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(54) Title: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

(57) Abrégé/Abstract:
The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

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COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FIELD OF THE INVENTION

The present invention is directed to compositions of matter useful for the diagnosis and treatment of tumor in mammals and to methods of using those compositions of matter for the same.

BACKGROUND OF THE INVENTION

Malignant tumors (cancers) are the second leading cause of death in the United States, after heart disease (Boring et al., *CA Cancel J. Clin.* 43:7 (1993)). Cancer is characterized by the increase in the number of abnormal, or neoplastic, cells derived from a normal tissue which proliferate to form a tumor mass, the invasion of adjacent tissues by these neoplastic tumor cells, and the generation of malignant cells which eventually spread via the blood or lymphatic system to regional lymph nodes and to distant sites via a process called metastasis. In a cancerous state, a cell proliferates under conditions in which normal cells would not grow. Cancer manifests itself in a wide variety of forms, characterized by different degrees of invasiveness and aggressiveness.

In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise membrane-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such membrane-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies. In this regard, it is noted that antibody-based therapy has proved very effective in the treatment of certain cancers. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. More specifically, HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells.

In other attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify (1) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (2) polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (3) polypeptides whose expression is specifically limited

to only a single (or very limited number of different) tissue type(s) in both the cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue). Such polypeptides may remain intracellularly located or may be secreted by the cancer cell. Moreover, such polypeptides may be expressed not by the cancer cell itself, but rather by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Such secreted polypeptides are often proteins that provide cancer cells with a growth advantage over normal cells and include such things as, for example, angiogenic factors, cellular adhesion factors, growth factors, and the like. Identification of antagonists of such non-membrane associated polypeptides would be expected to serve as effective therapeutic agents for the treatment of such cancers. Furthermore, identification of the expression pattern of such polypeptides would be useful for the diagnosis of particular cancers in mammals.

Despite the above identified advances in mammalian cancer therapy, there is a great need for additional diagnostic and therapeutic agents capable of detecting the presence of tumor in a mammal and for effectively inhibiting neoplastic cell growth, respectively. Accordingly, it is an objective of the present invention to identify: (1) cell membrane-associated polypeptides that are more abundantly expressed on one or more type(s) of cancer cell(s) as compared to on normal cells or on other different cancer cells, (2) non-membrane-associated polypeptides that are specifically produced by one or more particular type(s) of cancer cell(s) (or by other cells that produce polypeptides having a potentiating effect on the growth of cancer cells) as compared to by one or more particular type(s) of non-cancerous normal cell(s), (3) non-membrane-associated polypeptides that are produced by cancer cells at an expression level that is significantly higher than that of one or more normal non-cancerous cell(s), or (4) polypeptides whose expression is specifically limited to only a single (or very limited number of different) tissue type(s) in both a cancerous and non-cancerous state (e.g., normal prostate and prostate tumor tissue), and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals. It is also an objective of the present invention to identify cell membrane-associated, secreted or intracellular polypeptides whose expression is limited to a single or very limited number of tissues, and to use those polypeptides, and their encoding nucleic acids, to produce compositions of matter useful in the therapeutic treatment and diagnostic detection of cancer in mammals.

SUMMARY OF THE INVENTION

A. Embodiments

In the present specification, Applicants describe for the first time the identification of various cellular polypeptides (and their encoding nucleic acids or fragments thereof) which are expressed to a greater degree on the surface of or by one or more types of cancer cell(s) as compared to on the surface of or by one or more types of normal non-cancer cells. Alternatively, such polypeptides are expressed by cells which produce and/or secrete polypeptides having a potentiating or growth-enhancing effect on cancer cells. Again alternatively, such polypeptides may not be overexpressed by tumor cells as compared to normal cells of the same tissue type, but rather may be specifically expressed by both tumor cells and normal cells of only a single or very limited

number of tissue types (preferably tissues which are not essential for life, e.g., prostate, etc.). All of the above polypeptides are herein referred to as Tumor-associated Antigenic Target polypeptides ("TAT" polypeptides) and are expected to serve as effective targets for cancer therapy and diagnosis in mammals.

Accordingly, in one embodiment of the present invention, the invention provides an isolated nucleic acid molecule having a nucleotide sequence that encodes a tumor-associated antigenic target polypeptide or fragment thereof (a "TAT" polypeptide).

In certain aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule encoding a full-length TAT polypeptide having an amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide 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%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule comprising the coding sequence of a full-length TAT polypeptide cDNA as disclosed herein, the coding sequence of a TAT polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In further aspects, 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%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% nucleic acid sequence identity, to (a) a DNA molecule that encodes the same mature polypeptide encoded by the full-length coding region of any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect of the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a TAT 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(s) are disclosed herein. Therefore, soluble extracellular domains of the herein described TAT polypeptides are contemplated.

In other aspects, the present invention is directed to isolated nucleic acid molecules which hybridize to (a) a nucleotide sequence encoding a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular

domain of a transmembrane TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein, or (b) the complement of the nucleotide sequence of (a). In this regard, an embodiment of the present invention is directed to fragments of a full-length TAT polypeptide coding sequence, or the complement thereof, as disclosed herein, that may find use as, for example, hybridization probes useful as, for example, diagnostic probes, antisense oligonucleotide probes, or for encoding fragments of a full-length TAT polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-TAT polypeptide antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide. Such nucleic acid fragments are usually at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 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 TAT polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the TAT polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which TAT polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such novel fragments of TAT polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the TAT polypeptide fragments encoded by these nucleotide molecule fragments, preferably those TAT polypeptide fragments that comprise a binding site for an anti-TAT antibody, a TAT binding oligopeptide or other small organic molecule that binds to a TAT polypeptide.

In another embodiment, the invention provides isolated TAT polypeptides encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated TAT polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity, to a TAT polypeptide having a full-length amino acid sequence as disclosed herein, a TAT polypeptide amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane TAT polypeptide protein, with or without the signal peptide, as disclosed herein, an amino acid sequence encoded by any of the nucleic acid sequences disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated TAT polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid

sequence identity, to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated TAT polypeptide without the N-terminal signal sequence and/or without the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore 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 TAT polypeptide and recovering the TAT polypeptide from the cell culture.

Another aspect of the invention provides an isolated TAT 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 TAT polypeptide and recovering the TAT polypeptide from the cell culture.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cells comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli* cells, or yeast cells. 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 isolated chimeric polypeptides comprising any of the herein described TAT polypeptides fused to a heterologous (non-TAT) polypeptide. Example of such chimeric molecules comprise any of the herein described TAT polypeptides fused to a heterologous polypeptide such as, for example, an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, single-chain antibody or antibody that competitively inhibits the binding of an anti-TAT polypeptide antibody to its respective antigenic epitope. Antibodies of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the antibodies of the present invention may be detectably labeled, attached to a solid support, or the like.

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

In another embodiment, the invention provides oligopeptides ("TAT binding oligopeptides") which

bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding oligopeptides of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding oligopeptides of the present invention may optionally be produced in CHO cells or bacterial cells and preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding oligopeptides of the present invention may be detectably labeled, attached to a solid support, or the like.

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

In another embodiment, the invention provides small organic molecules ("TAT binding organic molecules") which bind, preferably specifically, to any of the above or below described TAT polypeptides. Optionally, the TAT binding organic molecules of the present invention may be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The TAT binding organic molecules of the present invention preferably induce death of a cell to which they bind. For diagnostic purposes, the TAT binding organic molecules of the present invention may be detectably labeled, attached to a solid support, or the like.

In a still further embodiment, the invention concerns a composition of matter comprising a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

In yet another embodiment, the invention concerns an article of manufacture comprising a container and a composition of matter contained within the container, wherein the composition of matter may comprise a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein. The article may further optionally comprise a label affixed to the container, or a package insert included with the container, that refers to the use of the composition of matter for the therapeutic treatment or diagnostic detection of a tumor.

Another embodiment of the present invention is directed to the use of a TAT polypeptide as described herein, a chimeric TAT polypeptide as described herein, an anti-TAT polypeptide antibody as described herein, a TAT binding oligopeptide as described herein, or a TAT binding organic molecule as described herein, for the preparation of a medicament useful in the treatment of a condition which is responsive to the TAT polypeptide, chimeric TAT polypeptide, anti-TAT polypeptide antibody, TAT binding oligopeptide, or TAT

binding organic molecule.

B. Additional Embodiments

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cell that expresses a TAT polypeptide, wherein the method comprises contacting the cell with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, and wherein the binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes inhibition of the growth of the cell expressing the TAT polypeptide. In preferred embodiments, the cell is a cancer cell and binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide causes death of the cell expressing the TAT polypeptide. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of determining the presence of a TAT polypeptide in a sample suspected of containing the TAT polypeptide, wherein the method comprises exposing the sample to an antibody, oligopeptide or small organic molecule that binds to the TAT polypeptide and determining binding of the antibody, oligopeptide or organic molecule to the TAT polypeptide in the sample, wherein the presence of such binding is indicative of the presence of the TAT polypeptide in the sample. Optionally, the sample may contain cells (which may be cancer cells) suspected of expressing the TAT polypeptide. The antibody, TAT binding oligopeptide or TAT binding organic molecule employed in the method may optionally be detectably labeled, attached to a solid support, or the like.

A further embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises detecting the level of expression of a gene encoding a TAT polypeptide (a) in a test sample of tissue cells obtained from said mammal, and (b) in a control sample of known normal non-cancerous cells of the same tissue origin or type, wherein a higher level of expression of the

TAT polypeptide in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

Another embodiment of the present invention is directed to a method of diagnosing the presence of a tumor in a mammal, wherein the method comprises (a) contacting a test sample comprising tissue cells obtained from the mammal with an antibody, oligopeptide or small organic molecule that binds to a TAT polypeptide and (b) detecting the formation of a complex between the antibody, oligopeptide or small organic molecule and the TAT polypeptide in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in the mammal. Optionally, the antibody, TAT binding oligopeptide or TAT binding organic molecule employed is detectably labeled, attached to a solid support, or the like, and/or the test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

Yet another embodiment of the present invention is directed to a method for treating or preventing a cell proliferative disorder associated with altered, preferably increased, expression or activity of a TAT polypeptide, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a TAT polypeptide. Preferably, the cell proliferative disorder is cancer and the antagonist of the TAT polypeptide is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide. Effective treatment or prevention of the cell proliferative disorder may be a result of direct killing or growth inhibition of cells that express a TAT polypeptide or by antagonizing the cell growth potentiating activity of a TAT polypeptide.

Yet another embodiment of the present invention is directed to a method of binding an antibody, oligopeptide or small organic molecule to a cell that expresses a TAT polypeptide, wherein the method comprises contacting a cell that expresses a TAT polypeptide with said antibody, oligopeptide or small organic molecule under conditions which are suitable for binding of the antibody, oligopeptide or small organic molecule to said TAT polypeptide and allowing binding therebetween.

Other embodiments of the present invention are directed to the use of (a) a TAT polypeptide, (b) a nucleic acid encoding a TAT polypeptide or a vector or host cell comprising that nucleic acid, (c) an anti-TAT polypeptide antibody, (d) a TAT-binding oligopeptide, or (e) a TAT-binding small organic molecule in the preparation of a medicament useful for (i) the therapeutic treatment or diagnostic detection of a cancer or tumor, or (ii) the therapeutic treatment or prevention of a cell proliferative disorder.

Another embodiment of the present invention is directed to a method for inhibiting the growth of a cancer cell, wherein the growth of said cancer cell is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide (wherein the TAT polypeptide may be expressed either by the cancer cell itself or a cell that produces polypeptide(s) that have a growth potentiating effect on cancer cells), wherein the method comprises contacting the TAT polypeptide with an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth-potentiating activity of the TAT polypeptide and, in turn, inhibiting the growth of the cancer cell. Preferably the growth of the cancer cell is completely inhibited. Even more preferably, binding of the antibody, oligopeptide or small organic molecule to the TAT polypeptide induces the death of the cancer cell. Optionally, the antibody is a monoclonal antibody, antibody fragment,

chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and TAT binding oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet another embodiment of the present invention is directed to a method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon the growth potentiating effect(s) of a TAT polypeptide, wherein the method comprises administering to the mammal a therapeutically effective amount of an antibody, an oligopeptide or a small organic molecule that binds to the TAT polypeptide, thereby antagonizing the growth potentiating activity of said TAT polypeptide and resulting in the effective therapeutic treatment of the tumor. Optionally, the antibody is a monoclonal antibody, antibody fragment, chimeric antibody, humanized antibody, or single-chain antibody. Antibodies, TAT binding oligopeptides and TAT binding organic molecules employed in the methods of the present invention may optionally be conjugated to a growth inhibitory agent or cytotoxic agent such as a toxin, including, for example, a maytansinoid or calicheamicin, an antibiotic, a radioactive isotope, a nucleolytic enzyme, or the like. The antibodies and oligopeptides employed in the methods of the present invention may optionally be produced in CHO cells or bacterial cells.

Yet further embodiments of the present invention will be evident to the skilled artisan upon a reading of the present specification.

BRIEF DESCRIPTION OF THE DRAWINGS

In the list of figures for the present application, specific cDNA sequences which are upregulated in certain tumor tissues as compared to their normal tissue counterparts are individually identified with a designation beginning with the letters "DNA" followed by a specific numerical designation. A full or partial length protein sequence that is encoded by a cDNA sequence identified and shown herein is individually identified with a designation beginning with the letters "PRO" followed by a specific numerical designation. Figures showing encoded amino acid sequences immediately follow the figure showing the cDNA sequence encoding that specific amino acid sequence. If start and/or stop codons have been identified in a cDNA sequence shown in the attached figures, they are shown in bold and underlined font.

List of Figures

Figure 1: DNA323717, XM_059201, gen.XM_059201
Figure 2: DNA323718, XM_117159, gen.XM_117159
Figure 3: DNA323719, XM_114062, gen.XM_114062
Figure 4: DNA323720, XM_086178, gen.XM_086178
Figure 5: PRO80480
Figure 6: DNA323721, XM_051556, gen.XM_051556
Figure 7: PRO80481
Figure 8: DNA323722, NM_017891, gen.NM_017891
Figure 9: PRO80482
Figure 10: DNA323723, NM_018188, gen.NM_018188
Figure 11: PRO80483
Figure 12: DNA323724, NM_002617, gen.NM_002617
Figure 13: PRO23746
Figure 14: DNA323725, XM_049742, gen.XM_049742
Figure 15: DNA323726, NM_033534, gen.NM_033534
Figure 16: PRO80484
Figure 17: DNA323727, NM_014188, gen.NM_014188
Figure 18: PRO80485
Figure 19: DNA323728, XM_086180, gen.XM_086180
Figure 20: DNA323729, XM_166599, gen.XM_166599
Figure 21: PRO80487
Figure 22: DNA323730, NM_017900, gen.NM_017900
Figure 23: PRO80488
Figure 24: DNA323731, XM_001589, gen.XM_001589
Figure 25: PRO80489
Figure 26: DNA323732, NM_016176, gen.NM_016176
Figure 27: PRO80490
Figure 28: DNA323733, XM_117692, gen.XM_117692
Figure 29: DNA323734, XM_086360, gen.XM_086360
Figure 30: PRO80492
Figure 31: DNA287173, NM_001428, gen.NM_001428
Figure 32: PRO69463
Figure 33: DNA323735, XM_001299, gen.XM_001299
Figure 34: DNA323736, NM_000983, gen.NM_000983
Figure 35: PRO80493
Figure 36A-B: DNA227821, NM_014851, gen.NM_014851
Figure 37: PRO38284
Figure 38A-B: DNA323737, XM_086204, gen.XM_086204
Figure 39: PRO80494
Figure 40: DNA323738, XM_030920, gen.XM_030920
Figure 41: DNA323739, NM_018948, gen.NM_018948
Figure 42: DNA273712, NM_007262, gen.NM_007262
Figure 43: PRO61679
Figure 44: DNA151148, NM_004781, gen.NM_004781
Figure 45: PRO12618
Figure 46: DNA323740, XM_086151, gen.XM_086151
Figure 47: PRO80497
Figure 48: DNA171408, NM_004401, gen.NM_004401
Figure 49: PRO20136
Figure 50: DNA323741, NM_003132, gen.NM_003132
Figure 51: PRO80498
Figure 52: DNA323742, XM_086586, gen.XM_086586
Figure 53: PRO80499
Figure 54: DNA323743, XM_086587, gen.XM_086587
Figure 55: DNA323744, XM_059230, gen.XM_059230
Figure 56: PRO80501
Figure 57A-B: DNA323745, XM_048780, gen.XM_048780
Figure 58: DNA323746, XM_053183, gen.XM_053183
Figure 59: DNA323747, XM_165442, gen.XM_165442
Figure 60: DNA323748, NM_033440, gen.NM_033440
Figure 61: PRO2269
Figure 62: DNA323749, NM_024329, gen.NM_024329
Figure 63: PRO80505
Figure 64: DNA323750, XM_018205, gen.XM_018205
Figure 65: PRO80506
Figure 66: DNA323751, XM_011650, gen.XM_011650
Figure 67: DNA323752, XM_017315, gen.XM_017315
Figure 68A-B: DNA323753, XM_030470, gen.XM_030470
Figure 69: DNA323754, NM_004930, gen.NM_004930
Figure 70: PRO80510
Figure 71: DNA323755, NM_003689, gen.NM_003689
Figure 72: PRO80511
Figure 73: DNA323756, NM_016183, gen.NM_016183
Figure 74: PRO80512
Figure 75: DNA323757, XM_015234, gen.XM_015234
Figure 76A-B: DNA323758, XM_027916, gen.XM_027916
Figure 77: DNA323759, XM_033683, gen.XM_033683
Figure 78: DNA323760, XM_001826, gen.XM_001826
Figure 79: DNA323761, XM_033654, gen.XM_033654
Figure 80: PRO80517
Figure 81: DNA323762, NM_001791, gen.NM_001791
Figure 82: PRO26194
Figure 83: DNA323763, NM_005826, gen.NM_005826
Figure 84: PRO60815
Figure 85: DNA323764, XM_086357, gen.XM_086357
Figure 86: PRO80518
Figure 87: DNA323765, NM_000975, gen.NM_000975
Figure 88: PRO80519
Figure 89: DNA323766, NM_007260, gen.NM_007260
Figure 90: PRO61250
Figure 91: DNA323767, NM_017761, gen.NM_017761
Figure 92: PRO80520
Figure 93: DNA323768, NM_006625, gen.NM_006625
Figure 94: PRO22196
Figure 95: DNA323769, NM_054016, gen.NM_054016
Figure 96: PRO80521
Figure 97: DNA323770, XM_086375, gen.XM_086375
Figure 98: DNA323771, XM_006290, gen.XM_006290
Figure 99: DNA323772, NM_015484, gen.NM_015484
Figure 100: PRO80524
Figure 101A-B: DNA323773, XM_001616, gen.XM_001616
Figure 102: DNA323774, XM_058240,

gen.XM_058240
Figure 103: DNA323775, XM_059117, gen.XM_059117
Figure 104: PRO80527
Figure 105: DNA226262, NM_005563, gen.NM_005563
Figure 106: PRO36725
Figure 107: DNA323776, NM_022778, gen.NM_022778
Figure 108: PRO80528
Figure 109: DNA323777, XM_017846, gen.XM_017846
Figure 110: DNA323778, NM_005517, gen.NM_005517
Figure 111: PRO80530
Figure 112A-C: DNA323779, XM_046918, gen.XM_046918
Figure 113: DNA323780, XM_002114, gen.XM_002114
Figure 114: DNA323781, XM_059066, gen.XM_059066
Figure 115: PRO80533
Figure 116: DNA323782, NM_018066, gen.NM_018066
Figure 117: PRO80534
Figure 118: DNA323783, NM_006600, gen.NM_006600
Figure 119: PRO80535
Figure 120: DNA323784, XM_059067, gen.XM_059067
Figure 121: PRO80536
Figure 122: DNA323785, NM_032872, gen.NM_032872
Figure 123: PRO80537
Figure 124: DNA196349, NM_006990, gen.NM_006990
Figure 125: PRO24856
Figure 126: DNA323788, XM_001640, gen.XM_001640
Figure 127: DNA323789, NM_002946, gen.NM_002946
Figure 128: PRO59099
Figure 129: DNA323790, XM_114044, gen.XM_114044
Figure 130: DNA323791, XM_059088, gen.XM_059088
Figure 131: DNA323792, NM_031459, gen.NM_031459
Figure 132: PRO80542
Figure 133: DNA323793, XM_010664, gen.XM_010664
Figure 134: DNA323794, XM_001812, gen.XM_001812
Figure 135: DNA323795, XM_001807, gen.XM_001807
Figure 136: DNA323796, XM_086444, gen.XM_086444
Figure 137: DNA323797, NM_024640, gen.NM_024640
Figure 138: PRO80547
Figure 139A-B: DNA323798, XM_049310, gen.XM_049310
Figure 140: DNA323799, XM_113374, gen.XM_113374
Figure 141: DNA323800, XM_002105, gen.XM_002105
Figure 142: DNA323801, NM_014571, gen.NM_014571
Figure 143: PRO80550
Figure 144: DNA323802, XM_165438, gen.XM_165438
Figure 145: DNA323803, XM_029844, gen.XM_029844
Figure 146: DNA188748, NM_006559, gen.NM_006559
Figure 147: PRO22304
Figure 148: DNA323804, NM_003757, gen.NM_003757
Figure 149: PRO80553
Figure 150: DNA323805, NM_004964, gen.NM_004964
Figure 151: PRO80554
Figure 152: DNA323806, NM_023009, gen.NM_023009
Figure 153: PRO80555
Figure 154: DNA323807, XM_030423, gen.XM_030423
Figure 155A-B: DNA323808, XM_036299, gen.XM_036299
Figure 156: PRO80557
Figure 157: DNA227213, NM_003680, gen.NM_003680
Figure 158: PRO37676
Figure 159: DNA323809, NM_006112, gen.NM_006112
Figure 160: PRO80558
Figure 161: DNA323810, XM_018136, gen.XM_018136
Figure 162: PRO80559
Figure 163: DNA323811, XM_117184, gen.XM_117184
Figure 164: PRO80560
Figure 165: DNA323812, NM_017825, gen.NM_017825
Figure 166: PRO80561
Figure 167: DNA189315, NM_014408, gen.NM_014408
Figure 168: PRO22262
Figure 169A-B: DNA323813, XM_029031, gen.XM_029031
Figure 170: PRO80562
Figure 171: DNA323814, XM_059171,

gen.XM_059171
Figure 172: PRO80563
Figure 173: DNA83085, NM_000760, gen.NM_000760
Figure 174: PRO2583
Figure 175: DNA323815, XM_165984,
gen.XM_165984
Figure 176: DNA323816, XM_029842,
gen.XM_029842
Figure 177: PRO2851
Figure 178: DNA323817, XM_086384,
gen.XM_086384
Figure 179: PRO80565
Figure 180A-C: DNA274487, NM_014747,
gen.NM_014747
Figure 181: PRO62389
Figure 182: DNA323818, XM_010712,
gen.XM_010712
Figure 183: DNA323819, NM_024664,
gen.NM_024664
Figure 184: PRO80567
Figure 185: DNA323820, XM_059214,
gen.XM_059214
Figure 186: PRO80568
Figure 187: DNA323821, XM_046349,
gen.XM_046349
Figure 188: DNA103253, NM_006516,
gen.NM_006516
Figure 189: PRO4583
Figure 190: DNA323822, XM_086543,
gen.XM_086543
Figure 191: PRO80570
Figure 192: DNA274745, NM_006824,
gen.NM_006824
Figure 193: PRO62518
Figure 194: DNA273060, NM_001255,
gen.NM_001255
Figure 195: PRO61125
Figure 196: DNA323823, NM_030587,
gen.NM_030587
Figure 197: PRO80571
Figure 198: DNA323824, XM_097649,
gen.XM_097649
Figure 199: DNA256503, NM_003780,
gen.NM_003780
Figure 200: PRO51539
Figure 201: DNA323825, XM_046450,
gen.XM_046450
Figure 202A-B: DNA272024, NM_014663,
gen.NM_014663
Figure 203: PRO60298
Figure 204: DNA323826, XM_046565,
gen.XM_046565
Figure 205: PRO80574
Figure 206: DNA323827, NM_024602,
gen.NM_024602
Figure 207: PRO80575
Figure 208: DNA323828, XM_046557,
gen.XM_046557
Figure 209: PRO80576
Figure 210: DNA323829, NM_001012,
gen.NM_001012
Figure 211: PRO10760
Figure 212: DNA323830, XM_046551,
gen.XM_046551
Figure 213A-B: DNA323831, XM_027983,
gen.XM_027983
Figure 214: DNA323832, XM_086324,
gen.XM_086324
Figure 215: PRO80579
Figure 216: DNA323833, XM_032391,
gen.XM_032391
Figure 217: PRO80580
Figure 218: DNA103214, NM_006066,
gen.NM_006066
Figure 219: PRO4544
Figure 220: DNA304686, NM_002574,
gen.NM_002574
Figure 221: PRO71112
Figure 222: DNA323834, NM_032756,
gen.NM_032756
Figure 223: PRO80581
Figure 224: DNA323835, XM_059133,
gen.XM_059133
Figure 225: PRO80582
Figure 226: DNA323836, XM_027313,
gen.XM_027313
Figure 227: PRO80583
Figure 228: DNA323837, XM_054868,
gen.XM_054868
Figure 229: DNA323838, NM_001262,
gen.NM_001262
Figure 230: PRO59546
Figure 231: DNA323839, XM_086391,
gen.XM_086391
Figure 232: PRO80584
Figure 233: DNA323840, XM_114798,
gen.XM_114798
Figure 234: PRO80585
Figure 235: DNA272748, NM_002979,
gen.NM_002979
Figure 236: PRO60860
Figure 237: DNA323841, XM_038911,
gen.XM_038911
Figure 238: PRO80586
Figure 239: DNA323842, NM_018070,
gen.NM_018070
Figure 240: PRO80587
Figure 241: DNA323843, NM_024603,
gen.NM_024603
Figure 242: PRO80588
Figure 243: DNA323844, XM_086389,
gen.XM_086389

Figure 244: DNA323845, XM_038852, gen.XM_038852
Figure 245: DNA323846, NM_032864, gen.NM_032864
Figure 246: PRO80591
Figure 247: DNA323847, NM_024586, gen.NM_024586
Figure 248: PRO80592
Figure 249A-B: DNA323848, XM_097565, gen.XM_097565
Figure 250: DNA323849, XM_001472, gen.XM_001472
Figure 251A-C: DNA323850, XM_055481, gen.XM_055481
Figure 252: PRO80593
Figure 253: DNA323851, XM_010615, gen.XM_010615
Figure 254A-B: DNA323852, XM_089138, gen.XM_089138
Figure 255: PRO80595
Figure 256A-B: DNA323853, XM_059180, gen.XM_059180
Figure 257: DNA323854, XM_015717, gen.XM_015717
Figure 258: PRO80597
Figure 259: DNA323855, XM_114125, gen.XM_114125
Figure 260: DNA323856, NM_015640, gen.NM_015640
Figure 261: PRO80599
Figure 262: DNA323857, NM_017768, gen.NM_017768
Figure 263: PRO80600
Figure 264: DNA323858, XM_165977, gen.XM_165977
Figure 265: DNA323859, XM_086343, gen.XM_086343
Figure 266: PRO80602
Figure 267: DNA269708, NM_007034, gen.NM_007034
Figure 268: PRO58118
Figure 269: DNA323860, NM_001554, gen.NM_001554
Figure 270: PRO80603
Figure 271: DNA226260, NM_006769, gen.NM_006769
Figure 272: PRO36723
Figure 273: DNA323861, NM_004261, gen.NM_004261
Figure 274: PRO80604
Figure 275: DNA323862, XM_165983, gen.XM_165983
Figure 276: DNA323863, XM_016164, gen.XM_016164
Figure 277: DNA323864, XM_086164, gen.XM_086164
Figure 278: PRO80607
Figure 279: DNA323865, XM_086165, gen.XM_086165
Figure 280: DNA323866, XM_086167, gen.XM_086167
Figure 281: DNA323867, XM_086166, gen.XM_086166
Figure 282: DNA323868, XM_086138, gen.XM_086138
Figure 283: PRO80611
Figure 284: DNA323869, NM_000969, gen.NM_000969
Figure 285: PRO80612
Figure 286: DNA323870, XM_088863, gen.XM_088863
Figure 287: PRO80613
Figure 288: DNA271003, NM_003729, gen.NM_003729
Figure 289: PRO59332
Figure 290: DNA323871, XM_165981, gen.XM_165981
Figure 291: PRO80614
Figure 292: DNA275139, NM_013296, gen.NM_013296
Figure 293: PRO62849
Figure 294: DNA323872, XM_058702, gen.XM_058702
Figure 295: DNA323873, XM_054978, gen.XM_054978
Figure 296: DNA323874, NM_032636, gen.NM_032636
Figure 297: PRO80617
Figure 298: DNA323875, NM_006513, gen.NM_006513
Figure 299: PRO80618
Figure 300: DNA323876, NM_006621, gen.NM_006621
Figure 301: PRO80619
Figure 302A-B: DNA323877, NM_007158, gen.NM_007158
Figure 303: PRO80620
Figure 304: DNA323878, XM_086132, gen.XM_086132
Figure 305: PRO80621
Figure 306: DNA323879, NM_004000, gen.NM_004000
Figure 307: PRO80622
Figure 308: DNA323880, NM_001688, gen.NM_001688
Figure 309: PRO80623
Figure 310: DNA323881, NM_019099, gen.NM_019099
Figure 311: PRO80624
Figure 312A-B: DNA323882, NM_000701, gen.NM_000701
Figure 313: PRO80625

Figure 314A-B: DNA323883, XM_018332, gen.XM_018332
Figure 315A-B: DNA323884, XM_040709, gen.XM_040709
Figure 316: PRO80627
Figure 317: DNA323885, XM_086518, gen.XM_086518
Figure 318A-D: DNA323886, XM_034671, gen.XM_034671
Figure 319: DNA323887, XM_034662, gen.XM_034662
Figure 320: PRO80630
Figure 321: DNA323888, XM_039721, gen.XM_039721
Figure 322: PRO80631
Figure 323A-B: DNA323889, XM_086397, gen.XM_086397
Figure 324A-B: DNA323890, XM_086515, gen.XM_086515
Figure 325: PRO80633
Figure 326: DNA323891, XM_016480, gen.XM_016480
Figure 327: DNA323892, XM_165975, gen.XM_165975
Figure 328: DNA323893, NM_016361, gen.NM_016361
Figure 329: PRO231
Figure 330: DNA323894, XM_059210, gen.XM_059210
Figure 331: DNA323895, XM_086296, gen.XM_086296
Figure 332: DNA323896, NM_030920, gen.NM_030920
Figure 333: PRO80638
Figure 334: DNA323897, NM_016022, gen.NM_016022
Figure 335: PRO80639
Figure 336: DNA323898, NM_031901, gen.NM_031901
Figure 337: PRO80640
Figure 338A-B: DNA323899, XM_088788, gen.XM_088788
Figure 339: PRO80641
Figure 340: DNA274759, NM_005620, gen.NM_005620
Figure 341: PRO62529
Figure 342: DNA323900, XM_001468, gen.XM_001468
Figure 343: PRO49642
Figure 344: DNA323901, NM_006862, gen.NM_006862
Figure 345: PRO80642
Figure 346: DNA227529, NM_002796, gen.NM_002796
Figure 347: PRO37992
Figure 348: DNA323902, NM_002810, gen.NM_002810
Figure 349: PRO61638
Figure 350: DNA290284, NM_005997, gen.NM_005997
Figure 351: PRO70433
Figure 352: DNA323903, XM_097639, gen.XM_097639
Figure 353: DNA323904, XM_041879, gen.XM_041879
Figure 354: DNA323905, XM_041884, gen.XM_041884
Figure 355: PRO80644
Figure 356: DNA225809, NM_000396, gen.NM_000396
Figure 357: PRO36272
Figure 358: DNA323906, NM_025150, gen.NM_025150
Figure 359: PRO80645
Figure 360: DNA323907, XM_114098, gen.XM_114098
Figure 361: DNA323908, XM_113369, gen.XM_113369
Figure 362: PRO80646
Figure 363: DNA323909, XM_099467, gen.XM_099467
Figure 364: DNA323910, NM_002965, gen.NM_002965
Figure 365: PRO80648
Figure 366: DNA323911, XM_086400, gen.XM_086400
Figure 367: DNA210134, NM_014624, gen.NM_014624
Figure 368: PRO33679
Figure 369: DNA304666, NM_002961, gen.NM_002961
Figure 370: PRO71093
Figure 371: DNA304720, NM_019554, gen.NM_019554
Figure 372: PRO71146
Figure 373: DNA323912, XM_165976, gen.XM_165976
Figure 374: DNA227577, NM_006271, gen.NM_006271
Figure 375: PRO38040
Figure 376: DNA323913, XM_114097, gen.XM_114097
Figure 377: DNA323914, XM_040009, gen.XM_040009
Figure 378: PRO80651
Figure 379: DNA323915, NM_024330, gen.NM_024330
Figure 380: PRO703
Figure 381: DNA323916, NM_012437, gen.NM_012437
Figure 382: PRO80652
Figure 383: DNA323917, XM_086271,

gen.XM_086271
Figure 384: DNA323918, XM_114055, gen.XM_114055
Figure 385: PRO37535
Figure 386: DNA323919, XM_113360, gen.XM_113360
Figure 387: PRO80654
Figure 388: DNA323920, XM_086564, gen.XM_086564
Figure 389: DNA323921, NM_005973, gen.NM_005973
Figure 390: PRO80656
Figure 391: DNA323922, XM_044077, gen.XM_044077
Figure 392: DNA323923, NM_001878, gen.NM_001878
Figure 393: PRO80657
Figure 394: DNA323924, NM_021948, gen.NM_021948
Figure 395: PRO6018
Figure 396: DNA273088, NM_006365, gen.NM_006365
Figure 397: PRO61146
Figure 398: DNA323925, XM_044127, gen.XM_044127
Figure 399: PRO80658
Figure 400: DNA323926, XM_053245, gen.XM_053245
Figure 401: PRO80659
Figure 402: DNA257916, NM_032323, gen.NM_032323
Figure 403: PRO52449
Figure 404: DNA323927, NM_005572, gen.NM_005572
Figure 405: PRO80660
Figure 406: DNA323928, XM_044166, gen.XM_044166
Figure 407: PRO80661
Figure 408: DNA323929, XM_044128, gen.XM_044128
Figure 409: DNA226125, NM_003145, gen.NM_003145
Figure 410: PRO36588
Figure 411A-B: DNA323930, XM_044172, gen.XM_044172
Figure 412: DNA323931, NM_032292, gen.NM_032292
Figure 413: PRO80664
Figure 414: DNA323932, NM_004632, gen.NM_004632
Figure 415: PRO80665
Figure 416: DNA323933, XM_044075, gen.XM_044075
Figure 417: PRO80666
Figure 418: DNA323934, NM_018253, gen.NM_018253
Figure 419: PRO80667
Figure 420: DNA323935, NM_018116, gen.NM_018116
Figure 421: PRO80668
Figure 422: DNA323936, NM_002004, gen.NM_002004
Figure 423: PRO80669
Figure 424: DNA323937, NM_005698, gen.NM_005698
Figure 425: PRO80670
Figure 426: DNA323938, NM_052837, gen.NM_052837
Figure 427: PRO80671
Figure 428: DNA194600, NM_006589, gen.NM_006589
Figure 429: PRO23942
Figure 430: DNA323939, XM_086567, gen.XM_086567
Figure 431: PRO80672
Figure 432: DNA323940, XM_086552, gen.XM_086552
Figure 433: DNA323941, XM_036744, gen.XM_036744
Figure 434: DNA323942, NM_130898, gen.NM_130898
Figure 435: PRO80675
Figure 436: DNA226793, NM_006694, gen.NM_006694
Figure 437: PRO37256
Figure 438: DNA294794, NM_002870, gen.NM_002870
Figure 439: PRO70754
Figure 440: DNA323943, NM_001030, gen.NM_001030
Figure 441: PRO80676
Figure 442: DNA323944, XM_036829, gen.XM_036829
Figure 443: PRO80677
Figure 444: DNA323945, NM_015449, gen.NM_015449
Figure 445: PRO80678
Figure 446: DNA323946, NM_014847, gen.NM_014847
Figure 447: PRO80679
Figure 448: DNA323947, XM_036934, gen.XM_036934
Figure 449: PRO80680
Figure 450A-B: DNA323948, XM_036845, gen.XM_036845
Figure 451: DNA323949, XM_010636, gen.XM_010636
Figure 452: DNA323950, NM_006556, gen.NM_006556
Figure 453: PRO62574
Figure 454: DNA323951, XM_034082, gen.XM_034082

Figure 455: DNA323952, NM_025207, gen.NM_025207
Figure 456: PRO80684
Figure 457: DNA103436, NM_003815, gen.NM_003815
Figure 458: PRO4763
Figure 459: DNA323953, NM_003516, gen.NM_003516
Figure 460: PRO80685
Figure 461: DNA323954, NM_005850, gen.NM_005850
Figure 462: PRO59725
Figure 463A-B: DNA323955, NM_014849, gen.NM_014849
Figure 464: PRO80686
Figure 465: DNA323956, XM_059094, gen.XM_059094
Figure 466: DNA323957, XM_058247, gen.XM_058247
Figure 467: PRO80688
Figure 468: DNA323958, NM_003779, gen.NM_003779
Figure 469: PRO80689
Figure 470: DNA323959, NM_004550, gen.NM_004550
Figure 471: PRO58974
Figure 472: DNA323960, XM_085581, gen.XM_085581
Figure 473: DNA323961, XM_113379, gen.XM_113379
Figure 474: DNA226619, NM_003564, gen.NM_003564
Figure 475: PRO37082
Figure 476A-B: DNA323962, XM_049680, gen.XM_049680
Figure 477: DNA323963, XM_165443, gen.XM_165443
Figure 478: PRO80693
Figure 479: DNA323964, XM_086381, gen.XM_086381
Figure 480: PRO80694
Figure 481A-B: DNA323965, NM_002857, gen.NM_002857
Figure 482: PRO80695
Figure 483A-B: DNA323966, XM_049690, gen.XM_049690
Figure 484: DNA323967, XM_114153, gen.XM_114153
Figure 485: DNA323968, XM_086378, gen.XM_086378
Figure 486: DNA323969, XM_001897, gen.XM_001897
Figure 487: PRO10002
Figure 488: DNA323970, NM_052862, gen.NM_052862
Figure 489: PRO80699
Figure 490: DNA323971, XM_086481, gen.XM_086481
Figure 491: PRO80700
Figure 492: DNA323972, XM_059191, gen.XM_059191
Figure 493: DNA323973, XM_086485, gen.XM_086485
Figure 494: DNA323974, XM_086484, gen.XM_086484
Figure 495: DNA323975, XM_047479, gen.XM_047479
Figure 496: PRO80704
Figure 497: DNA323976, NM_003617, gen.NM_003617
Figure 498: PRO37806
Figure 499: DNA254298, NM_025226, gen.NM_025226
Figure 500: PRO49409
Figure 501: DNA323977, XM_034000, gen.XM_034000
Figure 502: PRO80705
Figure 503: DNA323978, NM_032738, gen.NM_032738
Figure 504: PRO329
Figure 505: DNA323979, NM_000569, gen.NM_000569
Figure 506: PRO80706
Figure 507: DNA323980, XM_088945, gen.XM_088945
Figure 508: PRO80707
Figure 509: DNA323981, XM_060331, gen.XM_060331
Figure 510: PRO80708
Figure 511: DNA323982, NM_004905, gen.NM_004905
Figure 512: PRO80709
Figure 513: DNA323983, NM_017847, gen.NM_017847
Figure 514: PRO80710
Figure 515A-B: DNA323984, XM_051877, gen.XM_051877
Figure 516: PRO62077
Figure 517: DNA323985, NM_005717, gen.NM_005717
Figure 518: PRO80711
Figure 519A-B: DNA271986, NM_014837, gen.NM_014837
Figure 520: PRO60261
Figure 521A-B: DNA323986, XM_056923, gen.XM_056923
Figure 522: DNA323987, XM_046464, gen.XM_046464
Figure 523: DNA323988, XM_002068, gen.XM_002068
Figure 524A-B: DNA323989, XM_001289, gen.XM_001289

Figure 525: DNA323990, XM_114109, gen.XM_114109
Figure 526: PRO80714
Figure 527: DNA323991, NM_022371, gen.NM_022371
Figure 528: PRO80715
Figure 529: DNA323992, NM_004673, gen.NM_004673
Figure 530: PRO188
Figure 531: DNA323993, XM_060517, gen.XM_060517
Figure 532: DNA323994, XM_165978, gen.XM_165978
Figure 533: PRO80717
Figure 534: DNA323995, XM_117181, gen.XM_117181
Figure 535: DNA323996, NM_018122, gen.NM_018122
Figure 536: PRO80719
Figure 537: DNA323997, XM_042967, gen.XM_042967
Figure 538: DNA323998, XM_086494, gen.XM_086494
Figure 539: PRO80720
Figure 540: DNA290234, NM_002923, gen.NM_002923
Figure 541: PRO70333
Figure 542: DNA323999, XM_086328, gen.XM_086328
Figure 543: DNA324000, XM_086282, gen.XM_086282
Figure 544: DNA324001, XM_053633, gen.XM_053633
Figure 545: DNA256905, NM_138391, gen.NM_138391
Figure 546: PRO51836
Figure 547: DNA324002, XM_015434, gen.XM_015434
Figure 548: DNA324003, NM_006763, gen.NM_006763
Figure 549: PRO80725
Figure 550: DNA227246, NM_005686, gen.NM_005686
Figure 551: PRO37709
Figure 552: DNA324004, XM_058405, gen.XM_058405
Figure 553A-B: DNA226005, NM_000228, gen.NM_000228
Figure 554: PRO36468
Figure 555: DNA324005, NM_015714, gen.NM_015714
Figure 556: PRO11582
Figure 557: DNA324006, XM_086142, gen.XM_086142
Figure 558: DNA83046, NM_000574, gen.NM_000574
Figure 559: PRO2569
Figure 560A-B: DNA324007, XM_114030, gen.XM_114030
Figure 561: DNA324008, XM_097519, gen.XM_097519
Figure 562: DNA324009, XM_059120, gen.XM_059120
Figure 563: PRO80730
Figure 564: DNA324010, NM_016456, gen.NM_016456
Figure 565: PRO1248
Figure 566: DNA324011, XM_036556, gen.XM_036556
Figure 567: DNA324012, XM_001914, gen.XM_001914
Figure 568: DNA324013, XM_001916, gen.XM_001916
Figure 569: DNA324014, NM_018085, gen.NM_018085
Figure 570: PRO80734
Figure 571: DNA324015, NM_006335, gen.NM_006335
Figure 572: PRO80735
Figure 573: DNA324016, XM_036500, gen.XM_036500
Figure 574: PRO80736
Figure 575: DNA324017, XM_036507, gen.XM_036507
Figure 576: DNA196344, NM_004767, gen.NM_004767
Figure 577: PRO24851
Figure 578: DNA247474, NM_014176, gen.NM_014176
Figure 579: PRO44999
Figure 580A-B: DNA324018, XM_084055, gen.XM_084055
Figure 581: DNA324019, XM_010682, gen.XM_010682
Figure 582: DNA324020, XM_117185, gen.XM_117185
Figure 583: DNA324021, XM_055880, gen.XM_055880
Figure 584: PRO80740
Figure 585: DNA193882, NM_014184, gen.NM_014184
Figure 586: PRO23300
Figure 587: DNA324022, NM_018212, gen.NM_018212
Figure 588: PRO80741
Figure 589: DNA324023, XM_086431, gen.XM_086431
Figure 590: PRO80742
Figure 591: DNA324024, XM_037329, gen.XM_037329
Figure 592: DNA324025, XM_086432, gen.XM_086432
Figure 593A-B: DNA324026, XM_010732,

gen.XM_010732
Figure 594: DNA227504, NM_000447,
gen.NM_000447
Figure 595: PRO37967
Figure 596: DNA324027, NM_012486,
gen.NM_012486
Figure 597: PRO80745
Figure 598A-B: DNA324028, XM_113361,
gen.XM_113361
Figure 599A-B: DNA324029, XM_001958,
gen.XM_001958
Figure 600: DNA324030, XM_016199,
gen.XM_016199
Figure 601: DNA324031, XM_086244,
gen.XM_086244
Figure 602: DNA324032, XM_086245,
gen.XM_086245
Figure 603: DNA254346, NM_024709,
gen.NM_024709
Figure 604: PRO49457
Figure 605: DNA324033, XM_088107,
gen.XM_088107
Figure 606: DNA324034, NM_032890,
gen.NM_032890
Figure 607: PRO80752
Figure 608: DNA324035, XM_052974,
gen.XM_052974
Figure 609: PRO80753
Figure 610: DNA324036, XM_047499,
gen.XM_047499
Figure 611: PRO80754
Figure 612: DNA324037, NM_000858,
gen.NM_000858
Figure 613: PRO80755
Figure 614: DNA324038, NM_024319,
gen.NM_024319
Figure 615: PRO80756
Figure 616: DNA324039, XM_047545,
gen.XM_047545
Figure 617: PRO4914
Figure 618A-B: DNA324040, XM_056884,
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Figure 619: DNA324041, XM_098599,
gen.XM_098599
Figure 620: DNA324042, XM_165439,
gen.XM_165439
Figure 621: PRO80759
Figure 622: DNA324043, XM_089030,
gen.XM_089030
Figure 623: PRO80760
Figure 624: DNA82328, NM_000029, gen.NM_000029
Figure 625: PRO1707
Figure 626: DNA324044, NM_014236,
gen.NM_014236
Figure 627: PRO80761
Figure 628: DNA324045, XM_056970,
gen.XM_056970
Figure 629: PRO80762
Figure 630: DNA324046, NM_032324,
gen.NM_032324
Figure 631: PRO80763
Figure 632: DNA324047, XM_086257,
gen.XM_086257
Figure 633: PRO80764
Figure 634: DNA324048, XM_114137,
gen.XM_114137
Figure 635: PRO80765
Figure 636: DNA324049, NM_000143,
gen.NM_000143
Figure 637: PRO62607
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gen.XM_090833
Figure 639: DNA324051, NM_130398,
gen.NM_130398
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gen.XM_117196
Figure 642: DNA324053, XM_018041,
gen.XM_018041
Figure 643: DNA324054, NM_001011,
gen.NM_001011
Figure 644: PRO10692
Figure 645: DNA324055, NM_024027,
gen.NM_024027
Figure 646: PRO1182
Figure 647: DNA324056, NM_016030,
gen.NM_016030
Figure 648: PRO80770
Figure 649: DNA103217, NM_003310,
gen.NM_003310
Figure 650: PRO4547
Figure 651: DNA275195, NM_001034,
gen.NM_001034
Figure 652: PRO62893
Figure 653: DNA324057, XM_059368,
gen.XM_059368
Figure 654: PRO80771
Figure 655: DNA324058, NM_006826,
gen.NM_006826
Figure 656: PRO70258
Figure 657: DNA324059, NM_005378,
gen.NM_005378
Figure 658: PRO80772
Figure 659: DNA324060, NM_002539,
gen.NM_002539
Figure 660: PRO80773
Figure 661: DNA324061, XM_096149,
gen.XM_096149
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Figure 663: PRO62770
Figure 664A-B: DNA324062, XM_036450,

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Figure 665: DNA324063, XM_103946, gen.XM_103946
Figure 666: PRO80775
Figure 667: DNA324064, NM_014713, gen.NM_014713
Figure 668: PRO80776
Figure 669: DNA324065, XM_087206, gen.XM_087206
Figure 670: DNA324066, NM_106552, gen.NM_106552
Figure 671: PRO80778
Figure 672: DNA324067, XM_092135, gen.XM_092135
Figure 673: PRO80779
Figure 674: DNA324068, NM_017910, gen.NM_017910
Figure 675: PRO80780
Figure 676: DNA324069, XM_092517, gen.XM_092517
Figure 677: PRO80781
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Figure 680: DNA324071, XM_002480, gen.XM_002480
Figure 681: DNA324072, NM_002707, gen.NM_002707
Figure 682: PRO12199
Figure 683: DNA324073, XM_087151, gen.XM_087151
Figure 684: DNA227165, NM_014748, gen.NM_014748
Figure 685: PRO37628
Figure 686: DNA324074, NM_015636, gen.NM_015636
Figure 687: PRO80785
Figure 688: DNA273800, NM_001521, gen.NM_001521
Figure 689: PRO61761
Figure 690: DNA324075, XM_047175, gen.XM_047175
Figure 691: PRO80786
Figure 692A-B: DNA324076, NM_004341, gen.NM_004341
Figure 693: PRO80787
Figure 694: DNA324077, NM_016085, gen.NM_016085
Figure 695: PRO80788
Figure 696: DNA324078, NM_080592, gen.NM_080592
Figure 697: PRO80789
Figure 698: DNA227545, NM_021095, gen.NM_021095
Figure 699: PRO38008
Figure 700: DNA324079, XM_002435, gen.XM_002435
Figure 701: DNA324080, NM_000221, gen.NM_000221
Figure 702: PRO80790
Figure 703: DNA271243, NM_006488, gen.NM_006488
Figure 704: PRO59558
Figure 705: DNA324081, NM_007046, gen.NM_007046
Figure 706: PRO9886
Figure 707: DNA324082, NM_021831, gen.NM_021831
Figure 708: PRO80791
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Figure 710: PRO80792
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Figure 718: PRO80796
Figure 719: DNA324088, NM_024572, gen.NM_024572
Figure 720: PRO80797
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Figure 722: PRO80798
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Figure 727: DNA324093, NM_138801, gen.NM_138801
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Figure 735: PRO80806

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Figure 745: PRO62786
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Figure 747: PRO58543
Figure 748: DNA324102, XM_087051, gen.XM_087051
Figure 749: DNA324103, NM_002954, gen.NM_002954
Figure 750: PRO62239
Figure 751: DNA271060, NM_002453, gen.NM_002453
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Figure 754: PRO80811
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Figure 777: DNA324119, XM_065884, gen.XM_065884
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Figure 780: DNA324121, XM_031596, gen.XM_031596
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Figure 790: PRO80830
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Figure 804: PRO37991

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Figure 806: DNA150725, NM_001747, gen.NM_001747
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Figure 844: PRO80856
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Figure 868: PRO80868
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Figure 882: PRO60397
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Figure 911: DNA324191, XM_015922, gen.XM_015922
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Figure 934: DNA271608, NM_014670, gen.NM_014670
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Figure 937: PRO80900
Figure 938: DNA324207, XM_010852, gen.XM_010852
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Figure 941: DNA324209, NM_015934, gen.NM_015934
Figure 942: DNA324210, XM_087028, gen.XM_087028

Figure 943: PRO80903
Figure 944: DNA324211, XM_092346, gen.XM_092346
Figure 945: PRO80904
Figure 946: DNA324212, XM_002669, gen.XM_002669
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Figure 949: PRO23124
Figure 950: DNA324214, NM_001959, gen.NM_001959
Figure 951: PRO23124
Figure 952: DNA324215, XM_030834, gen.XM_030834
Figure 953: PRO80906
Figure 954A-C: DNA324216, XM_055254, gen.XM_055254
Figure 955: DNA324217, NM_004044, gen.NM_004044
Figure 956: PRO80908
Figure 957: DNA324218, XM_114298, gen.XM_114298
Figure 958: DNA324219, NM_021141, gen.NM_021141
Figure 959: PRO59313
Figure 960A-B: DNA324220, XM_098048, gen.XM_098048
Figure 961: PRO80910
Figure 962: DNA324221, XM_098047, gen.XM_098047
Figure 963: PRO80911
Figure 964: DNA324222, XM_002636, gen.XM_002636
Figure 965: DNA324223, XM_087181, gen.XM_087181
Figure 966: DNA324224, NM_000998, gen.NM_000998
Figure 967: PRO10498
Figure 968: DNA324225, XM_059422, gen.XM_059422
Figure 969: PRO9984
Figure 970: DNA324226, XM_092545, gen.XM_092545
Figure 971: DNA324227, XM_059461, gen.XM_059461
Figure 972: PRO80915
Figure 973: DNA324228, NM_018674, gen.NM_018674
Figure 974: PRO80916
Figure 975: DNA324229, XM_050962, gen.XM_050962
Figure 976: PRO80917
Figure 977: DNA194827, NM_012100, gen.NM_012100
Figure 978: PRO24091
Figure 979: DNA324230, XM_050638, gen.XM_050638
Figure 980A-B: DNA324231, NM_002846, gen.NM_002846
Figure 981: PRO2610
Figure 982: DNA324232, NM_006000, gen.NM_006000
Figure 983: PRO26228
Figure 984: DNA324233, XM_050891, gen.XM_050891
Figure 985: DNA324234, XM_087162, gen.XM_087162
Figure 986: DNA324235, XM_058098, gen.XM_058098
Figure 987: PRO80920
Figure 988: DNA324236, NM_022453, gen.NM_022453
Figure 989: PRO80921
Figure 990: DNA324237, NM_032726, gen.NM_032726
Figure 991: PRO70675
Figure 992: DNA324238, XM_010866, gen.XM_010866
Figure 993: DNA324239, XM_087166, gen.XM_087166
Figure 994: DNA254204, NM_001087, gen.NM_001087
Figure 995: PRO49316
Figure 996: DNA324240, NM_005731, gen.NM_005731
Figure 997: PRO80924
Figure 998: DNA189697, NM_004846, gen.NM_004846
Figure 999: PRO23123
Figure 1000: DNA324241, NM_025202, gen.NM_025202
Figure 1001: PRO80925
Figure 1002: DNA324242, XM_115825, gen.XM_115825
Figure 1003: PRO80926
Figure 1004: DNA324243, XM_010858, gen.XM_010858
Figure 1005: PRO80927
Figure 1006: DNA324244, XM_002540, gen.XM_002540
Figure 1007: DNA324245, XM_048690, gen.XM_048690
Figure 1008: PRO80929
Figure 1009: DNA324246, NM_030926, gen.NM_030926
Figure 1010: PRO80930
Figure 1011: DNA324247, XM_087218, gen.XM_087218
Figure 1012: DNA324248, NM_004509, gen.NM_004509
Figure 1013: PRO80932

