAAGGGAAAAGATAAAGACCAGAAATTCCCTTTTCACCTTTT
CAGGAAAATAACTTAGACTCTAGTATTTATGGGTGGATTTATCCTTTTGCCTTCTGGTATACTTCCTTACTTTTA
AGGATAAATCATAAAGTCAGTTGCTCAAAAAGAAATCAATAGTTGAATTAGTGAGTATAGTGGGGTTCCATGAGT
TATCATGAATTTTAAAGTATGCATTATTAAATTGTAAAACTCCAAGGTGATGTTGTACCTCTTTTGCTTGCCAAA
GTACAGAATTTGAATTATCAGCAAAGAAAAAAAAAAAAGCCAGCCAAGCTTTAAATTATGTGACCATAATGTACT
GATTTCAGTAAGTCTCATAGGTTAAAAAAAAAAGTCACCAAATAGTGTGAAATATATTACTTAACTGTCCGTAAG
CAGTATATTAGTATTATCTTGTTCAGGAAAAGGTTGAATAATATATGCCTTGTGTAATATTGAAAATTGAAAAGT
ACAACTAACGCAACCAAGTGTGCTAAAAATGAGCTTGATTAAATCAACCACCTATTTTTGACATGGAAATGAAGC
AGGGTTTCTTTTCTTCACTCAAATTTTGGCGAATCTCAAAATTAGATCCTAAGATGTGTTCTTATTTTTATAACA
TCTTTATTGAAATTCTATTTATAATACAGAATCTTGTTTTGAAAATAACCTAATTAATATATTAAAATTCCAAAT
TCATGGCATGCTTAAATTTTAACTAAATTTTAAAGCCATTCTGATTATTGAGTTCCAGTTGAAGTTAGTGGAAAT
CTGAACATTCTCCTGTGGAAGGCAGAGAAATCTAAGCTGTGTCTGCCCAATGAATAATGGAAAATGCCATGAATT
ACCTGGATGTTCTTTTTACGAGGTGACAAGAGTTGGGGACAGAACTCCCATTACAACTGACCAAGTTTCTCTTCT
AGATGATTTTTTGAAAGTTAACATTAATGCCTGCTTTTTGGAAAGTCAGAATCAGAAGATAGTCTTGGAAGCTGT
TTGGAAAAGACAGTGGAGATGAGGTCAGTTGTGTTTTTTAAGATGGCAATTACTTTGGTAGCTGGGAAAGCATAA

FIGURE 319B

AGCTCAAATGAAATGTATGCATTCACATTTAGAAAAGTGAATTGAAGTTTCAAGTTTTAAAGTTCATTGCAATTA
AACTTCCAAAGAAAGTTCTACAGTGTCCTAAGTGCTAAGTGCTTATTACATTTTATTAAGCTTTTTGGAATCTTT
GTACCAAAATTTTAAAAAAGGGAGTTTTTGATAGTTGTGTGTATGTGTGTGTGGGGTGGGGGGATGGTAAGAGAA
AAGAGAGAAACACTGAAAAGAAGGAAAGATGGTTAAACATTTTCCCACTCATTCTGAATTAATTAATTTGGAGCA
CAAAATTCAAAGCATGGACATTTAGAAGAAAGATGTTTGGCGTAGCAGAGTTAAATCTCAAATAGGCTATTAAAA
AAGTCTACAACATAGCAGATCTGTTTTGTGGTTTGGAATATTAAAAAACTTCATGTAATTTTATTTTAAAATTTC
ATAGCTGTACTTCTTGAATATAAAAAATCATGCCAGTATTTTTAAAGGCATTAGAGTCAACTACACAAAGCAGGC
TTGCCCAGTACATTTAAATTTTTTGGCACTTGCCATTCCAAAATATTATGCCCCACCAAGGCTGAGACAGTGAAT
TTGGGCTGCTGTAGCCTATTTTTTTAGATTGAGAAATGTGTAGCTGCAAAAATAATCATGAACCAATCTGGATGC
CTCATTATGTCAACCAGGTCCAGATGTGCTATAATCTGTTTTTACGTATGTAGGCCCAGTCGTCATCAGATGCTT
GCGGCAAAAGAAAGCTGTGTTTATATGGAAGAAAGTAAGGTGCTTGGAGTTTACCTGGCTTATTTAATATGCTTA
TAACCTAGTTAAAGAAAGGAAAAGAAAACAAAAAACGAATGAAAATAACTGAATTTGGAGGCTGGAGTAATCAGA
TTACTGCTTTAATCAGAAACCCTCATTGTGTTTCTACCGGAGAGAGAATGTATTTGCTGACAACCATTAAAGTCA
GAAGTTTTACTCCAGGTTATTGCAATAAAGTATAATGTTTATTAAATGCTTCATTTGTATGTCAAAGCTTTGACT
CTATAAGCAAATTGCTTTTTTCCAAAACAAAAAGATGTCTCAGGTTTGTTTTGTGAATTTTCTAAAAGCTTTCAT
GTCCCAGAACTTAGCCTTTACCTGTGAAGTGTTACTACAGCCTTAATATTTTCCTAGTAGATCTATATTAGATCA
AATAGTTGCATAGCAGTATATGTTAATTTGTGTGTTTTTAGCTGTGACACAACTGTGTGATTAAAAGGTATACTT
TAGTAGACATTTATAACTCAAGGATACCTTCTTATTTAATCTTTTCTTATTTTTGTACTTTATCATGAATGCTTT
TAGTGTGTGCATAATAGCTACAGTGCATAGTTGTAGACAAAGTACATTCTGGGGAAACAACATTTATATGTAGCC
TTTACTGTTTGATATACCAAATTAAAAAAAAATTGTATCTCATTACTTATACTGGGACACCATTACCAAAATAAT
AAAAATCACTTTCATAATCTTGAAAAAA

FIGURE 320

MGTSLSPNDPWPLNPLSIQQTTLLLLLSVLATVHVGQRLLRQRRRQLRSAPPGPFAWPLIGNAAAVGQAAHLSFA
RLARRYGDVFQIRLGSCPIVVLNGERAIHQALVQQGSAFADRPAFASFRVVSGGRSMAFGHYSEHWKVQRRAAHS
MMRNFFTRQPRSRQVLEGHVLSEARELVALLVRGSADGAFLDPRPLTVVAVANVMSAVCFGCRYSHDDPEFRELL
SHNEEFGRTVGAGSLVDVMPWLQYFPNPVRTVFREFEQLNRNFSNFILDKFLRHCESLRPGAAPRDMMDAFILSA
EKKAAGDSHGGGARLDLENVPATITDIFGASQDTLSTALQWLLLLFTRYPDVQTRVQAELDQVVGRDRLPCMGDQ
PNLPYVLAFLYEAMRFSSFVPVTIPHATTANTSVLGYHIPKDTVVFVNQWSVNHDPVKWPNPENFDPARFLDKDG
LINKDLTSRVMIFSVGKRRCIGEELSKMQLFLFISILAHQCDFRANPNEPAKMNFSYGLTIKPKSFKVNVTLRES
MELLDSAVQNLQAKETCQ