Figure 1014: DNA324249, NM_004510, gen.NM_004510
Figure 1015: PRO80933
Figure 1016: DNA324250, NM_080424, gen.NM_080424
Figure 1017: PRO80934
Figure 1018: DNA324251, NM_018410, gen.NM_018410
Figure 1019: PRO80935
Figure 1020: DNA324252, NM_017974, gen.NM_017974
Figure 1021: PRO80936
Figure 1022A-B: DNA324253, XM_096169, gen.XM_096169
Figure 1023: PRO80937
Figure 1024: DNA150884, NM_005855, gen.NM_005855
Figure 1025: PRO12520
Figure 1026A-B: DNA324254, NM_004735, gen.NM_004735
Figure 1027: PRO80938
Figure 1028A-C: DNA324255, XM_030203, gen.XM_030203
Figure 1029: DNA324256, XM_059372, gen.XM_059372
Figure 1030: DNA324257, NM_002712, gen.NM_002712
Figure 1031: PRO80941
Figure 1032A-B: DNA324258, XM_042326, gen.XM_042326
Figure 1033: PRO80942
Figure 1034: DNA324259, NM_004404, gen.NM_004404
Figure 1035: PRO80943
Figure 1036: DNA324260, XM_002742, gen.XM_002742
Figure 1037: DNA324261, NM_138483, gen.NM_138483
Figure 1038: PRO80945
Figure 1039: DNA324262, XM_115706, gen.XM_115706
Figure 1040: DNA324263, XM_115722, gen.XM_115722
Figure 1041: DNA324264, XM_084141, gen.XM_084141
Figure 1042: DNA324265, XM_005086, gen.XM_005086
Figure 1043: DNA324266, NM_015453, gen.NM_015453
Figure 1044: PRO80949
Figure 1045: DNA324267, NM_022485, gen.NM_022485
Figure 1046: PRO80950
Figure 1047A-B: DNA324268, XM_054520, gen.XM_054520
Figure 1048: PRO80951
Figure 1049: DNA324269, NM_006354, gen.NM_006354
Figure 1050: PRO80952
Figure 1051: DNA324270, NM_133480, gen.NM_133480
Figure 1052: PRO80953
Figure 1053: DNA324271, NM_133481, gen.NM_133481
Figure 1054: PRO80954
Figure 1055: DNA324272, NM_005718, gen.NM_005718
Figure 1056: PRO80955
Figure 1057: DNA324273, NM_015644, gen.NM_015644
Figure 1058: PRO80956
Figure 1059: DNA324274, XM_059561, gen.XM_059561
Figure 1060: DNA324275, XM_052310, gen.XM_052310
Figure 1061: PRO80958
Figure 1062: DNA269910, NM_006395, gen.NM_006395
Figure 1063: PRO58308
Figure 1064: DNA324276, NM_000994, gen.NM_000994
Figure 1065: PRO80959
Figure 1066: DNA151017, NM_004844, gen.NM_004844
Figure 1067: PRO12841
Figure 1068: DNA324277, XM_059557, gen.XM_059557
Figure 1069: PRO80960
Figure 1070A-B: DNA324278, XM_042860, gen.XM_042860
Figure 1071: PRO80961
Figure 1072: DNA324279, XM_042841, gen.XM_042841
Figure 1073: PRO80962
Figure 1074: DNA324280, XM_053712, gen.XM_053712
Figure 1075: DNA324281, XM_087284, gen.XM_087284
Figure 1076: DNA324282, NM_002948, gen.NM_002948
Figure 1077: PRO6360
Figure 1078: DNA324283, XM_053323, gen.XM_053323
Figure 1079A-B: DNA324284, NM_001068, gen.NM_001068
Figure 1080: PRO80966
Figure 1081: DNA252367, NM_017801, gen.NM_017801
Figure 1082: PRO48357
Figure 1083: DNA324285, XM_093624, gen.XM_093624
Figure 1084: PRO80967

Figure 1085: DNA324286, XM_046401, gen.XM_046401
Figure 1086: DNA324287, NM_022461, gen.NM_022461
Figure 1087: PRO80969
Figure 1088: DNA324288, XM_113410, gen.XM_113410
Figure 1089: DNA88100, NM_000404, gen.NM_000404
Figure 1090: PRO2172
Figure 1091: DNA324289, XM_091076, gen.XM_091076
Figure 1092: PRO80970
Figure 1093A-B: DNA271187, NM_005109, gen.NM_005109
Figure 1094: PRO59504
Figure 1095: DNA324290, NM_002468, gen.NM_002468
Figure 1096: PRO36735
Figure 1097: DNA269930, NM_001607, gen.NM_001607
Figure 1098: PRO58328
Figure 1099: DNA270401, NM_003149, gen.NM_003149
Figure 1100: PRO58784
Figure 1101: DNA324291, XM_087370, gen.XM_087370
Figure 1102: PRO80971
Figure 1103: DNA324292, XM_098158, gen.XM_098158
Figure 1104: PRO80972
Figure 1105: DNA324293, XM_017364, gen.XM_017364
Figure 1106: DNA324294, XM_087349, gen.XM_087349
Figure 1107: PRO80974
Figure 1108: DNA226547, NM_002295, gen.NM_002295
Figure 1109: PRO37010
Figure 1110: DNA324295, NM_003973, gen.NM_003973
Figure 1111: PRO80975
Figure 1112: DNA324296, XM_030417, gen.XM_030417
Figure 1113: DNA324297, NM_020347, gen.NM_020347
Figure 1114: PRO80977
Figure 1115: DNA324298, XM_087346, gen.XM_087346
Figure 1116: PRO80978
Figure 1117: DNA324299, XM_096198, gen.XM_096198
Figure 1118: PRO80979
Figure 1119: DNA324300, XM_003222, gen.XM_003222
Figure 1120: DNA324301, XM_087588, gen.XM_087588
Figure 1121: DNA324302, XM_166011, gen.XM_166011
Figure 1122A-B: DNA324303, XM_114364, gen.XM_114364
Figure 1123A-B: DNA324304, XM_033294, gen.XM_033294
Figure 1124: PRO80983
Figure 1125: DNA324305, NM_138614, gen.NM_138614
Figure 1126: PRO80984
Figure 1127: DNA324306, XM_002899, gen.XM_002899
Figure 1128: DNA225910, NM_004345, gen.NM_004345
Figure 1129: PRO36373
Figure 1130: DNA324307, XM_010953, gen.XM_010953
Figure 1131: DNA324308, XM_051518, gen.XM_051518
Figure 1132A-D: DNA324309, NM_001407, gen.NM_001407
Figure 1133: PRO50095
Figure 1134: DNA324310, NM_003365, gen.NM_003365
Figure 1135: PRO80988
Figure 1136: DNA324311, XM_003245, gen.XM_003245
Figure 1137: DNA324312, XM_047561, gen.XM_047561
Figure 1138: PRO80990
Figure 1139: DNA324313, XM_116853, gen.XM_116853
Figure 1140A-B: DNA324314, XM_113405, gen.XM_113405
Figure 1141: DNA324315, XM_114323, gen.XM_114323
Figure 1142: PRO80993
Figure 1143: DNA324316, XM_002828, gen.XM_002828
Figure 1144: PRO80994
Figure 1145: DNA150976, NM_022171, gen.NM_022171
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Figure 1147: DNA324317, XM_041507, gen.XM_041507
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Figure 1152: PRO80995
Figure 1153: DNA150562, NM_007275, gen.NM_007275
Figure 1154: PRO12779

Figure 1155: DNA254582, NM_004635, gen.NM_004635
Figure 1156: PRO49685
Figure 1157: DNA324319, NM_052859, gen.NM_052859
Figure 1158: PRO80996
Figure 1159: DNA324320, NM_001064, gen.NM_001064
Figure 1160: PRO80997
Figure 1161: DNA324321, XM_041211, gen.XM_041211
Figure 1162: DNA324322, XM_003213, gen.XM_003213
Figure 1163A-C: DNA324323, XM_037423, gen.XM_037423
Figure 1164: PRO80999
Figure 1165A-B: DNA227307, NM_007184, gen.NM_007184
Figure 1166: PRO37770
Figure 1167: DNA324324, NM_000688, gen.NM_000688
Figure 1168: PRO81000
Figure 1169: DNA324325, XM_067715, gen.XM_067715
Figure 1170: DNA324326, NM_000992, gen.NM_000992
Figure 1171: PRO62153
Figure 1172: DNA324327, NM_000666, gen.NM_000666
Figure 1173: PRO81002
Figure 1174: DNA324328, NM_032750, gen.NM_032750
Figure 1175: PRO81003
Figure 1176: DNA324329, NM_033008, gen.NM_033008
Figure 1177: PRO81004
Figure 1178: DNA324330, NM_033010, gen.NM_033010
Figure 1179: PRO81005
Figure 1180: DNA324331, NM_020418, gen.NM_020418
Figure 1181: PRO81006
Figure 1182: DNA273919, NM_004704, gen.NM_004704
Figure 1183: PRO61870
Figure 1184A-B: DNA324332, XM_087448, gen.XM_087448
Figure 1185: PRO81007
Figure 1186: DNA324333, XM_002855, gen.XM_002855
Figure 1187: DNA324334, XM_002854, gen.XM_002854
Figure 1188: DNA0, NM_002854, gen.NM_002854
Figure 1189: PRO
Figure 1190: DNA324335, XM_096195, gen.XM_096195
Figure 1191: PRO81010
Figure 1192: DNA324336, XM_166015, gen.XM_166015
Figure 1193: DNA324337, XM_113395, gen.XM_113395
Figure 1194: PRO81012
Figure 1195: DNA269730, NM_014814, gen.NM_014814
Figure 1196: PRO58140
Figure 1197: DNA324338, XM_036938, gen.XM_036938
Figure 1198: DNA324339, XM_029369, gen.XM_029369
Figure 1199: DNA324340, XM_076414, gen.XM_076414
Figure 1200: PRO81015
Figure 1201: DNA324341, XM_093546, gen.XM_093546
Figure 1202: DNA324342, XM_113409, gen.XM_113409
Figure 1203: DNA324343, XM_087268, gen.XM_087268
Figure 1204: DNA324344, XM_116071, gen.XM_116071
Figure 1205: DNA324345, XM_116072, gen.XM_116072
Figure 1206: DNA324346, NM_000986, gen.NM_000986
Figure 1207: PRO10602
Figure 1208: DNA324347, XM_015462, gen.XM_015462
Figure 1209: DNA324348, XM_167366, gen.XM_167366
Figure 1210: PRO81022
Figure 1211: DNA324349, XM_087331, gen.XM_087331
Figure 1212: PRO81023
Figure 1213: DNA324350, XM_039952, gen.XM_039952
Figure 1214: DNA324351, XM_045290, gen.XM_045290
Figure 1215: PRO81025
Figure 1216A-B: DNA324352, NM_007085, gen.NM_007085
Figure 1217: PRO2077
Figure 1218: DNA324353, NM_004547, gen.NM_004547
Figure 1219: PRO81026
Figure 1220: DNA324354, XM_027161, gen.XM_027161
Figure 1221A-B: DNA324355, XM_032269, gen.XM_032269
Figure 1222: PRO81028
Figure 1223: DNA88547, NM_006810, gen.NM_006810
Figure 1224: PRO2837

Figure 1225: DNA324356, XM_114301, gen.XM_114301
Figure 1226: PRO81029
Figure 1227: DNA324357, XM_098173, gen.XM_098173
Figure 1228: PRO81030
Figure 1229: DNA324358, XM_042618, gen.XM_042618
Figure 1230: PRO81031
Figure 1231: DNA324359, XM_084129, gen.XM_084129
Figure 1232: DNA324360, XM_098154, gen.XM_098154
Figure 1233: PRO81033
Figure 1234: DNA324361, XM_050552, gen.XM_050552
Figure 1235: DNA324362, NM_032343, gen.NM_032343
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Figure 1237: DNA324363, XM_051264, gen.XM_051264
Figure 1238A-B: DNA324364, NM_013336, gen.NM_013336
Figure 1239: PRO1314
Figure 1240: DNA324365, XM_067264, gen.XM_067264
Figure 1241: PRO81036
Figure 1242: DNA324366, XM_114309, gen.XM_114309
Figure 1243: DNA324367, XM_084111, gen.XM_084111
Figure 1244: DNA324368, XM_113397, gen.XM_113397
Figure 1245: DNA324369, XM_098111, gen.XM_098111
Figure 1246: DNA324370, NM_004637, gen.NM_004637
Figure 1247: PRO81040
Figure 1248: DNA324371, NM_020701, gen.NM_020701
Figure 1249: PRO81041
Figure 1250: DNA324372, NM_003418, gen.NM_003418
Figure 1251: PRO81042
Figure 1252: DNA324373, XM_059583, gen.XM_059583
Figure 1253: PRO81043
Figure 1254: DNA324374, XM_113417, gen.XM_113417
Figure 1255: DNA324375, XM_093487, gen.XM_093487
Figure 1256A-B: DNA324376, XM_030812, gen.XM_030812
Figure 1257: PRO58177
Figure 1258A-B: DNA324377, XM_039805, gen.XM_039805
Figure 1259: PRO81046
Figure 1260: DNA324378, NM_000532, gen.NM_000532
Figure 1261: PRO81047
Figure 1262: DNA324379, XM_036118, gen.XM_036118
Figure 1263: DNA324380, XM_084123, gen.XM_084123
Figure 1264: DNA324381, XM_018149, gen.XM_018149
Figure 1265: DNA324382, XM_087342, gen.XM_087342
Figure 1266: DNA324383, XM_059516, gen.XM_059516
Figure 1267: DNA324384, XM_087341, gen.XM_087341
Figure 1268: DNA324385, XM_165451, gen.XM_165451
Figure 1269: PRO81053
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Figure 1273: PRO51109
Figure 1274: DNA324387, XM_002859, gen.XM_002859
Figure 1275: DNA324388, XM_166014, gen.XM_166014
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Figure 1278: DNA324390, XM_058267, gen.XM_058267
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Figure 1281: PRO81057
Figure 1282: DNA324392, NM_015472, gen.NM_015472
Figure 1283: PRO81058
Figure 1284: DNA324393, NM_014445, gen.NM_014445
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Figure 1288A-B: DNA324395, XM_114356, gen.XM_114356
Figure 1289: DNA324396, XM_105236, gen.XM_105236
Figure 1290: DNA324397, XM_010978, gen.XM_010978
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Figure 1292A-B: DNA324399, XM_039796,

gen.XM_039796
Figure 1293: PRO81064
Figure 1294: DNA324400, XM_016334, gen.XM_016334
Figure 1295: DNA324401, XM_116058, gen.XM_116058
Figure 1296: DNA324402, XM_113408, gen.XM_113408
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Figure 1298: PRO81068
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Figure 1301: PRO69681
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Figure 1303: PRO81070
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Figure 1305: PRO81071
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Figure 1307: PRO81072
Figure 1308: DNA324409, XM_093423, gen.XM_093423
Figure 1309: PRO81073
Figure 1310: DNA324410, XM_029136, gen.XM_029136
Figure 1311: PRO81074
Figure 1312: DNA324411, XM_087322, gen.XM_087322
Figure 1313A-B: DNA324412, XM_029132, gen.XM_029132
Figure 1314A-B: DNA324413, XM_029104, gen.XM_029104
Figure 1315: DNA324414, XM_084120, gen.XM_084120
Figure 1316: DNA254620, NM_005787, gen.NM_005787
Figure 1317: PRO49722
Figure 1318: DNA324415, NM_032331, gen.NM_032331
Figure 1319: PRO81079
Figure 1320: DNA324416, XM_011074, gen.XM_011074
Figure 1321: PRO81080
Figure 1322: DNA324417, XM_087295, gen.XM_087295
Figure 1323: DNA324418, XM_087289, gen.XM_087289
Figure 1324: PRO81082
Figure 1325: DNA324419, XM_105658, gen.XM_105658
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Figure 1330: DNA225592, NM_001622, gen.NM_001622
Figure 1331: PRO36055
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Figure 1341: DNA324426, XM_038243, gen.XM_038243
Figure 1342: PRO81090
Figure 1343: DNA324427, XM_087359, gen.XM_087359
Figure 1344: DNA324428, XM_114328, gen.XM_114328
Figure 1345: DNA324429, XM_098109, gen.XM_098109
Figure 1346: PRO81093
Figure 1347: DNA324430, XM_087410, gen.XM_087410
Figure 1348: DNA324431, NM_033316, gen.NM_033316
Figure 1349: PRO81095
Figure 1350: DNA324432, XM_166017, gen.XM_166017
Figure 1351: PRO81096
Figure 1352: DNA79129, NM_001647, gen.NM_001647
Figure 1353: PRO2551
Figure 1354: DNA324433, NM_032288, gen.NM_032288
Figure 1355: PRO81097
Figure 1356: DNA324434, XM_086228, gen.XM_086228
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Figure 1358: DNA324435, XM_087278, gen.XM_087278
Figure 1359: DNA324436, XM_018523, gen.XM_018523
Figure 1360: DNA324437, XM_087297, gen.XM_087297

Figure 1361: DNA324438, XM_002255, gen.XM_002255
Figure 1362: PRO81102
Figure 1363: DNA324439, XM_053122, gen.XM_053122
Figure 1364: DNA324440, XM_042695, gen.XM_042695
Figure 1365: DNA324441, XM_011160, gen.XM_011160
Figure 1366: DNA324442, NM_007100, gen.NM_007100
Figure 1367: PRO81106
Figure 1368: DNA139747, NM_002477, gen.NM_002477
Figure 1369: PRO9785
Figure 1370: DNA253804, NM_032219, gen.NM_032219
Figure 1371: PRO49209
Figure 1372: DNA324443, NM_138385, gen.NM_138385
Figure 1373: PRO81107
Figure 1374: DNA324444, NM_006342, gen.NM_006342
Figure 1375: PRO81108
Figure 1376A-C: DNA324445, NM_133330, gen.NM_133330
Figure 1377: PRO81109
Figure 1378A-C: DNA324446, NM_014919, gen.NM_014919
Figure 1379: PRO81110
Figure 1380A-C: DNA324447, NM_133332, gen.NM_133332
Figure 1381: PRO81111
Figure 1382: DNA324448, NM_005663, gen.NM_005663
Figure 1383: PRO81112
Figure 1384A-B: DNA324449, XM_098248, gen.XM_098248
Figure 1385: PRO81113
Figure 1386: DNA270615, NM_002938, gen.NM_002938
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Figure 1388A-B: DNA324450, NM_014190, gen.NM_014190
Figure 1389: PRO81114
Figure 1390A-B: DNA324451, NM_014189, gen.NM_014189
Figure 1391: PRO81115
Figure 1392: DNA324452, XM_035572, gen.XM_035572
Figure 1393: PRO81116
Figure 1394A-B: DNA324453, NM_014556, gen.NM_014556
Figure 1395: PRO81117
Figure 1396: DNA324454, NM_001313, gen.NM_001313
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Figure 1398A-B: DNA324455, XM_052626, gen.XM_052626
Figure 1399: PRO81118
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Figure 1401: PRO81119
Figure 1402: DNA324457, XM_035824, gen.XM_035824
Figure 1403: PRO81120
Figure 1404: DNA324458, NM_033296, gen.NM_033296
Figure 1405: PRO81121
Figure 1406: DNA324459, NM_138699, gen.NM_138699
Figure 1407: PRO81122
Figure 1408: DNA324460, XM_116285, gen.XM_116285
Figure 1409: PRO81123
Figure 1410: DNA324461, XM_041221, gen.XM_041221
Figure 1411: PRO81124
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Figure 1413: DNA324463, XM_039165, gen.XM_039165
Figure 1414: DNA324464, NM_025205, gen.NM_025205
Figure 1415: PRO81127
Figure 1416: DNA324465, XM_039173, gen.XM_039173
Figure 1417: DNA324466, XM_039176, gen.XM_039176
Figure 1418: DNA324467, XM_087583, gen.XM_087583
Figure 1419: DNA324468, NM_017491, gen.NM_017491
Figure 1420: PRO12077
Figure 1421: DNA324469, NM_005112, gen.NM_005112
Figure 1422: PRO81131
Figure 1423: DNA324470, XM_011129, gen.XM_011129
Figure 1424A-B: DNA324471, XM_052530, gen.XM_052530
Figure 1425: DNA324472, NM_000661, gen.NM_000661
Figure 1426: PRO81134
Figure 1427A-B: DNA324473, NM_002913, gen.NM_002913
Figure 1428: PRO81135
Figure 1429A-B: DNA324474, XM_047477, gen.XM_047477
Figure 1430: DNA324475, NM_004181, gen.NM_004181
Figure 1431: PRO81137

Figure 1432: DNA324476, XM_003435, gen.XM_003435
Figure 1433: DNA324478, XM_010941, gen.XM_010941
Figure 1434: DNA324479, XM_059593, gen.XM_059593
Figure 1435: DNA324480, NM_001553, gen.NM_001553
Figure 1436: PRO81141
Figure 1437: DNA257511, NM_032313, gen.NM_032313
Figure 1438: PRO52083
Figure 1439: DNA324481, XM_071623, gen.XM_071623
Figure 1440A-B: DNA324482, XM_036002, gen.XM_036002
Figure 1441: DNA324483, XM_058927, gen.XM_058927
Figure 1442: DNA324484, XM_059628, gen.XM_059628
Figure 1443: DNA324485, XM_046057, gen.XM_046057
Figure 1444: PRO81146
Figure 1445: DNA324486, XM_031320, gen.XM_031320
Figure 1446: DNA225919, NM_001134, gen.NM_001134
Figure 1447: PRO36382
Figure 1448A-B: DNA324487, XM_003511, gen.XM_003511
Figure 1449: DNA324488, NM_006835, gen.NM_006835
Figure 1450: PRO4605
Figure 1451: DNA324489, XM_003305, gen.XM_003305
Figure 1452: DNA324490, XM_113425, gen.XM_113425
Figure 1453: DNA324491, XM_001389, gen.XM_001389
Figure 1454: PRO81148
Figure 1455: DNA324492, XM_087527, gen.XM_087527
Figure 1456: DNA324493, XM_035986, gen.XM_035986
Figure 1457A-B: DNA324494, NM_014933, gen.NM_014933
Figure 1458: PRO81150
Figure 1459: DNA290585, NM_000582, gen.NM_000582
Figure 1460: PRO70536
Figure 1461: DNA324495, XM_055551, gen.XM_055551
Figure 1462: PRO81151
Figure 1463: DNA324496, XM_087498, gen.XM_087498
Figure 1464: DNA324497, XM_096203, gen.XM_096203
Figure 1465: DNA324498, XM_084158, gen.XM_084158
Figure 1466: DNA324499, XM_034710, gen.XM_034710
Figure 1467: PRO81156
Figure 1468: DNA324500, XM_034713, gen.XM_034713
Figure 1469: DNA324501, XM_059633, gen.XM_059633
Figure 1470: DNA324502, XM_114426, gen.XM_114426
Figure 1471: DNA324503, XM_056957, gen.XM_056957
Figure 1472: DNA324504, XM_088472, gen.XM_088472
Figure 1473: DNA324505, XM_114424, gen.XM_114424
Figure 1474A-B: DNA324506, XM_042301, gen.XM_042301
Figure 1475: PRO81163
Figure 1476: DNA324507, XM_017925, gen.XM_017925
Figure 1477: DNA324508, XM_052336, gen.XM_052336
Figure 1478: DNA324509, NM_002106, gen.NM_002106
Figure 1479: PRO10297
Figure 1480: DNA324510, XM_085068, gen.XM_085068
Figure 1481: PRO81166
Figure 1482: DNA324511, XM_165473, gen.XM_165473
Figure 1483: DNA324512, XM_087514, gen.XM_087514
Figure 1484: DNA324513, XM_116247, gen.XM_116247
Figure 1485: DNA324514, NM_002358, gen.NM_002358
Figure 1486: PRO81169
Figure 1487: DNA324515, XM_050200, gen.XM_050200
Figure 1488: PRO81170
Figure 1489: DNA225584, NM_001154, gen.NM_001154
Figure 1490: PRO36047
Figure 1491: DNA324516, NM_024900, gen.NM_024900
Figure 1492: PRO81171
Figure 1493: DNA324517, XM_040752, gen.XM_040752
Figure 1494: DNA324518, NM_002413, gen.NM_002413
Figure 1495: PRO60956
Figure 1496: DNA324519, XM_114401, gen.XM_114401

Figure 1497: DNA324520, XM_068164, gen.XM_068164
Figure 1498: PRO81174
Figure 1499: DNA324521, XM_060067, gen.XM_060067
Figure 1500: DNA324522, XM_003555, gen.XM_003555
Figure 1501: PRO81176
Figure 1502: DNA324523, XM_034321, gen.XM_034321
Figure 1503: PRO81177
Figure 1504: DNA324524, NM_006439, gen.NM_006439
Figure 1505: PRO81178
Figure 1506: DNA324525, NM_001006, gen.NM_001006
Figure 1507: PRO81179
Figure 1508: DNA227575, NM_005141, gen.NM_005141
Figure 1509: PRO38038
Figure 1510: DNA324526, XM_114368, gen.XM_114368
Figure 1511A-B: DNA225920, NM_000508, gen.NM_000508
Figure 1512: PRO36383
Figure 1513: DNA324527, NM_021871, gen.NM_021871
Figure 1514: PRO81181
Figure 1515: DNA225921, NM_000509, gen.NM_000509
Figure 1516: PRO36384
Figure 1517: DNA324528, NM_021870, gen.NM_021870
Figure 1518: PRO81182
Figure 1519: DNA324529, XM_059623, gen.XM_059623
Figure 1520: DNA324530, XM_106246, gen.XM_106246
Figure 1521: PRO81184
Figure 1522: DNA324531, NM_002129, gen.NM_002129
Figure 1523: PRO81185
Figure 1524: DNA324532, XM_040321, gen.XM_040321
Figure 1525: DNA324533, XM_015563, gen.XM_015563
Figure 1526: DNA324534, NM_024748, gen.NM_024748
Figure 1527: PRO81188
Figure 1528: DNA324535, XM_165470, gen.XM_165470
Figure 1529: PRO81189
Figure 1530A-E: DNA324536, XM_003477, gen.XM_003477
Figure 1531: DNA324537, XM_165465, gen.XM_165465
Figure 1532: DNA324538, XM_116204, gen.XM_116204
Figure 1533: DNA324539, XM_116205, gen.XM_116205
Figure 1534: DNA324540, XM_098405, gen.XM_098405
Figure 1535: DNA324541, XM_052313, gen.XM_052313
Figure 1536: PRO81195
Figure 1537: DNA324542, XM_087659, gen.XM_087659
Figure 1538: PRO81196
Figure 1539: DNA324543, XM_029096, gen.XM_029096
Figure 1540: DNA324544, XM_003825, gen.XM_003825
Figure 1541: DNA324545, XM_057994, gen.XM_057994
Figure 1542: PRO81199
Figure 1543: DNA324546, XM_087686, gen.XM_087686
Figure 1544: DNA324547, XM_017641, gen.XM_017641
Figure 1545: DNA324548, NM_030782, gen.NM_030782
Figure 1546: PRO81202
Figure 1547: DNA324549, XM_084168, gen.XM_084168
Figure 1548: DNA324550, XM_057492, gen.XM_057492
Figure 1549: DNA324551, XM_087597, gen.XM_087597
Figure 1550: DNA324552, XM_087601, gen.XM_087601
Figure 1551: DNA324554, XM_087599, gen.XM_087599
Figure 1552: DNA324555, XM_114435, gen.XM_114435
Figure 1553: DNA324556, XM_087600, gen.XM_087600
Figure 1554: DNA324557, XM_016170, gen.XM_016170
Figure 1555: DNA324558, XM_114434, gen.XM_114434
Figure 1556: DNA324559, XM_113452, gen.XM_113452
Figure 1557: DNA324560, XM_071580, gen.XM_071580
Figure 1558: PRO81213
Figure 1559: DNA324561, XM_087713, gen.XM_087713
Figure 1560: PRO81214
Figure 1561: DNA324562, XM_094440, gen.XM_094440
Figure 1562: DNA324563, XM_106739, gen.XM_106739

Figure 1563: PRO81216
Figure 1564: DNA324564, XM_087614, gen.XM_087614
Figure 1565: DNA324565, XM_004009, gen.XM_004009
Figure 1566: PRO81219
Figure 1567: DNA324566, XM_114437, gen.XM_114437
Figure 1568: DNA324567, XM_043771, gen.XM_043771
Figure 1569: PRO81221
Figure 1570: DNA324568, NM_000997, gen.NM_000997
Figure 1571: PRO11077
Figure 1572: DNA324569, XM_003869, gen.XM_003869
Figure 1573: DNA227173, NM_001465, gen.NM_001465
Figure 1574: PRO37636
Figure 1575: DNA324570, NM_018034, gen.NM_018034
Figure 1576: PRO81223
Figure 1577: DNA324571, NM_032637, gen.NM_032637
Figure 1578: PRO81224
Figure 1579: DNA324572, NM_005983, gen.NM_005983
Figure 1580: PRO81225
Figure 1581A-B: DNA324573, XM_003896, gen.XM_003896
Figure 1582: DNA287282, NM_002130, gen.NM_002130
Figure 1583: PRO69554
Figure 1584: DNA324574, XM_114442, gen.XM_114442
Figure 1585: PRO81227
Figure 1586: DNA324575, XM_114439, gen.XM_114439
Figure 1587: DNA324576, XM_114440, gen.XM_114440
Figure 1588A-B: DNA324577, XM_032902, gen.XM_032902
Figure 1589: PRO81230
Figure 1590: DNA324578, XM_032895, gen.XM_032895
Figure 1591: DNA324579, XM_084179, gen.XM_084179
Figure 1592: DNA324580, XM_041712, gen.XM_041712
Figure 1593: DNA324581, XM_116439, gen.XM_116439
Figure 1594: PRO81234
Figure 1595: DNA324582, XM_087611, gen.XM_087611
Figure 1596: DNA324583, XM_059653, gen.XM_059653
Figure 1597: DNA324584, XM_087610, gen.XM_087610
Figure 1598: DNA288259, NM_031966, gen.NM_031966
Figure 1599: PRO4676
Figure 1600: DNA324585, XM_042025, gen.XM_042025
Figure 1601: PRO81238
Figure 1602: DNA324586, NM_005713, gen.NM_005713
Figure 1603: PRO81239
Figure 1604: DNA324587, XM_059709, gen.XM_059709
Figure 1605: PRO81240
Figure 1606: DNA324588, XM_116447, gen.XM_116447
Figure 1607: PRO81241
Figure 1608: DNA324589, XM_037260, gen.XM_037260
Figure 1609: DNA324590, XM_098351, gen.XM_098351
Figure 1610: DNA324591, XM_098354, gen.XM_098354
Figure 1611: DNA324592, XM_098352, gen.XM_098352
Figure 1612: DNA324593, XM_166037, gen.XM_166037
Figure 1613: PRO81246
Figure 1614: DNA324594, XM_041694, gen.XM_041694
Figure 1615: DNA324595, XM_165488, gen.XM_165488
Figure 1616: PRO81248
Figure 1617: DNA324596, XM_059669, gen.XM_059669
Figure 1618: PRO81249
Figure 1619: DNA324597, XM_027964, gen.XM_027964
Figure 1620: PRO81250
Figure 1621: DNA324598, XM_088020, gen.XM_088020
Figure 1622: DNA324599, XM_117387, gen.XM_117387
Figure 1623: DNA324600, XM_114469, gen.XM_114469
Figure 1624: DNA324601, NM_001207, gen.NM_001207
Figure 1625: PRO22771
Figure 1626A-B: DNA324602, XM_032553, gen.XM_032553
Figure 1627: DNA254147, NM_000521, gen.NM_000521
Figure 1628: PRO49262
Figure 1629: DNA324603, NM_031482, gen.NM_031482
Figure 1630: PRO81254

Figure 1631: DNA324604, XM_087790, gen.XM_087790
Figure 1632: DNA324605, NM_001025, gen.NM_001025
Figure 1633: PRO10685
Figure 1634: DNA324606, XM_098362, gen.XM_098362
Figure 1635: PRO81256
Figure 1636: DNA324607, NM_003401, gen.NM_003401
Figure 1637: PRO70327
Figure 1638: DNA290231, NM_022550, gen.NM_022550
Figure 1639: PRO70327
Figure 1640: DNA324608, XM_017857, gen.XM_017857
Figure 1641: DNA324609, XM_117398, gen.XM_117398
Figure 1642A-B: DNA257253, NM_032280, gen.NM_032280
Figure 1643: PRO51851
Figure 1644: DNA324610, XM_003771, gen.XM_003771
Figure 1645: PRO81259
Figure 1646A-B: DNA269816, NM_002397, gen.NM_002397
Figure 1647: PRO58219
Figure 1648: DNA324611, XM_116427, gen.XM_116427
Figure 1649: PRO81260
Figure 1650: DNA324612, NM_004772, gen.NM_004772
Figure 1651: PRO81261
Figure 1652: DNA324613, XM_016674, gen.XM_016674
Figure 1653: PRO81262
Figure 1654: DNA324614, XM_113463, gen.XM_113463
Figure 1655: DNA324615, XM_034744, gen.XM_034744
Figure 1656: DNA324616, XM_087745, gen.XM_087745
Figure 1657: PRO81264
Figure 1658: DNA324617, XM_018473, gen.XM_018473
Figure 1659: PRO81265
Figure 1660: DNA324618, XM_087635, gen.XM_087635
Figure 1661: PRO81266
Figure 1662: DNA324619, XM_087637, gen.XM_087637
Figure 1663: DNA324620, XM_166027, gen.XM_166027
Figure 1664: DNA324621, NM_014035, gen.NM_014035
Figure 1665: PRO1285
Figure 1666: DNA324622, XM_003830, gen.XM_003830
Figure 1667: PRO81269
Figure 1668: DNA324623, XM_037002, gen.XM_037002
Figure 1669: DNA324624, XM_166026, gen.XM_166026
Figure 1670: DNA324625, XM_041059, gen.XM_041059
Figure 1671: DNA83020, NM_000358, gen.NM_000358
Figure 1672: PRO2561
Figure 1673: DNA324626, NM_003687, gen.NM_003687
Figure 1674: PRO81272
Figure 1675: DNA324627, XM_034862, gen.XM_034862
Figure 1676: PRO34544
Figure 1677: DNA103380, NM_003374, gen.NM_003374
Figure 1678: PRO4710
Figure 1679: DNA324628, XM_017474, gen.XM_017474
Figure 1680: PRO63082
Figure 1681A-B: DNA324629, NM_014829, gen.NM_014829
Figure 1682: PRO81273
Figure 1683A-B: DNA324630, XM_114482, gen.XM_114482
Figure 1684: PRO81274
Figure 1685: DNA324631, NM_004893, gen.NM_004893
Figure 1686: PRO81275
Figure 1687: DNA269809, NM_006805, gen.NM_006805
Figure 1688: PRO58213
Figure 1689: DNA226872, NM_001964, gen.NM_001964
Figure 1690: PRO37335
Figure 1691: DNA324632, XM_116307, gen.XM_116307
Figure 1692: PRO81276
Figure 1693: DNA324633, NM_004134, gen.NM_004134
Figure 1694: PRO81277
Figure 1695: DNA324634, XM_038221, gen.XM_038221
Figure 1696: PRO81278
Figure 1697: DNA271931, NM_005754, gen.NM_005754
Figure 1698: PRO60207
Figure 1699: DNA324635, XM_003841, gen.XM_003841
Figure 1700: DNA324636, XM_032759, gen.XM_032759
Figure 1701: DNA324637, XM_017591,

gen.XM_017591
Figure 1702: DNA324638, NM_006058,
gen.NM_006058
Figure 1703: PRO81280
Figure 1704: DNA324639, NM_002084,
gen.NM_002084
Figure 1705: PRO81281
Figure 1706: DNA324640, NM_018047,
gen.NM_018047
Figure 1707: PRO81282
Figure 1708: DNA324641, NM_005617,
gen.NM_005617
Figure 1709: PRO10849
Figure 1710: DNA324642, XM_003937,
gen.XM_003937
Figure 1711: DNA324643, XM_087621,
gen.XM_087621
Figure 1712A-B: DNA324644, XM_003789,
gen.XM_003789
Figure 1713: DNA324645, XM_087652,
gen.XM_087652
Figure 1714: DNA324646, XM_068853,
gen.XM_068853
Figure 1715: PRO81286
Figure 1716: DNA324647, XM_116465,
gen.XM_116465
Figure 1717: PRO81287
Figure 1718: DNA302020, NM_005573,
gen.NM_005573
Figure 1719: PRO70993
Figure 1720: DNA324648, XM_113467,
gen.XM_113467
Figure 1721: DNA271626, NM_014773,
gen.NM_014773
Figure 1722: PRO59913
Figure 1723A-B: DNA324649, XM_056315,
gen.XM_056315
Figure 1724: DNA324650, NM_024668,
gen.NM_024668
Figure 1725: PRO81289
Figure 1726: DNA324651, NM_080670,
gen.NM_080670
Figure 1727: PRO81290
Figure 1728A-B: DNA324652, NM_002588,
gen.NM_002588
Figure 1729: PRO81291
Figure 1730A-B: DNA324653, NM_003735,
gen.NM_003735
Figure 1731: PRO81292
Figure 1732A-B: DNA150679, NM_003736,
gen.NM_003736
Figure 1733: PRO12416
Figure 1734A-B: DNA324654, NM_018912,
gen.NM_018912
Figure 1735: PRO36058
Figure 1736A-B: DNA324655, NM_018913,
gen.NM_018913
Figure 1737: PRO81293
Figure 1738A-B: DNA324656, NM_018914,
gen.NM_018914
Figure 1739: PRO81294
Figure 1740A-B: DNA324657, NM_018915,
gen.NM_018915
Figure 1741: PRO36020
Figure 1742A-B: DNA324658, NM_018916,
gen.NM_018916
Figure 1743: PRO81295
Figure 1744A-B: DNA324659, NM_018917,
gen.NM_018917
Figure 1745: PRO81296
Figure 1746A-B: DNA324660, NM_018918,
gen.NM_018918
Figure 1747: PRO81297
Figure 1748A-B: DNA324661, NM_018919,
gen.NM_018919
Figure 1749: PRO81298
Figure 1750A-B: DNA324662, NM_018920,
gen.NM_018920
Figure 1751: PRO81299
Figure 1752A-B: DNA324663, NM_018921,
gen.NM_018921
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Figure 1754A-B: DNA324664, NM_018922,
gen.NM_018922
Figure 1755: PRO81301
Figure 1756A-B: DNA324665, NM_018923,
gen.NM_018923
Figure 1757: PRO81302
Figure 1758A-B: DNA324666, NM_018924,
gen.NM_018924
Figure 1759: PRO81303
Figure 1760A-B: DNA324667, NM_018925,
gen.NM_018925
Figure 1761: PRO81304
Figure 1762A-B: DNA324668, NM_018926,
gen.NM_018926
Figure 1763: PRO81305
Figure 1764A-B: DNA324669, NM_018927,
gen.NM_018927
Figure 1765: PRO37091
Figure 1766A-B: DNA324670, NM_018928,
gen.NM_018928
Figure 1767: PRO81306
Figure 1768A-B: DNA324671, NM_018929,
gen.NM_018929
Figure 1769: PRO81307
Figure 1770A-B: DNA324672, NM_032088,
gen.NM_032088
Figure 1771: PRO81308
Figure 1772A-B: DNA324673, NM_032092,
gen.NM_032092
Figure 1773: PRO81309

Figure 1774: DNA324674, NM_032403, gen.NM_032403
Figure 1775: PRO81310
Figure 1776: DNA324675, NM_032402, gen.NM_032402
Figure 1777: PRO81311
Figure 1778: DNA324676, XM_098387, gen.XM_098387
Figure 1779: DNA324677, NM_002109, gen.NM_002109
Figure 1780: PRO4908
Figure 1781: DNA324678, XM_084180, gen.XM_084180
Figure 1782: PRO81313
Figure 1783: DNA324679, XM_039975, gen.XM_039975
Figure 1784: PRO81314
Figure 1785: DNA324680, NM_033551, gen.NM_033551
Figure 1786: PRO81315
Figure 1787: DNA324681, NM_004821, gen.NM_004821
Figure 1788: PRO81316
Figure 1789: DNA324682, XM_068395, gen.XM_068395
Figure 1790: PRO81317
Figure 1791: DNA226418, NM_004060, gen.NM_004060
Figure 1792: PRO36881
Figure 1793A-B: DNA324683, XM_056963, gen.XM_056963
Figure 1794: PRO81318
Figure 1795: DNA324684, NM_004219, gen.NM_004219
Figure 1796: PRO81319
Figure 1797: DNA324685, XM_094243, gen.XM_094243
Figure 1798A-B: DNA324686, XM_047964, gen.XM_047964
Figure 1799: DNA324687, XM_016345, gen.XM_016345
Figure 1800: DNA324688, NM_002887, gen.NM_002887
Figure 1801: PRO81323
Figure 1802: DNA324689, XM_166029, gen.XM_166029
Figure 1803: DNA324690, NM_002520, gen.NM_002520
Figure 1804: PRO58993
Figure 1805: DNA324691, XM_043340, gen.XM_043340
Figure 1806: PRO81325
Figure 1807: DNA324692, XM_116340, gen.XM_116340
Figure 1808A-B: DNA324693, XM_043388, gen.XM_043388
Figure 1809: PRO81327
Figure 1810: DNA324694, XM_116856, gen.XM_116856
Figure 1811: DNA324695, XM_003716, gen.XM_003716
Figure 1812: DNA227320, NM_003714, gen.NM_003714
Figure 1813: PRO37783
Figure 1814: DNA324696, NM_032361, gen.NM_032361
Figure 1815: PRO81330
Figure 1816: DNA324697, XM_087773, gen.XM_087773
Figure 1817: DNA324698, XM_114457, gen.XM_114457
Figure 1818: DNA324699, XM_165483, gen.XM_165483
Figure 1819: DNA324700, XM_114453, gen.XM_114453
Figure 1820: DNA324701, XM_165484, gen.XM_165484
Figure 1821: DNA324702, XM_030771, gen.XM_030771
Figure 1822: PRO19615
Figure 1823: DNA324703, XM_030777, gen.XM_030777
Figure 1824: DNA324704, XM_030782, gen.XM_030782
Figure 1825: PRO81336
Figure 1826: DNA324705, NM_030567, gen.NM_030567
Figure 1827: PRO81337
Figure 1828: DNA225909, NM_000505, gen.NM_000505
Figure 1829: PRO36372
Figure 1830: DNA274206, NM_006816, gen.NM_006816
Figure 1831: PRO62135
Figure 1832: DNA324706, NM_031300, gen.NM_031300
Figure 1833: PRO81338
Figure 1834: DNA324707, NM_013237, gen.NM_013237
Figure 1835: PRO81339
Figure 1836: DNA324708, NM_002011, gen.NM_002011
Figure 1837: PRO81340
Figure 1838: DNA324709, NM_022963, gen.NM_022963
Figure 1839: PRO81341
Figure 1840: DNA324710, XM_038946, gen.XM_038946
Figure 1841: DNA324711, XM_113454, gen.XM_113454
Figure 1842: DNA324712, XM_166028, gen.XM_166028

Figure 1843: DNA324713, NM_015043, gen.NM_015043
Figure 1844: PRO81345
Figure 1845: DNA324714, XM_113468, gen.XM_113468
Figure 1846: DNA324715, NM_014275, gen.NM_014275
Figure 1847: PRO1927
Figure 1848: DNA324716, NM_054013, gen.NM_054013
Figure 1849: PRO81347
Figure 1850: DNA270675, NM_005520, gen.NM_005520
Figure 1851: PRO59040
Figure 1852: DNA324717, NM_006098, gen.NM_006098
Figure 1853: PRO25849
Figure 1854: DNA269593, NM_005110, gen.NM_005110
Figure 1855: PRO58006
Figure 1856: DNA324718, XM_116365, gen.XM_116365
Figure 1857: DNA324719, XM_116511, gen.XM_116511
Figure 1858: DNA324720, XM_087823, gen.XM_087823
Figure 1859A-C: DNA324721, XM_053955, gen.XM_053955
Figure 1860: DNA324722, XM_113476, gen.XM_113476
Figure 1861: DNA324723, XM_116514, gen.XM_116514
Figure 1862: DNA324724, XM_094741, gen.XM_094741
Figure 1863: DNA324725, NM_025168, gen.NM_025168
Figure 1864: PRO81354
Figure 1865A-B: DNA324726, XM_165740, gen.XM_165740
Figure 1866: DNA272171, NM_002388, gen.NM_002388
Figure 1867: PRO60438
Figure 1868: DNA324727, XM_167169, gen.XM_167169
Figure 1869: PRO81355
Figure 1870: DNA324728, NM_014452, gen.NM_014452
Figure 1871: PRO868
Figure 1872: DNA324729, XM_166349, gen.XM_166349
Figure 1873: PRO81356
Figure 1874: DNA304680, NM_007355, gen.NM_007355
Figure 1875: PRO71106
Figure 1876: DNA324730, XM_165772, gen.XM_165772
Figure 1877: DNA324731, XM_168123, gen.XM_168123
Figure 1878: DNA324732, XM_166457, gen.XM_166457
Figure 1879: DNA324733, XM_166469, gen.XM_166469
Figure 1880: DNA324734, NM_018135, gen.NM_018135
Figure 1881: PRO81359
Figure 1882A-B: DNA324735, XM_166340, gen.XM_166340
Figure 1883: DNA324736, XM_087960, gen.XM_087960
Figure 1884: DNA324737, XM_166362, gen.XM_166362
Figure 1885: PRO81362
Figure 1886: DNA227204, NM_015388, gen.NM_015388
Figure 1887: PRO37667
Figure 1888: DNA324738, XM_166425, gen.XM_166425
Figure 1889: PRO81363
Figure 1890: DNA324739, NM_057161, gen.NM_057161
Figure 1891: PRO81364
Figure 1892: DNA270613, NM_006245, gen.NM_006245
Figure 1893: PRO58984
Figure 1894: DNA324740, NM_006586, gen.NM_006586
Figure 1895: PRO81365
Figure 1896: DNA324741, XM_166402, gen.XM_166402
Figure 1897: PRO81366
Figure 1898: DNA324742, NM_001760, gen.NM_001760
Figure 1899: PRO81367
Figure 1900: DNA287246, NM_004053, gen.NM_004053
Figure 1901: PRO69521
Figure 1902: DNA324743, NM_017601, gen.NM_017601
Figure 1903: PRO81368
Figure 1904: DNA275630, NM_006708, gen.NM_006708
Figure 1905: PRO63253
Figure 1906: DNA324744, NM_014341, gen.NM_014341
Figure 1907: PRO81369
Figure 1908: DNA304460, NM_016059, gen.NM_016059
Figure 1909: PRO4984
Figure 1910: DNA324745, XM_166412, gen.XM_166412
Figure 1911: PRO81370
Figure 1912: DNA304716, NM_078467,

gen.NM_078467
Figure 1913: PRO71142
Figure 1914: DNA324746, XM_166417, gen.XM_166417
Figure 1915: PRO81371
Figure 1916A-B: DNA324747, NM_003137, gen.NM_003137
Figure 1917: PRO81372
Figure 1918A-B: DNA324748, NM_004117, gen.NM_004117
Figure 1919: PRO36841
Figure 1920: DNA324749, XM_166419, gen.XM_166419
Figure 1921: DNA324750, XM_165794, gen.XM_165794
Figure 1922: DNA324751, NM_007104, gen.NM_007104
Figure 1923: PRO10360
Figure 1924: DNA324752, NM_024294, gen.NM_024294
Figure 1925: PRO81375
Figure 1926: DNA324753, NM_022758, gen.NM_022758
Figure 1927: PRO50582
Figure 1928: DNA324754, XM_168070, gen.XM_168070
Figure 1929: DNA324755, NM_012391, gen.NM_012391
Figure 1930: PRO81377
Figure 1931: DNA324756, XM_166459, gen.XM_166459
Figure 1932: DNA324757, XM_166333, gen.XM_166333
Figure 1933: PRO81379
Figure 1934: DNA324758, XM_058039, gen.XM_058039
Figure 1935: PRO81380
Figure 1936: DNA324759, XM_087990, gen.XM_087990
Figure 1937: DNA324760, XM_165743, gen.XM_165743
Figure 1938: DNA324761, XM_166360, gen.XM_166360
Figure 1939: DNA324763, XM_059801, gen.XM_059801
Figure 1940: DNA324764, XM_166363, gen.XM_166363
Figure 1941: DNA324765, XM_016857, gen.XM_016857
Figure 1942: DNA227442, NM_001350, gen.NM_001350
Figure 1943: PRO37905
Figure 1944: DNA324766, NM_005452, gen.NM_005452
Figure 1945: PRO81387
Figure 1946: DNA304661, NM_022551, gen.NM_022551
Figure 1947: PRO71088
Figure 1948: DNA324767, XM_165747, gen.XM_165747
Figure 1949: DNA324768, XM_165698, gen.XM_165698
Figure 1950: PRO4884
Figure 1951A-B: DNA324769, XM_165770, gen.XM_165770
Figure 1952: DNA287227, NM_004159, gen.NM_004159
Figure 1953: PRO69506
Figure 1954: DNA324770, XM_165717, gen.XM_165717
Figure 1955: DNA324771, XM_166480, gen.XM_166480
Figure 1956: DNA324772, XM_165801, gen.XM_165801
Figure 1957A-B: DNA324773, NM_000592, gen.NM_000592
Figure 1958: PRO36316
Figure 1959: DNA324774, NM_001710, gen.NM_001710
Figure 1960: PRO36305
Figure 1961: DNA227607, NM_005346, gen.NM_005346
Figure 1962: PRO38070
Figure 1963: DNA304668, NM_005345, gen.NM_005345
Figure 1964: PRO71095
Figure 1965: DNA324775, NM_021177, gen.NM_021177
Figure 1966: PRO81394
Figure 1967A-B: DNA272263, NM_006295, gen.NM_006295
Figure 1968: PRO70138
Figure 1969: DNA287319, NM_001288, gen.NM_001288
Figure 1970: PRO69584
Figure 1971: DNA324776, NM_001320, gen.NM_001320
Figure 1972: PRO63052
Figure 1973A-B: DNA324777, NM_004639, gen.NM_004639
Figure 1974: PRO81395
Figure 1975A-B: DNA324778, NM_080703, gen.NM_080703
Figure 1976: PRO81396
Figure 1977A-B: DNA324779, NM_080702, gen.NM_080702
Figure 1978: PRO81397
Figure 1979A-B: DNA324780, NM_004638, gen.NM_004638
Figure 1980: PRO81398
Figure 1981A-B: DNA324781, NM_080686, gen.NM_080686

Figure 1982: PRO81399
Figure 1983: DNA324782, XM_165771, gen.XM_165771
Figure 1984: DNA324783, NM_080598, gen.NM_080598
Figure 1985: PRO71125
Figure 1986: DNA304699, NM_004640, gen.NM_004640
Figure 1987: PRO71125
Figure 1988: DNA324784, XM_165765, gen.XM_165765
Figure 1989: PRO81400
Figure 1990: DNA324785, XM_087945, gen.XM_087945
Figure 1991: PRO81401
Figure 1992: DNA324786, XM_166381, gen.XM_166381
Figure 1993: PRO81402
Figure 1994: DNA324787, XM_168104, gen.XM_168104
Figure 1995: DNA324788, XM_166401, gen.XM_166401
Figure 1996: PRO81404
Figure 1997: DNA271040, NM_001517, gen.NM_001517
Figure 1998: PRO59365
Figure 1999A-B: DNA324789, XM_165738, gen.XM_165738
Figure 2000: DNA324790, XM_087939, gen.XM_087939
Figure 2001: PRO81406
Figure 2002: DNA324791, XM_166353, gen.XM_166353
Figure 2003: PRO1112
Figure 2004A-B: DNA324792, XM_166376, gen.XM_166376
Figure 2005: PRO81407
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Figure 2007: DNA290264, NM_025263, gen.NM_025263
Figure 2008: PRO70393
Figure 2009: DNA324794, XM_166361, gen.XM_166361
Figure 2010: PRO81409
Figure 2011: DNA324795, XM_165764, gen.XM_165764
Figure 2012: PRO81410
Figure 2013: DNA324796, XM_165758, gen.XM_165758
Figure 2014: PRO81411
Figure 2015: DNA324797, XM_166406, gen.XM_166406
Figure 2016: DNA324798, XM_165809, gen.XM_165809
Figure 2017: DNA324799, NM_018950, gen.NM_018950
Figure 2018: PRO81414
Figure 2019: DNA324800, XM_166392, gen.XM_166392
Figure 2020: PRO81415
Figure 2021: DNA324801, XM_166336, gen.XM_166336
Figure 2022: PRO81416
Figure 2023: DNA324802, XM_167128, gen.XM_167128
Figure 2024: PRO23797
Figure 2025: DNA324803, XM_167161, gen.XM_167161
Figure 2026: PRO81417
Figure 2027: DNA324804, NM_013375, gen.NM_013375
Figure 2028: PRO81418
Figure 2029: DNA324805, NM_007047, gen.NM_007047
Figure 2030: PRO81419
Figure 2031: DNA324806, XM_167179, gen.XM_167179
Figure 2032: DNA290785, NM_003107, gen.NM_003107
Figure 2033: PRO70544
Figure 2034: DNA150772, NM_003472, gen.NM_003472
Figure 2035: PRO12797
Figure 2036A-B: DNA324807, XM_165728, gen.XM_165728
Figure 2037: DNA324808, XM_165749, gen.XM_165749
Figure 2038: PRO81421
Figure 2039A-B: DNA324809, NM_004973, gen.NM_004973
Figure 2040: PRO81422
Figure 2041: DNA324810, XM_167196, gen.XM_167196
Figure 2042: DNA324811, XM_166446, gen.XM_166446
Figure 2043: PRO81424
Figure 2044A-C: DNA324812, XM_165777, gen.XM_165777
Figure 2045: DNA324813, XM_037875, gen.XM_037875
Figure 2046: PRO81426
Figure 2047: DNA324814, XM_167225, gen.XM_167225
Figure 2048: PRO81427
Figure 2049: DNA324815, XM_166357, gen.XM_166357
Figure 2050: DNA324816, NM_001069, gen.NM_001069
Figure 2051: PRO81429
Figure 2052: DNA324817, NM_001500, gen.NM_001500