FIGURE 321A

CTCTCACACACACACCCCTCCCCTGCCATCCCTCCCCGGACTCCGGCTCCGGCTCCGATTGCAATTTGCAACC
TCCGCTGCCGTCGCCGCAGCAGCCACCAATTCGCCAGCGGTTCAGGTGGCTCTTGCCTCGATGTCCTAGCCTAGG
GGCCCCCGGGCCGGACTTGGCTGGGCTCCCTTCACCCTCTGCGGAGTC**ATG**AGGGCGAACGACGCTCTGCAGGTG
CTGGGCTTGCTTTTCAGCCTGGCCCGGGGCTCCGAGGTGGGCAACTCTCAGGCAGTGTGTCCTGGGACTCTGAAT
GGCCTGAGTGTGACCGGCGATGCTGAGAACCAATACCAGACACTGTACAAGCTCTACGAGAGGTGTGAGGTGGTG
ATGGGGAACCTTGAGATTGTGCTCACGGGACACAATGCCGACCTCTCCTTCCTGCAGTGGATTCGAGAAGTGACA
GGCTATGTCCTCGTGGCCATGAATGAATTCTCTACTCTACCATTGCCCAACCTCCGCGTGGTGCGAGGGACCCAG
GTCTACGATGGGAAGTTTGCCATCTTCGTCATGTTGAACTATAACACCAACTCCAGCCACGCTCTGCGCCAGCTC
CGCTTGACTCAGCTCACCGAGATTCTGTCAGGGGGTGTTTATATTGAGAAGAACGATAAGCTTTGTCACATGGAC
ACAATTGACTGGAGGGACATCGTGAGGGACCGAGATGCTGAGATAGTGGTGAAGGACAATGGCAGAAGCTGTCCC
CCCTGTCATGAGGTTTGCAAGGGGCGATGCTGGGGTCCTGGATCAGAAGACTGCCAGACATTGACCAAGACCATC
TGTGCTCCTCAGTGTAATGGTCACTGCTTTGGGCCCAACCCCAACCAGTGCTGCCATGATGAGTGTGCCGGGGGC
TGCTCAGGCCCTCAGGACACAGACTGCTTTGCCTGCCGGCACTTCAATGACAGTGGAGCCTGTGTACCTCGCTGT
CCACAGCCTCTTGTCTACAACAAGCTAACTTTCCAGCTGGAACCCAATCCCCACACCAAGTATCAGTATGGAGGA
GTTTGTGTAGCCAGCTGTCCCCATAACTTTGTGGTGGATCAAACATCCTGTGTCAGGGCCTGTCCTCCTGACAAG
ATGGAAGTAGATAAAAATGGGCTCAAGATGTGTGAGCCTTGTGGGGGACTATGTCCCAAAGCCTGTGAGGGAACA
GGCTCTGGGAGCCGCTTCCAGACTGTGGACTCGAGCAACATTGATGGATTTGTGAACTGCACCAAGATCCTGGGC
AACCTGGACTTTCTGATCACCGGCCTCAATGGAGACCCCTGGCACAAGATCCCTGCCCTGGACCCAGAGAAGCTC
AATGTCTTCCGGACAGTACGGGAGATCACAGGTTACCTGAACATCCAGTCCTGGCCGCCCCACATGCACAACTTC
AGTGTTTTTTCCAATTTGACAACCATTGGAGGCAGAAGCCTCTACAACCGGGGCTTCTCATTGTTGATCATGAAG
AACTTGAATGTCACATCTCTGGGCTTCCGATCCCTGAAGGAAATTAGTGCTGGGCGTATCTATATAAGTGCCAAT
AGGCAGCTCTGCTACCACCACTCTTTGAACTGGACCAAGGTGCTTCGGGGGCCTACGGAAGAGCGACTAGACATC
AAGCATAATCGGCCGCGCAGAGACTGCGTGGCAGAGGGCAAAGTGTGTGACCCACTGTGCTCCTCTGGGGGATGC
TGGGGCCCAGGCCCTGGTCAGTGCTTGTCCTGTCGAAATTATAGCCGAGGAGGTGTCTGTGTGACCCACTGCAAC
TTTCTGAATGGGGAGCCTCGAGAATTTGCCCATGAGGCCGAATGCTTCTCCTGCCACCCGGAATGCCAACCCATG
GGGGGCACTGCCACATGCAATGGCTCGGGCTCTGATACTTGTGCTCAATGTGCCCATTTTCGAGATGGGCCCCAC
TGTGTGAGCAGCTGCCCCCATGGAGTCCTAGGTGCCAAGGGCCCAATCTACAAGTACCCAGATGTTCAGAATGAA
TGTCGGCCCTGCCATGAGAACTGCACCCAGGGGTGTAAAGGACCAGAGCTTCAAGACTGTTTAGGACAAACACTG
GTGCTGATCGGCAAAACCCATCTGACAATGGCTTTGACAGTGATAGCAGGATTGGTAGTGATTTTCATGATGCTG
GGCGGCACTTTTCTCTACTGGCGTGGGCGCCGGATTCAGAATAAAAGGGCTATGAGGCGATACTTGGAACGGGGT
GAGAGCATAGAGCCTCTGGACCCCAGTGAGAAGGCTAACAAAGTCTTGGCCAGAATCTTCAAAGAGACAGAGCTA
AGGAAGCTTAAAGTGCTTGGCTCGGGTGTCTTTGGAACTGTGCACAAAGGAGTGTGGATCCCTGAGGGTGAATCA
ATCAAGATTCCAGTCTGCATTAAAGTCATTGAGGACAAGAGTGGACGGCAGAGTTTTCAAGCTGTGACAGATCAT
ATGCTGGCCATTGGCAGCCTGGACCATGCCCACATTGTAAGGCTGCTGGGACTATGCCCAGGGTCATCTCTGCAG
CTTGTCACTCAATATTTGCCTCTGGGTTCTCTGCTGGATCATGTGAGACAACACCGGGGGGCACTGGGGCCACAG
CTGCTGCTCAACTGGGGAGTACAAATTGCCAAGGGAATGTACTACCTTGAGGAACATGGTATGGTGCATAGAAAC
CTGGCTGCCCGAAACGTGCTACTCAAGTCACCCAGTCAGGTTCAGGTGGCAGATTTTGGTGTGGCTGACCTGCTG
CCTCCTGATGATAAGCAGCTGCTATACAGTGAGGCCAAGACTCCAATTAAGTGGATGGCCCTTGAGAGTATCCAC
TTTGGGAAATACACACACCAGAGTGATGTCTGGAGCTATGGTGTGACAGTTTGGGAGTTGATGACCTTCGGGGCA
GAGCCCTATGCAGGGCTACGATTGGCTGAAGTACCAGACCTGCTAGAGAAGGGGGAGCGGTTGGCACAGCCCCAG
ATCTGCACAATTGATGTCTACATGGTGATGGTCAAGTGTTGGATGATTGATGAGAACATTCGCCCAACCTTTAAA
GAACTAGCCAATGAGTTCACCAGGATGGCCCGAGACCCACCACGGTATCTGGTCATAAAGAGAGAGAGTGGGCCT
GGAATAGCCCCTGGGCCAGAGCCCCATGGTCTGACAAACAAGAAGCTAGAGGAAGTAGAGCTGGAGCCAGAACTA
GACCTAGACCTAGACTTGGAAGCAGAGGAGGACAACCTGGCAACCACCACACTGGGCTCCGCCCTCAGCCTACCA
GTTGGAACACTTAATCGGCCACGTGGGAGCCAGAGCCTTTTAAGTCCATCATCTGGATACATGCCCATGAACCAG
GGTAATCTTGGGGGGTCTTGCCAGGAGTCTGCAGTTTCTGGGAGCAGTGAACGGTGCCCCCGTCCAGTCTCTCTA
CACCCAATGCCACGGGGATGCCTGGCATCAGAGTCATCAGAGGGGCATGTAACAGGCTCTGAGGCTGAGCTCCAG
GAGAAAGTGTCAATGTGTAGAAGCCGGAGCAGGAGCCGGAGCCCACGGCCACGCGGAGATAGCGCCTACCATTCC

FIGURE 321B

CAGCGCCACAGTCTGCTGACTCCTGTTACCCCACTCTCCCCACCCGGGTTAGAGGAAGAGGATGTCAACGGTTAT
GTCATGCCAGATACACACCTCAAAGGTACTCCCTCCTCCCGGGAAGGCACCCTTTCTTCAGTGGGTCTCAGTTCT
GTCCTGGGTACTGAAGAAGAAGATGAAGATGAGGAGTATGAATACATGAACCGGAGGAGAAGGCACAGTCCACCT
CATCCCCCTAGGCCAAGTTCCCTTGAGGAGCTGGGTTATGAGTACATGGATGTGGGGTCAGACCTCAGTGCCTCT
CTGGGCAGCACACAGAGTTGCCCACTCCACCCTGTACCCATCATGCCCACTGCAGGCACAACTCCAGATGAAGAC
TATGAATATATGAATCGGCAACGAGATGGAGGTGGTCCTGGGGGTGATTATGCAGCCATGGGGGCCTGCCCAGCA
TCTGAGCAAGGGTATGAAGAGATGAGAGCTTTTCAGGGGCCTGGACATCAGGCCCCCCATGTCCATTATGCCCGC
CTAAAAACTCTACGTAGCTTAGAGGCTACAGACTCTGCCTTTGATAACCCTGATTACTGGCATAGCAGGCTTTTC
CCCAAGGCTAATGCCCAGAGAACG**TAA**CTCCTGCTCCCTGTGGCACTCAGGGAGCATTTAATGGCAGCTAGTGCC
TTTAGAGGGTACCGTCTTCTCCCTATTCCCTCTCTCTCCCAGGTCCCAGCCCCTTTTCCCCAGTCCCAGACAATT
CCATTCAATCTTTGGAGGCTTTTAAACATTTTGACACAAAATTCTTATGGTATGTAGCCAGCTGTGCACTTTCTT
CTCTTTCCCAACCCCAGGAAAGGTTTTCCTTATTTTGTGTGCTTTCCCAGTCCCATTCCTCAGCTTCTTCACAGG
CACTCCTGGAGATATGAAGGATTACTCTCCATATCCCTTCCTCTCAGGCTCTTGACTACTTGGAACTAGGCTCTT
ATGTGTGCCTTTGTTTCCCATCAGACTGTCAAGAAGAGGAAAGGGAGGAAACCTAGCAGAGGAAAGTGTAATTTT
GGTTTATGACTCTTAACCCCCTAGAAAGACAGAAGCTTAAAATCTGTGAAGAAAGAGGTTAGGAGTAGATATTGA
TTACTATCATAATTCAGCACTTAACTATGAGCCAGGCATCATACTAAACTTCACCTACATTATCTCACTTAGTCC
TTTATCATCCTTAAAACAATTCTGTGACATACATATTATCTCATTTTACACAAAGGGAAGTCGGGCATGGTGGCT
CATGCCTGTAATCTCAGCACTTTGGGAGGCTGAGGCAGAAGGATTACCTGAGGCAAGGAGTTTGAGACCAGCTTA
GCCAACATAGTAAGACCCCCATCTC

FIGURE 322

MRANDALQVLGLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGHNADLS
FLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVMLNYNTNSSHALRQLRLTQLTEILSGGVYIE
KNDKLCHMDTIDWRDIVRDRDAEIVVKDNGRSCPPCHEVCKGRCWGPGSEDCQTLTKTICAPQCNGHCFGPNPNQ
CCHDECAGGCSGPQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFVVDQTS
CVRACPPDKMEVDKNGLKMCEPCGGLCPKACEGTGSGSRFQTVDSSNIDGFVNCTKILGNLDFLITGLNGDPWHK
IPALDPEKLNVFRTVREITGYLNIQSWPPHMHNFSVFSNLTTIGGRSLYNRGFSLLIMKNLNVTSLGFRSLKEIS
AGRIYISANRQLCYHHSLNWTKVLRGPTEERLDIKHNRPRRDCVAEGKVCDPLCSSGGCWGPGPGQCLSCRNYSR
GGVCVTHCNFLNGEPREFAHEAECFSCHPECQPMGGTATCNGSGSDTCAQCAHFRDGPHCVSSCPHGVLGAKGPI
YKYPDVQNECRPCHENCTQGCKGPELQDCLGQTLVLIGKTHLTMALTVIAGLVVIFMMLGGTFLYWRGRRIQNKR
AMRRYLERGESIEPLDPSEKANKVLARIFKETELRKLKVLGSGVFGTVHKGVWIPEGESIKIPVCIKVIEDKSGR
QSFQAVTDHMLAIGSLDHAHIVRLLGLCPGSSLQLVTQYLPLGSLLDHVRQHRGALGPQLLLNWGVQIAKGMYYL
EEHGMVHRNLAARNVLLKSPSQVQVADFGVADLLPPDDKQLLYSEAKTPIKWMALESIHFGKYTHQSDVWSYGVT
VWELMTFGAEPYAGLRLAEVPDLLEKGERLAQPQICTIDVYMVMVKCWMIDENIRPTFKELANEFTRMARDPPRY
LVIKRESGPGIAPGPEPHGLTNKKLEEVELEPELDLDLDLEAEEDNLATTTLGSALSLPVGTLNRPRGSQSLLSP
SSGYMPMNQGNLGGSCQESAVSGSSERCPRPVSLHPMPRGCLASESSEGHVTGSEAELQEKVSMCRSRSRSRSPR
PRGDSAYHSQRHSLLTPVTPLSPPGLEEEDVNGYVMPDTHLKGTPSSREGTLSSVGLSSVLGTEEEDEDEEYEYM
NRRRRHSPPHPPRPSSLEELGYEYMDVGSDLSASLGSTQSCPLHPVPIMPTAGTTPDEDYEYMNRQRDGGGPGGD
YAAMGACPASEQGYEEMRAFQGPGHQAPHVHYARLKTLRSLEATDSAFDNPDYWHSRLFPKANAQRT