Figure 2053: PRO81430
Figure 2054A-B: DNA324818, XM_166042, gen.XM_166042
Figure 2055: PRO51389
Figure 2056: DNA324819, XM_052721, gen.XM_052721
Figure 2057: DNA324820, XM_165499, gen.XM_165499
Figure 2058: DNA324821, XM_114497, gen.XM_114497
Figure 2059: DNA324822, XM_011117, gen.XM_011117
Figure 2060: DNA324823, XM_094855, gen.XM_094855
Figure 2061: PRO81435
Figure 2062: DNA324824, XM_059776, gen.XM_059776
Figure 2063: PRO81436
Figure 2064: DNA324825, XM_055641, gen.XM_055641
Figure 2065: DNA324826, XM_004151, gen.XM_004151
Figure 2066: DNA324827, NM_133645, gen.NM_133645
Figure 2067: PRO81439
Figure 2068: DNA324828, XM_097453, gen.XM_097453
Figure 2069: DNA324829, XM_029228, gen.XM_029228
Figure 2070: DNA103471, NM_006670, gen.NM_006670
Figure 2071: PRO4798
Figure 2072: DNA324830, XM_068963, gen.XM_068963
Figure 2073: PRO81441
Figure 2074: DNA324831, XM_040623, gen.XM_040623
Figure 2075: DNA324832, NM_020320, gen.NM_020320
Figure 2076: PRO81443
Figure 2077: DNA324833, NM_014107, gen.NM_014107
Figure 2078: PRO81444
Figure 2079A-B: DNA324834, XM_084204, gen.XM_084204
Figure 2080: DNA324835, XM_017517, gen.XM_017517
Figure 2081: DNA324836, NM_032929, gen.NM_032929
Figure 2082: PRO81446
Figure 2083: DNA324837, XM_003611, gen.XM_003611
Figure 2084: PRO81447
Figure 2085: DNA324838, XM_068919, gen.XM_068919
Figure 2086: PRO81448
Figure 2087: DNA324839, XM_167016, gen.XM_167016
Figure 2088: PRO81449
Figure 2089: DNA324840, XM_087855, gen.XM_087855
Figure 2090: DNA324841, XM_087853, gen.XM_087853
Figure 2091: DNA324842, XM_165669, gen.XM_165669
Figure 2092: DNA324843, XM_166303, gen.XM_166303
Figure 2093: PRO81453
Figure 2094: DNA324844, XM_167027, gen.XM_167027
Figure 2095: PRO81454
Figure 2096: DNA324845, XM_167037, gen.XM_167037
Figure 2097: PRO81455
Figure 2098: DNA324846, XM_018182, gen.XM_018182
Figure 2099: DNA227924, NM_000165, gen.NM_000165
Figure 2100: PRO38387
Figure 2101: DNA324847, XM_166310, gen.XM_166310
Figure 2102: PRO81457
Figure 2103: DNA324848, XM_168054, gen.XM_168054
Figure 2104: DNA271418, NM_003287, gen.NM_003287
Figure 2105: PRO59717
Figure 2106: DNA324849, XM_114492, gen.XM_114492
Figure 2107: DNA324850, XM_037056, gen.XM_037056
Figure 2108: DNA324851, XM_098468, gen.XM_098468
Figure 2109: PRO19933
Figure 2110: DNA324852, XM_004526, gen.XM_004526
Figure 2111: DNA324853, NM_001016, gen.NM_001016
Figure 2112: PRO81462
Figure 2113: DNA324854, XM_004297, gen.XM_004297
Figure 2114: DNA324855, XM_004256, gen.XM_004256
Figure 2115: PRO81464
Figure 2116: DNA324856, NM_014320, gen.NM_014320
Figure 2117: PRO81465
Figure 2118: DNA324857, XM_059741, gen.XM_059741
Figure 2119: DNA324858, XM_017831, gen.XM_017831
Figure 2120: PRO81467

Figure 2121: DNA324859, XM_049899, gen.XM_049899
Figure 2122: DNA324860, XM_004379, gen.XM_004379
Figure 2123A-C: DNA324861, XM_087834, gen.XM_087834
Figure 2124A-B: DNA324862, XM_087836, gen.XM_087836
Figure 2125: PRO81471
Figure 2126: DNA324863, NM_005389, gen.NM_005389
Figure 2127: PRO66279
Figure 2128A-C: DNA324864, XM_029746, gen.XM_029746
Figure 2129: PRO66282
Figure 2130: DNA324865, XM_004383, gen.XM_004383
Figure 2131: DNA324866, XM_059745, gen.XM_059745
Figure 2132: DNA324867, XM_033912, gen.XM_033912
Figure 2133: PRO81474
Figure 2134: DNA324868, XM_033910, gen.XM_033910
Figure 2135: DNA324870, NM_003181, gen.NM_003181
Figure 2136: PRO81476
Figure 2137: DNA324871, NM_002793, gen.NM_002793
Figure 2138: PRO81477
Figure 2139: DNA324872, XM_044866, gen.XM_044866
Figure 2140: DNA324873, XM_116524, gen.XM_116524
Figure 2141: DNA324874, XM_059773, gen.XM_059773
Figure 2142: DNA324875, XM_084998, gen.XM_084998
Figure 2143: PRO81481
Figure 2144: DNA324876, XM_058266, gen.XM_058266
Figure 2145: DNA324877, XM_042422, gen.XM_042422
Figure 2146A-B: DNA324878, XM_054706, gen.XM_054706
Figure 2147: DNA324879, XM_166049, gen.XM_166049
Figure 2148: DNA324880, XM_042473, gen.XM_042473
Figure 2149: PRO81486
Figure 2150: DNA324881, XM_167046, gen.XM_167046
Figure 2151: PRO23797
Figure 2152: DNA324882, XM_071937, gen.XM_071937
Figure 2153: PRO81487
Figure 2154: DNA324883, XM_087991, gen.XM_087991
Figure 2155: DNA324884, NM_005514, gen.NM_005514
Figure 2156: PRO81490
Figure 2157: DNA324885, XM_166327, gen.XM_166327
Figure 2158: PRO81491
Figure 2159: DNA324886, XM_165692, gen.XM_165692
Figure 2160: DNA324887, XM_117449, gen.XM_117449
Figure 2161: DNA324888, XM_086428, gen.XM_086428
Figure 2162: PRO81494
Figure 2163: DNA324889, NM_032350, gen.NM_032350
Figure 2164: PRO81495
Figure 2165: DNA324890, NM_013393, gen.NM_013393
Figure 2166: PRO81496
Figure 2167: DNA324891, XM_165860, gen.XM_165860
Figure 2168: DNA324892, XM_166541, gen.XM_166541
Figure 2169: PRO81498
Figure 2170A-B: DNA324893, XM_166523, gen.XM_166523
Figure 2171: PRO81499
Figure 2172: DNA324894, NM_016003, gen.NM_016003
Figure 2173: PRO81500
Figure 2174: DNA225631, NM_001101, gen.NM_001101
Figure 2175: PRO36094
Figure 2176: DNA274326, NM_003088, gen.NM_003088
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Figure 2178: DNA324895, NM_006303, gen.NM_006303
Figure 2179: PRO81501
Figure 2180: DNA324896, NM_014413, gen.NM_014413
Figure 2181: PRO60579
Figure 2182: DNA247595, NM_006908, gen.NM_006908
Figure 2183: PRO45014
Figure 2184: DNA324897, NM_006854, gen.NM_006854
Figure 2185: PRO12468
Figure 2186: DNA324898, NM_024067, gen.NM_024067
Figure 2187: PRO81502
Figure 2188: DNA324899, NM_002947, gen.NM_002947
Figure 2189: PRO81503

Figure 2190: DNA324900, XM_166531, gen.XM_166531
Figure 2191: DNA324901, XM_166540, gen.XM_166540
Figure 2192: PRO81505
Figure 2193: DNA193955, NM_002489, gen.NM_002489
Figure 2194: PRO23362
Figure 2195: DNA324902, XM_088264, gen.XM_088264
Figure 2196: PRO81506
Figure 2197: DNA324903, XM_165841, gen.XM_165841
Figure 2198: DNA324904, XM_166521, gen.XM_166521
Figure 2199: PRO81508
Figure 2200: DNA324905, XM_166506, gen.XM_166506
Figure 2201: PRO81509
Figure 2202: DNA324906, XM_166505, gen.XM_166505
Figure 2203: DNA324907, XM_166514, gen.XM_166514
Figure 2204: DNA324908, XM_166515, gen.XM_166515
Figure 2205: DNA324909, XM_166512, gen.XM_166512
Figure 2206: DNA227929, NM_019059, gen.NM_019059
Figure 2207: PRO38392
Figure 2208A-B: DNA324910, NM_018947, gen.NM_018947
Figure 2209: PRO81514
Figure 2210: DNA324911, NM_002137, gen.NM_002137
Figure 2211: PRO81515
Figure 2212: DNA324912, NM_031243, gen.NM_031243
Figure 2213: PRO6373
Figure 2214: DNA324913, NM_007276, gen.NM_007276
Figure 2215: PRO81516
Figure 2216: DNA324914, NM_016587, gen.NM_016587
Figure 2217: PRO81517
Figure 2218: DNA324915, XM_040853, gen.XM_040853
Figure 2219: DNA324916, XM_166509, gen.XM_166509
Figure 2220: DNA324917, XM_166513, gen.XM_166513
Figure 2221: PRO81520
Figure 2222: DNA324918, XM_166504, gen.XM_166504
Figure 2223: PRO81521
Figure 2224: DNA324919, XM_166494, gen.XM_166494
Figure 2225: DNA324920, XM_107825, gen.XM_107825
Figure 2226A-B: DNA324921, NM_022748, gen.NM_022748
Figure 2227: PRO81523
Figure 2228: DNA324922, NM_000598, gen.NM_000598
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Figure 2230A-B: DNA324923, XM_166594, gen.XM_166594
Figure 2231: PRO81524
Figure 2232A-B: DNA275334, NM_030900, gen.NM_030900
Figure 2233: PRO63009
Figure 2234: DNA324924, NM_031443, gen.NM_031443
Figure 2235: PRO81525
Figure 2236: DNA324925, NM_012412, gen.NM_012412
Figure 2237: PRO61812
Figure 2238: DNA324926, NM_021130, gen.NM_021130
Figure 2239: PRO7427
Figure 2240A-B: DNA324927, XM_165877, gen.XM_165877
Figure 2241: PRO81526
Figure 2242: DNA227268, NM_019082, gen.NM_019082
Figure 2243: PRO37731
Figure 2244: DNA324928, XM_015258, gen.XM_015258
Figure 2245: DNA324929, XM_165870, gen.XM_165870
Figure 2246: DNA273865, NM_006230, gen.NM_006230
Figure 2247: PRO61824
Figure 2248A-B: DNA324930, XM_165882, gen.XM_165882
Figure 2249: DNA324931, XM_165867, gen.XM_165867
Figure 2250: PRO61688
Figure 2251: DNA324932, NM_014063, gen.NM_014063
Figure 2252: PRO81529
Figure 2253: DNA324933, XM_165872, gen.XM_165872
Figure 2254: DNA304707, NM_002787, gen.NM_002787
Figure 2255: PRO71133
Figure 2256: DNA324934, XM_016733, gen.XM_016733
Figure 2257: PRO81531
Figure 2258: DNA324935, XM_165876, gen.XM_165876
Figure 2259A-B: DNA324936, NM_014800,

gen.NM_014800
Figure 2260: DNA324937, NM_130442, gen.NM_130442
Figure 2261: PRO81534
Figure 2262: DNA226416, NM_000385, gen.NM_000385
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Figure 2264A-B: DNA324938, XM_167339, gen.XM_167339
Figure 2265: DNA287189, NM_002047, gen.NM_002047
Figure 2266: PRO69475
Figure 2267: DNA324939, XM_170195, gen.XM_170195
Figure 2268: PRO81536
Figure 2269: DNA324940, XM_168378, gen.XM_168378
Figure 2270: PRO81537
Figure 2271: DNA324941, XM_168354, gen.XM_168354
Figure 2272: PRO81538
Figure 2273: DNA324942, XM_167494, gen.XM_167494
Figure 2274: DNA103588, NM_001762, gen.NM_001762
Figure 2275: PRO4912
Figure 2276: DNA324943, XM_037741, gen.XM_037741
Figure 2277: PRO81540
Figure 2278: DNA324944, XM_050265, gen.XM_050265
Figure 2279: PRO81541
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Figure 2281A-B: DNA324946, XM_018359, gen.XM_018359
Figure 2282: DNA324947, XM_059876, gen.XM_059876
Figure 2283: PRO81544
Figure 2284: DNA324948, NM_032951, gen.NM_032951
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Figure 2288: DNA324950, NM_022170, gen.NM_022170
Figure 2289: PRO81547
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Figure 2291: PRO81548
Figure 2292: DNA324952, XM_004901, gen.XM_004901
Figure 2293: DNA324953, NM_016328, gen.NM_016328
Figure 2294: PRO81550
Figure 2295A-B: DNA324954, NM_032999, gen.NM_032999
Figure 2296: PRO81551
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Figure 2298: PRO81552
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Figure 2300A-B: DNA324957, XM_167504, gen.XM_167504
Figure 2301: DNA324958, XM_167498, gen.XM_167498
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Figure 2303: PRO81556
Figure 2304: DNA324960, NM_031925, gen.NM_031925
Figure 2305: PRO81557
Figure 2306: DNA324961, NM_005918, gen.NM_005918
Figure 2307: PRO81558
Figure 2308: DNA304710, NM_001540, gen.NM_001540
Figure 2309: PRO71136
Figure 2310: DNA324962, XM_168470, gen.XM_168470
Figure 2311: DNA324963, XM_168461, gen.XM_168461
Figure 2312A-B: DNA324964, XM_167502, gen.XM_167502
Figure 2313: DNA324965, XM_017442, gen.XM_017442
Figure 2314: PRO81561
Figure 2315: DNA324966, XM_168450, gen.XM_168450
Figure 2316: DNA324967, XM_168435, gen.XM_168435
Figure 2317: DNA324968, XM_168464, gen.XM_168464
Figure 2318: DNA324969, XM_170427, gen.XM_170427
Figure 2319A-B: DNA324971, NM_015068, gen.NM_015068
Figure 2320: PRO81566
Figure 2321A-B: DNA324972, XM_167476, gen.XM_167476
Figure 2322: DNA324973, XM_168181, gen.XM_168181
Figure 2323: DNA324974, XM_168251, gen.XM_168251
Figure 2324: PRO81569
Figure 2325: DNA324975, XM_167477, gen.XM_167477
Figure 2326: DNA324976, NM_005837, gen.NM_005837
Figure 2327: PRO81571

Figure 2328: DNA324977, XM_167483, gen.XM_167483
Figure 2329: DNA324978, XM_167484, gen.XM_167484
Figure 2330: PRO81572
Figure 2331: DNA324979, NM_030935, gen.NM_030935
Figure 2332: PRO81573
Figure 2333: DNA324980, NM_019606, gen.NM_019606
Figure 2334: PRO81574
Figure 2335: DNA324981, NM_024070, gen.NM_024070
Figure 2336: PRO81575
Figure 2337: DNA324982, XM_084241, gen.XM_084241
Figure 2338: DNA324983, NM_006833, gen.NM_006833
Figure 2339: PRO22897
Figure 2340: DNA324984, NM_032164, gen.NM_032164
Figure 2341: PRO81578
Figure 2342: DNA304801, NM_004889, gen.NM_004889
Figure 2343: PRO71211
Figure 2344: DNA324985, NM_006693, gen.NM_006693
Figure 2345: PRO81579
Figure 2346: DNA324986, XM_165839, gen.XM_165839
Figure 2347: PRO81580
Figure 2348: DNA272090, NM_005720, gen.NM_005720
Figure 2349: PRO60360
Figure 2350: DNA324987, XM_165836, gen.XM_165836
Figure 2351A-B: DNA324988, XM_166482, gen.XM_166482
Figure 2352: DNA324989, XM_088180, gen.XM_088180
Figure 2353A-B: DNA324990, XM_166485, gen.XM_166485
Figure 2354: PRO81584
Figure 2355: DNA324991, NM_001673, gen.NM_001673
Figure 2356: PRO81585
Figure 2357: DNA324992, NM_133436, gen.NM_133436
Figure 2358: PRO81586
Figure 2359: DNA324993, XM_168586, gen.XM_168586
Figure 2360: PRO81587
Figure 2361: DNA83141, NM_000602, gen.NM_000602
Figure 2362: PRO2604
Figure 2363: DNA324994, NM_057089, gen.NM_057089
Figure 2364: PRO81588
Figure 2365: DNA324995, NM_001283, gen.NM_001283
Figure 2366: PRO41882
Figure 2367: DNA324996, NM_003378, gen.NM_003378
Figure 2368: PRO81589
Figure 2369: DNA324997, NM_001084, gen.NM_001084
Figure 2370: PRO58437
Figure 2371: DNA270711, NM_006349, gen.NM_006349
Figure 2372: PRO59074
Figure 2373: DNA324998, NM_024653, gen.NM_024653
Figure 2374: PRO81590
Figure 2375: DNA324999, XM_168548, gen.XM_168548
Figure 2376: DNA325000, NM_032958, gen.NM_032958
Figure 2377: PRO81591
Figure 2378: DNA325001, NM_002803, gen.NM_002803
Figure 2379: PRO81592
Figure 2380: DNA325002, XM_168572, gen.XM_168572
Figure 2381: DNA325003, XM_071605, gen.XM_071605
Figure 2382: PRO81594
Figure 2383: DNA325004, XM_033876, gen.XM_033876
Figure 2384: PRO81595
Figure 2385A-B: DNA325005, XM_027214, gen.XM_027214
Figure 2386: DNA325006, XM_088073, gen.XM_088073
Figure 2387: DNA325007, XM_072430, gen.XM_072430
Figure 2388: PRO81598
Figure 2389: DNA325008, XM_050430, gen.XM_050430
Figure 2390: PRO81599
Figure 2391: DNA325009, NM_001753, gen.NM_001753
Figure 2392: PRO81600
Figure 2393: DNA226560, NM_006136, gen.NM_006136
Figure 2394: PRO37023
Figure 2395: DNA325010, XM_012284, gen.XM_012284
Figure 2396: DNA325011, NM_005000, gen.NM_005000
Figure 2397: PRO59380
Figure 2398: DNA325012, NM_001662, gen.NM_001662

Figure 2399: PRO39773
Figure 2400: DNA325013, XM_011618, gen.XM_011618
Figure 2401: PRO81602
Figure 2402: DNA325014, XM_004627, gen.XM_004627
Figure 2403: DNA325015, XM_045401, gen.XM_045401
Figure 2404: DNA325016, XM_114602, gen.XM_114602
Figure 2405: PRO81605
Figure 2406: DNA325017, XM_117481, gen.XM_117481
Figure 2407A-C: DNA325018, XM_045856, gen.XM_045856
Figure 2408: PRO81607
Figure 2409A-B: DNA325019, XM_088105, gen.XM_088105
Figure 2410: PRO81608
Figure 2411: DNA325020, XM_011548, gen.XM_011548
Figure 2412: PRO81609
Figure 2413: DNA325021, XM_045952, gen.XM_045952
Figure 2414: DNA325022, XM_046001, gen.XM_046001
Figure 2415: PRO81611
Figure 2416: DNA325023, XM_088099, gen.XM_088099
Figure 2417: DNA325024, XM_040498, gen.XM_040498
Figure 2418: DNA325025, XM_088103, gen.XM_088103
Figure 2419: PRO81614
Figure 2420: DNA325026, XM_088122, gen.XM_088122
Figure 2421: PRO81615
Figure 2422: DNA325027, XM_088119, gen.XM_088119
Figure 2423: DNA325028, NM_001628, gen.NM_001628
Figure 2424: PRO81617
Figure 2425: DNA325029, NM_020299, gen.NM_020299
Figure 2426: PRO81618
Figure 2427: DNA325030, NM_024033, gen.NM_024033
Figure 2428: PRO81619
Figure 2429: DNA325031, XM_114555, gen.XM_114555
Figure 2430: DNA325032, XM_059839, gen.XM_059839
Figure 2431: PRO81621
Figure 2432: DNA325033, XM_095146, gen.XM_095146
Figure 2433: DNA325034, XM_016700, gen.XM_016700
Figure 2434: DNA325035, XM_042781, gen.XM_042781
Figure 2435: DNA304685, NM_003143, gen.NM_003143
Figure 2436: PRO71111
Figure 2437: DNA325036, NM_018238, gen.NM_018238
Figure 2438: PRO81625
Figure 2439: DNA325037, XM_035107, gen.XM_035107
Figure 2440: DNA325038, NM_003461, gen.NM_003461
Figure 2441: PRO10194
Figure 2442: DNA325039, NM_004911, gen.NM_004911
Figure 2443: PRO2733
Figure 2444A-B: DNA325040, XM_114578, gen.XM_114578
Figure 2445: PRO81627
Figure 2446: DNA325041, XM_088135, gen.XM_088135
Figure 2447: DNA325042, XM_098654, gen.XM_098654
Figure 2448: PRO81629
Figure 2449: DNA325043, NM_023942, gen.NM_023942
Figure 2450: PRO81630
Figure 2451: DNA325044, NM_138434, gen.NM_138434
Figure 2452: PRO81631
Figure 2453: DNA325045, XM_084238, gen.XM_084238
Figure 2454A-B: DNA325046, XM_032216, gen.XM_032216
Figure 2455A-B: DNA325047, XM_032121, gen.XM_032121
Figure 2456: DNA325048, NM_031434, gen.NM_031434
Figure 2457: PRO1555
Figure 2458: DNA226337, NM_005692, gen.NM_005692
Figure 2459: PRO36800
Figure 2460: DNA325049, NM_005614, gen.NM_005614
Figure 2461: PRO37938
Figure 2462A-B: DNA325050, NM_053043, gen.NM_053043
Figure 2463: PRO81634
Figure 2464: DNA325051, NM_022458, gen.NM_022458
Figure 2465: PRO81635
Figure 2466: DNA325052, XM_098669, gen.XM_098669
Figure 2467: DNA325053, NM_017760, gen.NM_017760

Figure 2468: PRO81637
Figure 2469: DNA325054, XM_036413, gen.XM_036413
Figure 2470A-B: DNA325055, XM_032944, gen.XM_032944
Figure 2471: DNA325056, XM_117444, gen.XM_117444
Figure 2472: DNA325057, XM_117452, gen.XM_117452
Figure 2473: DNA325058, XM_070203, gen.XM_070203
Figure 2474: PRO81641
Figure 2475: DNA325059, XM_095371, gen.XM_095371
Figure 2476: DNA325060, NM_004084, gen.NM_004084
Figure 2477: PRO2570
Figure 2478: DNA325061, NM_005217, gen.NM_005217
Figure 2479: PRO9980
Figure 2480: DNA325062, XM_070188, gen.XM_070188
Figure 2481: PRO81643
Figure 2482: DNA325063, XM_035680, gen.XM_035680
Figure 2483: DNA325064, XM_035662, gen.XM_035662
Figure 2484: PRO3344
Figure 2485: DNA325065, XM_005305, gen.XM_005305
Figure 2486: PRO81645
Figure 2487: DNA325066, XM_050293, gen.XM_050293
Figure 2488A-B: DNA325067, XM_027679, gen.XM_027679
Figure 2489: PRO81647
Figure 2490A-B: DNA325068, XM_027651, gen.XM_027651
Figure 2491: DNA274178, NM_005775, gen.NM_005775
Figure 2492: PRO62108
Figure 2493: DNA325069, XM_113557, gen.XM_113557
Figure 2494: PRO81649
Figure 2495: DNA83022, NM_001199, gen.NM_001199
Figure 2496: PRO2042
Figure 2497: DNA325070, NM_006128, gen.NM_006128
Figure 2498: PRO81650
Figure 2499: DNA325071, NM_006131, gen.NM_006131
Figure 2500: PRO81651
Figure 2501: DNA325072, NM_006132, gen.NM_006132
Figure 2502: PRO81652
Figure 2503: DNA325073, NM_025232, gen.NM_025232
Figure 2504: PRO81653
Figure 2505: DNA325074, XM_027440, gen.XM_027440
Figure 2506: DNA225671, NM_001831, gen.NM_001831
Figure 2507: PRO36134
Figure 2508: DNA325075, NM_024567, gen.NM_024567
Figure 2509: PRO81654
Figure 2510: DNA325076, NM_018250, gen.NM_018250
Figure 2511: PRO81655
Figure 2512: DNA227267, NM_018660, gen.NM_018660
Figure 2513: PRO37730
Figure 2514A-B: DNA325077, XM_095545, gen.XM_095545
Figure 2515: DNA325078, XM_088338, gen.XM_088338
Figure 2516: PRO81657
Figure 2517: DNA325079, XM_114617, gen.XM_114617
Figure 2518: PRO81658
Figure 2519: DNA325080, XM_088336, gen.XM_088336
Figure 2520: PRO81659
Figure 2521: DNA325081, XM_047083, gen.XM_047083
Figure 2522: PRO81660
Figure 2523: DNA325082, XM_114618, gen.XM_114618
Figure 2524: PRO81661
Figure 2525: DNA325083, XM_050215, gen.XM_050215
Figure 2526: DNA325084, XM_113531, gen.XM_113531
Figure 2527: DNA325085, NM_018310, gen.NM_018310
Figure 2528: PRO81664
Figure 2529: DNA325086, XM_088294, gen.XM_088294
Figure 2530: DNA325087, XM_013112, gen.XM_013112
Figure 2531: DNA325088, XM_059933, gen.XM_059933
Figure 2532: PRO1108
Figure 2533: DNA325089, XM_011629, gen.XM_011629
Figure 2534: DNA325090, NM_000930, gen.NM_000930
Figure 2535: PRO4
Figure 2536: DNA325091, NM_000931, gen.NM_000931
Figure 2537: PRO81668

Figure 2538: DNA325092, NM_033011, gen.NM_033011
Figure 2539: PRO81669
Figure 2540: DNA325093, XM_166063, gen.XM_166063
Figure 2541: DNA325094, NM_025070, gen.NM_025070
Figure 2542: PRO81671
Figure 2543A-B: DNA325095, XM_030268, gen.XM_030268
Figure 2544: DNA325096, XM_030274, gen.XM_030274
Figure 2545: PRO81673
Figure 2546: DNA151010, NM_003350, gen.NM_003350
Figure 2547: PRO12838
Figure 2548: DNA325097, XM_113540, gen.XM_113540
Figure 2549: PRO81674
Figure 2550: DNA325098, NM_006330, gen.NM_006330
Figure 2551: PRO59230
Figure 2552: DNA325099, NM_001023, gen.NM_001023
Figure 2553: PRO58263
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Figure 2555: PRO81675
Figure 2556: DNA325101, XM_114640, gen.XM_114640
Figure 2557: DNA325102, XM_057780, gen.XM_057780
Figure 2558: DNA325103, XM_166064, gen.XM_166064
Figure 2559: DNA325104, XM_088399, gen.XM_088399
Figure 2560: DNA325105, XM_088401, gen.XM_088401
Figure 2561: DNA325106, XM_042658, gen.XM_042658
Figure 2562: DNA325107, XM_011769, gen.XM_011769
Figure 2563: DNA325108, XM_044627, gen.XM_044627
Figure 2564: DNA325109, XM_098761, gen.XM_098761
Figure 2565: DNA226496, NM_006837, gen.NM_006837
Figure 2566: PRO36959
Figure 2567: DNA325110, NM_014294, gen.NM_014294
Figure 2568: PRO23248
Figure 2569: DNA325111, NM_000971, gen.NM_000971
Figure 2570: PRO81685
Figure 2571: DNA325112, XM_050731, gen.XM_050731
Figure 2572: DNA325113, XM_088325, gen.XM_088325
Figure 2573: PRO81687
Figure 2574: DNA325114, XM_088323, gen.XM_088323
Figure 2575: DNA325115, NM_001444, gen.NM_001444
Figure 2576: PRO81689
Figure 2577: DNA325116, XM_013127, gen.XM_013127
Figure 2578: PRO81690
Figure 2579: DNA325117, XM_165514, gen.XM_165514
Figure 2580: PRO81691
Figure 2581: DNA325118, XM_017816, gen.XM_017816
Figure 2582: DNA325119, XM_098747, gen.XM_098747
Figure 2583: DNA325120, XM_050506, gen.XM_050506
Figure 2584: DNA325121, NM_024613, gen.NM_024613
Figure 2585: PRO81695
Figure 2586: DNA325122, XM_011642, gen.XM_011642
Figure 2587: PRO81696
Figure 2588: DNA325123, NM_000989, gen.NM_000989
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Figure 2593: DNA131588, NM_002568, gen.NM_002568
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Figure 2595: DNA325126, XM_018287, gen.XM_018287
Figure 2596: DNA325127, NM_001568, gen.NM_001568
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Figure 2598: DNA325128, NM_003756, gen.NM_003756
Figure 2599: PRO81700
Figure 2600A-B: DNA272050, NM_006265, gen.NM_006265
Figure 2601: PRO60321
Figure 2602: DNA325129, NM_052886, gen.NM_052886
Figure 2603: PRO81701
Figure 2604: DNA325130, XM_016047, gen.XM_016047
Figure 2605: DNA325131, XM_005060, gen.XM_005060

Figure 2606: DNA325132, NM_005005, gen.NM_005005
Figure 2607: PRO81704
Figure 2608: DNA325133, XM_037657, gen.XM_037657
Figure 2609: DNA325134, XM_029567, gen.XM_029567
Figure 2610: PRO81705
Figure 2611: DNA325135, XM_088316, gen.XM_088316
Figure 2612: DNA325136, XM_051298, gen.XM_051298
Figure 2613: DNA325137, XM_088370, gen.XM_088370
Figure 2614: DNA325138, NM_016647, gen.NM_016647
Figure 2615: PRO23201
Figure 2616: DNA325139, NM_052963, gen.NM_052963
Figure 2617: PRO81708
Figure 2618: DNA325140, XM_049247, gen.XM_049247
Figure 2619: DNA325141, XM_058968, gen.XM_058968
Figure 2620: DNA325143, NM_023078, gen.NM_023078
Figure 2621: PRO81711
Figure 2622: DNA325144, XM_117487, gen.XM_117487
Figure 2623: DNA325145, XM_049226, gen.XM_049226
Figure 2624: PRO81714
Figure 2625: DNA325146, XM_114613, gen.XM_114613
Figure 2626: DNA325147, XM_035368, gen.XM_035368
Figure 2627: DNA325148, XM_113532, gen.XM_113532
Figure 2628: DNA325149, XM_088321, gen.XM_088321
Figure 2629: DNA325150, XM_035373, gen.XM_035373
Figure 2630: PRO81719
Figure 2631: DNA325151, XM_035370, gen.XM_035370
Figure 2632: PRO81720
Figure 2633: DNA325152, NM_000973, gen.NM_000973
Figure 2634: PRO22907
Figure 2635: DNA325153, NM_033301, gen.NM_033301
Figure 2636: PRO22907
Figure 2637: DNA325154, XM_049421, gen.XM_049421
Figure 2638: DNA325155, XM_034640, gen.XM_034640
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Figure 2643: PRO81725
Figure 2644: DNA325159, XM_059979, gen.XM_059979
Figure 2645: DNA325160, XM_167558, gen.XM_167558
Figure 2646: DNA325161, XM_039654, gen.XM_039654
Figure 2647: DNA325162, XM_060006, gen.XM_060006
Figure 2648: PRO81729
Figure 2649: DNA325163, NM_001122, gen.NM_001122
Figure 2650: PRO81730
Figure 2651: DNA325164, NM_001010, gen.NM_001010
Figure 2652: PRO10824
Figure 2653: DNA325165, NM_058195, gen.NM_058195
Figure 2654: PRO81731
Figure 2655: DNA325166, NM_000077, gen.NM_000077
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Figure 2657: DNA325167, NM_058196, gen.NM_058196
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Figure 2659: DNA325168, XM_017931, gen.XM_017931
Figure 2660: DNA271847, NM_001539, gen.NM_001539
Figure 2661: PRO60127
Figure 2662: DNA270991, NM_004323, gen.NM_004323
Figure 2663: PRO59321
Figure 2664: DNA325169, NM_016410, gen.NM_016410
Figure 2665: PRO81734
Figure 2666: DNA325170, XM_005543, gen.XM_005543
Figure 2667: PRO38028
Figure 2668: DNA325171, NM_001842, gen.NM_001842
Figure 2669: PRO21481
Figure 2670: DNA226345, NM_005866, gen.NM_005866
Figure 2671: PRO36808
Figure 2672: DNA325172, XM_088563, gen.XM_088563
Figure 2673: DNA325173, XM_059998, gen.XM_059998

Figure 2674: PRO59579
Figure 2675: DNA325174, NM_013442, gen.NM_013442
Figure 2676: PRO9819
Figure 2677: DNA325175, XM_114661, gen.XM_114661
Figure 2678: PRO81736
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Figure 2680: DNA290319, NM_003289, gen.NM_003289
Figure 2681: PRO70595
Figure 2682A-C: DNA325177, NM_006289, gen.NM_006289
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Figure 2684: DNA325178, XM_048518, gen.XM_048518
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Figure 2688: DNA325180, XM_114662, gen.XM_114662
Figure 2689: DNA325181, NM_001833, gen.NM_001833
Figure 2690: PRO81742
Figure 2691: DNA227491, NM_007096, gen.NM_007096
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Figure 2693: DNA254771, NM_012203, gen.NM_012203
Figure 2694: PRO49869
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Figure 2696: PRO2907
Figure 2697: DNA325182, XM_041020, gen.XM_041020
Figure 2698: PRO81743
Figure 2699: DNA325183, XM_114686, gen.XM_114686
Figure 2700: DNA325184, XM_088637, gen.XM_088637
Figure 2701: DNA287216, NM_021154, gen.NM_021154
Figure 2702: PRO69496
Figure 2703: DNA288247, NM_058179, gen.NM_058179
Figure 2704: PRO70011
Figure 2705: DNA325185, XM_071178, gen.XM_071178
Figure 2706: PRO81746
Figure 2707: DNA325186, XM_005490, gen.XM_005490
Figure 2708: DNA325187, NM_031263, gen.NM_031263
Figure 2709: PRO81748
Figure 2710: DNA325188, XM_018006, gen.XM_018006
Figure 2711: DNA325189, XM_017996, gen.XM_017996
Figure 2712: DNA325190, XM_016113, gen.XM_016113
Figure 2713: PRO81751
Figure 2714: DNA272655, NM_001827, gen.NM_001827
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Figure 2719: PRO81753
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Figure 2721: PRO81754
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Figure 2724: PRO63000
Figure 2725A-B: DNA325195, XM_098943, gen.XM_098943
Figure 2726: DNA325196, XM_016308, gen.XM_016308
Figure 2727: DNA325197, XM_005525, gen.XM_005525
Figure 2728: DNA325198, NM_003389, gen.NM_003389
Figure 2729: PRO81759
Figure 2730: DNA325199, NM_033219, gen.NM_033219
Figure 2731: PRO81760
Figure 2732: DNA325200, NM_006401, gen.NM_006401
Figure 2733: PRO81761
Figure 2734: DNA272213, NM_002486, gen.NM_002486
Figure 2735: PRO60475
Figure 2736: DNA325201, NM_001333, gen.NM_001333
Figure 2737: PRO81762
Figure 2738: DNA325202, XM_116818, gen.XM_116818
Figure 2739: PRO81763
Figure 2740: DNA254543, NM_006808, gen.NM_006808
Figure 2741: PRO49648
Figure 2742: DNA325203, XM_070873, gen.XM_070873
Figure 2743: PRO81764
Figure 2744: DNA325204, XM_042788, gen.XM_042788

Figure 2745: PRO81765
Figure 2746: DNA257309, NM_032342, gen.NM_032342
Figure 2747: PRO51901
Figure 2748: DNA325205, XM_088569, gen.XM_088569
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Figure 2750: DNA325206, XM_088571, gen.XM_088571
Figure 2751: DNA271722, NM_004697, gen.NM_004697
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Figure 2755A-C: DNA325208, XM_005348, gen.XM_005348
Figure 2756: DNA325209, XM_114646, gen.XM_114646
Figure 2757: DNA325210, XM_038391, gen.XM_038391
Figure 2758: PRO81771
Figure 2759A-B: DNA325211, XM_045296, gen.XM_045296
Figure 2760: DNA325212, XM_005365, gen.XM_005365
Figure 2761: DNA289530, NM_004435, gen.NM_004435
Figure 2762: PRO70290
Figure 2763: DNA287271, NM_032799, gen.NM_032799
Figure 2764: PRO69542
Figure 2765: DNA325213, XM_026987, gen.XM_026987
Figure 2766: DNA325214, XM_026985, gen.XM_026985
Figure 2767: DNA225630, NM_016174, gen.NM_016174
Figure 2768: PRO36093
Figure 2769: DNA325215, XM_026968, gen.XM_026968
Figure 2770: PRO81775
Figure 2771: DNA325216, XM_026951, gen.XM_026951
Figure 2772: DNA325217, NM_025072, gen.NM_025072
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Figure 2774: DNA325218, XM_033424, gen.XM_033424
Figure 2775: DNA325219, NM_004957, gen.NM_004957
Figure 2776: PRO81778
Figure 2777: DNA325220, XM_033457, gen.XM_033457
Figure 2778A-B: DNA325221, XM_033460, gen.XM_033460
Figure 2779: PRO81780
Figure 2780: DNA325222, NM_000976, gen.NM_000976
Figure 2781: PRO62236
Figure 2782: DNA218841, NM_012098, gen.NM_012098
Figure 2783: PRO34473
Figure 2784A-B: DNA325223, XM_052725, gen.XM_052725
Figure 2785: PRO81781
Figure 2786: DNA325224, XM_011752, gen.XM_011752
Figure 2787: DNA325225, XM_026944, gen.XM_026944
Figure 2788: PRO81783
Figure 2789: DNA325226, XM_116806, gen.XM_116806
Figure 2790A-B: DNA325227, NM_005347, gen.NM_005347
Figure 2791: PRO81785
Figure 2792: DNA325228, NM_005833, gen.NM_005833
Figure 2793: PRO81786
Figure 2794: DNA325229, NM_007209, gen.NM_007209
Figure 2795: PRO61897
Figure 2796: DNA88350, NM_000177, gen.NM_000177
Figure 2797: PRO2758
Figure 2798A-B: DNA325230, XM_011749, gen.XM_011749
Figure 2799: DNA325231, XM_114679, gen.XM_114679
Figure 2800: DNA325232, XM_087041, gen.XM_087041
Figure 2801: DNA325233, XM_114678, gen.XM_114678
Figure 2802: DNA325234, XM_114677, gen.XM_114677
Figure 2803: DNA325235, XM_087038, gen.XM_087038
Figure 2804: DNA325236, XM_059637, gen.XM_059637
Figure 2805: PRO81792
Figure 2806: DNA325237, NM_000368, gen.NM_000368
Figure 2807: PRO60115
Figure 2808: DNA325238, XM_033385, gen.XM_033385
Figure 2809A-B: DNA325239, XM_033380, gen.XM_033380
Figure 2810: PRO81794
Figure 2811: DNA325240, XM_033362, gen.XM_033362
Figure 2812: PRO81795
Figure 2813: DNA325241, XM_059986,

gen.XM_059986
Figure 2814: PRO81796
Figure 2815A-B: DNA325242, XM_033361, gen.XM_033361
Figure 2816: PRO81797
Figure 2817A-B: DNA325243, XM_033360, gen.XM_033360
Figure 2818: DNA325244, XM_033359, gen.XM_033359
Figure 2819A-B: DNA325245, XM_033355, gen.XM_033355
Figure 2820: DNA325246, NM_014285, gen.NM_014285
Figure 2821: PRO81800
Figure 2822: DNA325247, NM_054012, gen.NM_054012
Figure 2823: PRO81801
Figure 2824: DNA325248, XM_035103, gen.XM_035103
Figure 2825: DNA325249, XM_035109, gen.XM_035109
Figure 2826: DNA325250, NM_000972, gen.NM_000972
Figure 2827: PRO81804
Figure 2828: DNA325251, NM_033161, gen.NM_033161
Figure 2829: PRO81805
Figure 2830: DNA325252, NM_000787, gen.NM_000787
Figure 2831: PRO81806
Figure 2832A-B: DNA325253, XM_011778, gen.XM_011778
Figure 2833: DNA325254, XM_088426, gen.XM_088426
Figure 2834: DNA325255, NM_002003, gen.NM_002003
Figure 2835: PRO1910
Figure 2836: DNA325256, NM_058199, gen.NM_058199
Figure 2837: PRO81809
Figure 2838: DNA325257, XM_059945, gen.XM_059945
Figure 2839: DNA325258, XM_088422, gen.XM_088422
Figure 2840: PRO81811
Figure 2841: DNA325259, XM_029168, gen.XM_029168
Figure 2842: PRO81812
Figure 2843: DNA325260, XM_098913, gen.XM_098913
Figure 2844: PRO81813
Figure 2845: DNA325261, XM_114669, gen.XM_114669
Figure 2846: DNA325262, XM_113564, gen.XM_113564
Figure 2847A-B: DNA325263, XM_088459, gen.XM_088459
Figure 2848: PRO81815
Figure 2849: DNA325264, XM_054752, gen.XM_054752
Figure 2850: PRO81816
Figure 2851: DNA325265, XM_084270, gen.XM_084270
Figure 2852: DNA325266, XM_054763, gen.XM_054763
Figure 2853: PRO81817
Figure 2854: DNA325267, XM_114655, gen.XM_114655
Figure 2855: DNA325268, XM_038030, gen.XM_038030
Figure 2856: PRO59351
Figure 2857: DNA325269, XM_072526, gen.XM_072526
Figure 2858: PRO81819
Figure 2859: DNA325270, XM_059961, gen.XM_059961
Figure 2860: DNA325271, NM_032928, gen.NM_032928
Figure 2861: PRO81821
Figure 2862: DNA325272, NM_014172, gen.NM_014172
Figure 2863: PRO81822
Figure 2864: DNA325273, XM_038049, gen.XM_038049
Figure 2865: PRO62069
Figure 2866: DNA325274, XM_038063, gen.XM_038063
Figure 2867: PRO81823
Figure 2868: DNA325275, NM_000954, gen.NM_000954
Figure 2869: PRO81824
Figure 2870: DNA325276, XM_088461, gen.XM_088461
Figure 2871: DNA325277, XM_059966, gen.XM_059966
Figure 2872: PRO81826
Figure 2873: DNA325278, XM_114649, gen.XM_114649
Figure 2874: DNA325279, XM_117519, gen.XM_117519
Figure 2875: DNA325280, XM_053206, gen.XM_053206
Figure 2876: DNA325281, XM_040272, gen.XM_040272
Figure 2877: PRO58939
Figure 2878: DNA325282, XM_005724, gen.XM_005724
Figure 2879: DNA325283, XM_040267, gen.XM_040267
Figure 2880: PRO81831
Figure 2881: DNA325284, XM_048859, gen.XM_048859

Figure 2882: PRO62617
Figure 2883: DNA325285, NM_003739, gen.NM_003739
Figure 2884: PRO81832
Figure 2885: DNA325286, XM_060976, gen.XM_060976
Figure 2886: PRO81833
Figure 2887: DNA325287, XM_167626, gen.XM_167626
Figure 2888: PRO81834
Figure 2889: DNA325288, XM_165555, gen.XM_165555
Figure 2890: PRO81835
Figure 2891: DNA325289, NM_001494, gen.NM_001494
Figure 2892: PRO81836
Figure 2893: DNA325290, NM_032905, gen.NM_032905
Figure 2894: PRO81837
Figure 2895: DNA325291, NM_005174, gen.NM_005174
Figure 2896: PRO81838
Figure 2897: DNA325292, XM_165557, gen.XM_165557
Figure 2898: DNA325293, XM_167374, gen.XM_167374
Figure 2899: DNA273759, NM_006023, gen.NM_006023
Figure 2900: PRO61721
Figure 2901: DNA325294, XM_167411, gen.XM_167411
Figure 2902: DNA325295, NM_031453, gen.NM_031453
Figure 2903: PRO81841
Figure 2904: DNA325296, XM_167414, gen.XM_167414
Figure 2905: PRO12851
Figure 2906: DNA325297, XM_166717, gen.XM_166717
Figure 2907: PRO81842
Figure 2908: DNA325298, XM_005100, gen.XM_005100
Figure 2909: DNA325299, XM_038536, gen.XM_038536
Figure 2910A-B: DNA325300, XM_084420, gen.XM_084420
Figure 2911: DNA325301, XM_084429, gen.XM_084429
Figure 2912: PRO81846
Figure 2913A-C: DNA325302, XM_165551, gen.XM_165551
Figure 2914: DNA325303, XM_059720, gen.XM_059720
Figure 2915: PRO81848
Figure 2916A-B: DNA325304, NM_019619, gen.NM_019619
Figure 2917: PRO81849
Figure 2918: DNA325305, XM_166665, gen.XM_166665
Figure 2919A-B: DNA325306, NM_002211, gen.NM_002211
Figure 2920: PRO81851
Figure 2921A-B: DNA325307, XM_165567, gen.XM_165567
Figure 2922: DNA325308, XM_166157, gen.XM_166157
Figure 2923: DNA325309, NM_032023, gen.NM_032023
Figure 2924: PRO52537
Figure 2925: DNA325310, XM_165560, gen.XM_165560
Figure 2926: DNA325311, XM_165563, gen.XM_165563
Figure 2927: DNA325312, XM_113615, gen.XM_113615
Figure 2928: PRO81855
Figure 2929: DNA325313, XM_165890, gen.XM_165890
Figure 2930: DNA325314, XM_061126, gen.XM_061126
Figure 2931: DNA325315, XM_061125, gen.XM_061125
Figure 2932: PRO81858
Figure 2933: DNA325316, XM_054474, gen.XM_054474
Figure 2934: DNA325317, XM_165888, gen.XM_165888
Figure 2935: DNA325318, XM_054475, gen.XM_054475
Figure 2936: PRO81861
Figure 2937: DNA325319, XM_015652, gen.XM_015652
Figure 2938: PRO81862
Figure 2939: DNA325320, XM_036593, gen.XM_036593
Figure 2940: PRO81863
Figure 2941: DNA325321, XM_165891, gen.XM_165891
Figure 2942: DNA325322, XM_084450, gen.XM_084450
Figure 2943: PRO81865
Figure 2944: DNA325323, XM_084385, gen.XM_084385
Figure 2945: DNA325324, NM_021226, gen.NM_021226
Figure 2946: PRO81867
Figure 2947: DNA193957, NM_003055, gen.NM_003055
Figure 2948: PRO23364
Figure 2949: DNA325325, NM_032997, gen.NM_032997
Figure 2950: PRO81868

Figure 2951: DNA287642, NM_018464, gen.NM_018464
Figure 2952: PRO9902
Figure 2953: DNA325326, XM_084451, gen.XM_084451
Figure 2954: PRO81869
Figure 2955: DNA325327, NM_012207, gen.NM_012207
Figure 2956: PRO81870
Figure 2957: DNA325328, NM_024045, gen.NM_024045
Figure 2958: PRO81871
Figure 2959: DNA325329, NM_004728, gen.NM_004728
Figure 2960: PRO81872
Figure 2961: DNA88562, NM_002727, gen.NM_002727
Figure 2962: PRO2842
Figure 2963: DNA325330, XM_167395, gen.XM_167395
Figure 2964: DNA227172, NM_021129, gen.NM_021129
Figure 2965: PRO37635
Figure 2966A-B: DNA325331, XM_166125, gen.XM_166125
Figure 2967: PRO81874
Figure 2968: DNA325332, XM_044354, gen.XM_044354
Figure 2969: PRO81875
Figure 2970: DNA325333, XM_032520, gen.XM_032520
Figure 2971: DNA325334, NM_019058, gen.NM_019058
Figure 2972: PRO81877
Figure 2973: DNA325335, XM_045140, gen.XM_045140
Figure 2974: PRO2875
Figure 2975: DNA325336, XM_116863, gen.XM_116863
Figure 2976: DNA325337, XM_032476, gen.XM_032476
Figure 2977: DNA325338, XM_114894, gen.XM_114894
Figure 2978: DNA325339, NM_033022, gen.NM_033022
Figure 2979: PRO81881
Figure 2980: DNA325340, NM_001026, gen.NM_001026
Figure 2981: PRO11139
Figure 2982: DNA103421, NM_003375, gen.NM_003375
Figure 2983: PRO4749
Figure 2984A-B: DNA325341, XM_166093, gen.XM_166093
Figure 2985: PRO81882
Figure 2986: DNA304459, NM_005729, gen.NM_005729
Figure 2987: PRO37073
Figure 2988: DNA325342, XM_166629, gen.XM_166629
Figure 2989: PRO81883
Figure 2990: DNA103506, NM_001157, gen.NM_001157
Figure 2991: PRO4833
Figure 2992: DNA325343, XM_016093, gen.XM_016093
Figure 2993: PRO81884
Figure 2994: DNA325344, XM_084467, gen.XM_084467
Figure 2995: PRO81885
Figure 2996: DNA304488, NM_032333, gen.NM_032333
Figure 2997: PRO71057
Figure 2998: DNA325345, XM_043589, gen.XM_043589
Figure 2999: DNA325346, XM_043605, gen.XM_043605
Figure 3000: DNA325347, XM_087480, gen.XM_087480
Figure 3001: PRO81887
Figure 3002: DNA325348, NM_002921, gen.NM_002921
Figure 3003: PRO81888
Figure 3004: DNA226217, NM_005271, gen.NM_005271
Figure 3005: PRO36680
Figure 3006: DNA325349, XM_089551, gen.XM_089551
Figure 3007: PRO81889
Figure 3008: DNA287237, NM_001613, gen.NM_001613
Figure 3009: PRO39648
Figure 3010: DNA325350, XM_084477, gen.XM_084477
Figure 3011: PRO69523
Figure 3012: DNA325351, XM_084480, gen.XM_084480
Figure 3013A-B: DNA325352, NM_013451, gen.NM_013451
Figure 3014: PRO12813
Figure 3015: DNA325353, XM_018167, gen.XM_018167
Figure 3016: DNA325354, XM_084372, gen.XM_084372
Figure 3017: DNA325355, NM_020992, gen.NM_020992
Figure 3018: PRO81893
Figure 3019: DNA325356, XM_089514, gen.XM_089514
Figure 3020A-B: DNA325357, XM_058343, gen.XM_058343
Figure 3021: PRO81895

Figure 3022: DNA325358, XM_058602, gen.XM_058602
Figure 3023: PRO81896
Figure 3024A-B: DNA325359, NM_015179, gen.NM_015179
Figure 3025: PRO81897
Figure 3026: DNA325360, XM_083842, gen.XM_083842
Figure 3027: PRO69473
Figure 3028: DNA325361, XM_084413, gen.XM_084413
Figure 3029: DNA325362, NM_022362, gen.NM_022362
Figure 3030: PRO81899
Figure 3031: DNA325363, NM_032112, gen.NM_032112
Figure 3032: PRO81900
Figure 3033: DNA325364, NM_021830, gen.NM_021830
Figure 3034: PRO81901
Figure 3035A-B: DNA325365, XM_046743, gen.XM_046743
Figure 3036: PRO81902
Figure 3037: DNA325366, NM_013274, gen.NM_013274
Figure 3038: PRO81903
Figure 3039: DNA325367, NM_022039, gen.NM_022039
Figure 3040: PRO81904
Figure 3041A-B: DNA325368, XM_031866, gen.XM_031866
Figure 3042A-B: DNA325369, NM_015062, gen.NM_015062
Figure 3043: PRO81905
Figure 3044A-B: DNA325370, XM_031890, gen.XM_031890
Figure 3045A-B: DNA325371, NM_004193, gen.NM_004193
Figure 3046: PRO81907
Figure 3047: DNA325372, NM_024040, gen.NM_024040
Figure 3048: PRO81908
Figure 3049: DNA325373, XM_031949, gen.XM_031949
Figure 3050: PRO4900
Figure 3051A-B: DNA144601, NM_016169, gen.NM_016169
Figure 3052: PRO34073
Figure 3053: DNA325374, XM_005698, gen.XM_005698
Figure 3054: PRO81909
Figure 3055: DNA325375, NM_006523, gen.NM_006523
Figure 3056: PRO59043
Figure 3057: DNA325376, XM_018279, gen.XM_018279
Figure 3058A-B: DNA325377, XM_005938, gen.XM_005938
Figure 3059A-B: DNA325378, XM_031992, gen.XM_031992
Figure 3060: PRO81912
Figure 3061: DNA325379, NM_032747, gen.NM_032747
Figure 3062: PRO81913
Figure 3063: DNA325380, NM_005004, gen.NM_005004
Figure 3064: PRO81914
Figure 3065: DNA325381, XM_030447, gen.XM_030447
Figure 3066: DNA273521, NM_002079, gen.NM_002079
Figure 3067: PRO61502
Figure 3068A-B: DNA325382, NM_032211, gen.NM_032211
Figure 3069: PRO81916
Figure 3070: DNA325383, NM_031484, gen.NM_031484
Figure 3071: PRO81917
Figure 3072: DNA325384, XM_084632, gen.XM_084632
Figure 3073: DNA325385, XM_084359, gen.XM_084359
Figure 3074A-D: DNA325386, XM_045667, gen.XM_045667
Figure 3075: DNA325387, XM_109162, gen.XM_109162
Figure 3076: DNA227509, NM_000274, gen.NM_000274
Figure 3077: PRO37972
Figure 3078: DNA325388, XM_058361, gen.XM_058361
Figure 3079: PRO81922
Figure 3080: DNA325389, XM_084505, gen.XM_084505
Figure 3081: PRO81923
Figure 3082A-B: DNA325390, XM_049795, gen.XM_049795
Figure 3083: PRO81924
Figure 3084: DNA325391, XM_058406, gen.XM_058406
Figure 3085: PRO81925
Figure 3086: DNA325392, XM_055573, gen.XM_055573
Figure 3087: PRO60991
Figure 3088: DNA325393, XM_005969, gen.XM_005969
Figure 3089: DNA325394, NM_007190, gen.NM_007190
Figure 3090: PRO81926
Figure 3091: DNA325395, NM_000982, gen.NM_000982
Figure 3092: PRO81927