FIGURE 323A

GTCGGCCGTCCCCTTTAATTTTTAAATACACGGTCCCCTCTTTTCTCTGGGGGGGGCAAGCAAGAAATCAAAGAA
GGAGGAGACAAGCCGTCAATTTTCTCCAAAACAAACCCCACCGGGCAATTTGGTCTCGGGGTAGGGGGAGACGGG
GTGATTGCAAATTATTCCAGGACGAGATCCAGTTCTCCAGCGGGAAAGGGGCAAAGGAACGCCGCGCGTTGGAAG
GGCCAGGGTACGCAGCTCCCCTTGCAGCGCCCGCAGGACCCCCGCAAGCTCGTGCCGGCGAAATCGGAGACCGCC
GATCTGTCCTCGTTCTCTCCTGCACGTCTGGCTGCATTCGGAGGAAGACCTGGGGCGCGAGCGAGCGGCGACAGC
ATGAGCCTGTGCTGACCTCCGCGCGGCGGGCCGAGCCCAGGGCTTTGTCGCGGTACCTGCGCCCAGCCCGCGCCG
CAACTCTGTGCCCAGCTTTTGCAATCTTTTGTTGCAGCGCTGACCGCACCAAGTTAAATGCTCCCTTGCAATTTT
TCTTTTTTTTGTTTGTTTGTTTAATTTTTGGAGAGCTCGCGATCTTGGAAAAGCCTCAGACGCCATCTACAGTTA
AAACGTAGGTAACTGCCCTCTCCCGCACCCCCCCCTTACACGCCCCCCACCCTTTCCACCAAAAAAAGGGGGTGC
AGCGCGGATTCTGGCTGCCGTGCGTCGCCAGCCGGTAGACCCGTGCTTGTTTCCTTTCTCTTTTTGTTTGGCTTC
TAACGCGTTGGGACTGAGTCGCCGCCGTGAGCTCCCCGAAGACTGCACAAACTACCGCGGGCTCCTCCGCCCCGT
CTGCGATTCGGAAGCCGGCCTGGGGGTCGCGTCGGGAGCCCTGCGCTGCAGCTCCGCACCTTAGCAGCCCGGGTA
CTCATCCAGATCCACGCCGGGGACACACACACAGAGTAACTAAAAGTGCGGCGATTCTGCACATCGCCGACTGCT
TTGGGGTAACAAAAAGACCCGAGTTGCCTGCCGACCGAGGACCCCCGGGAGCCGGGCTCGGAGCAGACGAGGTAT
CCGGCGGCGCCCATTTGGGGGCTTCTAACTCTTTCTCCACGCAGCCCCTCTTCTGTCCCCTCCCCTCTCGCTCCC
TTTTAAAATCAGTGGCACCGAGGCGCCTGCAGCCGCACTCGCCAGCGACTCATCTCTCCAGCGGGTTTTTTTTTG
TTTGTCGTGTGCGATCCTCACACTC**ATG**AACATACACAGGTCTACCCCCATCACAATAGCGAGATATGGGAGATC
GCGGAACAAAACCCAGGATTTCGAAGAGTTGTCGTCTATAAGGTCCGCGGAGCCCAGCCAGAGTTTCAGCCCGAA
CCTCGGCTCCCCGAGCCCGCCCGAGACTCCGAACTTGTCGCATTGCGTTTCTTGTATCGGGAAATACTTATTGTT
GGAACCTCTGGAGGGAGACCACGTTTTTCGTGCCGTGCATCTGCACAGCGGAGAGGAGCTGGTGTGCAAGGTGTT
TGATATCAGCTGCTACCAGGAATCCCTGGCACCGTGCTTTTGCCTGTCTGCTCATAGTAACATCAACCAAATCAC
TGAAATTATCCTGGGTGAGACCAAAGCCTATGTGTTCTTTGAGCGAAGCTATGGGGACATGCATTCCTTCGTCCG
CACCTGCAAGAAGCTGAGAGAGGAGGAGGCAGCCAGACTGTTCTACCAGATTGCCTCGGCAGTGGCCCACTGCCA
TGACGGGGGGCTGGTGCTGCGGGACCTCAAGCTGCGGAAATTCATCTTTAAGGACGAAGAGAGGACTCGGGTCAA
GCTGGAAAGCCTGGAAGACGCCTACATTCTGCGGGGAGATGATGATTCCCTCTCCGACAAGCATGGCTGCCCGGC
TTACGTAAGCCCAGAGATCTTGAACACCAGTGGCAGCTACTCGGGCAAAGCAGCCGACGTGTGGAGCCTGGGGGT
GATGCTGTACACCATGTTGGTGGGGCGGTACCCTTTCCATGACATTGAACCCAGCTCCCTCTTCAGCAAGATCCG
GCGTGGCCAGTTCAACATTCCAGAGACTCTGTCGCCCAAGGCCAAGTGCCTCATCCGAAGCATTCTGCGTCGGGA
GCCCTCAGAGCGGCTGACCTCGCAGGAAATTCTGGACCATCCTTGGTTTTCTACAGATTTTAGCGTCTCGAATTC
AGCATATGGTGCTAAGGAAGTGTCTGACCAGCTGGTGCCGGACGTCAACATGGAAGAGAACTTGGACCCTTTCTT
TAAC**TGA**GCTCATGCCCCACGGAGACTTAGCAGGTTCCAGGAGTGAGCGAGGGCAGCGGAAAGGAGTTCTTCCGG
GGGACACGAATTGCCTGGCTGAGTAGCAAGAAAGACACACTCTTAAGTTTCTTGGTTCAGAGCAGGAAAACCTTC
AAGGAGCTGACTGACCACGTAGCATGGGGGCAAGAGGCGTGGGATGGGGATTGGGGTGAGATGGATGGGAGCCCG
CTGGAGCTTGTCTTCCCTAACATAGCCTGGGAGACCACCCCTTGCCACTTGGGCCACTTCCGCCTACCCCACTTT
TCATTTTGTTCCAAAATAGTTGCAGATCCTGACAGAATCAAAACTCTCTGCCTCAAACACACATCCTGGCATCGC
ACTGTTAGCATTTAACTTCTTGTTAGGATTCAGGGAAGGAACAGTTGGCCAAGAATTTTTTTTCTTTTAAACAAG
CCAACCACCTAGCTGGTAATTAATGAGGTTCACTTAAAAAAAAAATTCGGTGCACACAGACTGACATGAAACCTG
GGTGCTACAGTAAAAGAAAACAAAAGTCCAGTTTGTGTCTCTTAATCGCTCACTTCAACTCATTTCTTCTAAATA
AACTATTTAATATCCTGGTCAGGAAATGACATGTTAATGCTTTGCTCCCTGAAGGGGGAAAAAATCTGTCCTTTA
ACAAGCTATTCTGTTTTGTGTCAATTGGGTCCGTGGCAAGGAAGCTATTAGGAAGTCAAACGGTCCAGGATGCAT
TACCTGCTAATCCTTAGGTTTAAAGGGGGAAAGAAAAGGGAAGAAGAAAGGAAAAGAGAAATCCAACTCCTTTTT
CATGTTTTGCTTTTGAACAATGAGGGTTTGTGTGACAGGCATTCCTCTTTGCTGAGATGATAGCAATGGCCTGAG
ATTTTAGCAAGCTCCTGGAGTCTGATGCTTTTGCAGTACTCTGATCGCAACTAAACATTTGTCTTTGTTTTATTA
GAAACTAGTGAAACAAAGCAGGTTGTCCCACATGTATAAAATACAGGGCAGCTATTTAGTTTTCTTTACAGAGAA
TGATCCTTTTAAGGCTTGTAAGGCCCTCTGGTTTGGACAAAAACCCTCAGTAGAGACAAGCGGGAAGGATAATTA
GCTGAAAGCTATGATGATATAAATAAAAACAGCTCTCTATCCCAATACGCACCTTTGTATTTTCAAGAACTCTTC
TATTTATTAAGGAAAATGTCACATTGTGATGTATTAAGCCAGTACTTCAATTACGGGTTGACTTGGGATGACATA
TTACATGCTGTAGTTAACATTTATAATTCTTTTTCCTTGTTTGAGTATTTCTGTCTCTGAAATAACCTTTTACTT