Figure 3093: DNA269952, NM_004725, gen.NM_004725
Figure 3094: PRO58348
Figure 3095: DNA325396, NM_024942, gen.NM_024942
Figure 3096: PRO81928
Figure 3097: DNA325397, NM_016567, gen.NM_016567
Figure 3098: PRO81929
Figure 3099: DNA325398, NM_004092, gen.NM_004092
Figure 3100: PRO81930
Figure 3101: DNA269431, NM_006659, gen.NM_006659
Figure 3102: PRO57854
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Figure 3104: DNA325400, XM_114862, gen.XM_114862
Figure 3105: PRO81932
Figure 3106: DNA325401, XM_088009, gen.XM_088009
Figure 3107: DNA325402, NM_016526, gen.NM_016526
Figure 3108: PRO81934
Figure 3109: DNA255696, NM_021932, gen.NM_021932
Figure 3110: PRO50756
Figure 3111: DNA325403, XM_043220, gen.XM_043220
Figure 3112: PRO81935
Figure 3113: DNA255078, NM_006435, gen.NM_006435
Figure 3114: PRO50165
Figure 3115: DNA325404, NM_002339, gen.NM_002339
Figure 3116: PRO81936
Figure 3117: DNA325405, XM_028192, gen.XM_028192
Figure 3118: PRO81937
Figure 3119: DNA325406, XM_096544, gen.XM_096544
Figure 3120: DNA325407, NM_000612, gen.NM_000612
Figure 3121: PRO124
Figure 3122: DNA325408, XM_084742, gen.XM_084742
Figure 3123: PRO81939
Figure 3124: DNA325409, XM_084739, gen.XM_084739
Figure 3125: DNA325410, XM_058505, gen.XM_058505
Figure 3126: PRO81941
Figure 3127: DNA325411, XM_006139, gen.XM_006139
Figure 3128: PRO81942
Figure 3129: DNA325412, XM_044932, gen.XM_044932
Figure 3130: PRO81943
Figure 3131A-B: DNA325413, XM_044957, gen.XM_044957
Figure 3132: PRO81944
Figure 3133: DNA325414, NM_001909, gen.NM_001909
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Figure 3135: DNA325415, XM_006475, gen.XM_006475
Figure 3136: DNA325416, XM_006483, gen.XM_006483
Figure 3137: DNA325417, NM_001751, gen.NM_001751
Figure 3138: PRO69635
Figure 3139: DNA325418, XM_114981, gen.XM_114981
Figure 3140: PRO81945
Figure 3141: DNA325419, XM_083852, gen.XM_083852
Figure 3142: DNA325420, NM_000559, gen.NM_000559
Figure 3143: PRO81946
Figure 3144: DNA325421, NM_000184, gen.NM_000184
Figure 3145: PRO81947
Figure 3146: DNA325422, NM_005330, gen.NM_005330
Figure 3147: PRO81948
Figure 3148: DNA325423, XM_015243, gen.XM_015243
Figure 3149: DNA325424, NM_015324, gen.NM_015324
Figure 3150: PRO81950
Figure 3151: DNA325425, XM_006424, gen.XM_006424
Figure 3152: DNA325426, XM_113238, gen.XM_113238
Figure 3153A-C: DNA325427, XM_052786, gen.XM_052786
Figure 3154: PRO81953
Figure 3155: DNA325428, NM_000990, gen.NM_000990
Figure 3156: PRO25985
Figure 3157A-B: DNA325429, XM_045750, gen.XM_045750
Figure 3158: PRO81954
Figure 3159: DNA325430, XM_058414, gen.XM_058414
Figure 3160: PRO81955
Figure 3161A-B: DNA325431, XM_049197, gen.XM_049197
Figure 3162: PRO81956
Figure 3163A-B: DNA325432, NM_001418, gen.NM_001418

Figure 3164: PRO81957
Figure 3165: DNA325433, XM_096520, gen.XM_096520
Figure 3166: PRO81958
Figure 3167: DNA325434, XM_006212, gen.XM_006212
Figure 3168: PRO81959
Figure 3169: DNA325435, XM_084527, gen.XM_084527
Figure 3170: DNA325436, XM_016139, gen.XM_016139
Figure 3171: DNA325437, NM_001017, gen.NM_001017
Figure 3172: PRO11262
Figure 3173: DNA325438, NM_014267, gen.NM_014267
Figure 3174: PRO81962
Figure 3175: DNA97285, NM_005566, gen.NM_005566
Figure 3176: PRO3632
Figure 3177: DNA325439, XM_115081, gen.XM_115081
Figure 3178: DNA325440, XM_036339, gen.XM_036339
Figure 3179: PRO81964
Figure 3180: DNA325441, XM_084514, gen.XM_084514
Figure 3181: PRO81965
Figure 3182: DNA325442, XM_084516, gen.XM_084516
Figure 3183: DNA325443, XM_084515, gen.XM_084515
Figure 3184: DNA325444, XM_084517, gen.XM_084517
Figure 3185: DNA325445, XM_034431, gen.XM_034431
Figure 3186: PRO11691
Figure 3187: DNA325446, XM_030326, gen.XM_030326
Figure 3188: DNA325447, NM_057174, gen.NM_057174
Figure 3189: PRO81970
Figure 3190: DNA325448, NM_004813, gen.NM_004813
Figure 3191: PRO81971
Figure 3192: DNA325449, XM_167437, gen.XM_167437
Figure 3193: DNA325450, XM_054856, gen.XM_054856
Figure 3194: DNA325451, XM_004330, gen.XM_004330
Figure 3195: DNA325452, XM_084681, gen.XM_084681
Figure 3196: DNA325453, XM_006297, gen.XM_006297
Figure 3197: DNA325454, NM_003646, gen.NM_003646
Figure 3198: PRO81977
Figure 3199: DNA325455, NM_004551, gen.NM_004551
Figure 3200: PRO81978
Figure 3201: DNA325456, XM_006170, gen.XM_006170
Figure 3202: DNA325457, XM_037173, gen.XM_037173
Figure 3203: PRO81980
Figure 3204: DNA150974, NM_005693, gen.NM_005693
Figure 3205: PRO12224
Figure 3206: DNA226080, NM_001610, gen.NM_001610
Figure 3207: PRO36543
Figure 3208: DNA270134, NM_000107, gen.NM_000107
Figure 3209: PRO58523
Figure 3210: DNA325458, NM_016223, gen.NM_016223
Figure 3211: PRO81981
Figure 3212: DNA325459, XM_037147, gen.XM_037147
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Figure 3214: DNA325460, XM_015705, gen.XM_015705
Figure 3215: DNA272728, NM_003146, gen.NM_003146
Figure 3216: PRO60847
Figure 3217: DNA325461, XM_165611, gen.XM_165611
Figure 3218: DNA287417, NM_024098, gen.NM_024098
Figure 3219: PRO69674
Figure 3220: DNA227088, NM_014502, gen.NM_014502
Figure 3221: PRO37551
Figure 3222: DNA325462, XM_165610, gen.XM_165610
Figure 3223A-B: DNA325463, XM_165612, gen.XM_165612
Figure 3224: DNA325464, XM_166234, gen.XM_166234
Figure 3225: DNA325465, NM_015533, gen.NM_015533
Figure 3226: PRO81988
Figure 3227: DNA325466, XM_166232, gen.XM_166232
Figure 3228A-B: DNA325467, XM_167748, gen.XM_167748
Figure 3229: PRO81990
Figure 3230: DNA325468, NM_004739, gen.NM_004739
Figure 3231: PRO81991
Figure 3232: DNA325469, NM_014610,

gen.NM_014610
Figure 3233: PRO81992
Figure 3234: DNA325470, XM_167747, gen.XM_167747
Figure 3235: PRO81993
Figure 3236: DNA287254, NM_024099, gen.NM_024099
Figure 3237: PRO69528
Figure 3238: DNA325471, NM_015853, gen.NM_015853
Figure 3239: PRO81994
Figure 3240: DNA325472, NM_032667, gen.NM_032667
Figure 3241: PRO81995
Figure 3242: DNA325473, NM_006362, gen.NM_006362
Figure 3243: PRO81996
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Figure 3245: DNA75863, NM_002411, gen.NM_002411
Figure 3246: PRO2018
Figure 3247: DNA325475, XM_087710, gen.XM_087710
Figure 3248: DNA325476, XM_167726, gen.XM_167726
Figure 3249: DNA325477, NM_004265, gen.NM_004265
Figure 3250: PRO12878
Figure 3251A-B: DNA325478, NM_013402, gen.NM_013402
Figure 3252: PRO81999
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Figure 3254: PRO69568
Figure 3255: DNA325480, XM_048286, gen.XM_048286
Figure 3256: DNA325481, NM_004322, gen.NM_004322
Figure 3257: PRO20117
Figure 3258: DNA325482, NM_032989, gen.NM_032989
Figure 3259: PRO20117
Figure 3260: DNA325483, XM_011988, gen.XM_011988
Figure 3261: DNA325484, NM_031472, gen.NM_031472
Figure 3262: PRO82002
Figure 3263: DNA325485, XM_037808, gen.XM_037808
Figure 3264: DNA325486, NM_004074, gen.NM_004074
Figure 3265: PRO82004
Figure 3266: DNA325487, NM_017670, gen.NM_017670
Figure 3267: PRO82005
Figure 3268: DNA325488, XM_113223, gen.XM_113223
Figure 3269: DNA325489, XM_045642, gen.XM_045642
Figure 3270: DNA325490, XM_006533, gen.XM_006533
Figure 3271: DNA325491, XM_045613, gen.XM_045613
Figure 3272: PRO59721
Figure 3273A-B: DNA325492, XM_045612, gen.XM_045612
Figure 3274: PRO82009
Figure 3275: DNA325493, XM_113224, gen.XM_113224
Figure 3276: DNA325494, XM_045499, gen.XM_045499
Figure 3277: PRO82011
Figure 3278: DNA325495, XM_045525, gen.XM_045525
Figure 3279: DNA325496, NM_013265, gen.NM_013265
Figure 3280: PRO82013
Figure 3281: DNA325497, XM_006529, gen.XM_006529
Figure 3282: PRO60008
Figure 3283: DNA325498, XM_053787, gen.XM_053787
Figure 3284: DNA269803, NM_001667, gen.NM_001667
Figure 3285: PRO58207
Figure 3286: DNA325499, XM_115031, gen.XM_115031
Figure 3287: DNA325500, XM_084702, gen.XM_084702
Figure 3288: DNA325501, XM_053796, gen.XM_053796
Figure 3289: DNA325502, NM_002689, gen.NM_002689
Figure 3290: PRO82018
Figure 3291A-D: DNA325503, XM_167804, gen.XM_167804
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Figure 3295: DNA270721, NM_006842, gen.NM_006842
Figure 3296: PRO59084
Figure 3297: DNA189687, NM_000852, gen.NM_000852
Figure 3298: PRO25845
Figure 3299: DNA325506, NM_007103, gen.NM_007103
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Figure 3305: PRO82023
Figure 3306: DNA325510, NM_006053, gen.NM_006053
Figure 3307: PRO24831
Figure 3308: DNA325511, XM_166196, gen.XM_166196
Figure 3309: PRO82024
Figure 3310: DNA325512, XM_165600, gen.XM_165600
Figure 3311A-B: DNA325513, NM_053056, gen.NM_053056
Figure 3312: PRO4870
Figure 3313: DNA103474, NM_003824, gen.NM_003824
Figure 3314: PRO4801
Figure 3315: DNA325514, XM_096486, gen.XM_096486
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Figure 3318A-B: DNA325516, XM_167853, gen.XM_167853
Figure 3319: PRO82028
Figure 3320: DNA325517, NM_014042, gen.NM_014042
Figure 3321: PRO82029
Figure 3322A-B: DNA325518, NM_001567, gen.NM_001567
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Figure 3327: PRO57307
Figure 3328: DNA325522, XM_165631, gen.XM_165631
Figure 3329: DNA254186, NM_014752, gen.NM_014752
Figure 3330: PRO49298
Figure 3331: DNA325523, NM_001005, gen.NM_001005
Figure 3332: PRO82032
Figure 3333: DNA88176, NM_001235, gen.NM_001235
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Figure 3335A-B: DNA325524, XM_165627, gen.XM_165627
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Figure 3338: PRO82034
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Figure 3344A-B: DNA325530, NM_012296, gen.NM_012296
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Figure 3346: DNA325531, NM_032379, gen.NM_032379
Figure 3347: PRO82038
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Figure 3349: DNA325533, XM_166239, gen.XM_166239
Figure 3350: DNA325534, XM_084610, gen.XM_084610
Figure 3351: PRO82040
Figure 3352: DNA325535, XM_058450, gen.XM_058450
Figure 3353: DNA325536, XM_084601, gen.XM_084601
Figure 3354: PRO82042
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Figure 3356: PRO82043
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Figure 3359: DNA325540, NM_001467, gen.NM_001467
Figure 3360: PRO82045
Figure 3361: DNA325541, NM_001028, gen.NM_001028
Figure 3362: PRO82046
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Figure 3364: DNA325543, XM_115062, gen.XM_115062
Figure 3365: DNA325544, XM_115063, gen.XM_115063
Figure 3366: DNA325545, XM_113229, gen.XM_113229
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Figure 3368: PRO82050
Figure 3369: DNA325547, NM_022003, gen.NM_022003

Figure 3370: PRO82051
Figure 3371: DNA325548, XM_006432, gen.XM_006432
Figure 3372: PRO82052
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Figure 3374: DNA325550, NM_025164, gen.NM_025164
Figure 3375: PRO82054
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Figure 3378: DNA325551, XM_052113, gen.XM_052113
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Figure 3380: DNA271324, NM_006169, gen.NM_006169
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Figure 3394: DNA325556, XM_017369, gen.XM_017369
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Figure 3396: PRO82060
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Figure 3398: DNA325559, XM_051430, gen.XM_051430
Figure 3399: DNA325560, XM_006467, gen.XM_006467
Figure 3400: DNA325561, XM_113226, gen.XM_113226
Figure 3401: DNA325562, XM_165592, gen.XM_165592
Figure 3402: PRO82064
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Figure 3405: PRO82066
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Figure 3408: PRO82068
Figure 3409: DNA325567, XM_166174, gen.XM_166174
Figure 3410: PRO82069
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Figure 3419: PRO82072
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Figure 3421: PRO82073
Figure 3422: DNA325574, NM_058193, gen.NM_058193
Figure 3423: PRO82074
Figure 3424: DNA325575, XM_084522, gen.XM_084522
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Figure 3431: PRO82078
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Figure 3437: DNA325583, XM_113739, gen.XM_113739
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Figure 3447: PRO82084
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Figure 3449: PRO82085
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Figure 3451: DNA325591, XM_116926, gen.XM_116926
Figure 3452: DNA88114, NM_001734, gen.NM_001734
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Figure 3457A-B: DNA325594, XM_032588, gen.XM_032588
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Figure 3459: PRO38010
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Figure 3464: PRO82091
Figure 3465: DNA325599, XM_165910, gen.XM_165910
Figure 3466: DNA151827, NM_005439, gen.NM_005439
Figure 3467: PRO12902
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Figure 3485A-B: DNA325605, XM_006925, gen.XM_006925
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Figure 3496: DNA325612, NM_031289, gen.NM_031289
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Figure 3498: DNA226771, NM_003979, gen.NM_003979
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Figure 3501: DNA325614, NM_007178, gen.NM_007178
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Figure 3508: PRO82109
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Figure 3510: PRO82110
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Figure 3637: PRO82174
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Figure 3692: PRO82196
Figure 3693: DNA325716, NM_023033, gen.NM_023033
Figure 3694: PRO82197
Figure 3695: DNA325717, NM_005726, gen.NM_005726
Figure 3696: PRO82198
Figure 3697: DNA325718, NM_006576, gen.NM_006576
Figure 3698: PRO82199
Figure 3699A-B: DNA325719, XM_096038, gen.XM_096038
Figure 3700: DNA325720, XM_056681, gen.XM_056681
Figure 3701: PRO82201
Figure 3702: DNA325721, XM_084909, gen.XM_084909
Figure 3703: PRO82202
Figure 3704: DNA325722, XM_004098, gen.XM_004098
Figure 3705: DNA325723, XM_084912, gen.XM_084912
Figure 3706: PRO82204
Figure 3707: DNA325724, XM_040221, gen.XM_040221
Figure 3708: DNA325725, XM_016605, gen.XM_016605
Figure 3709: PRO82206
Figure 3710: DNA325726, XM_017508, gen.XM_017508
Figure 3711: PRO82207
Figure 3712: DNA325727, NM_032338, gen.NM_032338
Figure 3713: PRO82208
Figure 3714A-B: DNA325728, XM_052460, gen.XM_052460
Figure 3715: DNA325729, XM_083866, gen.XM_083866
Figure 3716: PRO82210
Figure 3717: DNA304694, NM_020401,

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Figure 3718: PRO71120
Figure 3719: DNA325730, XM_052474, gen.XM_052474
Figure 3720: DNA227474, NM_015646, gen.NM_015646
Figure 3721: PRO37937
Figure 3722: DNA325731, XM_053952, gen.XM_053952
Figure 3723: PRO82212
Figure 3724: DNA227171, NM_014515, gen.NM_014515
Figure 3725: PRO37634
Figure 3726: DNA325732, XM_046041, gen.XM_046041
Figure 3727: DNA271492, NM_006530, gen.NM_006530
Figure 3728: PRO59785
Figure 3729: DNA226014, NM_000239, gen.NM_000239
Figure 3730: PRO36477
Figure 3731: DNA325733, XM_084645, gen.XM_084645
Figure 3732A-B: DNA325734, XM_039395, gen.XM_039395
Figure 3733: PRO82213
Figure 3734: DNA325736, XM_040644, gen.XM_040644
Figure 3735: PRO82214
Figure 3736A-B: DNA325737, XM_006578, gen.XM_006578
Figure 3737: DNA325738, XM_038308, gen.XM_038308
Figure 3738: PRO82215
Figure 3739: DNA325739, XM_096597, gen.XM_096597
Figure 3740: DNA325740, NM_001920, gen.NM_001920
Figure 3741: PRO2841
Figure 3742: DNA325741, NM_133503, gen.NM_133503
Figure 3743: PRO2841
Figure 3744: DNA325742, NM_133504, gen.NM_133504
Figure 3745: PRO82218
Figure 3746: DNA325743, NM_133505, gen.NM_133505
Figure 3747: PRO82219
Figure 3748: DNA325744, NM_133507, gen.NM_133507
Figure 3749: PRO82220
Figure 3750: DNA325745, NM_133506, gen.NM_133506
Figure 3751: PRO82221
Figure 3752: DNA325746, NM_002345, gen.NM_002345
Figure 3753: PRO9987
Figure 3754: DNA325747, XM_167518, gen.XM_167518
Figure 3755: DNA325748, XM_052542, gen.XM_052542
Figure 3756: PRO82223
Figure 3757: DNA325749, NM_003877, gen.NM_003877
Figure 3758: PRO12839
Figure 3759: DNA325750, XM_012219, gen.XM_012219
Figure 3760: PRO69473
Figure 3761: DNA325751, XM_012145, gen.XM_012145
Figure 3762: PRO82224
Figure 3763: DNA274361, NM_000895, gen.NM_000895
Figure 3764: PRO62273
Figure 3765: DNA325752, XM_006887, gen.XM_006887
Figure 3766: DNA325753, XM_006589, gen.XM_006589
Figure 3767: DNA325754, XM_090458, gen.XM_090458
Figure 3768: PRO82227
Figure 3769: DNA325755, XM_052641, gen.XM_052641
Figure 3770: PRO82228
Figure 3771A-B: DNA325756, XM_049211, gen.XM_049211
Figure 3772: DNA325757, XM_049201, gen.XM_049201
Figure 3773: DNA325758, XM_058556, gen.XM_058556
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Figure 3775: DNA325760, XM_062437, gen.XM_062437
Figure 3776: PRO82232
Figure 3777: DNA254777, NM_014325, gen.NM_014325
Figure 3778: PRO49875
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Figure 3780: PRO82233
Figure 3781: DNA325762, NM_000970, gen.NM_000970
Figure 3782: PRO82234
Figure 3783: DNA325763, XM_084800, gen.XM_084800
Figure 3784: PRO82235
Figure 3785: DNA325764, NM_006817, gen.NM_006817
Figure 3786: PRO70694
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Figure 3788A-B: DNA325766, XM_084941, gen.XM_084941
Figure 3789: PRO82237
Figure 3790A-B: DNA325767, NM_057169, gen.NM_057169
Figure 3791: PRO82238
Figure 3792A-B: DNA325768, NM_014776, gen.NM_014776
Figure 3793: PRO82239
Figure 3794: DNA325769, NM_032904, gen.NM_032904
Figure 3795: PRO82240
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Figure 3797: DNA325771, XM_007002, gen.XM_007002
Figure 3798: DNA325772, XM_056996, gen.XM_056996
Figure 3799: PRO82243
Figure 3800: DNA325773, XM_084946, gen.XM_084946
Figure 3801: PRO82244
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Figure 3803: PRO82245
Figure 3804: DNA325776, XM_084948, gen.XM_084948
Figure 3805: DNA325777, NM_007062, gen.NM_007062
Figure 3806: PRO82247
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Figure 3809: DNA325779, XM_115197, gen.XM_115197
Figure 3810: DNA325780, NM_017901, gen.NM_017901
Figure 3811: PRO82250
Figure 3812: DNA325781, NM_032814, gen.NM_032814
Figure 3813: PRO82252
Figure 3814: DNA325782, XM_084889, gen.XM_084889
Figure 3815: PRO82253
Figure 3816: DNA325783, NM_002567, gen.NM_002567
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Figure 3818: DNA325784, XM_084808, gen.XM_084808
Figure 3819: DNA325785, XM_096572, gen.XM_096572
Figure 3820: PRO82255
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Figure 3827: DNA302016, NM_001002, gen.NM_001002
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Figure 3829: DNA325789, NM_053275, gen.NM_053275
Figure 3830: PRO70989
Figure 3831: DNA325790, NM_006253, gen.NM_006253
Figure 3832: PRO82259
Figure 3833: DNA325791, XM_045187, gen.XM_045187
Figure 3834: DNA325792, XM_045963, gen.XM_045963
Figure 3835: DNA325793, XM_006595, gen.XM_006595
Figure 3836: DNA325794, XM_012124, gen.XM_012124
Figure 3837: DNA325795, NM_002813, gen.NM_002813
Figure 3838: PRO82263
Figure 3839: DNA325796, NM_019887, gen.NM_019887
Figure 3840: PRO69471
Figure 3841A-B: DNA325797, XM_038791, gen.XM_038791
Figure 3842: PRO82264
Figure 3843: DNA325798, NM_016638, gen.NM_016638
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Figure 3845: DNA325799, XM_116913, gen.XM_116913
Figure 3846: PRO82266
Figure 3847: DNA325800, NM_006815, gen.NM_006815
Figure 3848: PRO4793
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Figure 3850: PRO82267
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Figure 3852: PRO82268
Figure 3853: DNA325803, XM_055013, gen.XM_055013
Figure 3854: PRO82269
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Figure 3856A-C: DNA325805, XM_045602, gen.XM_045602
Figure 3857: DNA325806, XM_087955, gen.XM_087955

Figure 3858: PRO82272
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Figure 3862: DNA325809, XM_113702, gen.XM_113702
Figure 3863: PRO82275
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Figure 3865: PRO58410
Figure 3866: DNA226853, NM_004004, gen.NM_004004
Figure 3867: PRO37316
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Figure 3869: DNA325811, XM_167918, gen.XM_167918
Figure 3870: DNA325812, XM_084982, gen.XM_084982
Figure 3871: PRO82278
Figure 3872: DNA325813, NM_024026, gen.NM_024026
Figure 3873: PRO82279
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Figure 3880: DNA325818, XM_169414, gen.XM_169414
Figure 3881A-B: DNA325819, NM_006646, gen.NM_006646
Figure 3882: PRO82285
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Figure 3886: DNA325822, XM_166273, gen.XM_166273
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Figure 3888: PRO71096
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Figure 3890: PRO82289
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Figure 3892: PRO82290
Figure 3893: DNA325825, XM_085017, gen.XM_085017
Figure 3894: PRO82291
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Figure 3897: PRO58642
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Figure 3900: DNA281436, NM_003295, gen.NM_003295
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Figure 3902: DNA325828, XM_038371, gen.XM_038371
Figure 3903A-B: DNA325829, XM_165636, gen.XM_165636
Figure 3904: DNA325830, XM_166266, gen.XM_166266
Figure 3905: PRO82295
Figure 3906: DNA325831, NM_014166, gen.NM_014166
Figure 3907: PRO82296
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Figure 3912: DNA274058, NM_016119, gen.NM_016119
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Figure 3917: DNA325836, XM_165639, gen.XM_165639
Figure 3918: DNA325837, XM_018399, gen.XM_018399
Figure 3919: PRO82300
Figure 3920: DNA325838, XM_058977, gen.XM_058977
Figure 3921: DNA325839, XM_015840, gen.XM_015840
Figure 3922: PRO82302
Figure 3923: DNA325840, XM_007199, gen.XM_007199
Figure 3924: DNA325841, XM_016351, gen.XM_016351
Figure 3925: DNA325842, XM_041209, gen.XM_041209
Figure 3926: DNA325843, XM_058611, gen.XM_058611

Figure 3927: PRO82305
Figure 3928: DNA325844, XM_041473, gen.XM_041473
Figure 3929: PRO82306
Figure 3930: DNA325845, XM_032443, gen.XM_032443
Figure 3931: DNA325847, XM_048957, gen.XM_048957
Figure 3932: DNA325848, XM_015842, gen.XM_015842
Figure 3933: DNA325849, XM_084997, gen.XM_084997
Figure 3934: PRO82311
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Figure 3937A-B: DNA325851, XM_049904, gen.XM_049904
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Figure 3942: DNA325854, NM_080687, gen.NM_080687
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Figure 3950: DNA325859, XM_046648, gen.XM_046648
Figure 3951: DNA325860, XM_046642, gen.XM_046642
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Figure 3953: DNA325861, XM_017914, gen.XM_017914
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Figure 3955: DNA325862, XM_085166, gen.XM_085166
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Figure 3957: DNA325863, XM_007316, gen.XM_007316
Figure 3958: DNA325864, XM_007315, gen.XM_007315
Figure 3959: DNA325865, XM_033251, gen.XM_033251
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Figure 3961: PRO82325
Figure 3962: DNA210180, NM_005132, gen.NM_005132
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Figure 3980: DNA325876, XM_033445, gen.XM_033445
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Figure 3983: DNA325878, XM_012377, gen.XM_012377
Figure 3984: DNA227321, NM_001344, gen.NM_001344
Figure 3985: PRO37784
Figure 3986: DNA325879, XM_058646, gen.XM_058646
Figure 3987: DNA325880, XM_085106, gen.XM_085106
Figure 3988: DNA325881, NM_019852, gen.NM_019852
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Figure 4002: PRO82344
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Figure 4036: PRO82364
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Figure 4041: PRO82367
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Figure 4043: PRO36112
Figure 4044: DNA325913, XM_085065, gen.XM_085065
Figure 4045: DNA325914, XM_007441, gen.XM_007441
Figure 4046: DNA325915, NM_006821, gen.NM_006821
Figure 4047: PRO82369
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Figure 4050A-B: DNA325917, XM_085151, gen.XM_085151
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Figure 4054: DNA325919, XM_085162, gen.XM_085162
Figure 4055: DNA325920, NM_012111, gen.NM_012111
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gen.NM_001275
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gen.XM_029288
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gen.XM_016487
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gen.XM_016486
Figure 4072: DNA325929, XM_007483,
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gen.XM_028347
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gen.XM_056317
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gen.NM_021966
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gen.XM_007272
Figure 4082: DNA325935, XM_090914,
gen.XM_090914
Figure 4083: PRO82383
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gen.NM_022747
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Figure 4086: DNA325937, XM_041014,
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gen.XM_040952
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gen.XM_058618
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gen.NM_005348
Figure 4093: PRO82388
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gen.XM_040942
Figure 4095: DNA226324, NM_014226,
gen.NM_014226
Figure 4096: PRO36787
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gen.XM_007254
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gen.NM_001969
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gen.XM_040898
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Figure 4104: PRO82393
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gen.XM_113759
Figure 4106: DNA325949, NM_006427,
gen.NM_006427
Figure 4107: PRO82395
Figure 4108: DNA325950, NM_021709,
gen.NM_021709
Figure 4109: PRO82396
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gen.NM_005163
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gen.NM_017955
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gen.XM_088588
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gen.XM_060012
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gen.XM_034953
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gen.XM_035014
Figure 4120: DNA325957, XM_088587,
gen.XM_088587
Figure 4121: DNA325958, XM_088589,
gen.XM_088589
Figure 4122: DNA325959, XM_071801,
gen.XM_071801
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gen.XM_018054
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gen.XM_091108
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gen.XM_039225
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gen.XM_165921
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gen.XM_007751
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gen.XM_085203
Figure 4131: PRO82411
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gen.XM_085204
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Figure 4134A-B: DNA325968, XM_036727, gen.XM_036727
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Figure 4136: DNA325970, NM_020149, gen.NM_020149
Figure 4137: PRO82415
Figure 4138A-B: DNA325971, XM_031617, gen.XM_031617
Figure 4139A-B: DNA325972, NM_001211, gen.NM_001211
Figure 4140: PRO82417
Figure 4141A-B: DNA151831, NM_004573, gen.NM_004573
Figure 4142: PRO12198
Figure 4143: DNA325973, NM_130468, gen.NM_130468
Figure 4144: PRO82418
Figure 4145: DNA325974, XM_031554, gen.XM_031554
Figure 4146: PRO82419
Figure 4147: DNA325975, XM_031515, gen.XM_031515
Figure 4148: DNA325976, NM_024111, gen.NM_024111
Figure 4149: PRO82421
Figure 4150: DNA325977, NM_032196, gen.NM_032196
Figure 4151: PRO82422
Figure 4152: DNA325978, NM_016359, gen.NM_016359
Figure 4153: PRO82423
Figure 4154: DNA325979, NM_018454, gen.NM_018454
Figure 4155: PRO82424
Figure 4156A-B: DNA325980, XM_007545, gen.XM_007545
Figure 4157: DNA325981, XM_091159, gen.XM_091159
Figure 4158: PRO82425
Figure 4159: DNA325982, XM_031718, gen.XM_031718
Figure 4160: DNA325983, XM_085307, gen.XM_085307
Figure 4161: DNA227559, NM_000070, gen.NM_000070
Figure 4162: PRO38022
Figure 4163A-B: DNA325984, XM_113823, gen.XM_113823
Figure 4164: PRO82428
Figure 4165: DNA325985, XM_016713, gen.XM_016713
Figure 4166: PRO82429
Figure 4167A-B: DNA325986, XM_007531, gen.XM_007531
Figure 4168: DNA325987, NM_014444, gen.NM_014444
Figure 4169: PRO82431
Figure 4170A-B: DNA227206, NM_005657, gen.NM_005657
Figure 4171: PRO37669
Figure 4172: DNA325988, NM_020990, gen.NM_020990
Figure 4173: PRO82432
Figure 4174: DNA325989, NM_005313, gen.NM_005313
Figure 4175: PRO2732
Figure 4176: DNA325990, NM_005770, gen.NM_005770
Figure 4177: PRO82433
Figure 4178: DNA325991, NM_004048, gen.NM_004048
Figure 4179: PRO4379
Figure 4180: DNA325992, XM_032403, gen.XM_032403
Figure 4181: PRO82434
Figure 4182: DNA219233, NM_014335, gen.NM_014335
Figure 4183: PRO34557
Figure 4184A-C: DNA325993, XM_034890, gen.XM_034890
Figure 4185: PRO82435
Figure 4186: DNA325994, XM_058684, gen.XM_058684
Figure 4187: DNA325995, NM_003104, gen.NM_003104
Figure 4188: PRO82437
Figure 4189: DNA325996, XM_007651, gen.XM_007651
Figure 4190: PRO82438
Figure 4191: DNA325997, XM_090991, gen.XM_090991
Figure 4192: PRO82439
Figure 4193: DNA325998, NM_016304, gen.NM_016304
Figure 4194: PRO82440
Figure 4195: DNA325999, NM_017610, gen.NM_017610
Figure 4196: PRO82441
Figure 4197: DNA326000, NM_004701, gen.NM_004701
Figure 4198: PRO82442
Figure 4199A-B: DNA326001, XM_012418, gen.XM_012418
Figure 4200: DNA326002, XM_039702, gen.XM_039702
Figure 4201: PRO82444
Figure 4202: DNA326003, XM_113266, gen.XM_113266

Figure 4203: DNA326004, NM_001218, gen.NM_001218
Figure 4204: PRO54594
Figure 4205: DNA326005, NM_015920, gen.NM_015920
Figure 4206: PRO82446
Figure 4207: DNA326006, XM_113268, gen.XM_113268
Figure 4208: DNA255340, NM_017684, gen.NM_017684
Figure 4209: PRO50409
Figure 4210: DNA326007, NM_002537, gen.NM_002537
Figure 4211: DNA326008, XM_085283, gen.XM_085283
Figure 4212: PRO82448
Figure 4213: DNA326009, XM_016985, gen.XM_016985
Figure 4214: DNA234442, NM_014736, gen.NM_014736
Figure 4215: PRO38852
Figure 4216: DNA326010, NM_022048, gen.NM_022048
Figure 4217: PRO82450
Figure 4218: DNA326011, NM_000942, gen.NM_000942
Figure 4219: PRO2720
Figure 4220: DNA326012, XM_050964, gen.XM_050964
Figure 4221: DNA326013, XM_007623, gen.XM_007623
Figure 4222A-B: DNA326014, NM_133375, gen.NM_133375
Figure 4223: PRO82453
Figure 4224: DNA226646, NM_017882, gen.NM_017882
Figure 4225: PRO37109
Figure 4226: DNA326015, NM_015322, gen.NM_015322
Figure 4227: PRO82454
Figure 4228: DNA326016, NM_001003, gen.NM_001003
Figure 4229: PRO82455
Figure 4230A-B: DNA326017, XM_051463, gen.XM_051463
Figure 4231: PRO82456
Figure 4232: DNA326018, NM_018357, gen.NM_018357
Figure 4233: PRO82457
Figure 4234: DNA326019, XM_063639, gen.XM_063639
Figure 4235: PRO82458
Figure 4236: DNA326020, XM_085249, gen.XM_085249
Figure 4237: DNA326021, XM_016076, gen.XM_016076
Figure 4238: PRO82460
Figure 4239: DNA326022, XM_015366, gen.XM_015366
Figure 4240: PRO82461
Figure 4241: DNA326023, XM_096060, gen.XM_096060
Figure 4242: DNA287331, NM_002654, gen.NM_002654
Figure 4243: PRO69595
Figure 4244: DNA326024, XM_037778, gen.XM_037778
Figure 4245: DNA326025, XM_096842, gen.XM_096842
Figure 4246: DNA326026, NM_022369, gen.NM_022369
Figure 4247: PRO82465
Figure 4248: DNA326027, NM_032907, gen.NM_032907
Figure 4249: PRO82466
Figure 4250: DNA326028, XM_058699, gen.XM_058699
Figure 4251: DNA326029, XM_118637, gen.XM_118637
Figure 4252: DNA326030, XM_053585, gen.XM_053585
Figure 4253: PRO82469
Figure 4254: DNA326031, XM_085239, gen.XM_085239
Figure 4255: PRO82470
Figure 4256: DNA326032, XM_034897, gen.XM_034897
Figure 4257A-B: DNA326033, XM_057020, gen.XM_057020
Figure 4258: PRO82472
Figure 4259: DNA326034, NM_000743, gen.NM_000743
Figure 4260: PRO61219
Figure 4261: DNA326035, NM_002789, gen.NM_002789
Figure 4262: PRO60499
Figure 4263: DNA326036, XM_091100, gen.XM_091100
Figure 4264: PRO82473
Figure 4265: DNA255370, NM_012170, gen.NM_012170
Figure 4266: PRO50438
Figure 4267: DNA273014, NM_000126, gen.NM_000126
Figure 4268: PRO61085
Figure 4269: DNA326037, XM_044565, gen.XM_044565
Figure 4270: DNA326038, NM_025234, gen.NM_025234
Figure 4271: PRO82475
Figure 4272: DNA326039, XM_044569, gen.XM_044569

Figure 4273: DNA326040, NM_005724, gen.NM_005724
Figure 4274: PRO730
Figure 4275: DNA326041, XM_049354, gen.XM_049354
Figure 4276: PRO82477
Figure 4277: DNA326042, NM_007364, gen.NM_007364
Figure 4278: DNA326043, XM_044593, gen.XM_044593
Figure 4279: DNA326044, NM_006791, gen.NM_006791
Figure 4280: PRO82479
Figure 4281: DNA326045, XM_060042, gen.XM_060042
Figure 4282: DNA326046, XM_085215, gen.XM_085215
Figure 4283: DNA326047, NM_001021, gen.NM_001021
Figure 4284: PRO82482
Figure 4285: DNA326048, XM_031404, gen.XM_031404
Figure 4286: DNA326049, XM_096844, gen.XM_096844
Figure 4287: DNA326050, XM_045681, gen.XM_045681
Figure 4288: PRO82485
Figure 4289: DNA326051, XM_085280, gen.XM_085280
Figure 4290: DNA326052, NM_022839, gen.NM_022839
Figure 4291: PRO82487
Figure 4292: DNA326053, XM_031354, gen.XM_031354
Figure 4293: DNA326054, NM_002168, gen.NM_002168
Figure 4294: PRO82489
Figure 4295: DNA326055, XM_031292, gen.XM_031292
Figure 4296: DNA326056, NM_022566, gen.NM_022566
Figure 4297: PRO82491
Figure 4298A-B: DNA326057, XM_051860, gen.XM_051860
Figure 4299: PRO82492
Figure 4300: DNA275144, NM_000137, gen.NM_000137
Figure 4301: PRO62852
Figure 4302: DNA326058, NM_016645, gen.NM_016645
Figure 4303: PRO82493
Figure 4304: DNA326059, XM_044523, gen.XM_044523
Figure 4305: DNA150485, NM_006384, gen.NM_006384
Figure 4306: PRO12774
Figure 4307A-B: DNA326060, XM_044533, gen.XM_044533
Figure 4308: PRO82495
Figure 4309A-C: DNA326061, XM_054900, gen.XM_054900
Figure 4310: DNA326062, NM_032162, gen.NM_032162
Figure 4311A-B: DNA326063, XM_015835, gen.XM_015835
Figure 4312: DNA326064, NM_018668, gen.NM_018668
Figure 4313: PRO82499
Figure 4314: DNA326065, XM_085262, gen.XM_085262
Figure 4315: DNA326066, NM_033544, gen.NM_033544
Figure 4316: PRO82501
Figure 4317: DNA326067, XM_049372, gen.XM_049372
Figure 4318: PRO82502
Figure 4319: DNA326068, XM_017971, gen.XM_017971
Figure 4320: DNA275181, NM_003090, gen.NM_003090
Figure 4321: PRO62882
Figure 4322: DNA326069, XM_012462, gen.XM_012462
Figure 4323A-B: DNA326070, XM_085525, gen.XM_085525
Figure 4324: PRO82505
Figure 4325: DNA326071, XM_165923, gen.XM_165923
Figure 4326: DNA326072, XM_113836, gen.XM_113836
Figure 4327: DNA326073, NM_017668, gen.NM_017668
Figure 4328: PRO82508
Figure 4329: DNA326074, XM_027309, gen.XM_027309
Figure 4330: PRO82509
Figure 4331: DNA326075, XM_018432, gen.XM_018432
Figure 4332: PRO82510
Figure 4333: DNA326076, XM_115352, gen.XM_115352
Figure 4334: DNA326077, XM_027365, gen.XM_027365
Figure 4335: DNA326078, NM_016641, gen.NM_016641
Figure 4336: PRO38464
Figure 4337: DNA326079, XM_058796, gen.XM_058796
Figure 4338: DNA326080, XM_017984, gen.XM_017984
Figure 4339: PRO82513
Figure 4340: DNA326081, NM_020677,

gen.NM_020677
Figure 4341: PRO82514
Figure 4342: DNA326082, XM_036680, gen.XM_036680
Figure 4343: PRO37961
Figure 4344A-B: DNA326083, XM_048119, gen.XM_048119
Figure 4345: PRO82515
Figure 4346: DNA326084, NM_024589, gen.NM_024589
Figure 4347: PRO82516
Figure 4348: DNA326085, XM_050534, gen.XM_050534
Figure 4349: PRO82517
Figure 4350: DNA326086, NM_024571, gen.NM_024571
Figure 4351: PRO82518
Figure 4352: DNA326087, XM_027558, gen.XM_027558
Figure 4353: DNA326088, XM_008126, gen.XM_008126
Figure 4354: DNA326089, NM_000517, gen.NM_000517
Figure 4355: PRO3629
Figure 4356: DNA326090, NM_000558, gen.NM_000558
Figure 4357: PRO3629
Figure 4358: DNA326091, NM_018032, gen.NM_018032
Figure 4359: PRO38311
Figure 4360: DNA273839, NM_006428, gen.NM_006428
Figure 4361: PRO61799
Figure 4362A-B: DNA256844, NM_005632, gen.NM_005632
Figure 4363: PRO51775
Figure 4364: DNA326092, XM_083939, gen.XM_083939
Figure 4365: PRO82521
Figure 4366: DNA326093, NM_058192, gen.NM_058192
Figure 4367: PRO82522
Figure 4368: DNA326094, XM_027412, gen.XM_027412
Figure 4369: PRO82523
Figure 4370: DNA256886, NM_014587, gen.NM_014587
Figure 4371: PRO51815
Figure 4372A-B: DNA326095, NM_001287, gen.NM_001287
Figure 4373: PRO38480
Figure 4374: DNA254781, NM_016111, gen.NM_016111
Figure 4375: PRO49879
Figure 4376: DNA326096, XM_034586, gen.XM_034586
Figure 4377: PRO82524
Figure 4378: DNA326097, NM_023936, gen.NM_023936
Figure 4379: PRO82525
Figure 4380: DNA326098, XM_034590, gen.XM_034590
Figure 4381: PRO82526
Figure 4382: DNA326099, NM_002952, gen.NM_002952
Figure 4383: PRO82527
Figure 4384: DNA326100, NM_006453, gen.NM_006453
Figure 4385: PRO82528
Figure 4386: DNA326101, NM_014353, gen.NM_014353
Figure 4387: PRO82529
Figure 4388: DNA326102, NM_032271, gen.NM_032271
Figure 4389: PRO82530
Figure 4390: DNA326103, XM_028848, gen.XM_028848
Figure 4391: PRO82531
Figure 4392: DNA326104, NM_006711, gen.NM_006711
Figure 4393: PRO82532
Figure 4394: DNA326105, NM_080594, gen.NM_080594
Figure 4395: PRO82533
Figure 4396: DNA326106, NM_024339, gen.NM_024339
Figure 4397: PRO82534
Figure 4398: DNA326107, NM_016639, gen.NM_016639
Figure 4399: PRO12683
Figure 4400: DNA326108, NM_021195, gen.NM_021195
Figure 4401: PRO82535
Figure 4402: DNA326109, NM_004203, gen.NM_004203
Figure 4403: PRO82536
Figure 4404: DNA326110, XM_058784, gen.XM_058784
Figure 4405: PRO82537
Figure 4406: DNA326111, NM_024507, gen.NM_024507
Figure 4407: PRO82538
Figure 4408: DNA326112, NM_006799, gen.NM_006799
Figure 4409: PRO303
Figure 4410A-C: DNA326113, XM_036528, gen.XM_036528
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Figure 4412: PRO82540
Figure 4413A-C: DNA326115, XM_165411, gen.XM_165411

Figure 4414: DNA326116, NM_016292, gen.NM_016292
Figure 4415: PRO82542
Figure 4416: DNA326117, NM_002484, gen.NM_002484
Figure 4417: PRO82543
Figure 4418: DNA326118, XM_113845, gen.XM_113845
Figure 4419: PRO82544
Figure 4420: DNA326119, XM_113843, gen.XM_113843
Figure 4421: DNA97293, NM_003366, gen.NM_003366
Figure 4422: PRO3640
Figure 4423: DNA326120, NM_006110, gen.NM_006110
Figure 4424: PRO82546
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Figure 4426: DNA326122, XM_113876, gen.XM_113876
Figure 4427A-B: DNA326123, XM_055195, gen.XM_055195
Figure 4428: PRO82548
Figure 4429: DNA326124, XM_113291, gen.XM_113291
Figure 4430A-B: DNA326125, XM_007988, gen.XM_007988
Figure 4431: DNA326126, XM_113874, gen.XM_113874
Figure 4432: DNA326127, XM_102377, gen.XM_102377
Figure 4433: PRO82551
Figure 4434: DNA326128, XM_086278, gen.XM_086278
Figure 4435: DNA326129, XM_085452, gen.XM_085452
Figure 4436: DNA326130, NM_018054, gen.NM_018054
Figure 4437: PRO82554
Figure 4438A-B: DNA326131, XM_056260, gen.XM_056260
Figure 4439: PRO82555
Figure 4440: DNA326132, NM_032626, gen.NM_032626
Figure 4441: PRO82556
Figure 4442: DNA326133, NM_005030, gen.NM_005030
Figure 4443: PRO82557
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Figure 4445: PRO82558
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Figure 4447: PRO70276
Figure 4448: DNA326135, XM_085340, gen.XM_085340
Figure 4449: DNA326136, NM_003752, gen.NM_003752
Figure 4450: PRO60325
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Figure 4452: PRO82560
Figure 4453A-B: DNA326138, XM_046035, gen.XM_046035
Figure 4454: DNA326139, NM_024671, gen.NM_024671
Figure 4455: PRO82562
Figure 4456: DNA326140, NM_033410, gen.NM_033410
Figure 4457: PRO82563
Figure 4458: DNA326141, NM_024031, gen.NM_024031
Figure 4459: PRO82564
Figure 4460A-B: DNA326142, XM_034375, gen.XM_034375
Figure 4461: DNA326143, XM_012569, gen.XM_012569
Figure 4462: DNA326144, XM_050194, gen.XM_050194
Figure 4463: DNA326145, XM_008106, gen.XM_008106
Figure 4464: PRO82567
Figure 4465: DNA326146, NM_004960, gen.NM_004960
Figure 4466: PRO82568
Figure 4467: DNA326147, XM_113293, gen.XM_113293
Figure 4468: DNA326148, NM_022744, gen.NM_022744
Figure 4469: PRO82570
Figure 4470: DNA326149, NM_024048, gen.NM_024048
Figure 4471: PRO82571
Figure 4472: DNA326150, XM_018088, gen.XM_018088
Figure 4473: PRO82572
Figure 4474: DNA326151, XM_007963, gen.XM_007963
Figure 4475: PRO82573
Figure 4476: DNA274002, NM_014321, gen.NM_014321
Figure 4477: PRO61948
Figure 4478: DNA326152, XM_015700, gen.XM_015700
Figure 4479: DNA326153, XM_051219, gen.XM_051219
Figure 4480: DNA326154, XM_085393, gen.XM_085393
Figure 4481: PRO82576
Figure 4482: DNA326155, XM_085395, gen.XM_085395

Figure 4483: DNA326156, XM_091270, gen.XM_091270
Figure 4484: DNA326157, XM_165656, gen.XM_165656
Figure 4485: DNA326158, NM_032330, gen.NM_032330
Figure 4486: PRO82579
Figure 4487: DNA254532, NM_001043, gen.NM_001043
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Figure 4489: DNA326159, XM_165658, gen.XM_165658
Figure 4490: DNA326160, XM_166285, gen.XM_166285
Figure 4491: DNA326161, XM_166282, gen.XM_166282
Figure 4492: PRO82582
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Figure 4494: PRO82583
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Figure 4496: PRO82584
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Figure 4498: DNA326165, NM_017458, gen.NM_017458
Figure 4499: PRO82585
Figure 4500: DNA326166, NM_005115, gen.NM_005115
Figure 4501: PRO82586
Figure 4502: DNA326167, NM_024516, gen.NM_024516
Figure 4503: PRO82587
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Figure 4505: DNA326169, XM_055771, gen.XM_055771
Figure 4506: PRO82589
Figure 4507: DNA271171, NM_007317, gen.NM_007317
Figure 4508: PRO59491
Figure 4509: DNA326170, XM_008064, gen.XM_008064
Figure 4510: PRO82590
Figure 4511: DNA326171, NM_003123, gen.NM_003123
Figure 4512: PRO2355
Figure 4513: DNA326172, XM_085442, gen.XM_085442
Figure 4514: DNA326173, XM_055132, gen.XM_055132
Figure 4515: PRO82592
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Figure 4517: PRO62110
Figure 4518: DNA326174, NM_002720, gen.NM_002720
Figure 4519: PRO42208
Figure 4520: DNA287355, NM_000034, gen.NM_000034
Figure 4521: PRO69617
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Figure 4523: PRO82593
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Figure 4525: PRO82594
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Figure 4529: PRO82597
Figure 4530: DNA194805, NM_014685, gen.NM_014685
Figure 4531: PRO24075
Figure 4532: DNA326180, XM_166277, gen.XM_166277
Figure 4533: PRO82598
Figure 4534: DNA326181, XM_165645, gen.XM_165645
Figure 4535: DNA326182, NM_018110, gen.NM_018110
Figure 4536: PRO82599
Figure 4537: DNA326183, XM_165648, gen.XM_165648
Figure 4538: DNA326184, XM_167453, gen.XM_167453
Figure 4539: DNA326185, NM_022770, gen.NM_022770
Figure 4540: PRO82602
Figure 4541: DNA326186, XM_167456, gen.XM_167456
Figure 4542: PRO82603
Figure 4543: DNA326187, XM_058745, gen.XM_058745
Figure 4544: DNA326188, XM_091420, gen.XM_091420
Figure 4545: DNA326189, NM_004691, gen.NM_004691
Figure 4546: PRO82606
Figure 4547: DNA326190, NM_000196, gen.NM_000196
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Figure 4549A-B: DNA326191, NM_004360, gen.NM_004360
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Figure 4551: DNA326192, XM_039306, gen.XM_039306
Figure 4552: PRO82608