FIGURE 323B

GGCTTTTCTAGATAGCTTTATTTGATTTCGAGTGGCAAAATGTTTTTTATTACGGCTTTTCTATTGCTGTATGAT
ACAGAACTCTTTTGGCATAAATATTTGTGTTCCCAGTACCTCACTTGTTCGGATTTGACTGCCTGTATATGTTTT
GTGAAATGGTCCTGTTTTTGGGTAGGTGACACGTGGACTCTAGTATGTAAATGTTACTTGAATCTGTGCTTCATA
ATAGTGTGTGGCATGTATGTGCAGACTCTTGGATGCTTTATGCCTGCGCACCAGGAGCCCTGTCCTCACGTTCCC
AGGAGGGCGGCTTCACCCTTCGTAACCAGGAGACAAGGCGGCCATGGATTTGCCCTTGATTCTATTTTGCTAATG
GAAGATAGAAAGGAGAGAAGGTTTTTTTTTTTTTTTAACATTCTGAAGATGGTGCTGTGTCAAGAAGGACCTTTT
TTTTCCCCTCTCCCCTATTTTTTAAGTACCTTGGAGGAGGAGAGGTTGGTGACATGCATGGTGGGGATCTATGGC
CTCTGGTGCTTTGTCCTGTATTTGGTTTAATGTTTTTGTCCTAATCTCTTCAATCAATAAAATTGTGCGTATTTA
ACTAAAAAAAAAAAAAAAAAA

FIGURE 324

MNIHRSTPITIARYGRSRNKTQDFEELSSIRSAEPSQSFSPNLGSPSPPETPNLSHCVSCIGKYLLLEPLEGDHV
FRAVHLHSGEELVCKVFDISCYQESLAPCFCLSAHSNINQITEIILGETKAYVFFERSYGDMHSFVRTCKKLREE
EAARLFYQIASAVAHCHDGGLVLRDLKLRKFIFKDEERTRVKLESLEDAYILRGDDDSLSDKHGCPAYVSPEILN
TSGSYSGKAADVWSLGVMLYTMLVGRYPFHDIEPSSLFSKIRRGQFNIPETLSPKAKCLIRSILRREPSERLTSQ
EILDHPWFSTDFSVSNSAYGAKEVSDQLVPDVNMEENLDPFFN

FIGURE 325

CGAGGTTCGGGTCGTGGGGCGGAGGGAAGAGCGGGCGGGCGGGAGGCGCCGGCGCCAGACGCGGAGGGAAGGAGC
TACGAGTAGCCGCCGAGAGGCCGCGGAGCCAGCGACGACCGACCCAGCCGAGCCGCCGCCGCCGCGCCCCCA
TGGCGGCCGCCAAGGACACTCATGAGGACCATGATACTTCCACTGAGAATACAGACGAGTCCAACCATGACCCTC
AGTTTGAGCCAATAGTTTCTCTTCCTGAGCAAGAAATTAAAACACTGGAAGAAGATGAAGAGGAACTTTTTAAAA
TGCGGGCAAAACTGTTCCGATTTGCCTCTGAGAACGATCTCCCAGAATGGAAGGAGCGAGGCACTGGTGACGTCA
AGCTCCTGAAGCACAAGGAGAAAGGGGCCATCCGCCTCCTCATGCGGAGGGACAAGACCCTGAAGATCTGTGCCA
ACCACTACATCACGCCGATGATGGAGCTGAAGCCCAACGCAGGTAGCGACCGTGCCTGGGTCTGGAACACCCACG
CTGACTTCGCCGACGAGTGCCCCAAGCCAGAGCTGCTGGCCATCCGCTTCCTGAATGCTGAGAATGCACAGAAAT
TCAAAACAAAGTTTGAAGAATGCAGGAAAGAGATCGAAGAGAGAGAAAAGAAAGCAGGATCAGGCAAAAATGATC
ATGCCGAAAAAGTGGCGGAAAAGCTAGAAGCTCTCTCGGTGAAGGAGGAGACCAAGGAGGATGCTGAGGAGAAGC
AATAAATCGTCTTATTTTATTTTCTTTTCCTCTCTTTCCTTTCCTTTTTTTAAAAAATTTTACCCTGCCCCTCTT
TTTCGGTTTGTTTTTATTCTTTCATTTTTACAAGGGACGTTATATAAAGAACTGAACTC

FIGURE 326

MAAAKDTHEDHDTSTENTDESNHDPQFEPIVSLPEQEIKTLEEDEEELFKMRAKLFRFASENDLPEWKERGTGDV
KLLKHKEKGAIRLLMRRDKTLKICANHYITPMMELKPNAGSDRAWVWNTHADFADECPKPELLAIRFLNAENAQK
FKTKFEECRKEIEEREKKAGSGKNDHAEKVAEKLEALSVKEETKEDAEEKQ