Figure 4553: DNA326193, NM_030579, gen.NM_030579
Figure 4554: PRO82609
Figure 4555: DNA326194, XM_012487, gen.XM_012487
Figure 4556: DNA326195, NM_014062, gen.NM_014062
Figure 4557: PRO82611
Figure 4558: DNA326196, XM_085471, gen.XM_085471
Figure 4559: PRO82612
Figure 4560: DNA326197, XM_113855, gen.XM_113855
Figure 4561: DNA326198, XM_085475, gen.XM_085475
Figure 4562: DNA326199, XM_028151, gen.XM_028151
Figure 4563: PRO82615
Figure 4564: DNA275408, NM_001605, gen.NM_001605
Figure 4565: PRO63068
Figure 4566: DNA326200, NM_007242, gen.NM_007242
Figure 4567: PRO82616
Figure 4568: DNA189703, NM_005548, gen.NM_005548
Figure 4569: PRO22637
Figure 4570: DNA326201, XM_113853, gen.XM_113853
Figure 4571: DNA326202, NM_032140, gen.NM_032140
Figure 4572: PRO82618
Figure 4573: DNA326203, NM_030819, gen.NM_030819
Figure 4574: PRO82619
Figure 4575: DNA304704, NM_005796, gen.NM_005796
Figure 4576: PRO71130
Figure 4577: DNA326204, XM_043047, gen.XM_043047
Figure 4578: PRO49967
Figure 4579: DNA88261, NM_001907, gen.NM_001907
Figure 4580: PRO2719
Figure 4581A-B: DNA326205, NM_005072, gen.NM_005072
Figure 4582: PRO4814
Figure 4583: DNA326206, XM_165410, gen.XM_165410
Figure 4584: DNA326207, NM_017803, gen.NM_017803
Figure 4585: PRO82621
Figure 4586A-B: DNA326208, NM_004555, gen.NM_004555
Figure 4587: PRO82622
Figure 4588A-B: DNA326209, NM_018124, gen.NM_018124
Figure 4589: PRO82623
Figure 4590: DNA326210, XM_091399, gen.XM_091399
Figure 4591: PRO82624
Figure 4592A-B: DNA326211, NM_014003, gen.NM_014003
Figure 4593: PRO82625
Figure 4594: DNA326212, NM_017853, gen.NM_017853
Figure 4595: PRO82626
Figure 4596: DNA326213, XM_042621, gen.XM_042621
Figure 4597: DNA326214, XM_064091, gen.XM_064091
Figure 4598: PRO82627
Figure 4599: DNA326215, XM_085981, gen.XM_085981
Figure 4600A-B: DNA326216, XM_051778, gen.XM_051778
Figure 4601: PRO82629
Figure 4602: DNA326217, NM_004483, gen.NM_004483
Figure 4603: PRO82630
Figure 4604: DNA326218, NM_020188, gen.NM_020188
Figure 4605: PRO82631
Figure 4606: DNA326219, XM_033922, gen.XM_033922
Figure 4607: PRO82632
Figure 4608: DNA326220, XM_113840, gen.XM_113840
Figure 4609: PRO82633
Figure 4610: DNA326221, NM_016095, gen.NM_016095
Figure 4611: PRO82634
Figure 4612: DNA326222, NM_006067, gen.NM_006067
Figure 4613: PRO50658
Figure 4614: DNA326223, NM_001861, gen.NM_001861
Figure 4615: PRO82635
Figure 4616A-B: DNA326224, XM_085483, gen.XM_085483
Figure 4617: DNA326225, NM_017566, gen.NM_017566
Figure 4618: PRO82637
Figure 4619: DNA326226, XM_057150, gen.XM_057150
Figure 4620: PRO82638
Figure 4621: DNA326227, XM_058739, gen.XM_058739
Figure 4622: DNA326228, XM_085327, gen.XM_085327
Figure 4623: PRO82640
Figure 4624: DNA326229, XM_047436,

gen.XM_047436
Figure 4625: PRO82641
Figure 4626: DNA227234, NM_002386, gen.NM_002386
Figure 4627: PRO37697
Figure 4628: DNA326230, NM_014972, gen.NM_014972
Figure 4629: PRO82642
Figure 4630: DNA326231, XM_071873, gen.XM_071873
Figure 4631: PRO82643
Figure 4632: DNA326232, XM_047525, gen.XM_047525
Figure 4633: DNA326233, NM_000977, gen.NM_000977
Figure 4634: PRO82645
Figure 4635: DNA326234, NM_033251, gen.NM_033251
Figure 4636: PRO82646
Figure 4637: DNA326235, XM_085408, gen.XM_085408
Figure 4638: DNA326236, NM_004933, gen.NM_004933
Figure 4639: PRO2198
Figure 4640: DNA326237, XM_113882, gen.XM_113882
Figure 4641: DNA326238, XM_010938, gen.XM_010938
Figure 4642: DNA326239, NM_006761, gen.NM_006761
Figure 4643: PRO39530
Figure 4644A-B: DNA326240, XM_017096, gen.XM_017096
Figure 4645: DNA326241, XM_033714, gen.XM_033714
Figure 4646A-B: DNA326242, XM_033689, gen.XM_033689
Figure 4647: DNA326243, NM_002615, gen.NM_002615
Figure 4648: DNA326244, XM_056082, gen.XM_056082
Figure 4649: PRO82654
Figure 4650: DNA326245, XM_008557, gen.XM_008557
Figure 4651: DNA326246, XM_045183, gen.XM_045183
Figure 4652: PRO82656
Figure 4653: DNA326247, XM_113901, gen.XM_113901
Figure 4654: DNA326248, NM_080822, gen.NM_080822
Figure 4655: PRO82658
Figure 4656A-B: DNA326249, XM_029438, gen.XM_029438
Figure 4657: PRO82659
Figure 4658: DNA326250, XM_008509, gen.XM_008509
Figure 4659: DNA326251, XM_085687, gen.XM_085687
Figure 4660: PRO82661
Figure 4661: DNA326252, XM_027825, gen.XM_027825
Figure 4662: PRO82662
Figure 4663: DNA326253, XM_053717, gen.XM_053717
Figure 4664: PRO82663
Figure 4665: DNA326254, NM_005022, gen.NM_005022
Figure 4666: PRO62780
Figure 4667A-B: DNA326255, XM_028398, gen.XM_028398
Figure 4668: PRO82664
Figure 4669: DNA326256, NM_000018, gen.NM_000018
Figure 4670: PRO66265
Figure 4671: DNA326257, XM_008334, gen.XM_008334
Figure 4672: DNA326258, NM_024297, gen.NM_024297
Figure 4673: PRO82665
Figure 4674: DNA326259, XM_113324, gen.XM_113324
Figure 4675: DNA326260, XM_012676, gen.XM_012676
Figure 4676: PRO82667
Figure 4677: DNA326261, XM_085691, gen.XM_085691
Figure 4678: DNA326262, XM_028417, gen.XM_028417
Figure 4679: PRO82669
Figure 4680A-B: DNA326263, XM_041964, gen.XM_041964
Figure 4681: PRO82670
Figure 4682: DNA326264, NM_019013, gen.NM_019013
Figure 4683: PRO82671
Figure 4684: DNA326265, XM_008538, gen.XM_008538
Figure 4685: PRO82672
Figure 4686: DNA326266, XM_008441, gen.XM_008441
Figure 4687: DNA97300, NM_001416, gen.NM_001416
Figure 4688: PRO3647
Figure 4689: DNA326267, NM_004870, gen.NM_004870
Figure 4690: PRO82674
Figure 4691: DNA326268, NM_006942, gen.NM_006942
Figure 4692: PRO82675
Figure 4693: DNA326269, XM_008679, gen.XM_008679

Figure 4694: DNA326270, XM_008231, gen.XM_008231
Figure 4695: DNA326271, XM_113328, gen.XM_113328
Figure 4696: DNA326272, XM_113929, gen.XM_113929
Figure 4697: DNA326273, NM_001970, gen.NM_001970
Figure 4698: PRO82678
Figure 4699: DNA297388, NM_004217, gen.NM_004217
Figure 4700: PRO70812
Figure 4701: DNA326274, XM_165421, gen.XM_165421
Figure 4702: PRO82679
Figure 4703: DNA326275, XM_113325, gen.XM_113325
Figure 4704: DNA326276, XM_165422, gen.XM_165422
Figure 4705: PRO49182
Figure 4706: DNA326277, XM_113931, gen.XM_113931
Figure 4707: DNA326278, XM_036659, gen.XM_036659
Figure 4708: DNA103401, NM_003876, gen.NM_003876
Figure 4709: PRO4729
Figure 4710A-B: DNA326279, XM_042698, gen.XM_042698
Figure 4711: PRO82683
Figure 4712A-B: DNA326280, XM_017234, gen.XM_017234
Figure 4713: DNA326281, XM_165418, gen.XM_165418
Figure 4714: DNA304715, NM_000987, gen.NM_000987
Figure 4715: PRO71141
Figure 4716A-B: DNA326282, NM_004618, gen.NM_004618
Figure 4717: PRO62981
Figure 4718: DNA326283, XM_085743, gen.XM_085743
Figure 4719A-B: DNA254198, NM_002018, gen.NM_002018
Figure 4720: PRO49310
Figure 4721A-B: DNA326284, XM_039910, gen.XM_039910
Figure 4722: PRO82687
Figure 4723A-C: DNA326285, XM_113310, gen.XM_113310
Figure 4724: DNA326286, XM_085613, gen.XM_085613
Figure 4725: DNA326287, NM_006470, gen.NM_006470
Figure 4726: PRO82689
Figure 4727: DNA326288, XM_051763, gen.XM_051763
Figure 4728: DNA290292, NM_018955, gen.NM_018955
Figure 4729: PRO70449
Figure 4730: DNA326289, XM_058900, gen.XM_058900
Figure 4731: PRO82691
Figure 4732: DNA326290, XM_039921, gen.XM_039921
Figure 4733: PRO82692
Figure 4734: DNA326291, XM_012549, gen.XM_012549
Figure 4735: DNA326292, XM_085548, gen.XM_085548
Figure 4736: PRO82694
Figure 4737: DNA326293, NM_018019, gen.NM_018019
Figure 4738: PRO82695
Figure 4739: DNA326294, NM_138427, gen.NM_138427
Figure 4740: PRO82696
Figure 4741: DNA326295, XM_085545, gen.XM_085545
Figure 4742A-B: DNA227084, NM_004176, gen.NM_004176
Figure 4743: PRO37547
Figure 4744: DNA326296, XM_012615, gen.XM_012615
Figure 4745: DNA326297, XM_085722, gen.XM_085722
Figure 4746: PRO82699
Figure 4747: DNA255414, NM_018242, gen.NM_018242
Figure 4748: PRO50481
Figure 4749: DNA326298, XM_045044, gen.XM_045044
Figure 4750: DNA326299, XM_008323, gen.XM_008323
Figure 4751: DNA326300, XM_045535, gen.XM_045535
Figure 4752A-B: DNA326301, XM_045551, gen.XM_045551
Figure 4753: PRO82702
Figure 4754: DNA326302, XM_097204, gen.XM_097204
Figure 4755: DNA326303, XM_058867, gen.XM_058867
Figure 4756: PRO82704
Figure 4757: DNA326304, XM_085672, gen.XM_085672
Figure 4758: DNA326305, XM_031536, gen.XM_031536
Figure 4759: PRO82706
Figure 4760: DNA326306, XM_008486, gen.XM_008486
Figure 4761: DNA326307, NM_015584,

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Figure 4762: PRO82707
Figure 4763: DNA326308, NM_000638, gen.NM_000638
Figure 4764: PRO82708
Figure 4765A-B: DNA326309, XM_031466, gen.XM_031466
Figure 4766: PRO82709
Figure 4767: DNA326310, XM_031415, gen.XM_031415
Figure 4768: DNA326311, XM_117066, gen.XM_117066
Figure 4769: DNA326312, XM_031427, gen.XM_031427
Figure 4770: PRO82712
Figure 4771: DNA326313, NM_032322, gen.NM_032322
Figure 4772: PRO82713
Figure 4773A-B: DNA326314, XM_050101, gen.XM_050101
Figure 4774: PRO82714
Figure 4775: DNA326315, XM_056730, gen.XM_056730
Figure 4776: PRO82715
Figure 4777: DNA326316, XM_008462, gen.XM_008462
Figure 4778: DNA287427, NM_002815, gen.NM_002815
Figure 4779: PRO69684
Figure 4780: DNA326317, NM_015544, gen.NM_015544
Figure 4781: PRO82717
Figure 4782: DNA188351, NM_005623, gen.NM_005623
Figure 4783: PRO21887
Figure 4784: DNA326318, NM_002878, gen.NM_002878
Figure 4785: PRO82718
Figure 4786: DNA326319, NM_133627, gen.NM_133627
Figure 4787: PRO82719
Figure 4788: DNA326320, NM_133630, gen.NM_133630
Figure 4789: PRO82720
Figure 4790: DNA326321, NM_133629, gen.NM_133629
Figure 4791: PRO82721
Figure 4792: DNA326322, NM_018096, gen.NM_018096
Figure 4793: PRO37791
Figure 4794A-B: DNA326323, XM_039474, gen.XM_039474
Figure 4795: PRO82722
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Figure 4797: PRO1204
Figure 4798: DNA326324, NM_000981, gen.NM_000981
Figure 4799: PRO4738
Figure 4800A-B: DNA326325, XM_008150, gen.XM_008150
Figure 4801: DNA326326, NM_000978, gen.NM_000978
Figure 4802: PRO82724
Figure 4803: DNA326327, XM_058830, gen.XM_058830
Figure 4804: PRO82725
Figure 4805: DNA270979, NM_002809, gen.NM_002809
Figure 4806: PRO59309
Figure 4807: DNA326328, NM_000422, gen.NM_000422
Figure 4808: PRO82726
Figure 4809: DNA326329, XM_008579, gen.XM_008579
Figure 4810: DNA326330, NM_002276, gen.NM_002276
Figure 4811: PRO82728
Figure 4812: DNA272889, NM_002275, gen.NM_002275
Figure 4813: PRO60979
Figure 4814: DNA326331, NM_002274, gen.NM_002274
Figure 4815: PRO82729
Figure 4816: DNA326332, NM_000526, gen.NM_000526
Figure 4817: PRO82730
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Figure 4819A-B: DNA326334, XM_113334, gen.XM_113334
Figure 4820: DNA226389, NM_000964, gen.NM_000964
Figure 4821: PRO36852
Figure 4822: DNA326335, NM_006455, gen.NM_006455
Figure 4823: PRO82732
Figure 4824: DNA326336, XM_113938, gen.XM_113938
Figure 4825: DNA326337, XM_036465, gen.XM_036465
Figure 4826: DNA326338, XM_055061, gen.XM_055061
Figure 4827A-B: DNA326339, XM_036462, gen.XM_036462
Figure 4828: PRO82736
Figure 4829: DNA326340, XM_048654, gen.XM_048654
Figure 4830: DNA326341, NM_025197, gen.NM_025197
Figure 4831: PRO82737
Figure 4832: DNA326342, XM_054038,

gen.XM_054038
Figure 4833: PRO82738
Figure 4834: DNA326343, NM_002265, gen.NM_002265
Figure 4835: PRO82739
Figure 4836: DNA326344, XM_032201, gen.XM_032201
Figure 4837: PRO82740
Figure 4838: DNA326345, NM_012138, gen.NM_012138
Figure 4839: PRO82741
Figure 4840: DNA326346, XM_018534, gen.XM_018534
Figure 4841: DNA227873, NM_001050, gen.NM_001050
Figure 4842: PRO38336
Figure 4843: DNA270975, NM_000386, gen.NM_000386
Figure 4844: PRO59305
Figure 4845: DNA88378, NM_002087, gen.NM_002087
Figure 4846: PRO2769
Figure 4847: DNA326347, NM_016016, gen.NM_016016
Figure 4848: PRO82743
Figure 4849: DNA326348, XM_012642, gen.XM_012642
Figure 4850A-B: DNA326349, NM_005474, gen.NM_005474
Figure 4851: PRO82745
Figure 4852: DNA326350, XM_045901, gen.XM_045901
Figure 4853: PRO82746
Figure 4854: DNA257428, NM_032376, gen.NM_032376
Figure 4855: PRO52010
Figure 4856: DNA326351, XM_008351, gen.XM_008351
Figure 4857: DNA326352, XM_032852, gen.XM_032852
Figure 4858: PRO82748
Figure 4859: DNA326353, NM_025233, gen.NM_025233
Figure 4860: PRO82749
Figure 4861: DNA326354, XM_032817, gen.XM_032817
Figure 4862: PRO82750
Figure 4863: DNA326355, XM_032813, gen.XM_032813
Figure 4864: DNA326356, XM_032766, gen.XM_032766
Figure 4865: DNA326357, NM_003766, gen.NM_003766
Figure 4866: PRO82753
Figure 4867: DNA326358, XM_008401, gen.XM_008401
Figure 4868: PRO82754
Figure 4869: DNA326359, XM_008402, gen.XM_008402
Figure 4870: PRO82755
Figure 4871: DNA326360, NM_017595, gen.NM_017595
Figure 4872: PRO82756
Figure 4873: DNA326361, XM_085636, gen.XM_085636
Figure 4874: PRO82757
Figure 4875: DNA326362, NM_006373, gen.NM_006373
Figure 4876: PRO82758
Figure 4877: DNA196642, NM_005440, gen.NM_005440
Figure 4878: PRO25115
Figure 4879A-B: DNA270901, NM_004247, gen.NM_004247
Figure 4880: DNA326363, XM_050159, gen.XM_050159
Figure 4881: DNA326364, XM_083983, gen.XM_083983
Figure 4882: PRO82760
Figure 4883A-B: DNA326365, NM_021079, gen.NM_021079
Figure 4884: PRO82761
Figure 4885: DNA326366, NM_133373, gen.NM_133373
Figure 4886: PRO82762
Figure 4887: DNA97290, NM_002512, gen.NM_002512
Figure 4888: PRO3637
Figure 4889: DNA227071, NM_000269, gen.NM_000269
Figure 4890: PRO37534
Figure 4891: DNA227764, NM_003971, gen.NM_003971
Figure 4892: PRO38227
Figure 4893A-B: DNA326367, NM_020038, gen.NM_020038
Figure 4894: PRO82763
Figure 4895A-B: DNA326368, NM_020037, gen.NM_020037
Figure 4896: PRO82764
Figure 4897: DNA326369, XM_037971, gen.XM_037971
Figure 4898: DNA254791, NM_018346, gen.NM_018346
Figure 4899: PRO49888
Figure 4900: DNA287425, NM_018509, gen.NM_018509
Figure 4901: PRO69682
Figure 4902A-B: DNA326370, XM_008432, gen.XM_008432
Figure 4903: DNA88554, NM_000250, gen.NM_000250

Figure 4904: PRO2839
Figure 4905: DNA326371, XM_113919, gen.XM_113919
Figure 4906: DNA326372, NM_017777, gen.NM_017777
Figure 4907: PRO82768
Figure 4908: DNA326373, NM_006924, gen.NM_006924
Figure 4909: PRO82769
Figure 4910: DNA326374, XM_115480, gen.XM_115480
Figure 4911: DNA326375, NM_005831, gen.NM_005831
Figure 4912: PRO59328
Figure 4913: DNA326376, XM_117061, gen.XM_117061
Figure 4914: PRO82771
Figure 4915: DNA326377, XM_008459, gen.XM_008459
Figure 4916A-B: DNA326378, XM_012651, gen.XM_012651
Figure 4917: DNA326379, NM_021626, gen.NM_021626
Figure 4918: PRO302
Figure 4919: DNA287291, NM_021213, gen.NM_021213
Figure 4920: PRO69561
Figure 4921A-B: DNA326380, NM_004859, gen.NM_004859
Figure 4922: PRO82774
Figure 4923: DNA326381, XM_083966, gen.XM_083966
Figure 4924: DNA326382, XM_044426, gen.XM_044426
Figure 4925: PRO82776
Figure 4926: DNA326383, XM_008253, gen.XM_008253
Figure 4927: DNA326384, XM_044394, gen.XM_044394
Figure 4928: PRO10400
Figure 4929: DNA326385, NM_017647, gen.NM_017647
Figure 4930: PRO82778
Figure 4931: DNA326386, NM_007372, gen.NM_007372
Figure 4932: PRO82779
Figure 4933: DNA326387, NM_002401, gen.NM_002401
Figure 4934: PRO37764
Figure 4935: DNA326388, XM_044376, gen.XM_044376
Figure 4936A-B: DNA150457, NM_006039, gen.NM_006039
Figure 4937: PRO12265
Figure 4938: DNA326389, XM_044367, gen.XM_044367
Figure 4939: DNA227055, NM_002634, gen.NM_002634
Figure 4940: PRO37518
Figure 4941: DNA326390, XM_011118, gen.XM_011118
Figure 4942: DNA326391, XM_055199, gen.XM_055199
Figure 4943A-B: DNA326392, XM_044372, gen.XM_044372
Figure 4944: DNA326393, XM_113315, gen.XM_113315
Figure 4945: DNA326394, XM_012609, gen.XM_012609
Figure 4946: DNA326395, NM_005220, gen.NM_005220
Figure 4947: PRO82787
Figure 4948: DNA326396, XM_085589, gen.XM_085589
Figure 4949: PRO82788
Figure 4950: DNA326397, XM_012634, gen.XM_012634
Figure 4951: DNA326398, XM_085627, gen.XM_085627
Figure 4952: PRO82790
Figure 4953: DNA150814, NM_002086, gen.NM_002086
Figure 4954: PRO12806
Figure 4955: DNA326399, NM_024844, gen.NM_024844
Figure 4956: PRO82791
Figure 4957: DNA326400, XM_041583, gen.XM_041583
Figure 4958: DNA326401, XM_046932, gen.XM_046932
Figure 4959: PRO82792
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Figure 4961: PRO82793
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Figure 4963A-B: DNA88430, NM_000213, gen.NM_000213
Figure 4964: PRO2788
Figure 4965A-B: DNA326404, XM_036104, gen.XM_036104
Figure 4966: PRO82794
Figure 4967: DNA326405, NM_000154, gen.NM_000154
Figure 4968: PRO82795
Figure 4969: DNA326406, NM_005324, gen.NM_005324
Figure 4970: PRO11403
Figure 4971A-B: DNA326407, XM_036115, gen.XM_036115
Figure 4972: PRO82796
Figure 4973: DNA326408, XM_054344,

gen.XM_054344
Figure 4974: PRO82797
Figure 4975: DNA274755, NM_002766,
gen.NM_002766
Figure 4976: PRO70703
Figure 4977A-B: DNA326409, XM_085531,
gen.XM_085531
Figure 4978: DNA326410, XM_113892,
gen.XM_113892
Figure 4979: PRO82799
Figure 4980: DNA326411, XM_017578,
gen.XM_017578
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Figure 4982: DNA326412, XM_036785,
gen.XM_036785
Figure 4983: PRO39201
Figure 4984: DNA326413, XM_097043,
gen.XM_097043
Figure 4985: DNA129504, NM_001168,
gen.NM_001168
Figure 4986: PRO7143
Figure 4987: DNA326414, XM_037196,
gen.XM_037196
Figure 4988: DNA326415, XM_037195,
gen.XM_037195
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Figure 4991: DNA326417, XM_085563,
gen.XM_085563
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gen.XM_085716
Figure 4993: PRO82805
Figure 4994A-B: DNA326419, XM_049934,
gen.XM_049934
Figure 4995: DNA326420, XM_049931,
gen.XM_049931
Figure 4996A-B: DNA326421, XM_045581,
gen.XM_045581
Figure 4997: PRO82807
Figure 4998: DNA326422, XM_113945,
gen.XM_113945
Figure 4999: DNA326423, XM_046481,
gen.XM_046481
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gen.XM_097195
Figure 5001: DNA326425, XM_097193,
gen.XM_097193
Figure 5002: DNA326426, NM_004309,
gen.NM_004309
Figure 5003: PRO61246
Figure 5004: DNA326427, XM_046472,
gen.XM_046472
Figure 5005: PRO82812
Figure 5006: DNA326428, NM_016286,
gen.NM_016286
Figure 5007: PRO82813
Figure 5008: DNA326429, NM_004127,
gen.NM_004127
Figure 5009: PRO82814
Figure 5010A-C: DNA326430, XM_113943,
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Figure 5011: DNA326431, XM_113330,
gen.XM_113330
Figure 5012: PRO82816
Figure 5013: DNA326432, XM_113303,
gen.XM_113303
Figure 5014: DNA287234, NM_031968,
gen.NM_031968
Figure 5015: PRO69513
Figure 5016: DNA326433, NM_022158,
gen.NM_022158
Figure 5017: PRO82818
Figure 5018: DNA326434, XM_038424,
gen.XM_038424
Figure 5019: DNA326435, XM_085735,
gen.XM_085735
Figure 5020: DNA326436, XM_046765,
gen.XM_046765
Figure 5021: DNA326437, XM_046769,
gen.XM_046769
Figure 5022: DNA326438, XM_046767,
gen.XM_046767
Figure 5023: DNA273694, NM_006101,
gen.NM_006101
Figure 5024: PRO61661
Figure 5025A-B: DNA326439, XM_028744,
gen.XM_028744
Figure 5026: DNA326440, XM_165954,
gen.XM_165954
Figure 5027: DNA326441, XM_041678,
gen.XM_041678
Figure 5028: DNA326442, XM_113343,
gen.XM_113343
Figure 5029: PRO82825
Figure 5030: DNA326443, XM_067325,
gen.XM_067325
Figure 5031: DNA326444, XM_012741,
gen.XM_012741
Figure 5032: DNA326445, NM_014214,
gen.NM_014214
Figure 5033: PRO82828
Figure 5034A-B: DNA326446, XM_035640,
gen.XM_035640
Figure 5035: PRO82829
Figure 5036: DNA326447, XM_016382,
gen.XM_016382
Figure 5037: DNA326448, NM_032933,
gen.NM_032933
Figure 5038: PRO82831
Figure 5039: DNA274690, NM_006938,
gen.NM_006938

Figure 5040A-B: DNA88457, NM_000227, gen.NM_000227
Figure 5041: PRO2799
Figure 5042: DNA326449, XM_085791, gen.XM_085791
Figure 5043: DNA326450, XM_085789, gen.XM_085789
Figure 5044: PRO82833
Figure 5045: DNA326451, XM_085790, gen.XM_085790
Figure 5046: DNA326452, XM_015755, gen.XM_015755
Figure 5047: PRO82835
Figure 5048: DNA326453, XM_097232, gen.XM_097232
Figure 5049: DNA326454, XM_085788, gen.XM_085788
Figure 5050: DNA88281, NM_001944, gen.NM_001944
Figure 5051: PRO2267
Figure 5052: DNA271841, NM_003787, gen.NM_003787
Figure 5053: PRO60121
Figure 5054: DNA326455, XM_008723, gen.XM_008723
Figure 5055: DNA326456, XM_084007, gen.XM_084007
Figure 5056: DNA256813, NM_018255, gen.NM_018255
Figure 5057: PRO51744
Figure 5058: DNA326457, XM_085775, gen.XM_085775
Figure 5059: PRO82840
Figure 5060: DNA326458, NM_138443, gen.NM_138443
Figure 5061: PRO82841
Figure 5062: DNA326459, XM_038872, gen.XM_038872
Figure 5063: PRO82842
Figure 5064: DNA326460, XM_086779, gen.XM_086779
Figure 5065: DNA326461, XM_167363, gen.XM_167363
Figure 5066: DNA326462, XM_031944, gen.XM_031944
Figure 5067: DNA326463, NM_000985, gen.NM_000985
Figure 5068: PRO82846
Figure 5069: DNA326464, NM_002396, gen.NM_002396
Figure 5070: PRO61113
Figure 5071: DNA326465, XM_166288, gen.XM_166288
Figure 5072: DNA326466, NM_004539, gen.NM_004539
Figure 5073: PRO60800
Figure 5074: DNA326467, XM_006937, gen.XM_006937
Figure 5075: DNA326468, XM_085779, gen.XM_085779
Figure 5076: DNA326469, XM_011089, gen.XM_011089
Figure 5077: PRO82850
Figure 5078: DNA326470, XM_169540, gen.XM_169540
Figure 5079: PRO82851
Figure 5080: DNA326471, XM_167008, gen.XM_167008
Figure 5081: PRO82852
Figure 5082: DNA326472, XM_048471, gen.XM_048471
Figure 5083A-B: DNA326473, XM_008812, gen.XM_008812
Figure 5084A-B: DNA326474, XM_117096, gen.XM_117096
Figure 5085: PRO82855
Figure 5086: DNA326475, NM_002385, gen.NM_002385
Figure 5087: PRO82856
Figure 5088: DNA326476, XM_015241, gen.XM_015241
Figure 5089A-B: DNA326477, XM_008695, gen.XM_008695
Figure 5090A-B: DNA326478, XM_041872, gen.XM_041872
Figure 5091: PRO82859
Figure 5092: DNA326479, XM_051586, gen.XM_051586
Figure 5093: DNA326480, NM_003712, gen.NM_003712
Figure 5094: PRO1077
Figure 5095: DNA326481, XM_042018, gen.XM_042018
Figure 5096: PRO2560
Figure 5097: DNA326482, XM_114018, gen.XM_114018
Figure 5098: DNA326483, NM_017876, gen.NM_017876
Figure 5099: PRO82861
Figure 5100: DNA326484, NM_031990, gen.NM_031990
Figure 5101: PRO82862
Figure 5102: DNA326485, NM_002819, gen.NM_002819
Figure 5103: PRO62899
Figure 5104: DNA326486, NM_005224, gen.NM_005224
Figure 5105: PRO82863
Figure 5106: DNA326487, XM_037565, gen.XM_037565
Figure 5107: PRO82864
Figure 5108: DNA326488, XM_092042,

gen.XM_092042
Figure 5109: DNA326489, XM_037572, gen.XM_037572
Figure 5110: DNA326490, XM_009279, gen.XM_009279
Figure 5111: PRO82867
Figure 5112: DNA326491, NM_002085, gen.NM_002085
Figure 5113A-B: DNA326492, XM_009277, gen.XM_009277
Figure 5114: DNA326493, XM_012913, gen.XM_012913
Figure 5115: DNA274101, NM_001687, gen.NM_001687
Figure 5116: PRO62039
Figure 5117: DNA326494, XM_028067, gen.XM_028067
Figure 5118: PRO82871
Figure 5119: DNA326495, XM_028064, gen.XM_028064
Figure 5120: DNA326496, NM_024407, gen.NM_024407
Figure 5121: PRO82872
Figure 5122: DNA326497, NM_000156, gen.NM_000156
Figure 5123: PRO58046
Figure 5124: DNA326498, NM_138924, gen.NM_138924
Figure 5125: PRO82873
Figure 5126: DNA326499, NM_001018, gen.NM_001018
Figure 5127: PRO10485
Figure 5128: DNA326500, XM_086101, gen.XM_086101
Figure 5129: PRO82874
Figure 5130: DNA326501, XM_086102, gen.XM_086102
Figure 5131: DNA326502, XM_047584, gen.XM_047584
Figure 5132A-B: DNA326503, XM_047600, gen.XM_047600
Figure 5133: PRO38496
Figure 5134: DNA326504, XM_097420, gen.XM_097420
Figure 5135A-B: DNA326505, XM_030721, gen.XM_030721
Figure 5136: PRO82877
Figure 5137: DNA326506, XM_030720, gen.XM_030720
Figure 5138: DNA326507, NM_031213, gen.NM_031213
Figure 5139: PRO82879
Figure 5140: DNA326508, XM_039723, gen.XM_039723
Figure 5141: DNA326509, NM_001319, gen.NM_001319
Figure 5142: PRO82881
Figure 5143: DNA326510, NM_017797, gen.NM_017797
Figure 5144: PRO82882
Figure 5145: DNA326511, XM_030714, gen.XM_030714
Figure 5146: DNA256555, NM_017572, gen.NM_017572
Figure 5147: PRO51586
Figure 5148A-B: DNA326512, NM_003938, gen.NM_003938
Figure 5149: PRO82884
Figure 5150A-B: DNA326513, XM_046822, gen.XM_046822
Figure 5151: PRO82885
Figure 5152: DNA326514, NM_007165, gen.NM_007165
Figure 5153: PRO82886
Figure 5154: DNA287636, NM_004152, gen.NM_004152
Figure 5155: DNA326515, NM_012458, gen.NM_012458
Figure 5156: PRO82887
Figure 5157: DNA326516, NM_032737, gen.NM_032737
Figure 5158: PRO82888
Figure 5159: DNA326517, XM_030485, gen.XM_030485
Figure 5160: DNA326518, XM_046934, gen.XM_046934
Figure 5161: DNA326519, NM_003021, gen.NM_003021
Figure 5162: PRO62302
Figure 5163: DNA326520, XM_055686, gen.XM_055686
Figure 5164: PRO37951
Figure 5165: DNA326521, XM_009222, gen.XM_009222
Figure 5166: DNA326522, XM_052635, gen.XM_052635
Figure 5167: PRO82892
Figure 5168: DNA326523, XM_052661, gen.XM_052661
Figure 5169: DNA326524, NM_016263, gen.NM_016263
Figure 5170: PRO82893
Figure 5171: DNA326525, NM_006339, gen.NM_006339
Figure 5172: PRO82894
Figure 5173: DNA326526, NM_032753, gen.NM_032753
Figure 5174: PRO82895
Figure 5175: DNA326527, XM_056421, gen.XM_056421
Figure 5176A-B: DNA326528, XM_031917, gen.XM_031917

Figure 5177: PRO82897
Figure 5178: DNA326529, NM_001961, gen.NM_001961
Figure 5179: PRO62225
Figure 5180: DNA326530, XM_016871, gen.XM_016871
Figure 5181: DNA326531, NM_016539, gen.NM_016539
Figure 5182: PRO82899
Figure 5183: DNA326532, XM_117122, gen.XM_117122
Figure 5184: DNA326533, XM_031857, gen.XM_031857
Figure 5185: PRO82901
Figure 5186: DNA326534, NM_024333, gen.NM_024333
Figure 5187: PRO82902
Figure 5188: DNA326535, NM_003025, gen.NM_003025
Figure 5189: PRO82903
Figure 5190: DNA326536, NM_025241, gen.NM_025241
Figure 5191: PRO82904
Figure 5192: DNA326537, XM_035638, gen.XM_035638
Figure 5193: PRO82905
Figure 5194A-B: DNA326538, XM_035636, gen.XM_035636
Figure 5195: DNA326539, XM_012862, gen.XM_012862
Figure 5196A-B: DNA326540, XM_035627, gen.XM_035627
Figure 5197A-B: DNA326541, XM_035625, gen.XM_035625
Figure 5198: PRO82909
Figure 5199: DNA274761, NM_014649, gen.NM_014649
Figure 5200: PRO62531
Figure 5201: DNA272421, NM_006012, gen.NM_006012
Figure 5202: PRO60674
Figure 5203: DNA326542, NM_003685, gen.NM_003685
Figure 5204: PRO82910
Figure 5205A-B: DNA326543, XM_009010, gen.XM_009010
Figure 5206: DNA270315, NM_004240, gen.NM_004240
Figure 5207: PRO58702
Figure 5208: DNA326544, NM_005490, gen.NM_005490
Figure 5209: PRO201
Figure 5210: DNA326546, XM_044619, gen.XM_044619
Figure 5211: PRO82912
Figure 5212: DNA326547, XM_012798, gen.XM_012798
Figure 5213: DNA326548, XM_044608, gen.XM_044608
Figure 5214: DNA326549, NM_003624, gen.NM_003624
Figure 5215: PRO82915
Figure 5216: DNA326550, NM_016579, gen.NM_016579
Figure 5217: PRO224
Figure 5218A-B: DNA326551, XM_048351, gen.XM_048351
Figure 5219: DNA326552, XM_048364, gen.XM_048364
Figure 5220: PRO82917
Figure 5221: DNA326553, XM_091938, gen.XM_091938
Figure 5222: DNA326554, XM_097300, gen.XM_097300
Figure 5223: DNA326555, XM_049282, gen.XM_049282
Figure 5224: PRO82920
Figure 5225: DNA326556, XM_058232, gen.XM_058232
Figure 5226: DNA326557, XM_045151, gen.XM_045151
Figure 5227A-B: DNA326558, XM_050435, gen.XM_050435
Figure 5228: PRO82923
Figure 5229: DNA326559, XM_113988, gen.XM_113988
Figure 5230: DNA326560, NM_058164, gen.NM_058164
Figure 5231: PRO82925
Figure 5232: DNA227280, NM_020230, gen.NM_020230
Figure 5233: PRO37743
Figure 5234: DNA270621, NM_003755, gen.NM_003755
Figure 5235: PRO58991
Figure 5236: DNA326561, XM_049502, gen.XM_049502
Figure 5237: DNA326562, NM_007065, gen.NM_007065
Figure 5238: PRO63226
Figure 5239: DNA326563, XM_049561, gen.XM_049561
Figure 5240: DNA326564, XM_017204, gen.XM_017204
Figure 5241: DNA326565, NM_005498, gen.NM_005498
Figure 5242: PRO62112
Figure 5243: DNA326566, XM_008887, gen.XM_008887
Figure 5244: DNA326567, XM_085862, gen.XM_085862
Figure 5245: PRO82930

Figure 5246: DNA326568, XM_084014, gen.XM_084014
Figure 5247A-B: DNA326569, XM_032710, gen.XM_032710
Figure 5248: DNA326570, XM_032719, gen.XM_032719
Figure 5249: PRO82933
Figure 5250: DNA326571, NM_024029, gen.NM_024029
Figure 5251: PRO23794
Figure 5252: DNA326572, XM_032724, gen.XM_032724
Figure 5253: PRO82934
Figure 5254A-B: DNA326573, NM_003072, gen.NM_003072
Figure 5255: PRO82935
Figure 5256A-B: DNA326574, XM_009082, gen.XM_009082
Figure 5257: DNA326575, XM_032774, gen.XM_032774
Figure 5258: DNA218271, NM_000121, gen.NM_000121
Figure 5259: PRO34323
Figure 5260: DNA326576, XM_057074, gen.XM_057074
Figure 5261: DNA326577, XM_032782, gen.XM_032782
Figure 5262: DNA326578, NM_032377, gen.NM_032377
Figure 5263: PRO82939
Figure 5264: DNA326579, XM_015697, gen.XM_015697
Figure 5265: PRO82940
Figure 5266: DNA326580, XM_010156, gen.XM_010156
Figure 5267: DNA326581, NM_001930, gen.NM_001930
Figure 5268: PRO58446
Figure 5269: DNA326582, NM_013406, gen.NM_013406
Figure 5270: DNA326583, NM_013407, gen.NM_013407
Figure 5271: PRO82943
Figure 5272: DNA103320, NM_002229, gen.NM_002229
Figure 5273: PRO4650
Figure 5274: DNA326584, XM_009063, gen.XM_009063
Figure 5275: PRO82944
Figure 5276: DNA326585, XM_085917, gen.XM_085917
Figure 5277: DNA274034, NM_006397, gen.NM_006397
Figure 5278: PRO61977
Figure 5279: DNA287243, NM_004461, gen.NM_004461
Figure 5280: PRO69518
Figure 5281: DNA326586, XM_032020, gen.XM_032020
Figure 5282: PRO2718
Figure 5283: DNA326587, NM_005053, gen.NM_005053
Figure 5284: PRO22613
Figure 5285: DNA326588, XM_085916, gen.XM_085916
Figure 5286: DNA326589, NM_017722, gen.NM_017722
Figure 5287: PRO82947
Figure 5288: DNA326590, NM_003765, gen.NM_003765
Figure 5289: PRO82948
Figure 5290: DNA326591, XM_051364, gen.XM_051364
Figure 5291: PRO82949
Figure 5292: DNA326592, XM_031345, gen.XM_031345
Figure 5293: PRO82950
Figure 5294: DNA326593, XM_113352, gen.XM_113352
Figure 5295: DNA326594, XM_058967, gen.XM_058967
Figure 5296: PRO82952
Figure 5297: DNA326595, XM_085909, gen.XM_085909
Figure 5298: DNA269894, NM_002730, gen.NM_002730
Figure 5299: PRO58292
Figure 5300: DNA326596, NM_018154, gen.NM_018154
Figure 5301: PRO82954
Figure 5302: DNA326597, XM_031276, gen.XM_031276
Figure 5303: DNA326598, XM_031273, gen.XM_031273
Figure 5304: PRO82956
Figure 5305: DNA326599, XM_031263, gen.XM_031263
Figure 5306: PRO82957
Figure 5307: DNA326600, XM_031251, gen.XM_031251
Figure 5308: DNA326601, NM_006844, gen.NM_006844
Figure 5309: PRO82958
Figure 5310A-C: DNA326602, XM_009303, gen.XM_009303
Figure 5311: DNA326603, XM_086074, gen.XM_086074
Figure 5312: DNA269630, NM_003290, gen.NM_003290
Figure 5313: PRO58042
Figure 5314: DNA326604, NM_005370, gen.NM_005370

Figure 5315: PRO12130
Figure 5316: DNA326605, XM_113348, gen.XM_113348
Figure 5317: DNA326606, NM_032207, gen.NM_032207
Figure 5318: PRO82962
Figure 5319A-B: DNA326607, NM_006387, gen.NM_006387
Figure 5320: PRO82963
Figure 5321: DNA326608, NM_024881, gen.NM_024881
Figure 5322: PRO82964
Figure 5323: DNA326609, NM_024104, gen.NM_024104
Figure 5324: PRO82965
Figure 5325A-C: DNA326610, XM_008854, gen.XM_008854
Figure 5326: DNA326611, NM_014173, gen.NM_014173
Figure 5327: PRO82967
Figure 5328: DNA287240, NM_004335, gen.NM_004335
Figure 5329: PRO29371
Figure 5330: DNA326612, XM_050660, gen.XM_050660
Figure 5331: DNA326613, XM_086116, gen.XM_086116
Figure 5332: DNA326614, NM_018174, gen.NM_018174
Figure 5333: PRO82970
Figure 5334: DNA326615, NM_000980, gen.NM_000980
Figure 5335: PRO82971
Figure 5336: DNA326616, XM_055230, gen.XM_055230
Figure 5337: DNA326617, XM_012179, gen.XM_012179
Figure 5338A-B: DNA326618, XM_009293, gen.XM_009293
Figure 5339: DNA326619, XM_038146, gen.XM_038146
Figure 5340: PRO82975
Figure 5341: DNA326620, XM_092046, gen.XM_092046
Figure 5342: PRO82976
Figure 5343: DNA326621, XM_038098, gen.XM_038098
Figure 5344: PRO82977
Figure 5345: DNA326622, NM_032627, gen.NM_032627
Figure 5346: PRO82978
Figure 5347: DNA326623, XM_165960, gen.XM_165960
Figure 5348: PRO82979
Figure 5349: DNA326624, XM_114004, gen.XM_114004
Figure 5350: DNA326625, NM_012181, gen.NM_012181
Figure 5351: PRO82980
Figure 5352: DNA227249, NM_007263, gen.NM_007263
Figure 5353: PRO37712
Figure 5354: DNA326626, XM_018515, gen.XM_018515
Figure 5355: DNA326627, NM_033415, gen.NM_033415
Figure 5356: PRO82982
Figure 5357: DNA326628, XM_009330, gen.XM_009330
Figure 5358: DNA326629, NM_134440, gen.NM_134440
Figure 5359: PRO82983
Figure 5360: DNA326630, NM_003721, gen.NM_003721
Figure 5361: PRO59220
Figure 5362: DNA326631, NM_015965, gen.NM_015965
Figure 5363: PRO82984
Figure 5364: DNA326632, XM_016378, gen.XM_016378
Figure 5365: PRO82985
Figure 5366: DNA326633, XM_114027, gen.XM_114027
Figure 5367: DNA326634, XM_165963, gen.XM_165963
Figure 5368: PRO82987
Figure 5369: DNA326635, XM_015769, gen.XM_015769
Figure 5370: DNA326636, XM_012812, gen.XM_012812
Figure 5371: DNA326637, XM_085971, gen.XM_085971
Figure 5372: DNA326638, XM_037662, gen.XM_037662
Figure 5373: PRO82991
Figure 5374: DNA326639, NM_001238, gen.NM_001238
Figure 5375: PRO82992
Figure 5376: DNA326640, NM_057182, gen.NM_057182
Figure 5377: PRO4756
Figure 5378: DNA326641, XM_009180, gen.XM_009180
Figure 5379: DNA326642, XM_117118, gen.XM_117118
Figure 5380: DNA326643, XM_092049, gen.XM_092049
Figure 5381: PRO82995
Figure 5382: DNA326644, XM_028672, gen.XM_028672
Figure 5383: DNA326645, XM_028666, gen.XM_028666

Figure 5384: DNA326646, XM_009338, gen.XM_009338
Figure 5385: DNA326647, XM_048258, gen.XM_048258
Figure 5386: PRO82998
Figure 5387: DNA256836, NM_018468, gen.NM_018468
Figure 5388: PRO51767
Figure 5389: DNA326648, NM_024321, gen.NM_024321
Figure 5390: PRO82999
Figure 5391A-B: DNA326649, XM_049237, gen.XM_049237
Figure 5392: PRO83000
Figure 5393: DNA326650, NM_032635, gen.NM_032635
Figure 5394: PRO23845
Figure 5395: DNA326651, XM_115615, gen.XM_115615
Figure 5396A-B: DNA326652, XM_091984, gen.XM_091984
Figure 5397: PRO83002
Figure 5398: DNA326653, XM_085986, gen.XM_085986
Figure 5399: DNA326654, XM_032285, gen.XM_032285
Figure 5400: PRO83004
Figure 5401: DNA326655, NM_002812, gen.NM_002812
Figure 5402: PRO83005
Figure 5403A-E: DNA326656, XM_029455, gen.XM_029455
Figure 5404: DNA326657, XM_029450, gen.XM_029450
Figure 5405: PRO83007
Figure 5406: DNA326658, XM_009149, gen.XM_009149
Figure 5407: PRO62500
Figure 5408: DNA326659, XM_056602, gen.XM_056602
Figure 5409: DNA326660, NM_012237, gen.NM_012237
Figure 5410: PRO83008
Figure 5411: DNA326661, NM_030593, gen.NM_030593
Figure 5412: PRO83009
Figure 5413: DNA326662, NM_017827, gen.NM_017827
Figure 5414: PRO83010
Figure 5415: DNA326663, NM_021107, gen.NM_021107
Figure 5416: PRO83011
Figure 5417: DNA326664, NM_033363, gen.NM_033363
Figure 5418: PRO83012
Figure 5419: DNA326665, XM_059045, gen.XM_059045
Figure 5420: PRO83013
Figure 5421: DNA273474, NM_005884, gen.NM_005884
Figure 5422: PRO61458
Figure 5423: DNA326666, XM_046090, gen.XM_046090
Figure 5424: PRO83014
Figure 5425: DNA326667, XM_086004, gen.XM_086004
Figure 5426: DNA272347, NM_001020, gen.NM_001020
Figure 5427: PRO60603
Figure 5428A-B: DNA326668, NM_003169, gen.NM_003169
Figure 5429: PRO12822
Figure 5430: DNA326669, XM_053074, gen.XM_053074
Figure 5431: PRO83016
Figure 5432: DNA326670, NM_016941, gen.NM_016941
Figure 5433: PRO83017
Figure 5434: DNA256840, NM_004714, gen.NM_004714
Figure 5435: PRO51771
Figure 5436: DNA326671, NM_001436, gen.NM_001436
Figure 5437: PRO83018
Figure 5438: DNA326672, XM_016410, gen.XM_016410
Figure 5439: DNA326673, XM_012860, gen.XM_012860
Figure 5440: DNA326674, XM_097365, gen.XM_097365
Figure 5441: DNA274139, NM_006503, gen.NM_006503
Figure 5442: PRO62075
Figure 5443: DNA326675, XM_009203, gen.XM_009203
Figure 5444: DNA326676, XM_047409, gen.XM_047409
Figure 5445: DNA326677, XM_047376, gen.XM_047376
Figure 5446A-B: DNA326678, XM_047374, gen.XM_047374
Figure 5447: DNA326679, XM_059052, gen.XM_059052
Figure 5448: DNA273600, NM_004596, gen.NM_004596
Figure 5449: PRO61575
Figure 5450: DNA326680, XM_030914, gen.XM_030914
Figure 5451: DNA326681, NM_052848, gen.NM_052848
Figure 5452: PRO83027
Figure 5453: DNA326682, XM_008912,

gen.XM_008912
Figure 5454: DNA326683, NM_020158, gen.NM_020158
Figure 5455: PRO83029
Figure 5456: DNA326684, XM_030901, gen.XM_030901
Figure 5457: PRO83030
Figure 5458: DNA326685, NM_018035, gen.NM_018035
Figure 5459: PRO83031
Figure 5460: DNA326686, XM_085874, gen.XM_085874
Figure 5461: DNA326687, XM_085875, gen.XM_085875
Figure 5462: DNA326688, XM_085876, gen.XM_085876
Figure 5463: DNA326689, XM_058949, gen.XM_058949
Figure 5464: PRO83035
Figure 5465: DNA326690, XM_030895, gen.XM_030895
Figure 5466: DNA326691, XM_115603, gen.XM_115603
Figure 5467: PRO83037
Figure 5468: DNA326692, NM_001022, gen.NM_001022
Figure 5469: PRO83038
Figure 5470: DNA326693, NM_004706, gen.NM_004706
Figure 5471: PRO83039
Figure 5472: DNA326694, XM_008878, gen.XM_008878
Figure 5473: PRO83040
Figure 5474: DNA326695, NM_022752, gen.NM_022752
Figure 5475: PRO83041
Figure 5476: DNA151808, NM_006494, gen.NM_006494
Figure 5477: PRO12892
Figure 5478: DNA326696, NM_001816, gen.NM_001816
Figure 5479: PRO34151
Figure 5480: DNA326697, NM_000554, gen.NM_000554
Figure 5481: PRO83042
Figure 5482: DNA326698, XM_049920, gen.XM_049920
Figure 5483: DNA326699, XM_055859, gen.XM_055859
Figure 5484A-B: DNA326700, XM_009125, gen.XM_009125
Figure 5485: DNA326701, XM_008860, gen.XM_008860
Figure 5486: DNA326702, XM_009036, gen.XM_009036
Figure 5487: DNA326703, XM_085950, gen.XM_085950
Figure 5488: DNA326704, XM_028263, gen.XM_028263
Figure 5489: DNA326705, XM_085928, gen.XM_085928
Figure 5490: PRO36963
Figure 5491: DNA326706, XM_028267, gen.XM_028267
Figure 5492: DNA326707, NM_013403, gen.NM_013403
Figure 5493: PRO83050
Figure 5494: DNA103580, NM_001743, gen.NM_001743
Figure 5495: PRO4904
Figure 5496: DNA326708, XM_009126, gen.XM_009126
Figure 5497: DNA326709, NM_006247, gen.NM_006247
Figure 5498: PRO25881
Figure 5499: DNA326710, NM_003370, gen.NM_003370
Figure 5500: PRO83052
Figure 5501: DNA326711, XM_085856, gen.XM_085856
Figure 5502: DNA150784, NM_001983, gen.NM_001983
Figure 5503: PRO12800
Figure 5504: DNA270931, NM_012099, gen.NM_012099
Figure 5505: PRO59264
Figure 5506A-B: DNA257531, NM_031417, gen.NM_031417
Figure 5507: PRO52101
Figure 5508: DNA326712, NM_001294, gen.NM_001294
Figure 5509: PRO83054
Figure 5510: DNA326713, XM_097274, gen.XM_097274
Figure 5511: DNA88084, NM_000041, gen.NM_000041
Figure 5512: PRO2644
Figure 5513: DNA256533, NM_006114, gen.NM_006114
Figure 5514: PRO51565
Figure 5515: DNA251057, NM_002856, gen.NM_002856
Figure 5516: PRO47354
Figure 5517: DNA226011, NM_005581, gen.NM_005581
Figure 5518: PRO36474
Figure 5519: DNA326714, NM_012116, gen.NM_012116
Figure 5520: PRO83056
Figure 5521: DNA326715, XM_097275, gen.XM_097275
Figure 5522: DNA326716, XM_008851,

gen.XM_008851
Figure 5523: DNA274289, NM_016440, gen.NM_016440
Figure 5524: PRO62212
Figure 5525: DNA326717, NM_012068, gen.NM_012068
Figure 5526: PRO83059
Figure 5527: DNA326718, XM_085927, gen.XM_085927
Figure 5528: DNA326719, XM_084023, gen.XM_084023
Figure 5529: DNA326720, XM_167530, gen.XM_167530
Figure 5530: DNA326721, XM_114025, gen.XM_114025
Figure 5531: DNA326722, XM_008985, gen.XM_008985
Figure 5532: DNA326723, NM_030973, gen.NM_030973
Figure 5533: PRO83065
Figure 5534: DNA326724, NM_025129, gen.NM_025129
Figure 5535: PRO83066
Figure 5536: DNA326725, NM_014203, gen.NM_014203
Figure 5537: DNA326726, XM_085934, gen.XM_085934
Figure 5538: PRO83068
Figure 5539: DNA326727, NM_001536, gen.NM_001536
Figure 5540: PRO83069
Figure 5541: DNA326728, XM_165432, gen.XM_165432
Figure 5542: DNA274823, NM_001571, gen.NM_001571
Figure 5543: PRO62582
Figure 5544A-B: DNA326729, XM_046313, gen.XM_046313
Figure 5545: PRO83071
Figure 5546: DNA326730, NM_015953, gen.NM_015953
Figure 5547: PRO83072
Figure 5548: DNA326731, XM_027904, gen.XM_027904
Figure 5549: DNA326732, XM_084026, gen.XM_084026
Figure 5550: DNA290260, NM_012423, gen.NM_012423
Figure 5551: PRO70385
Figure 5552: DNA326733, XM_058991, gen.XM_058991
Figure 5553: PRO83073
Figure 5554: DNA326734, NM_017916, gen.NM_017916
Figure 5555: PRO83074
Figure 5556: DNA326735, NM_003598, gen.NM_003598
Figure 5557: PRO83075
Figure 5558: DNA326736, NM_006666, gen.NM_006666
Figure 5559: PRO83076
Figure 5560: DNA326737, XM_114024, gen.XM_114024
Figure 5561: PRO83077
Figure 5562: DNA304658, NM_000146, gen.NM_000146
Figure 5563: PRO71085
Figure 5564: DNA326738, NM_004324, gen.NM_004324
Figure 5565: PRO38101
Figure 5566: DNA326739, NM_006184, gen.NM_006184
Figure 5567: PRO83078
Figure 5568: DNA273066, NM_001190, gen.NM_001190
Figure 5569: PRO61129
Figure 5570: DNA326740, XM_058987, gen.XM_058987
Figure 5571: DNA326741, NM_000979, gen.NM_000979
Figure 5572: PRO83080
Figure 5573: DNA326742, XM_085935, gen.XM_085935
Figure 5574: DNA326743, NM_031485, gen.NM_031485
Figure 5575: PRO61308
Figure 5576: DNA103239, NM_006801, gen.NM_006801
Figure 5577: PRO4569
Figure 5578: DNA326744, XM_046419, gen.XM_046419
Figure 5579: PRO83082
Figure 5580: DNA326745, NM_002691, gen.NM_002691
Figure 5581: PRO83083
Figure 5582: DNA326746, XM_056286, gen.XM_056286
Figure 5583: PRO83084
Figure 5584: DNA326747, XM_058990, gen.XM_058990
Figure 5585: PRO83085
Figure 5586: DNA326748, XM_091981, gen.XM_091981
Figure 5587: PRO83086
Figure 5588: DNA326749, NM_032712, gen.NM_032712
Figure 5589: PRO23238
Figure 5590: DNA83154, NM_001648, gen.NM_001648
Figure 5591: PRO2109
Figure 5592: DNA326750, XM_055658, gen.XM_055658

Figure 5593: DNA269481, NM_001985, gen.NM_001985
Figure 5594: PRO57901
Figure 5595: DNA326751, XM_091886, gen.XM_091886
Figure 5596: PRO83087
Figure 5597: DNA326752, XM_008830, gen.XM_008830
Figure 5598: DNA326753, XM_039908, gen.XM_039908
Figure 5599: PRO83089
Figure 5600: DNA326754, NM_015629, gen.NM_015629
Figure 5601: PRO83090
Figure 5602: DNA326755, XM_050236, gen.XM_050236
Figure 5603: DNA326756, XM_050589, gen.XM_050589
Figure 5604: PRO83092
Figure 5605: DNA326757, XM_117128, gen.XM_117128
Figure 5606: PRO83093
Figure 5607: DNA326758, XM_059321, gen.XM_059321
Figure 5608: DNA326759, NM_003283, gen.NM_003283
Figure 5609: PRO83095
Figure 5610A-B: DNA326760, NM_014931, gen.NM_014931
Figure 5611: PRO83096
Figure 5612: DNA326761, XM_035919, gen.XM_035919
Figure 5613: DNA326762, NM_000991, gen.NM_000991
Figure 5614: PRO83098
Figure 5615: DNA273346, NM_014501, gen.NM_014501
Figure 5616: PRO61349
Figure 5617: DNA326763, NM_013333, gen.NM_013333
Figure 5618: PRO83099
Figure 5619: DNA326764, NM_007279, gen.NM_007279
Figure 5620: PRO83100
Figure 5621: DNA326765, NM_016202, gen.NM_016202
Figure 5622: PRO83101
Figure 5623: DNA326766, XM_034377, gen.XM_034377
Figure 5624: PRO83102
Figure 5625: DNA272062, NM_014453, gen.NM_014453
Figure 5626: PRO60333
Figure 5627: DNA254548, NM_005762, gen.NM_005762
Figure 5628: PRO49653
Figure 5629: DNA326767, XM_085972, gen.XM_085972
Figure 5630: PRO83103
Figure 5631: DNA326768, NM_032792, gen.NM_032792
Figure 5632: PRO83104
Figure 5633: DNA326769, NM_001009, gen.NM_001009
Figure 5634: PRO83105
Figure 5635: DNA326770, XM_058125, gen.XM_058125
Figure 5636: DNA326771, NM_024691, gen.NM_024691
Figure 5637: PRO83107
Figure 5638: DNA297288, NM_021158, gen.NM_021158
Figure 5639: PRO70810
Figure 5640: DNA304662, NM_031229, gen.NM_031229
Figure 5641: PRO71089
Figure 5642: DNA326772, NM_031228, gen.NM_031228
Figure 5643: PRO83108
Figure 5644: DNA326773, XM_097749, gen.XM_097749
Figure 5645: PRO83109
Figure 5646: DNA326774, XM_055993, gen.XM_055993
Figure 5647: DNA326775, XM_009622, gen.XM_009622
Figure 5648: DNA326776, NM_000801, gen.NM_000801
Figure 5649: PRO59142
Figure 5650: DNA326777, NM_054014, gen.NM_054014
Figure 5651: PRO59142
Figure 5652: DNA326778, NM_016143, gen.NM_016143
Figure 5653: PRO83112
Figure 5654: DNA287270, NM_003091, gen.NM_003091
Figure 5655: PRO69541
Figure 5656: DNA326779, NM_052881, gen.NM_052881
Figure 5657: PRO83113
Figure 5658: DNA326780, XM_044914, gen.XM_044914
Figure 5659: PRO83114
Figure 5660: DNA326781, XM_044915, gen.XM_044915
Figure 5661: DNA326782, NM_006899, gen.NM_006899
Figure 5662: PRO83116
Figure 5663: DNA326783, NM_019609, gen.NM_019609
Figure 5664: PRO83117

Figure 5665: DNA326784, NM_021826, gen.NM_021826
Figure 5666: PRO83118
Figure 5667: DNA326785, XM_045418, gen.XM_045418
Figure 5668: DNA287261, NM_017874, gen.NM_017874
Figure 5669: PRO69533
Figure 5670: DNA326786, XM_086710, gen.XM_086710
Figure 5671: DNA326787, XM_045451, gen.XM_045451
Figure 5672: PRO83121
Figure 5673: DNA326788, XM_114174, gen.XM_114174
Figure 5674: DNA326789, XM_045460, gen.XM_045460
Figure 5675: DNA326790, XM_059268, gen.XM_059268
Figure 5676A-B: DNA271010, NM_014737, gen.NM_014737
Figure 5677: PRO59339
Figure 5678: DNA326791, XM_056035, gen.XM_056035
Figure 5679: DNA83170, NM_001819, gen.NM_001819
Figure 5680: PRO2615
Figure 5681: DNA227348, NM_019095, gen.NM_019095
Figure 5682: PRO37811
Figure 5683: DNA326792, NM_003092, gen.NM_003092
Figure 5684: PRO83125
Figure 5685: DNA287290, NM_014426, gen.NM_014426
Figure 5686: PRO69560
Figure 5687: DNA326793, XM_086701, gen.XM_086701
Figure 5688: DNA326794, XM_117209, gen.XM_117209
Figure 5689A-B: DNA326795, XM_046520, gen.XM_046520
Figure 5690: PRO83128
Figure 5691: DNA326796, XM_115846, gen.XM_115846
Figure 5692: PRO83129
Figure 5693: DNA326797, NM_080820, gen.NM_080820
Figure 5694: PRO83130
Figure 5695: DNA326798, XM_086715, gen.XM_086715
Figure 5696: DNA326799, XM_092760, gen.XM_092760
Figure 5697: PRO83132
Figure 5698: DNA326800, NM_012255, gen.NM_012255
Figure 5699: PRO83133
Figure 5700: DNA326801, XM_012970, gen.XM_012970
Figure 5701: DNA326802, XM_042765, gen.XM_042765
Figure 5702: PRO83135
Figure 5703: DNA150548, NM_001247, gen.NM_001247
Figure 5704: PRO12324
Figure 5705A-B: DNA326803, XM_009436, gen.XM_009436
Figure 5706: DNA326804, XM_114178, gen.XM_114178
Figure 5707: PRO83137
Figure 5708: DNA326805, XM_046160, gen.XM_046160
Figure 5709: PRO83138
Figure 5710: DNA326806, XM_046179, gen.XM_046179
Figure 5711: PRO83139
Figure 5712: DNA326807, XM_086745, gen.XM_086745
Figure 5713: DNA326808, NM_138578, gen.NM_138578
Figure 5714: PRO83141
Figure 5715: DNA326809, NM_012112, gen.NM_012112
Figure 5716: PRO83142
Figure 5717: DNA326810, XM_086736, gen.XM_086736
Figure 5718: PRO83143
Figure 5719: DNA326811, NM_030815, gen.NM_030815
Figure 5720: PRO83144
Figure 5721A-B: DNA150767, NM_014742, gen.NM_014742
Figure 5722: PRO12460
Figure 5723A-B: DNA326812, XM_047007, gen.XM_047007
Figure 5724: PRO83145
Figure 5725A-B: DNA326813, XM_047011, gen.XM_047011
Figure 5726: PRO83146
Figure 5727A-B: DNA326814, XM_047018, gen.XM_047018
Figure 5728: DNA326815, XM_009450, gen.XM_009450
Figure 5729: DNA326816, NM_033197, gen.NM_033197
Figure 5730: PRO83149
Figure 5731: DNA326817, XM_097772, gen.XM_097772
Figure 5732: PRO83150
Figure 5733: DNA326818, NM_016732, gen.NM_016732
Figure 5734: DNA97298, NM_003908,

gen.NM_003908
Figure 5735: PRO3645
Figure 5736: DNA326819, NM_000687, gen.NM_000687
Figure 5737: PRO83152
Figure 5738: DNA273517, NM_000178, gen.NM_000178
Figure 5739: PRO61498
Figure 5740: DNA326820, NM_018217, gen.NM_018217
Figure 5741: PRO83153
Figure 5742: DNA326821, NM_002212, gen.NM_002212
Figure 5743: PRO60945
Figure 5744A-C: DNA326822, NM_007186, gen.NM_007186
Figure 5745: DNA226758, NM_015966, gen.NM_015966
Figure 5746: PRO37221
Figure 5747: DNA194701, NM_003915, gen.NM_003915
Figure 5748: PRO24002
Figure 5749: DNA326823, XM_113380, gen.XM_113380
Figure 5750: DNA326824, NM_016558, gen.NM_016558
Figure 5751: PRO83155
Figure 5752: DNA326825, NM_015511, gen.NM_015511
Figure 5753: PRO83156
Figure 5754: DNA326826, XM_009501, gen.XM_009501
Figure 5755: PRO83157
Figure 5756: DNA326827, XM_057236, gen.XM_057236
Figure 5757: DNA326828, NM_024918, gen.NM_024918
Figure 5758: PRO83159
Figure 5759: DNA326829, XM_009642, gen.XM_009642
Figure 5760: DNA194807, NM_006698, gen.NM_006698
Figure 5761: PRO24077
Figure 5762: DNA326830, XM_009686, gen.XM_009686
Figure 5763: DNA326831, NM_030877, gen.NM_030877
Figure 5764: PRO83161
Figure 5765: DNA326832, XM_028806, gen.XM_028806
Figure 5766A-B: DNA326833, XM_028810, gen.XM_028810
Figure 5767: PRO83163
Figure 5768: DNA326834, XM_012931, gen.XM_012931
Figure 5769: DNA326835, NM_024855, gen.NM_024855
Figure 5770: PRO83165
Figure 5771A-B: DNA227472, NM_002660, gen.NM_002660
Figure 5772: PRO37935
Figure 5773: DNA326836, XM_097727, gen.XM_097727
Figure 5774: DNA103525, NM_002466, gen.NM_002466
Figure 5775: PRO4852
Figure 5776: DNA326837, XM_029810, gen.XM_029810
Figure 5777: PRO83167
Figure 5778: DNA326838, XM_029822, gen.XM_029822
Figure 5779: DNA326839, NM_002638, gen.NM_002638
Figure 5780: PRO2065
Figure 5781: DNA326840, NM_003064, gen.NM_003064
Figure 5782: PRO1720
Figure 5783: DNA326841, NM_015937, gen.NM_015937
Figure 5784: PRO83169
Figure 5785: DNA273320, NM_007019, gen.NM_007019
Figure 5786: PRO61327
Figure 5787: DNA326842, NM_033421, gen.NM_033421
Figure 5788: PRO83170
Figure 5789: DNA88569, NM_006227, gen.NM_006227
Figure 5790: PRO2420
Figure 5791: DNA88239, NM_004994, gen.NM_004994
Figure 5792: PRO2711
Figure 5793: DNA326843, XM_057374, gen.XM_057374
Figure 5794: DNA326844, XM_114163, gen.XM_114163
Figure 5795A-B: DNA326845, XM_097731, gen.XM_097731
Figure 5796A-B: DNA326846, XM_030044, gen.XM_030044
Figure 5797: PRO83174
Figure 5798: DNA326847, NM_017895, gen.NM_017895
Figure 5799: PRO83175
Figure 5800: DNA326848, XM_097713, gen.XM_097713
Figure 5801: PRO83176
Figure 5802: DNA326849, NM_005985, gen.NM_005985
Figure 5803: PRO83177
Figure 5804: DNA326850, NM_003349, gen.NM_003349

Figure 5805: PRO83178
Figure 5806: DNA326851, NM_022442, gen.NM_022442
Figure 5807: PRO83179
Figure 5808: DNA326852, NM_005194, gen.NM_005194
Figure 5809: DNA326853, NM_002827, gen.NM_002827
Figure 5810: PRO38066
Figure 5811: DNA326854, NM_003859, gen.NM_003859
Figure 5812: PRO83180
Figure 5813: DNA326855, XM_114165, gen.XM_114165
Figure 5814: DNA269526, NM_001324, gen.NM_001324
Figure 5815: PRO57942
Figure 5816: DNA326856, XM_009549, gen.XM_009549
Figure 5817: PRO83182
Figure 5818: DNA326857, XM_030621, gen.XM_030621
Figure 5819: DNA326858, XM_086648, gen.XM_086648
Figure 5820: PRO83183
Figure 5821: DNA326859, XM_009672, gen.XM_009672
Figure 5822: PRO83184
Figure 5823A-B: DNA326860, XM_009671, gen.XM_009671
Figure 5824: DNA326861, NM_004738, gen.NM_004738
Figure 5825: PRO983
Figure 5826: DNA326862, NM_016592, gen.NM_016592
Figure 5827: PRO83185
Figure 5828: DNA326863, NM_080425, gen.NM_080425
Figure 5829: PRO83186
Figure 5830: DNA304670, NM_000516, gen.NM_000516
Figure 5831: PRO71097
Figure 5832: DNA326864, NM_080426, gen.NM_080426
Figure 5833: PRO83187
Figure 5834: DNA326865, XM_030699, gen.XM_030699
Figure 5835: PRO83188
Figure 5836: DNA188229, NM_000114, gen.NM_000114
Figure 5837: PRO21728
Figure 5838: DNA326866, NM_002792, gen.NM_002792
Figure 5839: PRO83189
Figure 5840A-B: DNA326867, XM_037202, gen.XM_037202
Figure 5841: PRO83190
Figure 5842: DNA326868, XM_037206, gen.XM_037206
Figure 5843: PRO83191
Figure 5844: DNA103486, NM_007002, gen.NM_007002
Figure 5845: PRO4813
Figure 5846A-D: DNA326869, XM_037217, gen.XM_037217
Figure 5847: DNA326870, NM_001024, gen.NM_001024
Figure 5848: PRO83193
Figure 5849: DNA326871, NM_018270, gen.NM_018270
Figure 5850: PRO83194
Figure 5851: DNA326872, XM_028783, gen.XM_028783
Figure 5852: PRO83195
Figure 5853: DNA326873, NM_001853, gen.NM_001853
Figure 5854: PRO83196
Figure 5855: DNA326874, NM_080796, gen.NM_080796
Figure 5856: PRO83197
Figure 5857: DNA326875, NM_022105, gen.NM_022105
Figure 5858: PRO83198
Figure 5859: DNA326876, NM_080797, gen.NM_080797
Figure 5860: PRO83199
Figure 5861: DNA326877, NM_018209, gen.NM_018209
Figure 5862: PRO83200
Figure 5863A-C: DNA326878, XM_028834, gen.XM_028834
Figure 5864: PRO83201
Figure 5865: DNA326879, NM_024299, gen.NM_024299
Figure 5866: PRO83202
Figure 5867A-C: DNA326880, XM_028918, gen.XM_028918
Figure 5868: PRO83203
Figure 5869: DNA326881, NM_032527, gen.NM_032527
Figure 5870: PRO83204
Figure 5871A-B: DNA326882, XM_028966, gen.XM_028966
Figure 5872: PRO83205
Figure 5873: DNA269746, NM_012469, gen.NM_012469
Figure 5874: PRO58155
Figure 5875: DNA326883, XM_114154, gen.XM_114154
Figure 5876: DNA326884, XM_072173, gen.XM_072173
Figure 5877: DNA326885, XM_086759,

gen.XM_086759
Figure 5878: DNA326886, XM_086760, gen.XM_086760
Figure 5879: DNA326887, NM_021219, gen.NM_021219
Figure 5880: PRO28687
Figure 5881: DNA188732, NM_000484, gen.NM_000484
Figure 5882: PRO25302
Figure 5883: DNA326888, NM_016940, gen.NM_016940
Figure 5884: PRO83210
Figure 5885: DNA254572, NM_006585, gen.NM_006585
Figure 5886: PRO49675
Figure 5887: DNA326889, NM_005806, gen.NM_005806
Figure 5888: PRO83211
Figure 5889: DNA326890, XM_114185, gen.XM_114185
Figure 5890: DNA254994, NM_017613, gen.NM_017613
Figure 5891: PRO50083
Figure 5892: DNA274129, NM_001697, gen.NM_001697
Figure 5893: PRO62065
Figure 5894: DNA326891, NM_001757, gen.NM_001757
Figure 5895: PRO83212
Figure 5896A-C: DNA151898, NM_003316, gen.NM_003316
Figure 5897: PRO12135
Figure 5898: DNA326892, NM_003720, gen.NM_003720
Figure 5899: PRO83213
Figure 5900: DNA326893, NM_002606, gen.NM_002606
Figure 5901: PRO83214
Figure 5902: DNA326894, XM_033015, gen.XM_033015
Figure 5903: DNA326895, XM_033016, gen.XM_033016
Figure 5904: PRO59669
Figure 5905: DNA326896, NM_003681, gen.NM_003681
Figure 5906: PRO69486
Figure 5907: DNA326897, XM_035999, gen.XM_035999
Figure 5908: DNA326898, NM_020132, gen.NM_020132
Figure 5909: PRO83217
Figure 5910: DNA326899, XM_036011, gen.XM_036011
Figure 5911: DNA326900, NM_013369, gen.NM_013369
Figure 5912: PRO83219
Figure 5913: DNA326901, XM_036042, gen.XM_036042
Figure 5914: DNA326902, XM_086770, gen.XM_086770
Figure 5915: DNA326903, NM_004928, gen.NM_004928
Figure 5916: PRO83222
Figure 5917: DNA326904, XM_036087, gen.XM_036087
Figure 5918: PRO83223
Figure 5919: DNA326905, XM_009805, gen.XM_009805
Figure 5920: PRO83224
Figure 5921: DNA226409, NM_004339, gen.NM_004339
Figure 5922: PRO36872
Figure 5923: DNA326906, XM_036107, gen.XM_036107
Figure 5924A-B: DNA326907, XM_036175, gen.XM_036175
Figure 5925: DNA326908, XM_097817, gen.XM_097817
Figure 5926A-B: DNA326909, XM_054566, gen.XM_054566
Figure 5927: DNA326910, XM_036755, gen.XM_036755
Figure 5928: DNA326911, XM_086773, gen.XM_086773
Figure 5929: DNA326912, XM_097807, gen.XM_097807
Figure 5930: DNA326913, XM_086777, gen.XM_086777
Figure 5931: DNA326914, NM_002340, gen.NM_002340
Figure 5932: PRO83233
Figure 5933A-B: DNA326915, NM_003906, gen.NM_003906
Figure 5934: PRO83234
Figure 5935: DNA226617, NM_006272, gen.NM_006272
Figure 5936: PRO37080
Figure 5937: DNA326916, NM_033070, gen.NM_033070
Figure 5938: PRO83235
Figure 5939: DNA255046, NM_017829, gen.NM_017829
Figure 5940: PRO50134
Figure 5941: DNA326917, NM_001696, gen.NM_001696
Figure 5942: PRO83236
Figure 5943A-B: DNA326918, XM_032996, gen.XM_032996
Figure 5944: PRO83237
Figure 5945: DNA326919, XM_167538, gen.XM_167538
Figure 5946: DNA326920, XM_033090,

gen.XM_033090
Figure 5947: DNA225954, NM_000407, gen.NM_000407
Figure 5948: PRO36417
Figure 5949: DNA326921, XM_058918, gen.XM_058918
Figure 5950: DNA326922, XM_097833, gen.XM_097833
Figure 5951: DNA326923, NM_024627, gen.NM_024627
Figure 5952: PRO83242
Figure 5953: DNA326924, XM_086809, gen.XM_086809
Figure 5954: DNA326925, NM_006440, gen.NM_006440
Figure 5955: PRO83244
Figure 5956: DNA226561, NM_000754, gen.NM_000754
Figure 5957: PRO37024
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gen.XM_167395,2963
gen.XM_167411,2901
gen.XM_167414,2904
gen.XM_167433,3324
gen.XM_167437,3192
gen.XM_167439,3876
gen.XM_167453,4538
gen.XM_167456,4541
gen.XM_167476,2321
gen.XM_167477,2325
gen.XM_167483,2328
gen.XM_167484,2329
gen.XM_167494,2273
gen.XM_167498,2301
gen.XM_167500,2299
gen.XM_167502,2312
gen.XM_167504,2300
gen.XM_167518,3754
gen.XM_167530,5529
gen.XM_167538,5945
gen.XM_167558,2645
gen.XM_167626,2887
gen.XM_167716,3244
gen.XM_167726,3248
gen.XM_167747,3234
gen.XM_167748,3228
gen.XM_167780,3417
gen.XM_167804,3291
gen.XM_167853,3318
gen.XM_167892,3883
gen.XM_167906,3877
gen.XM_167911,3868
gen.XM_167918,3869
gen.XM_168054,2103
gen.XM_168070,1928
gen.XM_168104,1994
gen.XM_168123,1877
gen.XM_168181,2322
gen.XM_168251,2323
gen.XM_168354,2271
gen.XM_168378,2269
gen.XM_168435,2316
gen.XM_168450,2315
gen.XM_168454,2302
gen.XM_168461,2311
gen.XM_168464,2317
gen.XM_168470,2310
gen.XM_168548,2375
gen.XM_168572,2380
gen.XM_168586,2360
gen.XM_169414,3880
gen.XM_169540,5078
gen.XM_170195,2267
gen.XM_170427,2318

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "TAT polypeptide" and "TAT" as used herein and when immediately followed by a numerical designation, refer to various polypeptides, wherein the complete designation (i.e., TAT/number) refers to specific polypeptide sequences as described herein. The terms "TAT/number polypeptide" and "TAT/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides, polypeptide variants and fragments of native sequence polypeptides and polypeptide variants (which are further defined herein). The TAT 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 "TAT polypeptide" refers to each individual TAT/number polypeptide disclosed herein. All disclosures in this specification which refer to the "TAT 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, formation of TAT binding oligopeptides to or against, formation of TAT binding organic molecules to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "TAT polypeptide" also includes variants of the TAT/number polypeptides disclosed herein.

A "native sequence TAT polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding TAT polypeptide derived from nature. Such native sequence TAT polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TAT polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific TAT 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 certain embodiments of the invention, the native sequence TAT 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 (if indicated) are shown in bold font and underlined in the figures. Nucleic acid residues indicated as "N" in the accompanying figures are any nucleic acid residue. However, while the TAT polypeptides 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 TAT polypeptides.

The TAT polypeptide "extracellular domain" or "ECD" refers to a form of the TAT polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a TAT 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 TAT 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 TAT 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 TAT polypeptides disclosed herein may be 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.

"TAT polypeptide variant" means a TAT polypeptide, preferably an active TAT polypeptide, as defined herein having at least about 80% amino acid sequence identity with a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Such TAT polypeptide variants include, for instance, TAT 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 TAT polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity, to a full-length native sequence TAT polypeptide sequence as disclosed herein, a TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length TAT polypeptide sequence as disclosed herein. Ordinarily, TAT variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600 amino acids in length, or more. Optionally, TAT variant polypeptides will have no more than one conservative amino acid substitution as compared to the native TAT polypeptide sequence, alternatively no more than 2, 3, 4, 5, 6, 7, 8, 9, or 10 conservative amino acid substitution as compared to the native TAT polypeptide sequence.

"Percent (%) amino acid sequence identity" with respect to the TAT 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 TAT 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 "TAT", wherein "TAT" represents the amino acid sequence of a hypothetical TAT polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "TAT" 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.

"TAT variant polynucleotide" or "TAT variant nucleic acid sequence" means a nucleic acid molecule

which encodes a TAT polypeptide, preferably an active TAT polypeptide, as defined herein and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein (such as those encoded by a nucleic acid that represents only a portion of the complete coding sequence for a full-length TAT polypeptide). Ordinarily, a TAT variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence TAT polypeptide sequence as disclosed herein, a full-length native sequence TAT polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a TAT polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length TAT polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, TAT variant polynucleotides are at least about 5 nucleotides in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, or 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.

"Percent (%) nucleic acid sequence identity" with respect to TAT-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 TAT 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 "TAT-DNA", wherein "TAT-DNA" represents a hypothetical TAT-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "TAT-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.

In other embodiments, TAT variant polynucleotides are nucleic acid molecules that encode a TAT polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length TAT polypeptide as disclosed herein. TAT variant polypeptides may be those that are encoded by a TAT variant polynucleotide.

The term "full-length coding region" when used in reference to a nucleic acid encoding a TAT polypeptide refers to the sequence of nucleotides which encode the full-length TAT polypeptide of the invention (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures). The term "full-length coding region" when used in reference to an ATCC deposited nucleic acid refers to the TAT polypeptide-encoding portion of the cDNA that is inserted into the vector deposited with the ATCC (which is often shown between start and stop codons, inclusive thereof, in the accompanying figures).

"Isolated," when used to describe the various TAT 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 TAT polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" TAT 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.

"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) overnight hybridization in a solution that employs 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 a 10 minute wash at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) followed by a 10 minute 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 TAT polypeptide or anti-TAT antibody 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).

"Active" or "activity" for the purposes herein refers to form(s) of a TAT polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring TAT, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring TAT other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring TAT 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 TAT.

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 TAT 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 TAT 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 TAT polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a TAT polypeptide may comprise contacting a TAT polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities

normally associated with the TAT polypeptide.

"Treating" or "treatment" or "alleviation" 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. A subject or mammal is successfully "treated" for a TAT polypeptide-expressing cancer if, after receiving a therapeutic amount of an anti-TAT antibody, TAT binding oligopeptide or TAT binding organic molecule according to the methods of the present invention, the patient shows observable and/or measurable reduction in or absence of one or more of the following: reduction in the number of cancer cells or absence of the cancer cells; reduction in the tumor size; inhibition (i.e., slow to some extent and preferably stop) of cancer cell infiltration into peripheral organs including the spread of cancer into soft tissue and bone; inhibition (i.e., slow to some extent and preferably stop) of tumor metastasis; inhibition, to some extent, of tumor growth; and/or relief to some extent, one or more of the symptoms associated with the specific cancer; reduced morbidity and mortality, and improvement in quality of life issues. To the extent the anti-TAT antibody or TAT binding oligopeptide may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. Reduction of these signs or symptoms may also be felt by the patient.

The above parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician. For cancer therapy, efficacy can be measured, for example, by assessing the time to disease progression (TTP) and/or determining the response rate (RR). Metastasis can be determined by staging tests and by bone scan and tests for calcium level and other enzymes to determine spread to the bone. CT scans can also be done to look for spread to the pelvis and lymph nodes in the area. Chest X-rays and measurement of liver enzyme levels by known methods are used to look for metastasis to the lungs and liver, respectively. Other routine methods for monitoring the disease include transrectal ultrasonography (TRUS) and transrectal needle biopsy (TRNB).

For bladder cancer, which is a more localized cancer, methods to determine progress of disease include urinary cytologic evaluation by cystoscopy, monitoring for presence of blood in the urine, visualization of the urothelial tract by sonography or an intravenous pyelogram, computed tomography (CT) and magnetic resonance imaging (MRI). The presence of distant metastases can be assessed by CT of the abdomen, chest x-rays, or radionuclide imaging of the skeleton.

"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 the treatment of, alleviating the symptoms of or diagnosis of a cancer 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®.

By "solid phase" or "solid support" is meant a non-aqueous matrix to which an antibody, TAT binding oligopeptide or TAT binding organic molecule of the present invention can adhere or attach. 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 TAT polypeptide, an antibody thereto or a TAT binding oligopeptide) 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 or "small" organic molecule is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide, antibody, TAT binding oligopeptide, TAT binding organic molecule or an agonist or antagonist thereof as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

The term "therapeutically effective amount" refers to an amount of an antibody, polypeptide, TAT binding oligopeptide, TAT binding organic molecule or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating". To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic.

A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide

or TAT binding organic molecule is an amount capable of inhibiting the growth of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "growth inhibitory amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule is an amount capable of causing the destruction of a cell, especially tumor, e.g., cancer cell, either *in vitro* or *in vivo*. A "cytotoxic amount" of an anti-TAT antibody, TAT polypeptide, TAT binding oligopeptide or TAT binding organic molecule for purposes of inhibiting neoplastic cell growth may be determined empirically and in a routine manner.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-TAT monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-TAT antibody compositions with polyepitopic specificity, polyclonal antibodies, single chain anti-TAT antibodies, and fragments of anti-TAT antibodies (see below) as long as they exhibit the desired biological or immunological activity. The term "immunoglobulin" (Ig) is used interchangeable with antibody herein.

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.

The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to a H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_H1). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the

different classes of antibodies, see, e.g., Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

The L chain 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 (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α, δ, ϵ, γ, and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, e.g., humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and define specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the 110-amino acid span of the variable domains. Instead, the V regions consist of relatively invariant stretches called framework regions (FRs) of 15-30 amino acids separated by shorter regions of extreme variability called "hypervariable regions" that are each 9-12 amino acids long. The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g. around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L, and around about 1-35 (H1), 50-65 (H2) and 95-102 (H3) in the V_H; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (*e.g.* residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L, and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the V_H; Chothia and Lesk J. Mol. Biol. 196:901-917 (1987)).

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. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies.

The modifier "monoclonal" is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies useful in the present invention may be prepared by the hybridoma methodology first described by Kohler et al., Nature, 256:495 (1975), or may be made using recombinant DNA methods in bacterial, eukaryotic animal or plant cells (see, e.g., U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example.

The monoclonal antibodies herein include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see U.S. Patent No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.* Old World Monkey, Ape etc), and human constant region sequences.

An "intact" antibody is one which comprises an antigen-binding site as well as a C_L and at least heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains may be native sequence constant domains (*e.g.* human native sequence constant domains) or amino acid sequence variant thereof. Preferably, the intact antibody has one or more effector functions.

"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 (see U.S. Patent No. 5,641,870, Example 2; 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, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, i.e., it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large $F(ab')_2$ fragment which roughly corresponds to two disulfide linked Fab fragments having divalent antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having additional few residues at the carboxy terminus of the C_H1 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 Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides.

The effector functions of antibodies are determined by sequences in the Fc region, which region is also the part recognized by Fc receptors (FcR) found on certain types of cells.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and 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.

"Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv 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); Borrebaeck 1995, infra.

The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10 residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, resulting in a bivalent fragment, i.e., fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. 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).

"Humanized" forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. 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 hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see 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).

A "species-dependent antibody," e.g., a mammalian anti-human IgE antibody, is an antibody which

has a stronger binding affinity for an antigen from a first mammalian species than it has for a homologue of that antigen from a second mammalian species. Normally, the species-dependent antibody "bind specifically" to a human antigen (i.e., has a binding affinity (Kd) value of no more than about 1 x 10^{-7} M, preferably no more than about 1 x 10^{-8} and most preferably no more than about 1 x 10^{-9} M) but has a binding affinity for a homologue of the antigen from a second non-human mammalian species which is at least about 50 fold, or at least about 500 fold, or at least about 1000 fold, weaker than its binding affinity for the human antigen. The species-dependent antibody can be of any of the various types of antibodies as defined above, but preferably is a humanized or human antibody.

A "TAT binding oligopeptide" is an oligopeptide that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be chemically synthesized using known oligopeptide synthesis methodology or may be prepared and purified using recombinant technology. TAT binding oligopeptides are usually at least about 5 amino acids in length, alternatively at least about 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length or more, wherein such oligopeptides that are capable of binding, preferably specifically, to a TAT polypeptide as described herein. TAT binding oligopeptides may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening oligopeptide libraries for oligopeptides that are capable of specifically binding to a polypeptide target are well known in the art (see, e.g., U.S. Patent Nos. 5,556,762, 5,750,373, 4,708,871, 4,833,092, 5,223,409, 5,403,484, 5,571,689, 5,663,143; PCT Publication Nos. WO 84/03506 and WO84/03564; Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 81:3998-4002 (1984); Geysen et al., Proc. Natl. Acad. Sci. U.S.A., 82:178-182 (1985); Geysen et al., in Synthetic Peptides as Antigens, 130-149 (1986); Geysen et al., J. Immunol. Meth., 102:259-274 (1987); Schoofs et al., J. Immunol., 140:611-616 (1988), Cwirla, S. E. et al. (1990) Proc. Natl. Acad. Sci. USA, 87:6378; Lowman, H.B. et al. (1991) Biochemistry, 30:10832; Clackson, T. et al. (1991) Nature, 352: 624; Marks, J. D. et al. (1991), J. Mol. Biol., 222:581; Kang, A.S. et al. (1991) Proc. Natl. Acad. Sci. USA, 88:8363, and Smith, G. P. (1991) Current Opin. Biotechnol., 2:668).

A "TAT binding organic molecule" is an organic molecule other than an oligopeptide or antibody as defined herein that binds, preferably specifically, to a TAT polypeptide as described herein. TAT binding organic molecules may be identified and chemically synthesized using known methodology (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585). TAT binding organic molecules are usually less than about 2000 daltons in size, alternatively less than about 1500, 750, 500, 250 or 200 daltons in size, wherein such organic molecules that are capable of binding, preferably specifically, to a TAT polypeptide as described herein may be identified without undue experimentation using well known techniques. In this regard, it is noted that techniques for screening organic molecule libraries for molecules that are capable of binding to a polypeptide target are well known in the art (see, e.g., PCT Publication Nos. WO00/00823 and WO00/39585).

An antibody, oligopeptide or other organic molecule "which binds" an antigen of interest, e.g. a tumor-associated polypeptide antigen target, is one that binds the antigen with sufficient affinity such that the antibody, oligopeptide or other organic molecule is useful as a diagnostic and/or therapeutic agent in targeting a cell or tissue expressing the antigen, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antibody, oligopeptide or other organic molecule to a "non-target" protein will be less than about 10% of the binding of the antibody, oligopeptide or other organic molecule to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). With regard to the binding of an antibody, oligopeptide or other organic molecule to a target molecule, the term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term "specific binding" or "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a Kd for the target of at least about 10^{-4} M, alternatively at least about 10^{-5} M, alternatively at least about 10^{-6} M, alternatively at least about 10^{-7} M, alternatively at least about 10^{-8} M, alternatively at least about 10^{-9} M, alternatively at least about 10^{-10} M, alternatively at least about 10^{-11} M, alternatively at least about 10^{-12} M, or greater. In one embodiment, the term "specific binding" refers to binding where a molecule binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

An antibody, oligopeptide or other organic molecule that "inhibits the growth of tumor cells expressing a TAT polypeptide" or a "growth inhibitory" antibody, oligopeptide or other organic molecule is one which results in measurable growth inhibition of cancer cells expressing or overexpressing the appropriate TAT polypeptide. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferred growth inhibitory anti-TAT antibodies, oligopeptides or organic molecules inhibit growth of TAT-expressing tumor cells by greater

than 20%, preferably from about 20% to about 50%, and even more preferably, by greater than 50% (e.g., from about 50% to about 100%) as compared to the appropriate control, the control typically being tumor cells not treated with the antibody, oligopeptide or other organic molecule being tested. In one embodiment, growth inhibition can be measured at an antibody concentration of about 0.1 to 30 μg/ml or about 0.5 nM to 200 nM in cell culture, where the growth inhibition is determined 1-10 days after exposure of the tumor cells to the antibody. Growth inhibition of tumor cells *in vivo* can be determined in various ways such as is described in the Experimental Examples section below. The antibody is growth inhibitory in vivo if administration of the anti-TAT antibody at about 1 μg/kg to about 100 mg/kg body weight results in reduction in tumor size or tumor cell proliferation within about 5 days to 3 months from the first administration of the antibody, preferably within about 5 to 30 days.

An antibody, oligopeptide or other organic molecule which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which overexpresses a TAT polypeptide. Preferably the cell is a tumor cell, e.g., a prostate, breast, ovarian, stomach, endometrial, lung, kidney, colon, bladder cell. Various methods are available for evaluating the cellular events associated with apoptosis. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody, oligopeptide or other organic molecule which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor); and B cell activation.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express Fc γRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, Annu. Rev. Immunol. 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an in vitro ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, e.g., in a animal model such as that disclosed in Clynes et al.

(USA) 95:652-656 (1998).

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc γRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, Annu. Rev. Immunol. 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, Annu. Rev. Immunol. 9:457-492 (1991); Capel et al., Immunomethods 4:25-34 (1994); and de Haas et al., J. Lab. Clin. Med. 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer et al., J. Immunol. 117:587 (1976) and Kim et al., J. Immunol. 24:249 (1994)).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least Fc γRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source, e.g., from blood.

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro et al., J. Immunol. Methods 202:163 (1996), may be performed.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g., epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, multiple myeloma and B-cell lymphoma, brain, as well as head and neck cancer, and associated metastases.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are

associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

An antibody, oligopeptide or other organic molecule which "induces cell death" is one which causes a viable cell to become nonviable. The cell is one which expresses a TAT polypeptide, preferably a cell that overexpresses a TAT polypeptide as compared to a normal cell of the same tissue type. The TAT polypeptide may be a transmembrane polypeptide expressed on the surface of a cancer cell or may be a polypeptide that is produced and secreted by a cancer cell. Preferably, the cell is a cancer cell, e.g., a breast, ovarian, stomach, endometrial, salivary gland, lung, kidney, colon, thyroid, pancreatic or bladder cell. Cell death *in vitro* may be determined in the absence of complement and immune effector cells to distinguish cell death induced by antibody-dependent cell-mediated cytotoxicity (ADCC) or complement dependent cytotoxicity (CDC). Thus, the assay for cell death may be performed using heat inactivated serum (i.e., in the absence of complement) and in the absence of immune effector cells. To determine whether the antibody, oligopeptide or other organic molecule is able to induce cell death, loss of membrane integrity as evaluated by uptake of propidium iodide (PI), trypan blue (see Moore et al. Cytotechnology 17:1-11 (1995)) or 7AAD can be assessed relative to untreated cells. Preferred cell death-inducing antibodies, oligopeptides or other organic molecules are those which induce PI uptake in the PI uptake assay in BT474 cells.

A "TAT-expressing cell" is a cell which expresses an endogenous or transfected TAT polypeptide either on the cell surface or in a secreted form. A "TAT-expressing cancer" is a cancer comprising cells that have a TAT polypeptide present on the cell surface or that produce and secrete a TAT polypeptide. A "TAT-expressing cancer" optionally produces sufficient levels of TAT polypeptide on the surface of cells thereof, such that an anti-TAT antibody, oligopeptide ot other organic molecule can bind thereto and have a therapeutic effect with respect to the cancer. In another embodiment, a "TAT-expressing cancer" optionally produces and secretes sufficient levels of TAT polypeptide, such that an anti-TAT antibody, oligopeptide ot other organic molecule antagonist can bind thereto and have a therapeutic effect with respect to the cancer. With regard to the latter, the antagonist may be an antisense oligonucleotide which reduces, inhibits or prevents production and secretion of the secreted TAT polypeptide by tumor cells. A cancer which "overexpresses" a TAT polypeptide is one which has significantly higher levels of TAT polypeptide at the cell surface thereof, or produces and secretes, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. TAT polypeptide overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the TAT protein present on the surface of a cell, or secreted by the cell (e.g., via an immunohistochemistry assay using anti-TAT antibodies prepared against an isolated TAT polypeptide which may be prepared using recombinant DNA technology from an isolated nucleic acid encoding the TAT polypeptide; FACS analysis, etc.). Alternatively, or additionally, one may measure levels of TAT polypeptide-encoding nucleic acid or mRNA in the cell, e.g., via fluorescent *in situ* hybridization using a nucleic acid based probe corresponding to a TAT-encoding nucleic acid or the complement

thereof; (FISH; see WO98/45479 published October, 1998), Southern blotting, Northern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study TAT polypeptide overexpression by measuring shed antigen in a biological fluid such as serum, e.g, using antibody-based assays (see also, e.g., U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias et al., J. Immunol. Methods 132:73-80 (1990)). Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, e.g., a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, e.g., by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

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.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody, oligopeptide or other organic molecule so as to generate a "labeled" antibody, oligopeptide or other organic molecule. 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.

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., At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu), chemotherapeutic agents e.g. methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a TAT-expressing cancer cell, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of TAT-expressing cells 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), taxanes, and topoisomerase 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, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

"Doxorubicin" is an anthracycline antibiotic. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy-α-L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,11-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

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- 1a, 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-ß; 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.

The term "package insert" is used to refer to instructions customarily included in commercial packages of therapeutic products, that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products.

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,_M, 0, 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, 0,_M,_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,_M, 0, 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,_M, 0, 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, 0xFFFFFFFF, 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
         */
```

...nw

```
        id = xx - yy + len1 - 1;
        if (mis >= delx && mis >= dely[yy])
                col1[yy] = mis;
```

Table 1 (cont')

```
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')

```
/*
 * 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);
```

getmat

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()
{
        register  i;
        for (i = 0; i < 2; i++)
                *po[i]-- = '\0';
```

dumpblock

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

```
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

```
putline(ix)
        int     ix;                     {
```

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

```
cleanup(i)
        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)
        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';
```

getseq

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

```
        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--)
                                        ;
```

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')

writejmps

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejmps(ix)
        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

TAT	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 TAT polypeptide) =

5 divided by 15 = 33.3%

Table 3

TAT	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 TAT polypeptide) =

5 divided by 10 = 50%

Table 4

TAT-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLL	(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 TAT-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

DEMANDE OU BREVET VOLUMINEUX

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CECI EST LE TOME 1 DE 2
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JUMBO APPLICATIONS/PATENTS

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THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 267

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NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having a nucleotide sequence that has at least 80% nucleic acid sequence identity to:

(a) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a DNA molecule encoding the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a DNA molecule encoding an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

2. Isolated nucleic acid having:

(a) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleotide sequence that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleotide sequence that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

3. Isolated nucleic acid that hybridizes to:

(a) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) a nucleic acid that encodes the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) a nucleic acid that encodes an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(f) the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(g) the complement of (a), (b), (c), (d), (e) or (f).

4. The nucleic acid of Claim 3, wherein the hybridization occurs under stringent conditions.

5. The nucleic acid of Claim 3 which is at least about 5 nucleotides in length.

6. An expression vector comprising the nucleic acid of Claim 1, 2 or 3.

7. The expression vector of Claim 6, wherein said nucleic acid is operably linked to control sequences recognized by a host cell transformed with the vector.

8. A host cell comprising the expression vector of Claim 7.

9. The host cell of Claim 8 which is a CHO cell, an *E. coli* cell or a yeast cell.

10. A process for producing a polypeptide comprising culturing the host cell of Claim 8 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

12. An isolated polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

13. A chimeric polypeptide comprising the polypeptide of Claim 11 or 12 fused to a heterologous polypeptide.

14. The chimeric polypeptide of Claim 13, wherein said heterologous polypeptide is an epitope tag sequence or an Fc region of an immunoglobulin.

15. An isolated antibody that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

16. An isolated antibody that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

17. The antibody of Claim 15 or 16 which is a monoclonal antibody.

18. The antibody of Claim 15 or 16 which is an antibody fragment.

19. The antibody of Claim 15 or 16 which is a chimeric or a humanized antibody.

20. The antibody of Claim 15 or 16 which is conjugated to a growth inhibitory agent.

21. The antibody of Claim 15 or 16 which is conjugated to a cytotoxic agent.

22. The antibody of Claim 21, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

23. The antibody of Claim 21, wherein the cytotoxic agent is a toxin.

24. The antibody of Claim 23, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

25. The antibody of Claim 23, wherein the toxin is a maytansinoid.

26. The antibody of Claim 15 or 16 which is produced in bacteria.

27. The antibody of Claim 15 or 16 which is produced in CHO cells.

28. The antibody of Claim 15 or 16 which induces death of a cell to which it binds.

29. The antibody of Claim 15 or 16 which is detectably labeled.

30. An isolated nucleic acid having a nucleotide sequence that encodes the antibody of Claim 15 or 16.

31. An expression vector comprising the nucleic acid of Claim 30 operably linked to control sequences recognized by a host cell transformed with the vector.

32. A host cell comprising the expression vector of Claim 31.

33. The host cell of Claim 32 which is a CHO cell, an *E. coli* cell or a yeast cell.

34. A process for producing an antibody comprising culturing the host cell of Claim 32 under conditions suitable for expression of said antibody and recovering said antibody from the cell culture.

35. An isolated oligopeptide that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

36. An isolated oligopeptide that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355

(SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

37. The oligopeptide of Claim 35 or 36 which is conjugated to a growth inhibitory agent.

38. The oligopeptide of Claim 35 or 36 which is conjugated to a cytotoxic agent.

39. The oligopeptide of Claim 38, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

40. The oligopeptide of Claim 38, wherein the cytotoxic agent is a toxin.

41. The oligopeptide of Claim 40, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

42. The oligopeptide of Claim 40, wherein the toxin is a maytansinoid.

43. The oligopeptide of Claim 35 or 36 which induces death of a cell to which it binds.

44. The oligopeptide of Claim 35 or 36 which is detectably labeled.

45. A TAT binding organic molecule that binds to a polypeptide having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

46. The organic molecule of Claim 45 that binds to a polypeptide having:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown

in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

47. The organic molecule of Claim 45 or 46 which is conjugated to a growth inhibitory agent.

48. The organic molecule of Claim 45 or 46 which is conjugated to a cytotoxic agent.

49. The organic molecule of Claim 48, wherein the cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

50. The organic molecule of Claim 48, wherein the cytotoxic agent is a toxin.

51. The organic molecule of Claim 50, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

52. The organic molecule of Claim 50, wherein the toxin is a maytansinoid.

53. The organic molecule of Claim 45 or 46 which induces death of a cell to which it binds.

54. The organic molecule of Claim 45 or 46 which is detectably labeled.

55. A composition of matter comprising:

(a) the polypeptide of Claim 11;

(b) the polypeptide of Claim 12;

(c) the chimeric polypeptide of Claim 13;

(d) the antibody of Claim 15;

(e) the antibody of Claim 16;

(f) the oligopeptide of Claim 35;

(g) the oligopeptide of Claim 36;

(h) the TAT binding organic molecule of Claim 45; or

(i) the TAT binding organic molecule of Claim 46; in combination with a carrier.

56. The composition of matter of Claim 55, wherein said carrier is a pharmaceutically acceptable carrier.

57. An article of manufacture comprising:

(a) a container; and

(b) the composition of matter of Claim 55 contained within said container.

58. The article of manufacture of Claim 57 further comprising a label affixed to said container, or a package insert included with said container, referring to the use of said composition of matter for the therapeutic treatment of or the diagnostic detection of a cancer.

59. A method of inhibiting the growth of a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-

6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody, oligopeptide or organic molecule that binds to said protein, the binding of said antibody, oligopeptide or organic molecule to said protein thereby causing an inhibition of growth of said cell.

60. The method of Claim 59, wherein said antibody is a monoclonal antibody.

61. The method of Claim 59, wherein said antibody is an antibody fragment.

62. The method of Claim 59, wherein said antibody is a chimeric or a humanized antibody.

63. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

64. The method of Claim 59, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

65. The method of Claim 64, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

66. The method of Claim 64, wherein the cytotoxic agent is a toxin.

67. The method of Claim 66, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

68. The method of Claim 66, wherein the toxin is a maytansinoid.

69. The method of Claim 59, wherein said antibody is produced in bacteria.

70. The method of Claim 59, wherein said antibody is produced in CHO cells.

71. The method of Claim 59, wherein said cell is a cancer cell.

72. The method of Claim 71, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

73. The method of Claim 71, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

74. The method of Claim 71, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

75. The method of Claim 59 which causes the death of said cell.

76. The method of Claim 59, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures

1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

77. A method of therapeutically treating a mammal having a cancerous tumor comprising cells that express a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to said mammal a therapeutically effective amount of an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said mammal.

78. The method of Claim 77, wherein said antibody is a monoclonal antibody.

79. The method of Claim 77, wherein said antibody is an antibody fragment.

80. The method of Claim 77, wherein said antibody is a chimeric or a humanized antibody.

81. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

82. The method of Claim 77, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

83. The method of Claim 82, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

84. The method of Claim 82, wherein the cytotoxic agent is a toxin.

85. The method of Claim 84, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

86. The method of Claim 84, wherein the toxin is a maytansinoid.

87. The method of Claim 77, wherein said antibody is produced in bacteria.

88. The method of Claim 77, wherein said antibody is produced in CHO cells.

89. The method of Claim 77, wherein said tumor is further exposed to radiation treatment or a chemotherapeutic agent.

90. The method of Claim 77, wherein said tumor is a breast tumor, a colorectal tumor, a lung tumor, an ovarian tumor, a central nervous system tumor, a liver tumor, a bladder tumor, a pancreatic tumor, or a cervical tumor.

91. The method of Claim 77, wherein said protein is more abundantly expressed by the cancerous cells of said tumor as compared to a normal cell of the same tissue origin.

92. The method of Claim 77, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

93. A method of determining the presence of a protein in a sample suspected of containing said protein, wherein said protein has at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising exposing said sample to an antibody, oligopeptide or organic molecule that binds to said protein and determining binding of said antibody, oligopeptide or organic molecule to said protein in said sample, wherein binding of the antibody, oligopeptide or organic molecule to said protein is indicative of the presence of said protein in said sample.

94. The method of Claim 93, wherein said sample comprises a cell suspected of expressing said protein.

95. The method of Claim 94, wherein said cell is a cancer cell.

96. The method of Claim 93, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

97. The method of Claim 93, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

98. A method of diagnosing the presence of a tumor in a mammal, said method comprising determining the level of expression of a gene encoding a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), in a test sample of tissue cells obtained from said mammal and in a control sample of known normal cells of the same tissue origin, wherein a higher level of expression of said protein in the test sample, as compared to the control sample, is indicative of the presence of tumor in the mammal from which the test sample was obtained.

99. The method of Claim 98, wherein the step of determining the level of expression of a gene encoding said protein comprises employing an oligonucleotide in an *in situ* hybridization or RT-PCR analysis.

100. The method of Claim 98, wherein the step determining the level of expression of a gene encoding said protein comprises employing an antibody in an immunohistochemistry or Western blot analysis.

101. The method of Claim 98, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

102. A method of diagnosing the presence of a tumor in a mammal, said method comprising contacting a test sample of tissue cells obtained from said mammal with an antibody, oligopeptide or organic molecule that binds to a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), and detecting the formation of a complex between said antibody, oligopeptide or organic molecule and said protein in the test sample, wherein the formation of a complex is indicative of the presence of a tumor in said mammal.

103. The method of Claim 102, wherein said antibody, oligopeptide or organic molecule is detectably labeled.

104. The method of Claim 102, wherein said test sample of tissue cells is obtained from an individual suspected of having a cancerous tumor.

105. The method of Claim 102, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

106. A method for treating or preventing a cell proliferative disorder associated with increased expression or activity of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising administering to a subject in need of such treatment an effective amount of an antagonist of said protein, thereby effectively treating or preventing said cell proliferative disorder.

107. The method of Claim 106, wherein said cell proliferative disorder is cancer.

108. The method of Claim 106, wherein said antagonist is an anti-TAT polypeptide antibody, TAT binding oligopeptide, TAT binding organic molecule or antisense oligonucleotide.

109. A method of binding an antibody, oligopeptide or organic molecule to a cell that expresses a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said cell with an antibody,

oligopeptide or organic molecule that binds to said protein and allowing the binding of the antibody, oligopeptide or organic molecule to said protein to occur, thereby binding said antibody, oligopeptide or organic molecule to said cell.

110. The method of Claim 109, wherein said antibody is a monoclonal antibody.

111. The method of Claim 109, wherein said antibody is an antibody fragment.

112. The method of Claim 109, wherein said antibody is a chimeric or a humanized antibody.

113. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

114. The method of Claim 109, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

115. The method of Claim 114, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

116. The method of Claim 114, wherein the cytotoxic agent is a toxin.

117. The method of Claim 116, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

118. The method of Claim 116, wherein the toxin is a maytansinoid.

119. The method of Claim 109, wherein said antibody is produced in bacteria.

120. The method of Claim 109, wherein said antibody is produced in CHO cells.

121. The method of Claim 109, wherein said cell is a cancer cell.

122. The method of Claim 121, wherein said cancer cell is further exposed to radiation treatment or a chemotherapeutic agent.

123. The method of Claim 121, wherein said cancer cell is selected from the group consisting of a breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a cervical cancer cell, a melanoma cell and a leukemia cell.

124. The method of Claim 123, wherein said protein is more abundantly expressed by said cancer cell as compared to a normal cell of the same tissue origin.

125. The method of Claim 109 which causes the death of said cell.

126. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

127. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treating a tumor.

128. Use of a nucleic acid as claimed in any of Claims 1 to 5 or 30 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

129. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

130. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of

medicament for treating a tumor.

131. Use of an expression vector as claimed in any of Claims 6, 7 or 31 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

132. Use of a host cell as claimed in any of Claims 8, 9, 32, or 33 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

133. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treating a tumor.

134. Use of a host cell as claimed in any of Claims 8, 9, 32 or 33 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

135. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

136. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treating a tumor.

137. Use of a polypeptide as claimed in any of Claims 11 to 14 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

138. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

139. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treating a tumor.

140. Use of an antibody as claimed in any of Claims 15 to 29 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

141. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

142. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treating a tumor.

143. Use of an oligopeptide as claimed in any of Claims 35 to 44 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

144. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

145. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treating a tumor.

146. Use of a TAT binding organic molecule as claimed in any of Claims 45 to 54 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

147. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

148. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treating a tumor.

149. Use of a composition of matter as claimed in any of Claims 55 or 56 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

150. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for the therapeutic treatment or diagnostic detection of a cancer.

151. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treating a tumor.

152. Use of an article of manufacture as claimed in any of Claims 57 or 58 in the preparation of a medicament for treatment or prevention of a cell proliferative disorder.

153. A method for inhibiting the growth of a cell, wherein the growth of said cell is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, there by inhibiting the growth of said cell.

154. The method of Claim 153, wherein said cell is a cancer cell.

155. The method of Claim 153, wherein said protein is expressed by said cell.

156. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

157. The method of Claim 153, wherein the binding of said antibody, oligopeptide or organic molecule to said protein induces the death of said cell.

158. The method of Claim 153, wherein said antibody is a monoclonal antibody.

159. The method of Claim 153, wherein said antibody is an antibody fragment.

160. The method of Claim 153, wherein said antibody is a chimeric or a humanized antibody.

161. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

162. The method of Claim 153, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

163. The method of Claim 162, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

164. The method of Claim 162, wherein the cytotoxic agent is a toxin.

165. The method of Claim 164, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

166. The method of Claim 164, wherein the toxin is a maytansinoid.

167. The method of Claim 153, wherein said antibody is produced in bacteria.

168. The method of Claim 153, wherein said antibody is produced in CHO cells.

169. The method of Claim 153, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

170. A method of therapeutically treating a tumor in a mammal, wherein the growth of said tumor is at least in part dependent upon a growth potentiating effect of a protein having at least 80% amino acid sequence identity to:

(a) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(c) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide;

(d) an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide;

(e) a polypeptide encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) a polypeptide encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), said method comprising contacting said protein with an antibody, oligopeptide or organic molecule that binds to said protein, thereby effectively treating said tumor.

171. The method of Claim 170, wherein said protein is expressed by cells of said tumor.

172. The method of Claim 170, wherein the binding of said antibody, oligopeptide or organic molecule to said protein antagonizes a cell growth-potentiating activity of said protein.

173. The method of Claim 170, wherein said antibody is a monoclonal antibody.

174. The method of Claim 170, wherein said antibody is an antibody fragment.

175. The method of Claim 170, wherein said antibody is a chimeric or a humanized antibody.

176. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a growth inhibitory agent.