FIGURE 327

GGGGGCGTGGCCCCGAGAAGGCGGAGACAAGATGGCCGCCCATAGCGCTTGGAGGACCTAAGAGGCGGTGGCCGG
GGCCACGCCCCGGGCAGGAGGGCCGCTCTGTGCGCGCCCGCTCTATGATGCTTGCGCGCGTCCCCCGCGCGCCGC
GCTGCGGGCGGGGCGGGTCTCCGGGATTCCAAGGGCTCGGTTACGGAAGAAGCGCAGCGCCGGCTGGGGAGGGGG
CTGG**ATG**CGCGCGCACCCGGGGGGAGGCCGCTGCTGCCCGGAGCAGGAGGAGGGGGAGAGTGCGGCGGGCGGCAG
CGGCGCTGGCGGCGACTCCGCCATAGAGCAGGGGGGCCAGGGCAGCGCGCTCGCCCCGTCCCCGGTGAGCGGCGT
GCGCAGGGAAGGCGCTCGGGGCGGCGGCCGTGGCCGGGGGCGGTGGAAGCAGGCGGGCCGGGGCGGCGGCGTCTG
TGGCCGTGGCCGGGGCCGGGGCCGTGGCCGGGGACGGGGACGGGGCCGGGGCCGGGGCCGCGGCCGTCCCCCGAG
TGGCGGCAGCGGCCTTGGCGGCGACGGCGGCGGCTGCGGCGGCGGCGGCAGCGGTGGCGGCGGCGCCCCCCGGCG
GGAGCCGGTCCCTTTCCCGTCGGGGAGCGCGGGGCCGGGGCCCAGGGGACCCCGGGCCACGGAGAGCGGGAAGAG
GATGGATTGCCCGGCCCTCCCCCCCGGATGGAAGAAGGAGGAAGTGATCCGAAAATCTGGGCTAAGTGCTGGCAA
GAGCGATGTCTACTACTTCAGTCCAAGTGGTAAGAAGTTCAGAAGCAAGCCTCAGTTGGCAAGGTACCTGGGAAA
TACTGTTGATCTCAGCAGTTTTGACTTCAGAACTGGAAAGATGATGCCTAGTAAATTACAGAAGAACAAACAGAG
ACTGCGAAACGATCCTCTCAATCAAAATAAGCTGCGCTGGAACACTCATCGTCCTGCACCATGGCATGCGCTTTC
AAGACTCTGCTTGCTCATACGCTGTTTGCTCTGCTTGGAATGTGCTTACCCCCTTCCCCTTCATCTGGTGAACTC
CTACTCATCCAAGACCCAGCTTCATTGTCTCCATCTCTGGGAAGCCTGCCCTGCATACTCCAGGCAGAACCAATC
CTTTCCTCCA**TAA**GGGTAAACCAGACTTGAATACAACATTGCCAATTAGACAAACAGCATCAATTTTCAAACAAC
CGGTAACCAAAGTCACAAATCATCCTAGTAATAAAGTGAAATCAGACCCACAACGAATGAATGAACAGCCACGTC
AGCTTTTCTGGGAGAAGAGGCTACAAGGACTTAGTGCATCAGATGTAACAGAACAAATTATAAAAACCATGGAAC
TACCCAAAGGTCTTCAAGGAGTTGGTCCAGGTAGCAATGATGAGACCCTTTTATCTGCTGTTGCCAGTGCTTTGC
ACACAAGCTCTGCGCCAATCACAGGGCAAGTCTCCGCTGCTGTGGAAAAGAACCCTGCTGTTTGGCTTAACACAT
CTCAACCCCTCTGCAAAGCTTTTATTGTCACAGATGAAGACATCAGGAAACAGGAAGAGCGAGTACAGCAAGTAC
GCAAGAAATTGGAAGAAGCACTGATGGCAGACATCTTGTCGCGAGCTGCTGATACAGAAGAGATGGATATTGAAA
TGGACAGTGGAGATGAAGCCTAAGAATATGATCAGGTAACTTTCGACCGACTTTCCCCAAGAGAAAATTCCTAGA
AATTGAACAAAAATGTTTCCACTGGCTTTTGCCTGTAAGAAAAAAAATGTACCCGAGCACATAGAGCTTTTTAAT
AGCACTAACCAATGCCTTTTTAGATGTATTTTTGATGTATATATCTATTATTCAAAAAATCATGTTTATTTTGAG
TCCTAGGACTTAAAATTAGTCTTTTGTAATATCAAGCAGGACCCTAAGATGAAGCTGAGCTTTTGATGCCAGGTG
CAATCTACTGGAAATGTAGCACTTACGTAAAACATTTGTTTCCCCCACAGTTTTAATAAGAACAGATCAGGAATT
CTAAATAAATTTCCCAGTTAAAGATTATTGTGACTTCACTGTATATAAACATATTTTTATACTTTATTGAAAGGG
GACACCTGTACATTCTTCCATCATCACTGTAAAGACAAATAAATGATTATATTCACAGACTGATTGGAATTCTTT
CTGTTGAAAAGCACACACAATAAAGAACCCCTCGTTAGCCTTCCTCTGATTTACATTCAACTCTGATCCCTGGGC
CTTAGGTTTGACATGGAGGTGGAGGAAGATAGCGCATATATTTGCAGTATGAACTATTGCCTCTGGACGTTGTGA
GAATTGTGCTTTCACCAGAATTTCTAAGAATTTCTGCTAAATATCACCTAGCATGTGTAATTTTTTTTCCTTGCC
TGTGACTTGGACTTTTGATAGTTCTATAAGAATAAGGCTTTTTCTTCCCTTGGGCATGAGTCAGATACACAAGGA
CCCTTCAGGTGTTACTAGAAGGCGTCCATGTTTATTGTTTTTTAAAGAATGTTTGGCACTCTCTAACGTCCACTA
GCTTACTGAGTTATCAGGTGCAGGTCAGACTCTTGGCTACAGTGAGAGGCAGCTTCTAGGCAGAGTTGCTTAATG
AAAGGGTTTGTAATACTTTACAAACCATTACCTGTACCTGGCCTGGCCTCCAAAATATTAACATTCTTTTTCTGT
TGAAACTCGCGAGTGTAACTTTCATACCACTTGAATTTATTGATATTTAATTATGAAAACTAGCATTACATTATT
AAACGATTTCTAAAATC

FIGURE 328

MRAHPGGGRCCPEQEEGESAAGGSGAGGDSAIEQGGQGSALAPSPVSGVRREGARGGGRGRGRWKQAGRGGGVCG
RGRGRGRGRGRGRGRGRGRGRPPSGGSGLGGDGGGCGGGGSGGGGAPRREPVPFPSGSAGPGPRGPRATESGKRM
DCPALPPGWKKEEVIRKSGLSAGKSDVYYFSPSGKKFRSKPQLARYLGNTVDLSSFDFRTGKMMPSKLQKNKQRL
RNDPLNQNKLRWNTHRPAPWHALSRLCLLIRCLLCLECAYPLPLHLVNSYSSKTQLHCLHLWEACPAYSRQNQSF
PP

FIGURE 329A

CGGACGCGTGGGAACGAAGCCACCCATTACGGTATGATGATGTCAAACGTGATGCTGATGCTACAGTTACAGCCC
CTGCTGGCGCAGCCTCTCTGATTCTCTCTCCCTCTCCGCGTCCAGTGCTGGGCTTTTTCAGACAAGTGCATCTCC
TAACCAGGTCACATTTCAGCCGCGACCCACTCTCCGCCAGTCACCGGAGGCAGACCGCGGGAGGAGAGCTGAGGA
CAGCCGCGTGCGCTTCGCCAGCAGCGGGGTGGGAGGAAGGACATTAAAATACTGCAGAAGTCAAGACCCCCCAGG
TCGAACCCAGACCACG**ATG**CGCGCCCCGGGCTGCGGGCGGCTGGTGCTGCCGCTGCTGCTCCTGGCCGCGGCAGC
CCTGGCCGAAGGCGACGCCAAGGGGCTCAAGGAGGGCGAGACCCCCGGCAATTTCATGGAGGACGAGCAATGGCT
GTCGTCCATCTCGCAGTACAGCGGCAAGATCAAGCACTGGAACCGCTTCCGAGACGAAGTGGAGGATGACTATAT
CAAGAGCTGGGAGGACAATCAGCAAGGAGATGAAGCCCTGGATACCACCAAGGACCCCTGCCAGAAGGTGAAGTG
CAGCCGCCACAAGGTGTGCATTGCCCAGGGCTACCAGCGGGCCATGTGCATCAGTCGCAAGAAGCTGGAGCACAG
GATCAAGCAGCCGACCGTGAAACTCCATGGAAACAAAGACTCCATCTGCAAGCCCTGCCACATGGCCCAGCTTGC
CTCTGTCTGCGGCTCAGATGGCCACACTTACAGCTCTGTGTGTAAGCTGGAGCAACAGGCGTGCCTGAGCAGCAA
GCAGCTGGCGGTGCGATGCGAGGGCCCCTGCCCCTGCCCCACGGAGCAGGCTGCCACCTCCACCGCCGATGGCAA
ACCAGAGACTTGCACCGGTCAGGACCTGGCTGACCTGGGAGATCGGCTGCGGGACTGGTTCCAGCTCCTTCATGA
GAACTCCAAGCAGAATGGCTCAGCCAGCAGTGTAGCCGGCCCGGCCAGCGGGCTGGACAAGAGCCTGGGGGCCAG
CTGCAAGGACTCCATTGGCTGGATGTTCTCCAAGCTGGACACCAGTGCTGACCTCTTCCTGGACCAGACGGAGCT
GGCCGCCATCAACCTGGACAAGTACGAGGTCTGCATCCGTCCCTTCTTCAACTCCTGTGACACCTACAAGGATGG
CCGGGTCTCTACTGCTGAGTGGTGCTTCTGCTTCTGGAGGGAGAAGCCCCCCTGCCTGGCAGAGCTGGAGCGCAT
CCAGATCCAGGAGGCCGCCAAGAAGAAGCCAGGCATCTTCATCCCGAGCTGCGACGAGGATGGCTACTACCGGAA
GATGCAGTGTGACCAGAGCAGCGGTGACTGCTGGTGTGTGGACCAGCTGGGCCTGGAGCTGACTGGCACGCGCAC
GCATGGGAGCCCCGACTGCGATGACATCGTGGGCTTCTCGGGGGACTTTGGAAGCGGTGTCGGCTGGGAGGATGA
GGAGGAGAAGGAGACGGAGGAAGCAGGCGAGGAGGCCGAGGAGGAGGAGGGCGAGGCAGGCGAGGCTGACGACGG
GGGCTACATCTGG**TAG**ACGCCCTCAGAAGCCGGCTGCCGGGGGGGACTCAACAGCAGAGCTCTGAGCAGCAGCAG
GCAACTTCGAGAACGGATCCAGAAATGCAGTCAGAAGGACCCTGCTCCACCTGGGGGGACTGGGAGTGTGAGTGT
GCATGGCATGTGTGTGGCACAGATGGCTGGGACGGGTGACAGTGTGAGTGCATGTGTGCATGCATGTGTGTATGT
GTGTGTGTGTGTGGCATGCGCTGACAAATGTGTCCTTGATCCACACTGCTCCTGGCAGAGTGAGTAACCCAAAGG
CCCCTTCGGCCTCCTTGTAGCTGTTTTCTTTCCTTTTGTTGTTGGTTTTAAAATACATTCACACACAAATACAAA
TTGACAGGTCAAAATCCATGAAATGAGATCCCCCAGCCGTGTCCTCCAGCCCAGCCCTGACCCCTTGGTTTCTAC
CCTGGCTCCCCTTGGTTTCTACCCTGGCTCAACCGACCCCTGTCTGCCCTTCTCCCTCCTGCTTCTGAGGTCAAG
CTCTGGCCTGCGAGCCTGTCCCCATTGCAAAGGGGAGGGAGGGGCAGGGAGCTGTCTACCAGCTGAGGTCCTCCC
AAAACTGGGCCGATGTGGTGTGACATCCCCACCAGCCTCAGATGAGACGGGCCAGGACGCCCAGCCACAGCAAGC
CCTGTCCCTTTGCCGGATCCCCAAACACTAGAGAAGCTCTCCTAACCCAAGGCGGAGAATGAAGGTGGTGGCGGC
AGAGGAGGAGGGCAGCAGCTGAGAGGCCAGGGACAGGGTGCCTCGCCAAGCTGTCTGAGGTCTGTCCCAGGTGGC
CCAGGTGGTGCAGGTAGAACAGGGTGAGGAGAGGGGGTCGGCTCAACAGGAGGAGGCTGTGGCTGCAGAGCCTGG
AGGAGCTTTTAGGTGTTGAGATGGGGCAGCTCTGAATCCTAGACCCTGGAATAGCCTGTCCCTTTTCTCTGGGTC
TCGTGGTGGAGCCATGATCTGGGCTGCTCTCTTGGGGACACTGGGTGGTGGTTACACAGTTGACCTCTGCCTGGC
TCCCCCTTGGTGCAACTCCTGCCTCCATCCCCCTTGCTGGGGTCCCCTCATCCACTTGAGGGCGCCTGAGGGCCA
GGAGCAGCAGGCAAGGAGCCTGGGTCTAGGCTAAGGGGGTGTGTGCCCACCTCCTCCCTGACCCTTAACACTCCT
GTCCTGCCCAGACCAACAGAGAGAGCTGTCCCTGAGACCCCGGAGAGAAGCAGCTGCCGAAAGCTGCAGCCTTTC
CGCACTCTGAGACCATGATCTTCCTCCTGCCAGGGGAGAGCCACCCACAGGCCATGTCCAGCCCCACTTCCCTCA
GCCCCCAGGGCTTCCTTCTGGCCCCTCTGAGGATTCCCTAGGGCTGCCCCGCAGAGGGGCTTCCCCAAGCTCTGT
TTTGAAGCCTGCAATGTGGAAAAGTGAGAAGTCAGAGGGAACAGGACAGGTGCAGCCGGGCTCTGAGGCCACACC
TCACACCTCGCTGTTCCCCAACATCCCCTGAGCAGTGTGAGCTCATCTCACCAGATGAGAAGAGGCCCTGTGCAT
TTCTTTTGTTTGTTTGTTGCTGTTTTCCCCCACCCATCCAGTTCTCCTCAGCAAAGCAAATTCCTTAACACCTTT
GGTGGAGAATTTCTTACCCAGACTTGGGGCTGTGATGCCCTTCAGTGCGTGGTGAGTGCAGCGTGTGTGCGTGTG
CCTGTGTGTGAACCTGGGGGCCATCCTGGTGGCCTGGGAGCGTGAGGAGAGGCCCCCTGTGTGCTGGGTGAGTGG
TGGGTGTGGGGTCAATGCAGTGAGGCTCTCTGGGTGAGGCTCCCAACCTGGCAGTCCCCAGCCTCCCAGCATCTG
TGAGCGTCTGTTGGACTTTACAGAAGAGCCTCATCCCGTCTGCCCCTCACTCTGCCCTGGAATCAACATCTTCCG
AGTCCTTCTTGGGGGAAATAGCAGAGCCCCACTTAACTCCATAAACTGCTTCCCATTCCGCAGCCCAGTTCTGAT