177. The method of Claim 170, wherein said antibody, oligopeptide or organic molecule is conjugated to a cytotoxic agent.

178. The method of Claim 177, wherein said cytotoxic agent is selected from the group consisting of toxins, antibiotics, radioactive isotopes and nucleolytic enzymes.

179. The method of Claim 177, wherein the cytotoxic agent is a toxin.

180. The method of Claim 179, wherein the toxin is selected from the group consisting of maytansinoid and calicheamicin.

181. The method of Claim 179, wherein the toxin is a maytansinoid.

182. The method of Claim 170, wherein said antibody is produced in bacteria.

183. The method of Claim 170, wherein said antibody is produced in CHO cells.

184. The method of Claim 170, wherein said protein has:

(a) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355);

(b) the amino acid sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), with its associated signal peptide sequence;

(d) an amino acid sequence of an extracellular domain of the polypeptide shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355), lacking its associated signal peptide sequence;

(e) an amino acid sequence encoded by the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355); or

(f) an amino acid sequence encoded by the full-length coding region of the nucleotide sequence shown in any one of Figures 1-6355 (SEQ ID NOS:1-6355).

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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1/6881

FIGURE 1

ATCACATGCCTATCATATAGTAAAACCCAGCCCATGGCCCCTAACAGGGGCCCTCTCAGCCCTCCTAATGACCTC
CGGCCTAGCCATGTGATTTCACTTCCACTCCACAACCCTCCTCATACTAGGCCTACTAACCAACACACTAACCAT
ATACCAATGATGGCGCGATGTAACACGAGAAAGCACATACCAAGGCCACCACACACCACCTGTCCAGAAAGGCCT
TCGATACGGGATAATCCTATTTATTACCTCAGAAGTTTTTTTCTTCGCAGGATTTTTCTGAGCCTTTTACCACTC
CAGCCTAGCTCCCACCCCCCAACTAGGGGGACACTGGCCCCCAACAGGCATCACCCCGCTAAATCCCCTAGAAGT
CCCACTCCTAAACACATCCGTATTACTCGCATCAGGGGTATCAATCACCTGAGCTCACCATAGTCTAATAGTCTA
TTTTACCCTCCTACAAGCCTCAGAGTACTTCGAG

FIGURE 2

TCTAATACCTATTGATCTGTCACTTTCTCCCATCACGCTCAGGTGGGACCATTCAGTTGCAGGAAAACAAGCTTA
ACACGCCCACTAATTCTACATTATGGTGAGTTCTATAATTATTTTATTATATATTACAGTGTAATAATGGAAATA
AAGTGCCTAATAAATGCAAATGTGCTTACATCTTTTGGCCCAGCTCCTACCTCCCGGCAGCCTCTCCAGGCCCAG
AACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTATGTCAC
GGCAGCCTCCGCAGATGAGGCTACTGCCTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTT
TAGACCCAGCTCCTGCCTCCCAGCCTTCTCTCCAGGCCCTGAACTTTCTCAAGTCGACCTCACCAGGCCCAGCTC
ATGCTTCTTTGCAGCCTCTCCAGGCCCAGCTCCTGCATCTTGGTGGCCCCTCCAGGCCCAGCCTCTGCCTCCCGT
CAGCCTCTACAGTCCCAAAGTCTGCCTCACAGCAGATTCTTCACGCCCAGCATCTACCTCACTTGGACCCTCCAG
ACCCAGATGGTGTCTCACTGTGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCT
CCTGCCTCCCAGTGGCCTCTTTCGGCCCAGCCCAGCTCATGCCTCCCGGCGGCCTTCCCAAGCCCCGCTTTTGAC
TTTCGGTGGCCTCTGCAGGCCTCGACAAGGCCCAGCCTCCTGCCTCCCGAAGGCCTGCACAGGCCCAGCCTCTGC
CTCACAGCGGACTCTC

FIGURE 3

CAAGCTCATGACTCACAATGGCCTATTTAGGCCCATACCCTACGTCACGGCAGCCTCCGCAGATGAGCCTACTGC
CTCACAACAGCCTCCACAGGCACAGCTCCATCGTTACAATGGCCTCTTTAGACCCAGCTCCTGCCTCCCAGCCTT
CTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAGTGCTATCGCAGCTGA
CTGCAGCCTCAACCTTCCAGGCTGAAGCGATCCTCCCACCTCAACCTCCCACGTGGCTGAGACTACAGGTGCTTG
CCACTATGCCCAACTAACATTTGGAATTTTCGTATACGTGGATTCCAGAGGGGTGACAGCGAAACGTGGGACCAT
TCAGTTGCAGGAAAACAAGCTTAACACGCCCACTAATTCTACATTATGCTCCTACCTCCCGGCAGCCTCTCCAGG
CCCAGAACTTTCTCCAGTCAGCCTCTACAGACCAAGCTCATGACTCACAATG

FIGURE 4

CGTCGGCCCCCGGCCCCCCAGCAGCCTCCAAAGCCCTGTGACTCACAGCCCTGCTTCCACGGGGGGACCTGCCAG
GACTGGGCATTGGGCGGGGGCTTCACCTGCAGCTGCCCGGCAGGCAGGGGAGGCGCCGTCTGTGAGAAGGTGCTT
GGCGCCCCTGTGCCGGCCTTCGAGGGCCGCTCCTTCCTGGCCTTCCCCACTCTCCGCGCCTACCACACGCTGCGC
CTGGCACTGGAATTCCGGGCGCTGGAGCCTCAGGGGCTGCTGCTGTACAATGGCAACGCCCGGGGCAAGGACTTC
CTGGCATTGGCGCTGCTAGATGGCCGCGTGCAGCTCAGGTTTGACACAGGTTCGGGGCCGGCGGTGCTGACCAGT
GCCGTGCCGGTAGAGCCGGGCCAGTGGCACCGCCTGGAGCTGTCCCGGCACTGGCGCCGGGGCACCCTCTCGGTG
GATGGTGAGACCCCTGTTCTGGGCGAGAGTCCCAGTGGCACCGACGGCCTCAACCTGGACACAGACCTCTTTGTG
GGCGGCGTACCCGAGGACCAGGCTGCCGTGGCGCTGGAGCGGACCTTCGTGGGCGCCGGCCTGAGGGGGTGCATC
CGTTTGCTGGACGTCAACAACCAGCGCCTGGAGCTTGGCATTGGGCCGGGGGCTGCCACCCGAGGCTCTGGCGTG
GGCAAGTGCGGGGACCACCCCTGCCTGCCCAACCCCTGCCATGGCGGGGCCCCATGCCAGAACCTGGAGGCTGGA
AGGTTCCATTGCCAGTGCCCGCCCGGCCGCGTCGGACCAACCTGTGCCGATGAGAAGAGCCCCTGCCAGCCCAAC
CCCTGCCATGGGGCGGCGCCCTGCCGTGTGCTGCCCGAGGGTGGTGCTCAGTGCGAGTGCCCCCTGGGGCGTGAG
GGCACCTTCTGCCAGACAGCCTCGGGGCAGGACGGCTCTGGGCCCTTCCTGGCTGACTTCAACGGCTTCTCCCAC
CTGGAGCTGAGAGGCCTGCACACCTTTGCACGGGACCTGGGGGAGAAGATGGCGCTGGAGGTCGTGTTCCTGGCA
CGAGGCCCCAGCGGCCTCCTGCTCTACAACGGGCAGAAGACGGACGGCAAGGGGGACTTCGTGTCGCTGGCACTG
CGGGACCGCCGCCTGGAGTTCCGCTACGACCTGGGCAAGGGGGCAGCGGTCATCAGGAGCAGGGAGCCAGTCACC
CTGGGAGCCTGGACCAGGGTCTCACTGGAGCGAAACGGCCGCAAGGGTGCCCTGCGTGTGGGCGACGGCCCCCGT
GTGTTGGGGGAGTCCCCGGTTCCGCACACCGTCCTCAACCTGAAGGAGCCGCTCTACGTAGGGGGCGCTCCCGAC
TTCAGCAAGCTGGCCCGTGCTGCTGCCGTGTCCTCTGGCTTCGACGGTGCCATCCAGCTGGTCTCCCTCGGAGGC
CGCCAGCTGCTGACCCCGGAGCACGTGCTGCGGCAGGTGGACGTCACGTCCTTTGCAGGTCACCCCTGCACCCGG
GCCTCAGGCCACCCCTGCCTCAATGGGGCCTCCTGCGTCCCGAGGGAGGCTGCCTATGTGTGCCTGTGTCCCGGG
GGATTCTCAGGACCGCACTGCGAGAAGGGGCTGGTGGAGAAGTCAGCGGGGGACGTGGATACCTTGGCCTTTGAC
GGGCGGACCTTTGTCGAGTACCTCAACGCTGTGACCGAGAGCGAGAAGGCACTGCAGAGCAACCACTTTGAACTG
AGCCTGCGCACTGAGGCCACGCAGGGGCTGGTGCTCTGGAGTGGCAAGGCCACGGAGCGGGCAGACTATGTGGCA
CTGGCCATTGTGGACGGGCACCTGCAACTGAGCTACAACCTGGGCTCCCAGCCCGTGGTGCTGCGTTCCACCGTG
CCCGTCAACACCAACCGCTGGTTGCGGGTCGTGGCACATAGGGAGCAGAGGGAAGGTTCCCTGCAGGTGGGCAAT
GAGGCCCCTGTGACCGGCTCCTCCCCGCTGGGCGCCACGCAGCTGGACACTGATGGAGCCCTGTGGCTTGGGGGC
CTGCCGGAGCTGCCCGTGGGCCCAGCACTGCCCAAGGCCTACGGCACAGGCTTTGTGGGCTGCTTGCGGGACGTG
GTGGTGGGCCGGCACCCGCTGCACCTGCTGGAGGACGCCGTCACCAAGCCAGAGCTGCGGCCCTGCCCCACCCCA
TGAGCTGGCACCAGAGCCCCGCGCCCGCTGTAATTATTTTCTATTTTTGTAAACTTGTTGCTTTTTGATATGATT
TTCTTGCCTGAGTGTTGGCCGGAGGGACTGCTGGCCCGGCCTCCCTTCCGTCCAGGCAGCCGTGCTGCAGACAGA
CCTAGTGCCGAGGGATGGACAGGCGAGGTGGCAGCGTGGAGGGCTCGGCGTGGATGGCAGCCTCAGGACACACAC
CCCTGCCTCAAGGTGCTGAGCCCCCGCCTTGCACTGCGCCTGCCCCACGGTGTCCCCGCCGGGAAGCAGCCCCGG
CTCCTGAATCACCCTCGCTCCGTCAGGCGGGACTCGTGTCCCAGAGAGGAAGGGGCTGCTGAGGTCTGATGGGGC
CCTTCCTCCGGGTGACCCCACAGGGCCTTTCCAAGCCCCCATTTGAGCTGCTCCTTCCTGTGTGTGCTCTGGGCC
CTGCCTCGGCCTCCTGCGCCAATACTGTGACTTCCAAACAATGTTACTGCTGGGCACAGCTCTGCGTTGCTCCCG
TGCTGCCTGCGCCAGCCCCAGGCTGCTGAGGAGCAGAGGCCAGACCAGGGCCGATCTGGGTGTCCTGACCCTCAG
CTGGCCCTGCCCAGCCACCCTGGACATGACCGTATCCCTCTGCCACACCCCAGGCCCTGCGAGGGGCTATCGAGA
GGAGCTCACTGTGGGATGGGGTTGACCTCTGCCGCCTGCCTGGGTATCTGGGCCTGGCCATGGCTGTGTTCTTCA
TGTGTTGATTTTATTTGACCCCTGGAGTGGTGGGTCTCATCTTTCCCATCTCGCCTGAGAGCGGCTGAGGGCTGC
CTCACTGCAAATCCTCCCCACAGCGTCAGTGAAAGTCGTCCTTGTCTCAGAATGACCAGGGGCCAGCCAGTGTCT
GACCAAGGTCAAGGGGCAGGTGCAGAGGTGGCAGGGATGGCTCCGAAGCCAGAAATGCCTTAAACTGCAACGTCC
CGTCCCTTCCCCACCCCCATCCCATCCCCACCCCCAGCCCCAGCCCAGTCCTCCTAGGAGCAGGACCCGATGAAG
CGGGCGGCGGTGGGGCTGGGTGCCGTGTTACTAACTCTAGTATGTTTCTGTGTCAATCGCTGTGAAATAAAGTCT
GAAAACTTT

FIGURE 5

MLNSSLMRITLRNLEEVEFCVEDKPGTHFTPVPPTPPDACRGMLCGFGAVCEPNAEGPGRASCVCKKSPCPSVVA
PVCGSDASTYSNECELQRAQCSQQRRIRLLSRGPCGSRDPCSNVTCSFGSTCARSADGLTASCLCPATCRGAPEG
TVCGSDGADYPGECQLLRRACARQENVFKKFDGPCDPCQGALPDPSRSCRVNPRTRRPEMLLRPESCPARQAPVC
GDDGVTYENDCVMGRSGAARGLLLQKVRSGQCQGRDQCPEPCRFNAVCLSRRGRPRCSCDRVTCDGAYRPVCAQD
GRTYDSDCWRQQAECRQQRAIPSKHQGPCDQAPSPCLGVQCAFGATCAVKNGQAACECLQACSSLYDPVCGSDGV
TYGSACELEATACTLGREIQVARKGPCDRCGQCRFGALCEAETGRCVCPSECVALAQPVCGSDGHTYPSECMLHV
HACTHQISLHVASAGPCETCGDAVCAFGAVCSAGQCVCPRCEHPPPGPVCGSDGVTYGSACELREAACLQQTQIE
EARAGPCEQAECGSGGSGSGEDGDCEQELCRQRGGIWDEDSEDGPCVCDFSCQSVPGSPVCGSDGVTYSTECELK
KARCESQRGLYVAAQGACRGPTFAPLPPVAPLHCAQTPYGCCQDNITAARGVGLAGCPSACQCNPHGSYGGTCDP
ATGQCSCRPGVGGLRCDRCEPGFWNFRGIVTDGRSGCTPCSCDPQGAVRDDCEQMTGLCSCKPGVAGPKCGQCPD
GRALGPAGCEADASAPATCAEMRCEFGARCVEESGSAHCVCPMLTCPEANATKVCGSDGVTYGNECQLKTIACRQ
GLQISIQSLGPCQEAVAPSTHPTSASVTVTTPGLLLSQALPAPPGALPLAPSSTAHSQTTPPPSSRPRTTASVPR
TTVWPVLTVPPTAPSPAPSLVASAFGESGSTDGSSDEELSGDQEASGGGSGGLEPLEGSSVATPGPPVERASCYN
SALGCCSDGKTPSLDAEGSNCPATKVFQGVLELEGVEGQELFYTPEMADPKSELFGETARSIESTLDDLFRNSDV
KKDFRSVRLRDLGPGKSVRAIVDVHFDPTTAFRAPDVARALLRQIQVSRRRSLGVRRPLQEHVRFMDFDWFPAFI
TGATSGAIAAGATARATTASRLPSSAVTPRAPHPSHTSQPVAKTTAAPTTRRPPTTAPSRVPGRRPPAPQQPPKP
CDSQPCFHGGTCQDWALGGGFTCSCPAGRGGAVCEKVLGAPVPAFEGRSFLAFPTLRAYHTLRLALEFRALEPQG
LLLYNGNARGKDFLALALLDGRVQLRFDTGSGPAVLTSAVPVEPGQWHRLELSRHWRRGTLSVDGETPVLGESPS
GTDGLNLDTDLFVGGVPEDQAAVALERTFVGAGLRGCIRLLDVNNQRLELGIGPGAATRGSGVGKCGDHPCLPNP
CHGGAPCQNLEAGRFHCQCPPGRVGPTCADEKSPCQPNPCHGAAPCRVLPEGGAQCECPLGREGTFCQTASGQDG
SGPFLADFNGFSHLELRGLHTFARDLGEKMALEVVFLARGPSGLLLYNGQKTDGKGDFVSLALRDRRLEFRYDLG
KGAAVIRSREPVTLGAWTRVSLERNGRKGALRVGDGPRVLGESPVPHTVLNLKEPLYVGGAPDFSKLARAAAVSS
GFDGAIQLVSLGGRQLLTPEHVLRQVDVTSFAGHPCTRASGHPCLNGASCVPREAAYVCLCPGGFSGPHCEKGLV
EKSAGDVDTLAFDGRTFVEYLNAVTESEKALQSNHFELSLRTEATQGLVLWSGKATERADYVALAIVDGHLQLSY
NLGSQPVVLRSTVPVNTNRWLRVVAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALWLGGLPELPVGPALPK
AYGTGFVGCLRDVVVGRHPLHLLEDAVTKPELRPCPTP

FIGURE 6

ACAGAGACCCCGAGTTCTACAAGTTCCTGCAGGAGAATGACCAGAGCCTGCTAAACTTCAGCGACTCGGACAGCT
CTGAGGAGGAAGAGGGGCCGTTCCACTCCCTGCCAGATGTGCTGGAGGAAGCCAGTGAGGAGGAGGATGGAGCGG
AGGAAGGAGAAGATGGGGACAGAGTCCCCAGAGGGCTGAAGGGGAAGAAGAATTCTGTTCCTGTGACCGTCGCCA
TGGTTGAGAGATGGAAGCAGGCAGCAAAGCAACGCCTCACTCCAAAGCTGTTCCATGAAGTGGTACAGGCGTTCC
GAGCAGCTGTGGCCACCACCCGAGGGGACCAGGAAAGTGCTGAGGCCAACAAATTCCAGGTCACGGACAGTGCTG
CATTCAATGCTCTGGTTACCTTCTGCATCAGAGACCTCATTGGCTGTCTCCAGAAGCTGCTGTTTGGAAAGGTGG
CAAAGGATAGCAGCAGGATGCTGCAGCCGTCCAGCAGCCCGCTCTGGGGGAAGCTTCGTGTGGACATCAAGGCTT
ACCTGGGCTCGGCCATACAGCTGGTGTCCTGTCTGTCGGAGACGACGGTGTTGGCGGCCGTGCTGCGGCACATCA
GCGTGCTGGTGCCCTGCTTCCTGACCTTCCCCAAGCAGTGCCGCATGCTGCTCAAGAGAATGGTGATCGTATGGA
GCACTGGGGAAGAGTCTCTGCGGGTGCTGGCTTTCCTGGTCCTCAGCAGAGTCTGCCGGCACAAGAAGGACACTT
TCCTTGGCCCCGTCCTCAAGCAAATGTACATCACGTATGTGAGGAACTGCAAGTTCACCTCGCCTGGTGCCCTCC
CCTTCATCAGTTTCATGCAGTGGACCTTGACGGAGCTGCTGGCCCTGGAGCCGGGTGTGGCCTACCAGCACGCCT
TCCTCTACATCCGCCAGCTCGCCATACACCTGCGCAACGCCATGACCACTCGCAAGAAGGAAACATACCAGTCTG
TGTACAACTGGCAGTATGTGCACTGCCTCTTCCTGTGGTGCCGGGTCCTGAGCACTGCGGGCCCCAGCGAAGCCC
TCCAGCCCTTGGTCTACCCCCTTGCCCAAGTCATCATTGGCTGTATCAAGCTCATCCCCACTGCCCGCTTCTACC
CGCTGCGAATGCACTGCATCCGTGCCCTGACGCTGCTCTCGGGGAGCTCGGGGGCCTTCATCCCGGTGCTGCCTT
TCATCCTGGAGATGTTCCAGCAGGTCGACTTCAACAGGAAGCCAGGGCGCATGAGCTCCAAGCCCATCAACTTCT
CCGTGATCCTGAAGCTGTCCAATGTCAACCTGCAGGAGAAGGCGTACCGGGACGGCCTGGTGGAGCAGCTGTACG
ACCTCACCCTGGAGTACCTGCACAGCCAGGCACACTGCATCGGCTTCCCGGAGCTGGTGCTGCCTGTGGTCCTGC
AGCTGAAGTCGTTCCTCCGGGAGTGCAAGGTGGCCAACTACTGCCGGCAGGTGCAGCAGCTGCTTGGGAAGGTTC
AGGAGAACTCGGCATACATCTGCAGCCGCCGCCAGAGGGTTTCCTTCGGCGTCTCTGAGCAGCAGGCAGTGGAAG
CCTGGGAGAAGCTGACCCGGGAAGAGGGGACACCCCTGACCTTGTACTACAGCCACTGGCGCAAGCTGCGTGACC
GGGAGATCCAGCTGGAGATCAGTGGCAAAGAGCGGCTGGAAGACCTGAACTTCCCTGAGATCAAACGAAGGAAGA
TGGCTGACAGGAAGGATGAGGACAGGAAGCAATTTAAAGACCTCTTTGACCTGAACAGCTCTGAAGAGGACGACA
CCGAGGGATTCTCGGAGAGAGGGATACTGAGGCCCCTGAGCACTCGGCATGGGGTGGAAGACGATGAAGAGGACG
AGGAGGAGGGCGAGGAGGACAGCAGCAACTCGGAGGATGGAGACCCAGACGCAGAGGCGGGGCTGGCCCCTGGGG
AGCTGCAGCAGCTGGCCCAGGGGCCGGAGGACGAGCTGGAGGATCTGCAGCTCTCAGAGGACGACTGAGGCAGCC
CATCTGGGGGGCCTGTAGGGGCTGCCGGGCTGGTGGCCAGTGTTTCCACCTCCCTGGCAGTCAGGCCTAGAGGCT
GGCGTCTGTGCAGTTGGGGGAGGCAGTAGACACGGGACAGGCTTTATTATTTATTTTTCAGCATGAAAGACCAAA
CGTATCGAGAGCTGGGCTGGGCTGGGCTGGTGTGGCTGCTGAAGCCCCACAGCTGTGGGCTGCTGAAGTCAGCTC
CGCGGGGGAGCTGACCCTGACGTCAGCAGACCGAGACCAGTCCCAGTTCCAGGGGGAGGCCTGCAGGCCCCTGGC
CCCTTCCACCACCTCTGCCCTCCGTCTGCAGACCTCGTCCATCTGCACCAGGCTCTGCCTTCACTCCCCCAAGTC
TTTGAAAATTTGTTCCTTTCCTTTGAAGTCACATTTTCTTTTAAAATTTTTTGTTTTGCATCCGAAACCGAAAGA
AATAAAGCGGTGGGAGGCAGGGCCATTGTGTTG

FIGURE 7

MAAAGSRKRRLAELTVDEFLASGFDSESESESENSPQAETREAREAARSPDKPGGSPSASRRKGRASEHKDQLSR
LKDRDPEFYKFLQENDQSLLNFSDSDSSEEEEGPFHSLPDVLEEASEEEDGAEEGEDGDRVPRGLKGKKNSVPVT
VAMVERWKQAAKQRLTPKLFHEVVQAFRAAVATTRGDQESAEANKFQVTDSAAFNALVTFCIRDLIGCLQKLLFG
KVAKDSSRMLQPSSSPLWGKLRVDIKAYLGSAIQLVSCLSETTVLAAVLRHISVLVPCFLTFPKQCRMLLKRMVI
VWSTGEESLRVLAFLVLSRVCRHKKDTFLGPVLKQMYITYVRNCKFTSPGALPFISFMQWTLTELLALEPGVAYQ
HAFLYIRQLAIHLRNAMTTRKKETYQSVYNWQYVHCLFLWCRVLSTAGPSEALQPLVYPLAQVIIGCIKLIPTAR
FYPLRMHCIRALTLLSGSSGAFIPVLPFILEMFQQVDFNRKPGRMSSKPINFSVILKLSNVNLQEKAYRDGLVEQ
LYDLTLEYLHSQAHCIGFPELVLPVVLQLKSFLRECKVANYCRQVQQLLGKVQENSAYICSRRQRVSFGVSEQQA
VEAWEKLTREEGTPLTLYYSHWRKLRDREIQLEISGKERLEDLNFPEIKRRKMADRKDEDRKQFKDLFDLNSSEE
DDTEGFSERGILRPLSTRHGVEDDEEDEEEGEEDSSNSEDGDPDAEAGLAPGELQQLAQGPEDELEDLQLSEDD

FIGURE 8

GTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAGCTGAGCCCATGAGCTC
CCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGGTAGTCCCCATCCTGGAGGGGCAGGCTCT
GCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTCGCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGT
CCATGGAGAACACGGCCCAGCTGCCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAA
GTCTGTGTGGTCCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGAA
CCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCGGGTGCGCCATTCCCCATGAACAGAAGCT
CAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCCCTCTTCCTGGGCACGTTCTTCATTA
GCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTACCTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACA
GAAGAAACAAAGCTCCGGCCCTGCAGCCTGGCGAAGCCGCTGCAATGATCCCCCCGCCACAGTCCTCAGTACGGA
AGCCGCGCTACGTCAGGCGGGAGCGGCCCCTGGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTA
TCAGCAATGTC**TGA**CCTGGAGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGC
GGGAACCAGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGTCCCTC
CGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCACAGCCATCTCGTTTATCG
GACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGCCTTGGGGGGTCCGGGCCCCCCCAGGAAAC
ACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGGCACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCA
GGGGCTCTGCTGCCGTGCCCTCCAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGA
GACCCCTCTGAGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGCCT
AGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCCTCCCGCGTGGCGGAGACCCCAAGCACGCAGCCAC
CCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAGCAGAAATTCATTGTGCTGAAAAGTC
CTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACCCCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGC
CCACATCTAACCCCCACAAGTCACTGCCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCT
CCCGGAGTTCCTGGGAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCA
GACGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCCTTCGGGGTCC
CCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTGGGCCAGCGGGAACGTGGGGGCA
CTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAAAAAAAAAAAA

FIGURE 9

MALRHLALLAGLLVGVASKSMENTAQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGSASCVRCGNGTLPAYN
GSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFISSGLILSVAGFFYLKRSSKLPRACYRRNKAP
ALQPGEAAAMIPPPQSSVRKPRYVRRERPLDRATDPAAFPGEARISNV

FIGURE 10

AAAAAAAAAAAAAAAACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCGCGAGTCAGACTCGGGTGGGGG
TCCCGGCGGCGGTAGCGGCGGCGGCGGTGCGAGC**ATG**TCGTGGCTCTTCGGCATTAACAAGGGCCCCAAGGGTGA
AGGCGCGGGGCCGCCGCCGCCTTTGCCGCCCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGCTTGGGAGA
CCGGCCGGCGCCCAAGGACAAATGGAGCAACTTCGACCCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGA
GCTGGAGCACTCGCGTTATGCCAAGGACGCCCTGAATCTGGCACAGATGCAGGAGCAGACGCTGCAGTTGGAGCA
ACAGTCCAAGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGA
GAGGAGGAAGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCGGCA
GCGCTACGAGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCA
GAAGCAGGAAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGT
GGAGGCCGAGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAA
GGCGGCCGAGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGC
CTTTGTGACAGACTGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTTGGGGTCTACTCAGC
CAAGAATGCCACGCTTGTCGCCGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTC
CCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGC
GCTGGAGGGTGTTGTGCTCAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACAAGGAACACCAA
GAAGAACCGCAGCCTGTACAGGAACATCCTGATGTACGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAA
ACTCGCCCTGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGT
GACCGCCATGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGA
CGCCTTCCTTCGGAAGCGAGCCACCGAGAAGATAAGCGAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCG
CACGGGCCAGCACAGCAACAAGTTCATGCTGGTCCTGGCCAGCAACCAACCAGAGCAGTTCGACTGGGCCATCAA
TGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGGAGGAACGGGAGCGCCTGGTGAGAATGTATTT
TGACAAGTATGTTCTTAAGCCGGCCACAGAAGGAAAGCAGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAA
GTGCTCGGAGGTCGCTCGGCTGACGGAGGGCATGTCGGGCCGGGAGATCGCTCAGCTGGCCGTGTCCTGGCAGGC
CACGGCGTATGCCTCCGAGGACGGGGTCCTGACCGAGGCCATGATGGACACCCGCGTGCAAGATGCTGTCCAGCA
GCACCAGCAGAAGATGTGCTGGCTGAAGGCGGAAGGGCCTGGGCGTGGGGACGAGCCTTCCCCATCC**TGA**GTCCA
CAGGGAGATCCACAGCTCACGGAGCCTGGCCGCGGACCCCTCCCACCCCTGCCTTGCCGGCCCCTGCACATTTAG
GATATGCTCCTGGGTGGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCCAGGATGTCTTGTGGTGCGGGTCGGCC
GTTCTGCCCCCCAGGGCACCCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCCTGCCCCTCGAGAC
ACTCTTGGGAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGCACCCCAGCCCCTGCCCAGGCC
ACTGTGAGGGTGGGTGCTGGCTGACCCCCCGGGGCAGCAGGAGCCAGGCAGGTGATGTCTTTGTTCTCGGCTCCC
ACAGCAGAGCCAGGTGAGGGGGCGCCTGCCAGGGCCAGACCCAGGTGGGGCAGCCTGAACCCTGCTTCCCCCTGT
GGCCGGCATGCCCCGATCTTTCACACACTGGTGACCCTGAGAGAGGAGGGAGGAGGGAACCTGGCGGGGGTGTCT
GAGGCCGCACTGTCAGCTGGCCGGTCCAAGCCTGTGGCTGGAGCTGGGGTCTGTTTACCTAATAAAGTCCCACAG
GTGCCTCATT

FIGURE 11

MSWLFGINKGPKGEGAGPPPPLPPAQPGAEGGGDRGLGDRPAPKDKWSNFDPTGLERAAKAARELEHSRYAKDAL
NLAQMQEQTLQLEQQSKLKEYEAAVEQLKSEQIRAQAEERRKTLSEETRQHQARAQYQDKLARQRYEDQLKQQQL
LNEENLRKQEESVQKQEAMRRATVEREMELRHKNEMLRVEAEARARAKAERENADIIREQIRLKAAEHRQTVLES
IRTAGTLFGEGFRAFVTDWDKVTATVAGLTLLAVGVYSAKNATLVAGRFIEARLGKPSLVRETSRITVLEALRHP
IQVSRRLLSRPQDALEGVVLSPSLEARVRDIAIATRNTKKNRSLYRNILMYGPPGTGKTLFAKKLALHSGMDYAI
MTGGDVAPMGREGVTAMHKLFDWANTSRRGLLLFVDEADAFLRKRATEKISEDLRATLNAFLYRTGQHSNKFMLV
LASNQPEQFDWAINDRINEMVHFDLPGQEERERLVRMYFDKYVLKPATEGKQRLKLAQFDYGRKCSEVARLTEGM
SGREIAQLAVSWQATAYASEDGVLTEAMMDTRVQDAVQQHQQKMCWLKAEGPGRGDEPSPS

FIGURE 12

ATCAGTTCTCGCCCGTCTGGGCGTGGGCGTGGCCGGCGTGGCTGCTCGGGACCACCCGAACCCGCGGCC**ATG**GCC
CCGGCCGCCGCCAGCCCCCCGGAGGTGATCCGCGCGGCGCAGAAGGACGAGTACTACCGCGGTGGGCTGCGGAGC
GCGGCGGGCGGCGCCCTGCACAGCCTGGCGGGTGCGAGGAAGTGGCTGGAGTGGAGGAAGGAGGTTGAGCTGCTC
TCAGATGTGGCCTACTTTGGCCTCACCACACTTGCAGGCTACCAGACCCTGGGGGGAGGAGTACGTCAGCATCATC
CAGGTGGACCCATCGCGGATACATGTGCCCTCCTCGCTGCGCCGTGGCGTGCTGGTGACGCTGCATGCCGTCCTG
CCCTACCTGCTGGACAAGGCCCTGCTCCCCCTGGAGCAGGAGCTGCAGGCTGACCCCGACAGTGGGCGACCCTTG
CAGGGGAGCCTGGGGCCAGGTGGGCGTGGCTGCTCAGGGGCGCGGCGCTGGATGCGTCACCACACGGCCACCCTG
ACTGAGCAGCAGAGGAGGGCGCTGCTGCGGGCGGTCTTCGTCCTCAGACAGGGCCTCGCCTGCCTCCAGCGGCTA
CATGTTGCCTGGTTTTACATCCACGGTGTCTTCTACCACCTGGCCAAGAGGCTCACGGGGATCACGTACCTCCGT
GTCCGCAGCCTGCCCGGAGAGGACCTGAGGGCCCGTGTTAGCTACAGGCTGCTGGGGGTCATCTCACTGCTGCAC
CTGGTGCTGTCCATGGGGCTGCAGCTGTACGGTTTCAGGCAGCGGCAGCGAGCCAGGAAGGAGTGGAGGCTGCAC
CGCGGCCTGTCTCACCGCAGGGCCTCCTTGGAGGAGAGAGCCGTTTCCAGAAACCCCCTGTGCACCCTGTGCCTG
GAGGAGCGCAGGCACCCAACAGCCACGCCCTGCGGCCACCTGTTCTGCTGGGAGTGCATCACCGCGTGGTGCAGC
AGCAAGGCGGAGTGTCCCCTCTGCCGGGAGAAGTTCCCTCCCCAGAAGCTCATCTACCTTCGGCACTACCGC**TGA**

GCCGGCGCCCGGGTGGGCCTGGACACAGATGACCTCTACGGGAGTCTGAACGCCAAGATTTAGTCTCAGGATTAA
CCTTGCTTGCACAGAAGTTAGAACACTCTCAGTTTTTTGTCATGTAAGATACTAACCTAGCCACCCTGGGAGAGA
ACAGAAAGCTGTCCCTGGCTGCGCTTTCTCAGCCCTGGGAGGGGCGCCTGAACCCAGAACATTTCCCTAACCCCA
ACCTGGTAGGACTCAGCCACTTCTTCAGGAATTTCACTTATTTGGACGGGATTTTAGGTTTCCCTCCCTTCCCCA
AACCATACAGTTGAGAAGTAATTCAGAAGTAGGCCAGAAGACACTTTATTCGTTTATATTGTGAGAAAACAGCCC
CATCAGGCTTGTGTTAAGGCAATGGACTGAATGAGTGCGTGCTGGGTGGGGTGGGGCACGGAGGCTGGCGGGTTG
CTTCAGCCAGTGCAGTGAGAACAGCAGCCCCACGGCCCCATGGGAGGCGGCGCTGCTCTCCCCGAGGGCGGCTGG
GCAGAGCACATCCCCCAGGACTTGATGACCACACGGGGCAGAGAGAAACCAACCAAGGCCAGCACCTCCGTCGGA
AGCATTTGGCACACACACCTTCAATACACGTCAAGGTCGCTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGC
CTGAGACGCACAGAGAGGTCTCTTCCTGACCCAGACGCACTCACGAGCCAGGTCCTGGGGGGTATGGGGGCTGCCA
GGGGCGCCCGAGCCCTCTCCTGGGGGGCCTGCTGGGCAGGCGACCTGCTGACCCACGGTCACTGCTGTGTTCAGC
CCCTCAGCTCGGCCCCAGCCTATTTCCCGCCTCCATTTGATGTTTCCAGGTTTTCAAAACTGCATTTAACCTGCG
CCAGAGAGTTCACCGTAGGCATCTTTAATAAACTAACTCCAGCAAAAAAAAAAAAAAA

FIGURE 13

MAPAAASPPEVIRAAQKDEYYRGGLRSAAGGALHSLAGARKWLEWRKEVELLSDVAYFGLTTLAGYQTLGEEYVS
IIQVDPSRIHVPSSLRRGVLVTLHAVLPYLLDKALLPLEQELQADPDSGRPLQGSLGPGGRGCSGARRWMRHHTA
TLTEQQRRALLRAVFVLRQGLACLQRLHVAWFYIHGVFYHLAKRLTGITYLRVRSLPGEDLRARVSYRLLGVISL
LHLVLSMGLQLYGFRQRQRARKEWRLHRGLSHRRASLEERAVSRNPLCTLCLEERRHPTATPCGHLFCWECITAW
CSSKAECPLCREKFPPQKLIYLRHYR

FIGURE 14

GGGCGGCGAGTGGGGAGCGGGGCCGGGAGTGGAGCAGCCGCCGCGGCGGGACTGGACCGAGCCTCGCCGGCGCGC
ACCTGCCCGCAGCGCCCGCGGAGCGCGCAGCGCGGCCCGAGCGCGACGACCTGCCGAGCGGCGGCCGAGGCGGCG
GTGTGGGCGCGTCAGGCCGCGACGAGGGCGCTGAGACAAATTTACATGTATTGGAGACCAGACCAGAAGCCCTTC
TGAATTAAGATCTCACATTCTTGAAGGTGGCATTGAAGAGCACTAAGATCGGAAGATGAGTGAGCTTGACCAGTT
ACGGCAGGAGGCCGAGCAACTTAAGAACCAGATTCGAGACGCCAGGAAAGCATGTGCAGATGCAACTCTCTCTCA
GATCACAAACAACATCGACCCAGTGGGAAGAATCCAAATGCGCACGAGGAGGACACTGCGGGGGCACCTGGCCAA
GATCTACGCCATGCACTGGGGCACAGACTCCAGGCTTCTCGTCAGTGCCTCGCAGGATGGTAAACTTATCATCTG
GGACAGCTACACCACCAACAAGGTCCACGCCATCCCTCTGCGCTCCTCCTGGGTCATGACCTGTGCATATGCCCC
TTCTGGGAACTATGTGGCCTGCGGTGGCCTGGATAACATTTGCTCCATTTACAATCTGAAAACTCGTGAGGGGAA
CGTGCGCGTGAGTCGTGAGCTGGCAGGACACACAGGTTACCTGTCCTGCTGCCGATTCCTGGATGACAATCAGAT
CGTCACCAGCTCTGGAGACACCACGTGTGCCCTGTGGGACATCGAGACCGGCCAGCAGACGACCACGTTTACCGG
ACACACTGGAGATGTCATGAGCCTTTCTCTTGCTCCTGACACCAGACTGTTCGTCTCTGGTGCTTGTGATGCTTC
AGCCAAACTCTGGGATGTGCGAGAAGGCATGTGCCGGCAGACCTTCACTGGCCACGAGTCTGACATCAATGCCAT
TTGCTTCTTTCCAAATGGCAATGCATTTGCCACTGGCTCAGACGACGCCACCTGCAGGCTGTTTGACCTTCGTGC
TGACCAGGAGCTCATGACTTACTCCCATGACAACATCATCTGCGGGATCACCTCTGTCTCCTTCTCCAAGAGCGG
GCGCCTCCTCCTTGCTGGGTACGACGACTTCAACTGCAACGTCTGGGATGCACTCAAAGCCGACCGGGCAGGTGT
CTTGGCTGGGCATGACAACCGCGTCAGCTGCCTGGGCGTGACTGACGATGGCATGGCTGTGGCGACAGGGTCCTG
GGATAGCTTCCTCAAGATCTGGAACTAACGCCAGTAGCATGTGGATGCCATGGAGACTGGAAGACCATTCCAACT
TGGACGCGTTACCATGAGAGCATATCCTATCCAACCGTACTAACGTGGACACCCTACACCTCCCCTCAGAACTTC
AAAAGGGCAAGATCTTTTTTCCTTCACTTATTGCTGAAACCAAGAGCACAATTCCCATTGAGAGAAAGATCTCTG
TGCTGTAAACTAAAACAAATTGTGCATTCCTTCCGGGGCCATCGTCTTTGTTTTCTTTTTTGTCTTGAATGAATT
TTAAAAGGAAATATATAATAAAAATGTTAACCAGAAGGTAAACTTGAGTGTAATTGTCAGACAGACACACTTTTC
CACCAGTGTATTTGAATTTTAGACCAGTGACCCTGTTTTGTGGCATTCATGCAAAACATGCTGAGGGCTTTGTTC
ATCTGGTCATCGTGTCCAAATTTCAGTCATGTTTGTAGCAAGATTTTGGAAGCATTCATATTTCCTTTTTAAAAT
GTATTCCTTTGTGTTCAACAGTTAATCAAAACCAGAGAGTCTAGGGCAGCCTCTCTGATGTTGTCAATGATGTAA
ATTCAGTCCCTGGTTTTTAATTTTCTGTCTGATGTCACAGATCATTGTTGCACACAAACGTGGCATAGAAAAGAA
CATGTTCAGAAGCCATGGGGCCAAGCACATGCGGGGACGGTCTCAAATGCGTGATCAGAGAATCCTTCACCTTTG
CTGAAAAGTGAGCTCAGATCCAGCACCATGTTCCTCCTGACCCATCCTGTCTATCTTCTCAGTTGAGTTTTTAAT
CTCACTTTGGGTTTCCTTGTGAAGTTGGAGGGAAGTTTATAATAGCCTAACACTACCCCACCCCCAACTAGGAGG
AACCTCTGTTTTCAAGAGAGATGCCTGTCCTGTGCTTGGATAGTCAGTCAATTATTTGTGTATGAAACAATGTAC
AAATCAATGTTTTGAAAATAATGATCTCAGACTTTCTAAGTTAAATTTTAAAAATTTTGATTGTTTGCCATATTG
GGTGGGTTTACTCTTAGAATCGCATGCTGTAGAAATGCTCAAAAGTGCATATGGGACTCAGTCCTTAGGTGTTCT
TTTTCTTTTAAGAAATAACCTCTTACAGTTGTAACCATTGCGGCTCTGTCCACTTCTCGTTGCTGCTCTGTGGCA
CATATCGGAAGCAGTACAGCGCGCGGCTCTACACGCTTGGGTAGCGGGATAAGTCACTGTTTTCTTTATTTCTTT
AAAAAAAAAAAAGTTCTGTTGCAAACGACTGCTGTTGGATTCTGAGGGTGGGGAGGGAGAGAGAGGGAGGGAGAG
GGAGTGAAGAGCCTGCCCTCCTATATGGATTCTTCAGGGCCCTCCACATCTGAGGTGGCTCATTCCCATCACACA
CAGATTGTCCTGGTGTTCATTTCAAGGCCAGTGTTCAGCAGCAGCGTTTGGAAAGCAGGTTCTGTGGGACCCCCC
GCCCCGCCCCCCGCACTCCTTCATAGCAGCAGTAGTGGCTTCTCCATCCTGTTTTCTGCAACATTCTATACAAAA
CTGTGCTGTGACCTTGCGGTAGGCCTGGATCTGGCAAAGAGAATACAAATGAAACCCCTTCTTTCTCTTTCCGTC
CAACAACTCTGTAGAGCTCTCTGCACCCTTACCCCTTTCCACCTTTTGTATTTAATTTTAAAGTCAGTGTACTGC
AAGGAAGCTGGATGCAAGATAGATACTATATTAAACTGTACTGTTATTTAAGATGTAATAAAGCAGTTTGACATG

FIGURE 15

ATCAAACCACCCCAGCAAATGTCTCGGAAAGAAAAAGTTCATCACAGAAAAGATGAAAAGAGAAAAGAAAAATGT
AGGCATCATAGCCATTCAGCAGAAGGGGGGAAGCATGCTAGAGTGAAAGAAAGAGAGCACGAACGTCGGAAACGA
CATCGAGAAGAACAGGATAAAGCTCGCCGGGA**ATG**GGAAAGACAGAAGAGAAGGGAAATGGCAAGGGAGCATTCC
AGGAGAGAAAGGGACCGCTTGGAGCAGTTAGAAAGGAAGCGGGAGCGGGAGCGCAAGATGCGGGAGCAGCAGAAG
GAGCAGCAGTCAAGAAGATGACCTTCAGCGAGCACCCCTACAACAACCTCCGCAAGCGCTTCGGGGCTCTGCTCT
CAGACCAGGGCTTCGACCTCATGAACAAGTTCCTGACCTACTTCCCCGGGAGGAGGATCAGCGCTGAGGACGGCC
TCAAGCATGAGTATTTCCGCGAGACCCCCCTCCCCATCGACCCCTCCATGTTCCCCACGTGGCCCGCCAAGAGCG
AGCAGCAGCGTGTGAAGCGGGGCACCAGCCCGAGGCCCCCTGAGGGAGGCCTGGGCTACAGCCAGCTGGGTGACG
ACGACCTGAAGGAGACGGGCTTCCACCTTACCACCACGAACCAGGGGGCCTCTGCCGCGGGCCCCGGCTTCAGCC
TCAAGTTC**TGA**AGGTCAGAGTGGACCCCGTCATGGGG

FIGURE 16

MGKTEEKGNGKGAFQERKGPLGAVRKEAGAGAQDAGAAEGAAVKKMTFSEHPYNNLRKRFGALLSDQGFDLMNKF
LTYFPGRRISAEDGLKHEYFRETPLPIDPSMFPTWPAKSEQQRVKRGTSPRPPEGGLGYSQLGDDDLKETGFHLT
TTNQGASAAGPGFSLKF

FIGURE 17

TCGCGCGGAAGCCGCGGTAGGGTGGGAACCCAAGCGGGAGAGCCGCGGGATTTGCGGCCGCCGCC**ATG**CCGTCGT
CCCCGCTGCGGGTGGCGGTGGTGTGCTCGAGCAACCAGAACCGGAGCATGGAGGCGCACAACATCCTCAGCAAAC
GGGGATTCAGCGTCCGATCCTTTGGAACAGGGACTCACGTGAAGCTTCCAGGACCAGCTCCCGACAAGCCCAATG
TTTATGATTTCAAAACCACATATGACCAGATGTACAATGATCTTCTTAGGAAAGACAAAGAACTCTATACACAGA
ATGGGATTTTACATATGCTGGACAGAAATAAGAGAATCAAGCCCCGGCCAGAAAGATTCCAGAACTGCAAAGACC
TGTTTGATCTGATCCTCACTTGCGAAGAGAGAGTGTATGACCAGGTGGTGGAAGATCTGAATTCCAGAGAACAGG
AGACCTGCCAGCCCGTGCACGTGGTCAATGTGGACATCCAGGACAACCACGAGGAGGCCACCCTGGGGGCGTTTC
TCATCTGTGAGCTCTGCCAGTGTATCCAGCACACGGAAGACATGGAGAACGAGATCGACGAGCTGCTGCAGGAGT
TCGAGGAGAAGAGTGGCCGCACCTTTCTGCACACCGTCTGCTTCTAC**TGA**GCCCAGCGCCCGCATGGAGCCGCCT
CTGGAGCTTCCTGTTGTTCATACTTTTTCCTTCCTGACATTTGTTTTTACTTACAGGTGTTCTGCTGGTGACGGT
AGCATTACCCAAATAAACTGTGCATATGAAATGGGAGAGGAGATGCCAAAACGCCAGATGAAAGCAATCAAGTTT
CTTCTTTTCCACTTTTACTTATGAGCGGGATATTGATTACAAAGTTTTTCTTCTTTAACCAAAAAGGAAAGACAA
CGGTTTGTGTGCACTTCCCGACATACCTGTGTCTTCGTGTGCCTGCCTTCCCTCCCTCCTCCCCACCGGGCCGGA
CTGTACAGAGCCCTGCTGCGGCGTGTTAGGAATGACCTGGAATTGTCAATAAACAGATGCTGCTGTCAAAAAAAA
AAAAAAAAA

FIGURE 18

MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDKEL
YTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYDQVVEDLNSREQETCQPVHVVNVDIQDNHEEATL
GAFLICELCQCIQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY

FIGURE 19

CCTGGCCACCGGCTCGCGGCGCGTGGAGGCTGCTCCCAGCCGCGCCCGAGTCAGACTCGGGTGGGGGTCCCGGCG
GCGGTAGCGGCGGCGGCGGTGCGAGCATGTCGTGGCTCTTCGGCGTTAACAAGGGCCCCAAGGGTGAAGGCGCGG
GGCCGCCGCCGCCTTTGCCGCCCGCGCAGCCCGGGGCCGAGGGCGGCGGGGACCGCGGTTTGGGAGACCGGCCGG
CGCCCAAGGACAAATGGAGCAACTTCGACCCCACCGGCCTGGAGCGCGCCGCCAAGGCGGCGCGCGAGCTGGAGC
ACTCGCGTTACGCCAAGGAGGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCA
AGCTCAAAGAGTATGAGGCCGCCGTGGAGCAGCTCAAGAGCGAGCAGATCCGGGCGCAGGCTGAGGAGAGGAGGA
AGACCCTGAGCGAGGAGACCCGGCAGCACCAGGCCAGGGCCCAGTATCAAGACAAGCTGGCCCGGCAGCGCTACG
AGGACCAACTGAAGCAGCAGCAACTTCTCAATGAGGAGAATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCAGG
AAGCCATGCGGCGAGCCACCGTGGAGCGGGAGATGGAGCTGCGGCACAAGAATGAGATGCTGCGAGTGGAGACCG
AGGCCCGGGCGCGCGCCAAGGCCGAGCGGGAGAATGCAGACATCATCCGCGAGCAGATCCGCCTGAAGGCGTCCG
AGCACCGTCAGACCGTCTTGGAGTCCATCAGGACGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGA
CAGACCGGGACAAAGTGACAGCCACGGTGGCTGGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATG
CGACAGCCGTCACTGGCCGCTTCATCGAGGCTCGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCA
CGGTGCTGGAGGCGCTGCGGCACCCCATCCAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGG
GTGTTGTGCTTAGTCCCAGCCTGGAAGCACGGGTGCGCGACATCGCCATAGCAACCAGGAACACCAAGAAGAACC
GGGGCCTGTACAGGCACATCCTGCTGTATGGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAAACTCGCCC
TGCACTCAGGCATGGACTACGCCATCATGACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCA
TGCACAAGCTCTTTGACTGGGCCAATACCAGCCGGCGCGGCCTCCTGCTCTTCATGGATGAAGCAGACGCCTTCC
TTCGGAAGCGAGCCACTGAGGAGATAAGCAAGGACCTCAGAGCCACACTGAACGCCTTCCTGTACCACATGGGCC
AACACAGCAACAAATTCATGCTGGTCCTGGCCAGCAATCTGCCTGAGCAGTTCGACTGTGCCATCAACAGCCGCA
TTGACGTGATGGTCCACTTCGACCTGCCGCAGCAGGAGGAGCGGGAGCGCCTGGTGAGACTGCATTTTGACAACT
GTGTTCTTAAGCCGGCCACAGAAGGAAAACGGCGCCTGAAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTCGG
AGGTCGCTCGGCTGACGGAGGGCATGTCGGGCCGGGAGATCGCTCAGCTGGCCGTGTCCTGGCAGGCCACGGCAT
ATGCCTCCAAGGACGGGGTCCTCACTGAGGCCATGATGGACGCCTGTGTGCAAGATGCTGTCCAGCAGTACCGAC
AGAAGATGCGCTGGCTGAAGGCGGAGGGGCCTGGGCGCGGGGTCGAGCACCCCCTATCCGGAGTCCAAGGCGAGA
CCCTCACCTCATGGAGCCTGGCCACGGACCCCTCCTACCCCTGCCTTGCCGGCCCCTGCACATTTAGGATATGCT
CCTGGATGGGGACTGGGCTGTGCCCAGGGCCTCTGTCCCCCAGGATGTCTTGTGGTGGCGGTCGGCCGTTCTGCC
CCCCAGGGCACCCCCTGTTGTAGGCACTGGCTAGGGAGGGGCAGGCCTCCTTCCTGCCCCTCGAGACACTCTTGG
GAGATGCATTTTCCGTCTGGCTCACAGGGGGAGGGTGAGGCTTTGTACCCCAGCCCCTGCCCAGGCCACTGTGAG
GGTGGGTGCTGGCTGAGCCCCTGGGGCAGAAGGAGTGGGGCAGGCGGGGTCTTTGTTCTCGGCTCCCACAGCAGA
GCCAGGTGAGGGGGGGCCTGCCAGGACTAGACAGAAGTGGGGCGGC

FIGURE 20

ATGAGGCTGCAGAGTGATGTGGGGGCCAGCGGTGACTTCATGACCACACTGCGCCCAGGTGTAAGAGGGCACGCT
TCTGCCCAGGCATCGTCCATGGAAGACACGCAGTCGGCCACTGCAGCCTCGGTCCTGGGTGCCCTGGGGCTGGGT
CACTGGGGGCCACAGGCCACACTGAGAGACCACAGTCCTGGCATGCCATGCAGCTCCCTGTCCCCAGAGGCCATG
TCAAAGGACGCCCTGAATCTGGCGCAGATGCAGGAGCAGACGCTGCAGTTGGAGCAACAGTCCAAGCTCAAACAA
CTTGTCAATGAGGATTTACGGAAGCAGGAGGAGTCCGTGCAGAAGCACCATCAGACCTTCTTGGAGTCCATCAGG
GCGGCTGGCACCTTGTTTGGGGAAGGATTCCGTGCCTTTGTGACAGACCGGGACAAAGTGACAGCCACGGTGGCT
GGGCTGACGCTGCTGGCTGTCGGGGTCTACTCAGCCAAGAATGCGACAGCCGTCACTGGCCGCTACATCGAGGCT
CGGCTGGGGAAGCCGTCCCTAGTGAGGGAGACGTCCCGCATCACGGTGCTTGAGGCGCTGCGGCACCCCATCCAG
CAGGTCAGCCGGCGGCTCCTCAGTCGACCCCAGGACGTGCTGGAGGGTGTTGTGCTTAGTCCCAGCCTGGAAGCA
CGGGTGCGCGACATCGCCATAATGACAAGGAACATCAAGAAGAACCGGGGCCTGTACAGGCACATCCTGCTGTAC
GGGCCACCAGGCACCGGGAAGACGCTGTTTGCCAAGAAACTCGCCCTGCACTCAGGCATGGACTACGCCATCATG
ACAGGCGGGGACGTGGCCCCCATGGGGCGGGAAGGCGTGACCGCCATGCACAAGCTCTTTGACTGGGCCAATACC
AGCCGGCGCGGCCTCCTGCTCTTTGTGGATGAAGCGGACGCCTTCCTTCGGAAGCGAGCCACTGAGAAGATAAGC
GAGGACCTCAGGGCCACACTGAACGCCTTCCTGTACCGCACGGGCCAGCACAGCAACAAATTCATGCTGATCCTG
GCCAGCTGCCACCCCGAGCAGTTCGACTGGGCCATCAATGCCTGCATCGACGTGATGGTCCACTTCGACCTGCCA
GGGCAGGAGGAGCGGGCGCGCCTGGGATTGGAGGGAGAGGCTCCTCATGAGACCCCCATGTCGGGACTAGAGGGA
GAGGCTCCTCATGGTCCACTGCTGGCTTCTGGCCTGGCCTCCCTGCAGCTGCCACACCCGGCCCTGGAGCCTCGT
GGTGTGGGGCGCGGCTCTTGCTTCCTGCTGCACATGTGCCTTGAGGCTGTCAGGCTCCCTGTTGCTGGCGGGCCC
CGGTTTCTGAGTCCTTCTGTGCACCTGACCCAAATCCCTGCTGTCGCCAGTGACGACAAAAGCTGCTCTGTTCCA
AAGAGAGCCTGGTTCTCCCCTGCCGACCCCTCCACTGCCGCCTGCTCCATGCTAGACCAGCTTTCCGGGCGTCTG
AAGCTGGCCCAGTTTGACTACGGGAGGAAGTGCTTAGAGATCGCTCGGCTGACAGAGGGCATGTCATGCCGGAAG
ATCGCACAGCTGGCCGTGTCCTGGCAGGCCACGGCGTATGCCTCCAAGGACGGGGTCCTGACCGAGGCCATGATG
GACGCCTGCGTGCAAGACTTTGTCCAGCAGCACCAGCAGATGATGCGCTGGCTGAAGGGGGAGAGGCCTGGGCCC
GAGGACGAGCAACCCTCATCC**TGA**