FIGURE 329B

TGTTGAGGTGTCGCGTCGTTCCAGGTCCCCCAGTCCCCTCTTTCTCCTGTCCTCTCTCTGTCCTTCACCTCCCCA
CTCCAGCCCCGGCTCAGTTCAGGGAAATGCTGTTCCATATCAGCCCTCTGCTCTCTGAGGCAGCCGCGCCTCTGA
CTCGGAGCTACTTGAAACTTCTGCTCTTGCTAGGATTGGAGTCTACCTATCTCTTCCATTTGTCCCAGCTGGAGT
TCTGGAACTTTCCTCCTCGGGGTGGGGGTGGGGGTTGTTAAGGATGCTGGGGGGCCTGGGGAAGGAAGGAGTTCA
GAGGAAGGGTGTCCCCTGTCCTCTTGATGTCACCCTCCGCTCCTGGGACACGTGCTCTCTCTGTCTCTGGGTCTT
CTGGCTGTGCACGTTTGTGTGTCCTTGTAAATATGTTTTAGGAAGAAAGCAAAAGGGACTGAACTAGCCTCTGGT
AGGATTGCAGGGGTCCAGCCTTGCCTGTTTCCGAAGCCCCCACACTGCCTTTCGCCCCACTGAGACTGGTCCCCT
CAAAAGGTAGACAAAACAGCAGCTCCCTGTGGAGCTGAAGGGCGGCCTCAAAGTGGCTTTTTGTTAGACAAGGTT
AAGGTTTCCTCATGAGCAAGGTTGCAGATCGGTCCTTCCTCAGCTCCTTGATTTGTGACCTTGACCAAGGGGCCT
GCCACCCAGCCCCTCCAGTGCCCTCTCCTCGATGCCTCGCTCCTTCCTGCCCCCACTCCCCTGGCTTAGGCAGGT
AGGGGAATTAGGGCCATGCTGGAAGAAGCTTAACCATGTGTTCAAAGAACGGTTTCTTGCTTGCTTGGTCCTGGA
ACTCCCCTTGGCTGCCCCAGGCCTCCTTGGCCCATGGGTGCTGGGGGAGGTGGATGTCAGATCTGGTAGGTTGCA
GCAGAGAAAATAAATGTGCCTTGAGAGACCACTCAGAGAGGGTCCAAGGGTGATGGAGAAGGAAGCATGGCCTGG
GAGCTTGGAAGGGAGGGGTGGTGGGTGGCGGCATCTTGACTGCCCCCTGTTGTCCCACACGTGGGGGGTGGTCAC
CCCCCTTCACTCCAGCCCGCCTGCCTTCAGCCTTCCATGAGCTTCACCTGCTTCCAACTTCACTTTGGAGGGGGT
GGGGTCCGTTGGCATCAACACGGGGACCCTCTGCTTCACCAAAGCCCGAGCCCTCAGCCCCTGGGGAGAACAAAT
GGCTGAGCTTTGATACCTGGGGTCGTCGAGAGGCTGCGGGCTGGCGGCAGTCCCAGGGGAGAGACACCACAGAAG
GAGACCCAGACATCCCGAGGAAGTTCCCAGCAGAGCAAACTGCTTTCCAGCCTGAAGCCTGCTTAAACTGTGTGA
TGTGCAATAACTGAGCTTAGAGTTAGGAATTGTGTTCAAGTGCTTGGATTTCCGTCTGTAGATTTAACTGCTGAA
ATTGTATCTCTCAGTAATTTTAGATGTCTTTTAAAAAATTGAAAAACAAAGTGTTAGACTGTGTGCGTGTGCGTT
GATGGGCACTCAAGAGTCCCGTGAGTCATCCAGCCCTGCCTTTCCCCTGCGCCCCCATCCTCTCACGTCCCGCCC
TGCCTCCACTTGGGGACCCTGCCTCGTGTCGTCTTTATCTGCCTATTACTCAGCCTAAGGAAACAAGTACACTCC
ACACATGCATAAAGGAAATCAAATGTTATTTTTAAGAAAATGGAAAATAAAAACTTTATAAACACC

FIGURE 330

MRAPGCGRLVLPLLLLAAAALAEGDAKGLKEGETPGNFMEDEQWLSSISQYSGKIKHWNRFRDEVEDDYIKSWED
NQQGDEALDTTKDPCQKVKCSRHKVCIAQGYQRAMCISRKKLEHRIKQPTVKLHGNKDSICKPCHMAQLASVCGS
DGHTYSSVCKLEQQACLSSKQLAVRCEGPCPCPTEQAATSTADGKPETCTGQDLADLGDRLRDWFQLLHENSKQN
GSASSVAGPASGLDKSLGASCKDSIGWMFSKLDTSADLFLDQTELAAINLDKYEVCIRPFFNSCDTYKDGRVSTA
EWCFCFWREKPPCLAELERIQIQEAAKKKPGIFIPSCDEDGYYRKMQCDQSSGDCWCVDQLGLELTGTRTHGSPD
CDDIVGFSGDFGSGVGWEDEEEKETEEAGEEAEEEEGEAGEADDGGYIW

FIGURE 331

TCTTGACTCACGCCTTCGCCGTAGCATCTTTCGCAGCGGACCGAAGAGAAGAAAAGTAGGCCAGAGCCGAACTCT
CTTCCTGCCAAG**ATG**TCTATTGGTGTGCCGATTAAAGTACTGCATGAGGCCGAGGGCCACATTGTGACATGTGAG
ACGAACACCGGTGAGGTATATCGGGGGAAGCTCATTGAAGCAGAGGACAACATGAACTGCCAGATGTCCAACATC
ACAGTCACATACAGAGATGGCCGAGTGGCACAGCTGGAGCAGGTATACATCCGTGGCAGCAAAATCCGCTTTCTG
ATTTTGCCTGACATGCTGAAGAACGCACCCATGTTAAAGAGCATGAAAAATAAAAACCAAGGCTCAGGGGCTGGC
CGAGGAAAAGCTGCCATTCTCAAGGCCCAAGTGGCCGCAAGAGGAAGAGGACGTGGAATGGGACGTGGAAACATC
TTTCAAAAGCGAAGA**TAA**TTTTCTAAGTTGAACAGAACTTTGTCCTTTTTTCTTTCAGGTTATCTGAGTTCATTG
GAGTGGGTGCTTGTGCATATATCTAGGTATCTTTTGCCATCTTTCTCTTTAGATCAGGGGAAATGTTTAAGCTAA
ATAAATCTGGGGGGTTTTTTGTTCTG

FIGURE 332

MSIGVPIKVLHEAEGHIVTCETNTGEVYRGKLIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGSKIRFLILPD
MLKNAPMLKSMKNKNQGSGAGRGKAAILKAQVAARGRGRGMGRGNIFQKRR

FIGURE 333

CCTGCGTGGCTGGGCTGCTCGGGTTAGATCGTCAGGAAAAGCCTAAAGATTAGACTGTAAGAAAAGAAAATAGAA
GCC**ATG**TTTCGAAGACCTGTATTACAGGTACTTCGTCAGTTTGTAAGACATGAGTCCGAAACAACTACCAGTTTG
GTTCTTGAAAGATCCCTGAATCGTGTGCACTTACTTGGGCGAGTGGGTCAGGACCCTGTCTTGAGACAGGTGGAA
GGAAAAAATCCAGTCACAATATTTTCTCTAGCAACTAATGAGATGTGGCGATCAGGGGATAGTGAAGTTTACCAA
CTGGGTGATGTCAGTCAAAAGACAACATGGCACAGAATATCAGTATTCCGGCCAGGCCTCAGAGACGTGGCATAT
CAATATGTGAAAAAGGGGTCTCGAATTTATTTGGAAGGGAAAATAGACTATGGTGAATACATGGATAAAAATAAT
GTGAGGCGACAAGCAACAACAATCATAGCTGATAATATTATATTTCTGAGTGACCAGACGAAAGAGAAGGAG**TAG**

AAAGGATGATTCTTCTTTGGCCATCATTTGGTACAGTCTCATTTCCAAGTCATGTATAATCTTTATGGCTTCCAA
GGACAAGAATTAAAATACTCTTTTACGT

DEMANDE OU BREVET VOLUMINEUX

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