FIGURE 21

MRLQSDVGASGDFMTTLRPGVRGHASAQASSMEDTQSATAASVLGALGLGHWGPQATLRDHSPGMPCSSLSPEAM
SKDALNLAQMQEQTLQLEQQSKLKQLVNEDLRKQEESVQKHHQTFLESIRAAGTLFGEGFRAFVTDRDKVTATVA
GLTLLAVGVYSAKNATAVTGRYIEARLGKPSLVRETSRITVLEALRHPIQQVSRRLLSRPQDVLEGVVLSPSLEA
RVRDIAIMTRNIKKNRGLYRHILLYGPPGTGKTLFAKKLALHSGMDYAIMTGGDVAPMGREGVTAMHKLFDWANT
SRRGLLLFVDEADAFLRKRATEKISEDLRATLNAFLYRTGQHSNKFMLILASCHPEQFDWAINACIDVMVHFDLP
GQEERARLGLEGEAPHETPMSGLEGEAPHGPLLASGLASLQLPHPALEPRGVGRGSCFLLHMCLEAVRLPVAGGP
RFLSPSVHLTQIPAVASDDKSCSVPKRAWFSPADPSTAACSMLDQLSGRLKLAQFDYGRKCLEIARLTEGMSCRK
IAQLAVSWQATAYASKDGVLTEAMMDACVQDFVQQHQQMMRWLKGERPGPEDEQPSS

FIGURE 22

AAGTGCCCGAGGGCGGCCGCAGAACGGTCAATTTGAGCCGCGTCGAGCTCCCCTGGGACCTGTGGCCGCCGCCCA
CAGACC**ATG**CTCCTGGGGCGCCTGACTTCCCAGCTGTTGAGGGCCGTTCCTTGGGCAGGCGGCCGCCCGCCTTGG
CCCGTCTCTGGAGTGCTGGGCAGCCGGGTCTGCGGGCCCCTTTACAGCACATCGCCGGCCGGCCCAGGTAGGGCG
GCCTCTCTCCCTCGCAAGGGGGCCCAGCTGGAGCTGGAGGAGATGCTGGTCCCCAGGAAGATGTCCGTCAGCCCC
CTGGAGAGCTGGCTCACGGCCCGCTGCTTCCTGCCCAGACTGGATACCGGGACCGCAGGGACTGTGGCTCCACCG
CAATCCTACCAGTGTCCGCCCAGCCAGATAGGGGAAGGGGCCGAGCAGGGGGATGAAGGCGTCGCGGATGCGCCT
CAAATTCAGTGCAAAAACGTGCTGAAGATCCGCCGGCGGAAGATGAACCACCACAAGTACCGGAAGCTGGTGAAG
AAGACGCGGTTCCTGCGGAGGAAGGTCCAGGAGGGACGCCTGAGACGCAAGCAGATCAAGTTCGAGAAAGACCTG
AGGCGCATCTGGCTGAAGGCGGGGCTAAAGGAAGCCCCCGAAGGCTGGCAGACCCCCAAGATCTACCTGCGGGGC
AAA**TGA**GTCTGGCGCCGCCCTTCCCGCCCGTTGCTGCTGTGATCCGTAGTAATAAATTCTCAGAGGACTCAGCCT
TTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 23

MLLGRLTSQLLRAVPWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPGRAASLPRKGAQLELEEMLVPRKMSVSPLE
SWLTARCFLPRLDTGTAGTVAPPQSYQCPPSQIGEGAEQGDEGVADAPQIQCKNVLKIRRRKMNHHKYRKLVKKT
RFLRRKVQEGRLRRKQIKFEKDLRRIWLKAGLKEAPEGWQTPKIYLRGK

FIGURE 24

GCGGTGCGGGCCGGGCGGGGCGCAGGCGGGCGGGCGGGTAGCGCCCCGCGTCCGAGCCCCGGGCCGGGCCCTGAG
CGCGCGGGCTCCGCGCCGCCGCCGCGCC**ATG**GCGGAGACCAAGATTATCTACCACATGGACGAGGAGGAGACGCC
GTACCTGGTCAAGCTGCCCGTGGCCCCCGAGCGCGTCACGCTGGCCGACTTCAAGAACGTGCTCAGCAACCGGCC
CGTGCACGCCTACAAATTCTTCTTTAAGTCCATGGACCAGGACTTCGGGGTGGTGAAGGAGGAGATCTTTGATGA
CAATGCCAAGCTTCCCTGCTTCAACGGCCGCGTGGTCTCCTGGCTGGTCCTGGCTGAGGGTGCTCACTCGGATGC
GGGGTCCCAGGGCACGGACAGCCACACAGACCTGCCCCCGCCTCTTGAGCGGACAGGCGGCATCGGGGACTCCCG
GCCCCCCTCCTTCCACCCAAATGTGGCCAGCAGCCGTGACGGGATGGACAACGAGACAGGCACGGAGTCCATGGT
CAGTCACCGGCGGGAGCGTGCCCGACGCCGGAACCGCGAGGAGGCCGCCCGGACCAATGGGCACCCAAGGGGAGA
CCGACGGCGGGATGTGGGGCTGCCCCCAGACAGCGCGTCCACCGCCCTCAGCAGCGAGCTTGAGTCCAGCAGCTT
TGTGGACTCGGACGAGGATGGCAGCACGAGCAGGCTCAGCAGCTCCACGGAGCAGAGCACCTCATCCAGACTCAT
CCGGAAGCACAAACGCCGGCGGAGGAAGCAGCGCCTTCGGCAGGCGGACCGGGCCTCCTCCTTCAGCAGCATAAC
CGACTCCACCATGTCCCTCAACATCGTCACTGTCACGCTCAACATGGAAAGACATCACTTTCTGGGCATCAGCAT
CGTGGGGCAGAGCAACGACCGTGGAGACGGCGGCATCTACATTGGCTCCATCATGAAGGGCGGGGCTGTGGCCGC
TGACGGCCGCATCGAGCCCGGCGACATGTTGCTGCAGGTGAATGACGTGAACTTTGAGAACATGAGCAATGACGA
TGCCGTGCGGGTGCTGCGGGAGATCGTTTCCCAGACGGGGCCCATCAGCCTCACTGTGGCCAAGTGCTGGGACCC
AACGCCCCGAAGCTACTTCACCGTCCCACGGGCTGACCCGGTGCGGCCCATCGACCCCGCCGCCTGGCTGTCCCA
CACGGCGGCACTGACAGGAGCCCTGCCCCGCTACGAGCTGGAAGAGGCGCCGCTGACGGTGAAGAGTGACATGAG
CGCCGTCGTCCGGGTCATGCAGCTGCCAGACTCGGGACTGGAGATCCGCGACCGCATGTGGCTCAAGATCACCAT
CGCCAATGCCGTCATCGGGGCGGACGTGGTGGACTGGCTGTACACACACGTGGAGGGCTTCAAGGAGCGGCGGGA
GGCCCGGAAGTACGCCAGCAGCTTGCTGAAGCACGGCTTCCTGCGGCACACGGTCAACAAGATCACCTTCTCCGA
GCAGTGCTACTACGTCTTCGGGGATCTCTGCAGCAATCTCGCCACCCTGAACCTCAACAGTGGCTCCAGTGGGAC
TTCGGATCAGGACACGCTGGCCCCGCTGCCCCACCCGGCTGCCCCCTGGCCTCTGGGTCAGGGCTACCCCTACCA
GTACCCGGGACCCCCACCCTGCTTCCCGCCTGCCTACCAGGACCCGGGCTTTAGCTATGGCAGCGGCAGCACCGG
GAGTCAGCAGAGTGAAGGGAGCAAAAGCAGTGGGTCCACCCGGAGCAGCCGCCGGGCCCCGGGCCGTGAGAAGGA
GCGTCGGGCGGCGGGAGCTGGGGGCAGTGGCAGTGAATCGGATCACACGGCACCGAGTGGGGTGGGGAGCAGCTG
GCGAGAGCGTCCGGCCGGCCAGCTCAGCCGTGGCAGCAGCCCACGCAGTCAGGCCTCGGCTACCGCCCCGGGGCT
CCCCCCGCCCCACCCCACGACCAAGGCCTATACAGTGGTGGGGGGGCCACCCGGGGGACCCCCTGTCCGGGAGCT
GGCTGCCGTCCCCCCGGAATTGACAGGCAGCCGCCAGTCCTTCCAGAAGGCTATGGGGAACCCCTGCGAGTTCTT
CGTGGACATCATG**TGA**CTCGTGGCGCATGCCCCAGCCCTGCCTGAGGTGGGGAGCTGGCGGTCCTGCCGCATGCA
GAGCTCGCGTGGGCTTGCCTTCGTGGGGGCCAGGACGGGAGGCAGGGTGGGGGGCAGGCTGGACCACCACCATCT
GCCCTGGCAGCCTGGCTGCTCCAGCTCCTGACAGCACCTGTGTCTGAGCAGCCGTGTTGGGGGCGCTCCCTCTCT
GCCCCTCAGCGAGAGCCTCGGACCTCCCAACCCCTTGTGTCTGGTGGGGATCCCTCCTGGGATGAGGAAGACCCC
CTCGGGCTCTCGGCTGACCCCCACCTCCTGCACAGCTGTGCCCAGGCCCCCAGGGTGGTCCATGCGGGGCAACCC
CCTGCGGTGCACAGGCCCCCTGTCTGGAGTAGGGATCTAATTTATTTATTTATTGCCTGGCCGGTGACTCGGGGG
AGGAGGCGACCCTGTCATCTGTCCCACCTGCTGCTGCCCCTTGGAGCAGCCTGCACCTTCTCTCCTCCCATCCGG
CAACAGTCTGAAAGTACGTGGAGGACGGGACCGGAAGACGAGAGAGGGCTGGACATCCTGCCCACCGTGTCCCAG
CCAGGGCAGGGAGGGACCATGGCCCGCAGGGTCAAGGGGCCCCGATGTGCACAGCTGCCACAGGGAGGGAGGTCT
TGGGGAGATGGGCAGTCAGGTGGCCCGTCCTTGGTGAGTGCACACACTGCGCGCACACATCGCGGCCTTCCTGGC
TTCTCTGGCCCCCACGTGTCTGTGCTGTAGATACTGTATCAAAGTCCCAGCGTTTAGATGGTTAACATAGAGCTG
CTTCTGTGTAAATGCTGCTTATTTTAAACACTAAAAAGCGTTTAATTTTATGGG

FIGURE 25

MAETKIIYHMDEEETPYLVKLPVAPERVTLADFKNVLSNRPVHAYKFFFKSMDQDFGVVKEEIFDDNAKLPCFNG
RVVSWLVLAEGAHSDAGSQGTDSHTDLPPPLERTGGIGDSRPPSFHPNVASSRDGMDNETGTESMVSHRRERARR
RNREEAARTNGHPRGDRRRDVGLPPDSASTALSSELESSSFVDSDEDGSTSRLSSSTEQSTSSRLIRKHKRRRRK
QRLRQADRASSFSSITDSTMSLNIVTVTLNMERHHFLGISIVGQSNDRGDGGIYIGSIMKGGAVAADGRIEPGDM
LLQVNDVNFENMSNDDAVRVLREIVSQTGPISLTVAKCWDPTPRSYFTVPRADPVRPIDPAAWLSHTAALTGALP
RYELEEAPLTVKSDMSAVVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYASSLL
KHGFLRHTVNKITFSEQCYYVFGDLCSNLATLNLNSGSSGTSDQDTLAPLPHPAAPWPLGQGYPYQYPGPPPCFP
PAYQDPGFSYGSGSTGSQQSEGSKSSGSTRSSRRAPGREKERRAAGAGGSGSESDHTAPSGVGSSWRERPAGQLS
RGSSPRSQASATAPGLPPPHPTTKAYTVVGGPPGGPPVRELAAVPPELTGSRQSFQKAMGNPCEFFVDIM

FIGURE 26

GCACCGCCCCCGCCCGCAAGAAAGATGGCAGTGGCCTGATCCGGGCCCGTTGGCGGCGTCACTGACGCTTCGCTC
CGGTCCTCGGATCCCGAGCGCGGGGAGGCAGACCGACTGTGAGCTGCTTGTCCCCATCCTGCGGCCGTCCTGGGG
ACACAGAGCCCTCCGTGGTGCCCGGGGATTGGATTGGAGCCAGGACCTCACTTCCTCCTCTGCCCCTGCCCCTGC
CCCTCCCAGCACCTGGCCCACACCCTGCAGCCCGCCCC**ATG**GTCTGGCCCTGGGTGGCGATGGCGTCCAGGTGGG
GTCCCCTCATTGGCCTGGCTCCGTGCTGCCTCTGGCTCCTGGGGGCAGTCCTTCTGATGGACGCGTCTGCACGGC
CTGCCAACCACTCGTCCACTCGAGAGAGAGTAGCCAACAGGGAGGAGAATGAGATCCTGCCCCCAGACCACCTGA
ACGGGGTGAAGCTGGAGATGGACGGGCACCTCAATCGCGGCTTCCACCAGGAGGTCTTCCTAGGCAAGGACCTGG
GTGGCTTTGATGAGGACGCGGAGCCGCGGCGGAGCCGGAGGAAGCTGATGGTCATCTTTTCCAAGGTGGATGTGA
ACACTGACCGGAAGATCAGTGCCAAGGAGATGCAGCGCTGGATCATGGAGAAGACGGCCGAGCACTTCCAGGAGG
CCATGGAGGAGAGCAAGACACACTTCCGCGCCGTGGACCCTGACGGGGACGGTCACGTGTCTTGGGACGAGTATA
AGGTGAAGTTTTTGGCGAGTAAAGGCCATAGCGAGAAGGAGGTTGCCGACGCCATCAGGCTCAACGAGGAACTCA
AAGTGGACGAGGAAACACAGGAAGTCCTGGAGAACCTGAAGGACCGCTGGTACCAGGCGGACAGCCCCCCTGCAG
ACCTGCTGCTGACGGAGGAGGAGTTCCTGTCGTTCCTCCACCCCGAGCACAGCCGGGGAATGCTCAGGTTCATGG
TGAAGGAGATCGTCCGGGACCTGGACCAGGACGGTGACAAGCAGCTCTCTGTGCCCGAGTTCATCTCCCTGCCCG
TGGGCACCGTGGAGAACCAGCAGGGCCAGGACATTGACGACAACTGGGTGAAAGACAGAAAAAAGGAGTTTGAGG
AGCTCATTGACTCCAACCACGACGGCATCGTGACCGCCGAGGAGCTGGAGAGCTACATGGACCCCATGAACGAGT
ACAACGCGCTGAACGAGGCCAAGCAGATGATCGCCGTCGCCGACGAGAACCAGAACCACCACCTGGAGCCCGAGG
AGGTGCTCAAGTACAGCGAGTTCTTCACGGGCAGCAAGCTGGTGGACTACGCGCGCAGCGTGCACGAGGAGTTT**T**
GAGCGCCCGGCCGCGCCCCGCGCCGCCCCCCACGCACCACCGGGGCGGCCTCGCGGGTGACTCCGGGCTCCGTGG
CTGTCCCGGACCCCACCTCTTCCCTGCCGCCCGCCACCGGCCGACCGACCGCGGCTGCCCCAGTTGATGAGCGGC
GTGTCCCCTCTGCAGCGCGCACCCCGGCGGGGCTTTGGCTGTGACGCGGTCGGGGCGCGGGGCTGGGCTGTGGCC
CCGCGGCGCCGCCTCCTCCCTGGTCCCTCGAAATCGTGGCATCTCACTTCTGAGAACGAAATCTCGCTTCAGTCA
CTCTGCCGAAGGCGCTGACGGCATCGCGGCCGGAACCTCTGGGCCCGGCCCCTCCCAGGGCCGCCGCTCCGTGGG
AAAAAACAGCTCCTCCATTTCCTTGAAAACTGAACGATTATTAAAAATAGATTAAACTTCGCTGGAAATGAGTAG
CCAGGAAGTTCAGGGGAGGGTGCCGGGTCCTTCCCGGGCCTGGCGTGTCGGAGCCACCCAGGTCCCGCAGCTGCC
GCTGAGAAAATGCAAATATTTGTTGTGACAAGAATCACATACATTTACTTTAAATATAGTTGCCTTTTTTGGTCA
GCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 27

MVWPWVAMASRWGPLIGLAPCCLWLLGAVLLMDASARPANHSSTRERVANREENEILPPDHLNGVKLEMDGHLNR
GFHQEVFLGKDLGGFDEDAEPRRSRRKLMVIFSKVDVNTDRKISAKEMQRWIMEKTAEHFQEAMEESKTHFRAVD
PDGDGHVSWDEYKVKFLASKGHSEKEVADAIRLNEELKVDEETQEVLENLKDRWYQADSPPADLLLTEEEFLSFL
HPEHSRGMLRFMVKEIVRDLDQDGDKQLSVPEFISLPVGTVENQQGQDIDDNWVKDRKKEFEELIDSNHDGIVTA
EELESYMDPMNEYNALNEAKQMIAVADENQNHHLEPEEVLKYSEFFTGSKLVDYARSVHEEF

FIGURE 28

AAGGGGCCAAAAGGTCCACCTGATGAACCTGTTGCACGCGAAAAGTTCAGAACCACTGCTGCCAAGATGCTGACA
GAAGCCTTGAGAAGCACCTGCTGCGGGAAAAGACGTGCAGGCCTCACAGGTGCAGTGCGGTCTTCAGCGCGCTTG
AAAGCACGAAGTTGTTCGGCAGCCAGGTTGGCCTCTGCCCAGGAAGTTGCTGGTTCCACGTCTGCCAAGACAGCA
TGTCTGACCCGGGCCCTGATCCTAGCACCCGCCCACCCGTGTACTTCCTCATCCCACAAAGCCACAGACACGCGA
ACGTCCAAGAAGTTCAAATGTGACAAAGGACATCTTGTGAAGTCAGAATTACAGAAGCTTGTCCCTAAGAATGAC
AGCGCTTCTTTGCCAAAAGTGACACCTGAGACCCCTTGTGAAAATGAGTTTGCTGAAGGCAGTGCCTTGCTTCCA
GGCAGCGAGGCTGGCGTTTCTGTGCAGCAGGGGGCTGCAAGTCTTCCTCTCGGTGGCTGCAGAGTTGTGAGTGAC
TCTCGCTTAGCAAAGACTAGAGATGGCCTGTCCGTGCCAAAACACAGTGCCGGGTCCGGAGCAGAAGAATCCAAC
AGCAGCTCCACTGTGCAGAAGCAGAATGAGCCAGGGCTACAGACAGAGGATGTGCAGAAGCCACCACTTCAGATG
GACAACAGCGTCTTTCTAGATGACGACAGCAATCAGCCAATGCCCGTGAGCCGGTTCTTTGGAAACGTTGAGCTC
ATGCAGGCCATAGAGAGGTCCGTGTGCAGCTGCCTGACGAGAACTGCATTCCCCAGCCCCAGCGGCGTCAGGGAG
CACCTCACCGTGTGTTCTCGCCCAGGGCAGTGGAGACAAGCCATTGGGAGTGCTCTCTCCATGGCCTCTTCCTGC
CGCCACCTGCACATAGAAGCTGAGTGGACCAACCAGGAGCAAGCTGGGGTCCCCGGGTGA

FIGURE 29

AGAGGCGAGAACGACCCCGGGACCGACCAAAGCCCGCGCGCCGCCGCATCCCGCGTACAGCACCTACATCCCGCC
ACCGTCACCGCCACCACCATGCCCAAGAGAAAGGCTGAAGGGGATGCTAAAGGAGGTAAAGCCAAGGTGAAGGAC
GAACCACAGAGAAGGTCTGCAAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCAAGCCTAAAAAGACC
CCTGCAAAGAAGGCAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCCCAGGAGGAGGGATTCCCTGAC
TTTGACACACATGGCCACCTTGGCACAAAAGCCTTGTGGTGTGGAAAAACAAATTTGTTTTTATGTCCTCTTCTC
CCTTTCCATCTTTCAGCATAGACTTAACTCCTTTAATCCCAGGCATCTGTTGGGACCTGACCCCTAGTCATTGGT
TACCAGTGTGTCAGGCAATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCA
TTTCTAGATTGTGGATCTTCAGATAAATTCTGCCATTTTCATTTCACTTCCTGAAAGTCAGAGTCGGCTTGTGAA
AAGTTGTTAAACAACATGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTCAGAGCATGAGATGA
AGACTTCTTTGGGTTTTATAGCGGCTTTCTGATTTTTCGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTA
TACTGTTAACAATTGTCTGCCCATGTCCTGCCTGAAATACCA

FIGURE 30

MPKRKAEGDAKGGKAKVKDEPQRRSARLSAKPAPPKPEPKPKKTPAKKAEKVPKGKKGKADVDTHGHLGTKALWC
GKTNLFLCPLLPFHLSA

FIGURE 31

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 32

MSILKIHAREIFDSRGNPTVEVDLFTSKGLFRAAVPSGASTGIYEALELRDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLNVTEQEKIDKLMIEMDGTENKSKFGANAILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVPAF
NVINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDQLADLYKSFIKDYPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGVMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEELGSKAKFAGRNFRNPLAK

FIGURE 33

TGGTCCCAAGGCGCGTGCTTTGCAGCAGATGTGTGACCTGGCGTTCCCCTGAGTGCTCGGAAAATGGCCTTGTCT
CCGGTCGTTCCCGTTCAGGAGCAGAATTTTCCCACTGTAAAAAACCGAGCAAGTCTGGATAAGTGAGGCTGGCTC
CATGTATCCAGAATCAACGACGGGCTCCCCGGCTCGGCTCTCGCTGCGGCAGACGGGCTCCCCCGGGATGATCTA
CAGTACTCGGTATGGGAGTCCCAAAAGACAGCTCCAGTTTTACAGGAACCTGGGCAAGTCTGGCCTGCGGGTCTC
CTGCCTGGGACTTGGAACATGGGTGACCTTCGGAGGCCAGATCACCGATGAGATGGCAGAGCAGCTCATGACCTT
GGCCTATGATAATGGCATCAACCTCTTCGATACAGCAGAAGTCTACGCAGCCGGCAAGGCTGAAGTGGTACTGGG
AAACATCATTAAGAAGAAAGGATGGAGGCGGTCCAGCCTCGTCATCACCACCAAGATCTTCTGGGGCGGAAAGGC
GGAGACGGAGCGGGGCCTGTCCAGGAAGCACATAATCGAAGGTCTGAAAGCTTCCCTGGAGCGACTGCAGCTGGA
GTACGTGGATGTGGTGTTTGCCAACCGCCCGGACCCCAACACCCCGATGGAAGAGACCGTCCGCGCCATGACCCA
CGTCATCAACCAGGGGATGGCCATGTACTGGGGCACGTCACGCTGGAGCTCCATGGAGATCATGGAGGCCTACTC
CGTGGCCCGGCAGTTCAACCTGACCCCGCCCATCTGCGAGCAGGCTGAGTACCACATGTTCCAGCGTGAGAAAGT
GGAGGTGCAGCTGCCGGAGCTGTTCCACAAGATAGGAGTGGGCGCCATGACCTGGTCCCCTCTGGCCTGTGGCAT
TGTTTCTGGCAAGTACGACAGTGGCATCCCACCCTACTCAAGAGCCTCCTTGAAGGGCTACCAGTGGCTGAAGGA
CAAGATCCTCAGTGAGGAGGGCCGGCGCCAGCAAGCCAAGCTGAAGGAGCTGCAGGCCATCGCCGAGCGCCTGGG
CTGCACCCTGCCCCAGCTGGCCATAGCCTGGTGCCTGAGGAATGAGGGAGTCAGCTCCGTGCTCCTGGGGGCCTC
CAATGCGGACCAGCTCATGGAGAACATTGGGGCAATACAGGTCCTTCCGAAACTGTCATCTTCCATTATCCACGA
GATTGATAGTATTTTGGGCAATAAACCCTACAGCAAAAAGGACTACAGATCCTAAGCCGCCCCCGCCCGCCTGCT
CGGACAGTTTCCGTTCCCTCCTAGTCTCTGTTCGCTCGCTTAAGCTGTTTTGAAGCCAAGTGAAGAGTGTGGTTT
GCATCCAAGAGAAAACACCACACTGTGATGTCATCGGGAAATGATCTCCCAAGTCGCTGCCAGACACCACCCACT
GCTTCGCCGGACAATGTCGAAGTCCAGTCTGTGCCGGGGAAGGCACTGGTTAGGAAGGATGTTCAAACGGTCCCA
CCCAAGCCTGTCACCTCTGCTCATCCTCCAAGACCACCCAGCTTTCTCCCAGCCACAGCCAAGATTCCCAAAGTC
AAGGCCCAAAGATTTCCAAGGTTCCCAAAGTCAAGGCCAGGCCAAGGCCTGGTTGGGTCCTTGGGGCGGGCAGGG
CCAGCCTCTCCTCTGCTGAGAATCCCCACTTGGTGTAGGGGGAGAGGGGAAAGGGGTCTGGCCCATCGAGGGGCC
CCTTCTGCCAGGGCCTTGGTTGCTGGGGCAGGGCCTCCCCACTGGGGGTCTTCCTCCACCTCCCACTTTCCAAGG
GCTCCAGGAATCTGGGGCCTGACCACAGATTCCTCTCCCATCCTTTTCTGCTCCAACCTGCCCCACTGGGTCCCG
GCAGGGGCCATGCCTACCAAGCTCGAGCTGGCCCTTGACCCCCACCCACCCCCACCCTTGCTGGCAGGGGCAGGG
ACCCCAGGGGGATTGACTCTGCAGTTTGGGAGCCACAAAAAGCGTAGCGGTGTGATTTCTAGCTCAGCCTCCCAC
CGTCTTCCTCCTACACACCAATGATGAGCCTCATGCCAGTGAGGCCCGGAGCGCTTGGGAGGGGTCCCAGTGGGG
CAGGCCCCTCTGTCTGGCCACCCCTCTGTCCTGGCCCCGGAAGGCCCTGTGGTCATGTGCTCCTAGCTGCACGGT
GGCTGCTGGCCACACCACGGCAAGTGGCAGCAGGGGCCGGCCCTGTGCACAAGGATGCACTCCTCTCGGCCCCTG
TAGACTTTCTCTAAAGCCGCCCGCCAGCCCAGGCCGCTGCTCTGCACCGAGCTGGTGGGCTTGGGTTTTGTGGAG
CGCATGCTTGGACCCTTTCAGTAAGGAAGGGTCTTTGGGGTTTTCTGTGCCCATGACTTGGGGGCTGCACCCCCA
CAGCACCCCCACAATGTAGGAAAAGACCTCAGGGAACCTCTCCCTGGAAAGACGGGCAGGGCTGGTTAGCCCCTC
CCACTGCCTGACACCTGGGACAGGCTGGGCAGAGGGGAGAGAGGGCAGGACAGGCCAGAGTGACGCCCCCGTGCA
GCTTGGGCCGGAGGGCAAGGGATGCCAGTAAGTCTGCAGGTGCGGGGTGCCACCTACAGGCCCAGGCCTGTGTCC
CAAGCAGTACCCAGGCTTTGCAGACCACGCGGGGCAGGGCTCCACTGAAGCCACCCCCACCCCTCGCCAGCTAGC
TCCATAGGGAAGCCTGTGTCTCCTGCCCCCAGGGCGCACCCTCAGTGCAGGCACCTCTGTTCCCGCTTTGCCCCT
GGAGGAGCCACTATTCCAGAAGGCTCCACCCTGCCGTCCTGCGGGAGCCTGCTGTCCAGTCCTGGCCGGGCCAAG
GCCTGGGAAACTGTGAAAGTCAGAAAGGCCAGCGGGGAGAGGCTGGGGCGAGGGGAGGAGGGGGATCAGCTTCTG
CTATTACCGACCCCCCTTCATGCTGCCCCTGGCGCCTAGAACCCTTGCCCCTCCTCATAGACCAAGTCCCGGGGGG
TCTCCACTCAGTCCTGCTGCCTGCTTCACCAGAAGCAGCCCTGTGAGTGTGGGGTGGGGAAGTCCCTTCCCAACG
GAGGTCCCAGCCTATGGCCCTGGGCCCAGGTGGGGGTCGCCTGCTTCCTTCCCGGACAGGGTCCTGCAG

FIGURE 34

CCTTTCTAACTCCGCTGCCGCC**ATG**GCTCCTGTGAAAAAGCTTGTGGTGAAGGGGGGCAAAAAAAAGAAGCAAGT
TCTGAAGTTCACTCTTGATTGCACCCACCCTGTAGAAGATGGAATCATGGATGCTGCCAATTTTGAGCAGTTTTT
GCAAGAAAGGATCAAAGTGAACGGAAAAGCTGGGAACCTTGGTGGAGGGGTGGTGACCATCGAAAGGAGCAAGAG
CAAGATCACCGTGACATCCGAGGTGCCTTTCTCCAAAAGGTATTTGAAATATCTCACCAAAAAATATTTGAAGAA
GAATAATCTACGTGACTGGTTGCGCGTAGTTGCTAACAGCAAAGAGAGTTACGAATTACGTTACTTCCAGATTAA
CCAGGACGAAGAAGAGGAGGAAGACGAGGAT**TAA**ATTTCATTTATCTGGAAAATTTTGTATGAGTTCTTGAATAA
AACTTGGGAACCAAAATGGTGGTTTATCCTTGTATCTCTGCAGTGTGGATTGAACAGAAAATTGGAAATCATAGT
CAAAGGGCTTCCCTTGGTTCGCCACTCATTTATTTGTAACTTGACTTCT

FIGURE 35

MAPVKKLVVKGGKKKKQVLKFTLDCTHPVEDGIMDAANFEQFLQERIKVNGKAGNLGGGVVTIERSKSKITVTSE
VPFSKRYLKYLTKKYLKKNNLRDWLRVVANSKESYELRYFQINQDEEEEEDED

FIGURE 36A

CGCGCTCGCGGGGGGCGGTGGCGCCCGGCACAGAGGGGTTAAGGGGGCGGTGCAGACGTCTCCCCGCCCATCCCG
CCCCTCGAGAGCCGCGGCGCCCCGCCCTATTTATAGCAGCGGTGCCTAGCGCGCCGCGTCTCTCCGCAGGCCCCG
GCCGCGGCGTCCTCGACAACCTATCGAAGGCGCC**ATG**GAGCGACCGGCGCCCCTGGCCGTGCTTCCCTTCTCGGA
CCCCGCGCACGCCCTGAGCCTGCTGCGCGGCCTGAGCCAGCTGCGCGCCGAGCGCAAGTTCCTGGACGTGACCCT
GGAGGCGGCGGGCGGGCGCGACTTCCCGGCGCACCGTGCGGTGCTGGCCGCCGCCAGCCCCTACTTCCGCGCCAT
GTTCGCGGGGCAGCTGCGCGAGAGCCGCGCCGAGCGGGTGCGCCTGCACGGAGTGCCTCCCGACATGCTGCAGCT
GCTGCTGGACTTCAGCTACACGGGCCGCGTGGCGGTAAGCGGCGACAACGCTGAGCCGCTGCTGCGCGCCGCCGA
CCTGCTGCAGTTCCCGGCCGTGAAGGAGGCGTGCGGGGCCTTCCTGCAGCAGCAGCTCGACCTGGCCAACTGCCT
GGACATGCAGGACTTCGCTGAGGCCTTCAGCTGCTCGGGACTGGCGAGCGCGGCGCAGCGGTTCATTCTGCGCCA
CGTGGGCGAGCTGGGCGCCGAGCAGCTGGAGCGGCTGCCACTGGCGCGCCTGCTGCGCTACCTGCGGGACGACGG
GCTGTGTGTGCCCAAGGAGGAGGCCGCCTACCAGCTGGCGCTGCGCTGGGTCCGCGCTGACCCGCCGCGCCGCGC
CGCGCACTGGCCGCAGCTGCTGGAGGCCGTGCGCCTGCCCTTCGTGCGCCGCTTCTACCTGTTGGCGCACGTCGA
GGCCGAGCCGCTGGTGGCGCGCTGCCCACCCTGCCTGCGCCTGCTGCGCGAGGCGCGCGACTTCCAGGCGGCGCG
CTACGACCGCCACGACCGCGGGCCCTGTCCCCGAATGCGTCCTCGCCCGTCCACCGGTCTCGCCGAGATCCTCGT
GCTCGTGGGCGGCTGCGACCAGGACTGTGACGAGCTGGTCACTGTCGACTGCTACAACCCGCAGACGGGTCAGTG
GCGCTACCTGGCCGAGTTCCCAGACCACCTGGGCGGAGGCTACAGCATCGTGGCGCTGGGCAATGACATCTACGT
GACGGGTGGGTCCGATGGCTCCCGGCTCTATGACTGCGTGTGGAGGTACAACTCAAGCGTGAATGAGTGGGCGGA
GGTGGCGCCCATGCTGAAGGCCCGCGAGTACCACAGCTCCTCTGTGCTGGACGGACTGCTGTACGTGGTGGCCGC
CGACAGCACCGAGCGCTATGACCACACCACTGACTCCTGGGAGGCCCTGCAGCCCATGACCTACCCCATGGACAA
CTGCTCCACCACTGCGTGCCGTGGCCGGCTCTATGCCATCGGCTCCCTGGCTGGCAAGGAGACCATGGTGATGCA
GTGCTACGACCCGGACACCGACCTGTGGTCGCTGGTGGACTGCGGCCAGCTCCCGCCCTGGTCCTTCGCCCCCAA
GACTGCGACTCTAAACGGACTCATGTACTTTGTCAGGGATGACTCCGCTGAGGTGGACGTGTACAACCCGACGAG
GAACGAATGGGACAAGATCCCGTCCATGAATCAGGTAAATTTTCAGGCGGGCCAGCATTGGAAGCACAGGCTGGT
CCTGATTTTGCAACCCAAGTGTCATCGTGATGAGTGTTTGGGATCCACAGCCATGATGGATGGGTCTCATCTCAA
T**TAA**TAGAAGGCTGCTCTTACCCTTATTTTGCACTTAAGGCTCACTGAGACACAGATGTTAAGTAATACCCTATG
ATTACACAGCTTAGTACACATTTGAGCAGTGTTTATTGAGTATCTGCTGTGAGCCAGAGAGCAGAAGGAAGTGAG
GGAGCAAGGCATACAGTCATCTGGGGACACCTGTTCCAGAGAGGGACAGCAGGTACAGAGGCCCTGCAGCAGGGC
ACCCTGGCGTGTTCTTAGATACACCAGCAGCCCATGTGGCCGGAGCAGAGTCAGCATGAGGTCTGTGACCTACCT
TTTTTATTTTTGAGACAGGGTCTTGCTCTGTCACCCAGGCTGGAGTGCAGTGGTACAATCATGGCTCACTGCAGC
CTCCACCTCCTTGACTCGCAGTCCTCCCACCGCACCTTCCTGAATAGCTGAGACTACAGGCGTGTGCCACCACAC
CCAGTAATTTTTTTTCTCATATGTAGATACAAAAGGATATTCTTAAAATTTTTATAGAGACAGGGTCTTGCTGTG
TTACCCAGGCTGGTCTCACACTCCTGGCCTCAAGTGACCCTCCTGTCTCAGCCTCCCAAAGTGCTAGGATTATAG
GCGTGAACCACCACGCCCAGCTGGTTCCTGAGGAAGTCAGTGTGGGAATACTTTTTTTTTTTTTTATACGGAGTCT
CGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCCATCTCCCAGGTTCACGCCA
TTCTCCGGCCTCAACCTCCCGAGTAGCTGGGACTACAGGTACCCACCACCACGCCCAGCTAATTTTGTTTGTGTA
TTTTTAGTAGAGACGGGATTTCACTGTGTTAGCCAGGATGGTCTGGATCTCCTGACCTTGTGATCTGCCTGGCTC
AGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCCAGCCCACTGTGGGAATACTTGTGTTGAGCAC
TTGCTGTGTGTTCTGAATAGGACAACCAGGGTCCACCCCTTCTCTCTGGGCTTGTTGAGAAGAGGGGTGCCCAGC
CTGACAGTGATGGGACAGGGAGGCTTCAGTGCCATTTGGCCATGTGAGCAGTGTTAGTCTGAGGTACACATCATA
TTGCCTACAGCCTTCTTTCCTGTGTGTCTGTTAACATTTCCAAACCTACACTCCGTGACATCCAGCCTCACAGCT
TACATCACAGCTTAATGTCCTGGCATTTAAGAGACCCAGCGTTCTGTTTTCCCCGCAGTAAGCTGCACATAGTCA
TAGCGAATTTGGGAAAGATGGAAGGAATCATCCAGCCTCGCGGTTCAGAGCCCAGCTCTGCCACTGTCAGCCATG
CAAGCCTCAGTTTTCCCATCTGTAACATGGGGAGAACAGCACTGCTCAGCCCAGAGGGCCACTGCAGAGATTCTG
AGAGAGAACGTAGGAAGCGCTGCTCGGCACGACCTGCACACGGGGAGGCCTGGCGCTGCAGCGGGCACCCTCATC
ACCATAGGGAAGGCCCAGCTGCCTCCGGGGAGGCCCGTTCTCCTAGGCAGGGTGTTGGAAAGGGGTTGGCCTCTC
TGCTGCTTTCTGGGAGAGCCAAGGCCACCCCTCTGGGGTACTGACAGGGCATGCCTTGTCTCCAGTGGTTCCCCA
GGTGGGGCCCTGCCCTACCCTCTCCTCTGACCTCCACTCACTCATCCCTTTGGCCCACAGGTACATGTGGGGGGC
AGCCTGGCCGTCCTTGGGGGGAAGCTGTACGTCTCTGGGGGATACGACAATACATTTGAACTCTCGGACGTGGTA

FIGURE 36B

GAGGCCTATGACCCAGAGACTCGCGCGTGGAGCGTGGTGGGGCGGCTCCCAGAACCCACCTTCTGGCATGGCAGT
GTCAGCATCTTCCGCCAGTTCATGCCCCAGACCTTCTCGGGTGGGCGTGGCTTCGAGTTGGACAGTGGCAGCGAT
GACATGGACCCAGGCCGACCCCGGCCGCCGCGGGACCCCGATGAGCTGCACTAGCCCCAGTCTGGCCCGGCACGG
GCCTCGGTGCAGGTAACTGGCACCTCTGCGGGGCAGTGCCCCACTCCTTTGTGCACAAGGACACGTTGGGCTCAC
AGGAGGAGCACAGGCTCTTGGGTGGCGAAGCCAGCCCAGGATCCATTACCTGGAAGGTTTCTGTACCTTGAGAGC
CTGAATCAGAGGCCGTCGGGAACGCCCTCCCTGCAGTTGAGGAAGAGCCACTTTCCTGCCAGCACATGTTTCTGG
GTCTTGGAGGTCACCCCCACCCCGCGGATCACAGCTCACCCACGCGGCGCACACCCCTCCTGCCGTTGTCATCTG
CACCTACTTGTTCCCACCTTGGGAGAGGACGATGACTTGGGAGGGACGCGTGAAGGGAGAAGGGGTCCTCCCATG
AGGCTGAGGATGGCCTGAACCTGGAGCAGCGGACCAGGCAGACGGGCTGAAGTGGGGTCCCAAATTCCATGTCCA
GAGGTGTGGGGAGCCTGCCTCCCTAGCTCCTGGCCCCTGCCAGGGGCTTACATCAAAACACCTCAGAGGGCTGCC
CTCCAGAGGCTGCACCCAGAACAGTGGGACATGAGCAGGGGTGTGGGCTTGGAGGGTGAAGAGGATGTGGTCCTA
TCAGATGCTGGGCCTCCTCAGCCATAGCCCCCTGCTCCTACCCCCTGACTGGCTCTTGCGTCCTCACCTCTCACC
CTCTCCTTCCCGGGAGGCCCTGGGAGGTGATCATTGACACCCAGCCAAGCAGACAGCTGCGGGTGCCCAAGCCCT
TGCTGGGCCTGCGCGTGAGGAGTCCCACTGCTTCTAAAGGAAGTCCTGGGCAGGAGGTGGCTTTGGTGGTTGGTT
CCAAAGTTGAAAATGCTTGCAGTTTGACCTTAGAAGAAGTGGGAAGAAGAAGGAGCTCTACAGGGTCAGCTTTGT
TTGATTTGTCCAGTCTAAGAAGTCCCATTGCCAAAGCTTTCTGCAGGAGGGTGAATGCCGCAGCTTGGCAGCCCC
TGGGTTTCTCTTGGAAATGGTCAGTTTCCCCTCAAAGTACCCAAAGTAGCCTTGGCTTGAGTTTTTGTCCTTGCC
TCCTTTTTAGAGAAGAGGGCATTTAGACTGCATTTTCCTGGTTAAAGAAGGTTAAAGCAAATGTTTATTGCCTTT
TCTAGTGAACTAACTCGTAGAGATGTTCTCAGCAGGAAGACAGTCTTAGCACTGTCACTTAGCAGATTGCACTTA
AGTCCCTTGTGCTGGCCAGATGGCGTGGCTGGTTGCCTTAATATGTCCCAGGACCCCTGACAGGGCTGCCTGGCC
TCTCCCTCGTGCTCCTCAAGAGCCCAGTCCATACACTGTGGATGTCATTGCTGTCGGGTTAGGAAGTCTTGTCCT
AGAACGCCCTGGCTGGTATGACCACAGTTCATGGCGGCTCTTCTCGCTTGGGTCATGGTCATCTTCCAGCACCTG
CTGTGCTGGGAAGGCCGAGGATGGGGGCCCAGCACTGTCCAGGCCTGCTGGGGCCTGGCTGGGAGTCCTGTGGGC
AGCATGGAACATGCAGCTGGGCTTCCTGTGACCAGGCACCCTCTGGCACTGTTGCTTGCCCTGTGCCCTGGACCT
TTTCCTGCCCTTCTCCTTCCTCTGCTCCCTTGGGGCTACCCCTTGGCCCCTCCTGGTCTGTGCAAACTCCCTCAG
GGAGCCCCCCTGCCCTGTAGCTCTCGCTTAACTTCCTAGGGGCTGCTGAGCCCACCCAGAGGTTGTTGGAGTTCA
GCGGGGCAGCTTGTCTCCCTTGTCAGCAGGGGCGTAAGGGCTGGGTTTGGCCATACAAGGTTGGCTACGCCCTCA
ATCCCTGACCGTTCCAGGCACTGAGCTGGGCACCCACGGAAGGACATGCTGTCCAGACTGTGATGACTGCCAGCA
CAGGGCATCTCGGGCTTGGCTGGTCTGCGAGGCCTTGCCCCTGTGGAACTCTGGGTTCCTGTTTTCTCAGTCTTT
TTTGCGGCTTTGCTGTGGTTGGCAGCTGCCGTACTCCAGGCTTGTGTCGGCCACTCAGATGAGGGCTGTGGTGCG
AGCCAGTGCAGGAGAGCTGCGCTTGGGATTGTGCCCTCTCCTGTGTCTGTCCTCCGGACCTACCCAGGTCTCCAC
CATCAGGACCCTGTCTTTGGGTTTAGAAGACCAAGTATGGGGAAAACCAGGCACCAGCCTCTGCAGCAATGGGTC
CCTCTAGCCTGTGGACACCAGCTGGGGGATCCAGGGTCAGGCCCCCTCCTCTCCCCAGTTTCCCTCTGCTGTGGG
TTCTGGGCTGTCATGTCTCCACCACTTAAGGATGTCTTTACACTGACTTCAGGATAGATGTTGGGATGCCTGGGC
ATGGCCACATGTTACATGTACAGAACTTTGTCTACAGCACAAATTAAGTTATATAAACACAGTGACTGGTATTTA
ATGCTGATCTACTATAAGGTATTCTATATTTATATGACTTCAGAGACGCGTATGTAATAAAGGACGCCCTCCCTC
CAGTGTCCACATCCAGTTCACCCCAGAGGGTCGGGCAGGTTGACATATTTATTTTTGTCTATTCTGTAGGCTTCC
ATGTCCAGAATCCTGCTTAAGGTTTTAGGGTACCTTCAGTACTTTTTGCAATAAAAGTATTTCCTATCCATTTGG

FIGURE 37

MERPAPLAVLPFSDPAHALSLLRGLSQLRAERKFLDVTLEAAGGRDFPAHRAVLAAASPYFRAMFAGQLRESRAE
RVRLHGVPPDMLQLLLDFSYTGRVAVSGDNAEPLLRAADLLQFPAVKEACGAFLQQQLDLANCLDMQDFAEAFSC
SGLASAAQRFILRHVGELGAEQLERLPLARLLRYLRDDGLCVPKEEAAYQLALRWVRADPPRRAAHWPQLLEAVR
LPFVRRFYLLAHVEAEPLVARCPPCLRLLREARDFQAARYDRHDRGPCPRMRPRPSTGLAEILVLVGGCDQDCDE
LVTVDCYNPQTGQWRYLAEFPDHLGGGYSIVALGNDIYVTGGSDGSRLYDCVWRYNSSVNEWAEVAPMLKAREYH
SSSVLDGLLYVVAADSTERYDHTTDSWEALQPMTYPMDNCSTTACRGRLYAIGSLAGKETMVMQCYDPDTDLWSL
VDCGQLPPWSFAPKTATLNGLMYFVRDDSAEVDVYNPTRNEWDKIPSMNQVNFQAGQHWKHRLVLILQPKCHRDE
CLGSTAMMDGSHLN

FIGURE 38A

CCCGCGGCCGAGCCGGCGCGGGCCCCCGCACCTCCCCCGCTCGCGCGGCCTCGAGTCCAGAAGACCCGCCTCCAC
ACACCGGGGCCGCCGCCGCGGAGCCTCATGGGGGTTGGAGTCCCCAAGGTTTCCTTTGTGCGCAGTATTGGCGGG
GCCTTGGACTACCACTCCCACAAGGCACCGCGCCCGCCTCCCGCGCCACGCCCCCTCGCCGCTGGCTTCCAGTCG
CCACCCAGACTACATTTCCCGACAGGCCTCCCGGCTCTCCCGCCCTCCCTCCCGAGACACGAGCCGAACTGGGCG
TCAGGTCGGGGAGCCGGTCGGGTTCCCGCTCACCGCCGCCGCCGCCGCCCCCTGCAGCCACTCTCCCGCCTCTAC
CGCCGCGGGAGCTGCATCGTCCACTCCGGTCGGCGGTGGAACCGCCAGTCCGGGGTCACAGAGCTTGAGAAGCGA
CGCGCTGAGCCCCCCATCACCTCCAGCCCGGGCGACCCCTCCCGGGTCCGCCCTCGCCCTGCGCAGCCGCCCGAG
CCCCCAGCCCCGGGCGGCCCCGCTCCAGCATCCCAGCTCCTGCACTCTCGCAGCCGCCGCCGCCCCCCGCCCGGA
AC**ATG**GACTCTGACTCTTGCGCCGCCGCCTTCCACCCGGAGGAATACTCCCCCAGTTGCAAGAGGCGCAGGACCG
TGGAAGACTTCAACAAATTCTGCACCTTTGTCTTGGCCTATGCTGGCTACATCCCTTATCCGAAGGAGGAACTCC
CTTTAAGGAGCAGCCCCAGCCCTGCTAACAGCACTGCTGGTACCATTGACAGCGACGGCTGGGACGCGGGTTTCT
CAGACATCGCGTCCTCAGTGCCCTTGCCAGTCTCTGACCGCTGCTTTAGCCACCTGCAGCCTACTCTCTTGCAGC
GAGCCAAGCCCAGTAACTTCCTGCTGGACAGAAAGAAAACGGACAAGCTGAAGAAGAAGAAGAAGAGGAAGCGCA
GGGACAGTGATGCGCCTGGGAAAGAGGGGTACAGGGGGGGCTTGCTGAAGCTGGAAGCCGCTGACCCCTACGTGG
AGACCCCCACGAGTCCCACCTTGCAGGATATCCCCCAGGCTCCCAGCGACCCCTGCTCGGGCTGGGACTCCGATA
CTCCCTCGAGTGGATCTTGTGCCACTGTGTCACCTGATCAGGTCAAAGAAATAAAAACTGAAGGCAAACGGACTA
TCGTCCGGCAGGGAAAGCAGGTGGTGTTCCGAGATGAGGACAGCACTGGCAATGATGAGGACATCATGGTGGACT
CAGATGACGATTCCTGGGACCTCGTGACCTGCTTCTGCATGAAGCCATTTGCCGGCCGCCCCATGATCGAGTGTA
ATGAGTGCCACACCTGGATTCACCTGTCCTGTGCGAAAATCCGGAAATCCAATGTTCCAGAAGTGTTTGTCTGCC
AAAAGTGCCGGGACTCCAAGTTTGACATCCGCCGTTCCAACCGCTCGCGGACGGGCTCCCGGAAGCTGTTCCTGG
AC**TGA**CTGCTGGCTGGCGAGGAGGCTGCGAGCGTGGAATCGGAAGCGACCGCGGGCTTTTTTGCCCTTCTCTTAG
TTGAGCACAGAACCCTCAGCTCTGGTGCGGGCAGATCCCTGCCATTTAGGTGCCTAAGCAAAAGGACAGGCTGTC
CAAGGTAGAAACTGTACATAGCCGGTGACCGAATGCGACCTTTGCCAGCCAGAGCTGCTGCCAGAGCTGCGTTCC
CTGCAGTGGAGGTGGACTGGACACCCACGTGCAGCGGGTTTGGCTCATTTGAAAATGAGGGTCCGTGGTAGCTGT
GCGTTTTGCTATCATTGCTAAGAGATTCCCGCTGATTGGGCTCAGTGCCAGCTGTTATTCTGCTTCCACTGTGTT
GGGGAGAGGTGTTCGGTTTCCCCAGCCTGTTAATGAACAGCCATACGTGTAAGCTTTTTCTTGAGTGTTAAGTCT
TTTACCAAAAGTGTCTGTACAGCAGCCATCCAAGTTGCCCCTACTTAGTGGCTTGCCCTCTGCCTGCCTCAGCTG
CTGCCTGACCGGCTGGGGGAGGCACTGGCGGGAGGCCTCGGGCTCCCCTGGAAGGGCGCTGGGCTGGCGGGTCAG
CTGGTGGTTCTTAGGTTTCCTTCTGTTTGTTAAAAGGGACAATGTGGCCACTTCTCTGTGGAAAGGGAGTTGGTT
GGGGGGTTGAGATGGCCCGTGTTCATAACTCAGTTTCCTGTTTTGCACGATGTAAAAACCCTGTCTTTTTGCACG
ATACAGCCAAAAGTATTGGCTGATTTCTTGCTGAGTGCCCTCTTAGTTGGTGTGTGAGGTCTTGGTGGGCTCAGG
CCAGCTGTTTGCGAGTGTGGGAACTCATAGGTTCTGTCTTTGTCTCTTCCTTTCACCTCATTCTGGTAGCAGCAT
AAAGGTTAGGCAATCACTGGGACCCGCATGGTGTTCCTCCAAAGAATAGGGTAAAGGAGAGCTGGGAGGGAGCCC
TCTCCGTTGGGTGACTCTTGTGTGCCCTTTAGACAGGCTGGCCTGCCGGTTCCACAGGGTACAGTTAGGACTTGA
GTCTTTCTTTTTCTGTTTTGAGTTGGTGAGTGAGTGATAGGGTAACATGGGCCTTCAGGATGACCCCTTGGAACT
GTGCCGAGTTCCTTAAATCTCAGCTGGGATCCTGGACCTGGGAGGCCCCTGTGAGGGCCAGCTCTGGAAAAACCT
GGGAGTTGATGCCGGAGGCTGTGGAAGAACTCTGCTCGAGGGCAGGGTGCCCTGGAACACTGGTAGTTCTGGGGC
TGGGAGGGAGAGGGGCTCCGGCTTTCTCTGAAATGAACACTGCTCTTCAGCAGTTCAAGTACTTGTTCTCAAAAC
ATTTTCTAATTGATTGGTAGGTTTTCATAAGCATTGTTTCTTTAAGGCATGGAAAGGGAAGAATGCTCAAGCAAG
TCATGTTTGTTTTCAGTGGGATGGGCCCGCGTTCTCACTGCTGGGGGCTTCCCCTTCATGTGGCACCTTTGTGCC
AGGCCACCAGGCAGACTCTTCCCACCTTCTCCCACTGAAGCACCAAGGGGCTTGAACCGTAATTTGGCTAATCAG
AGGCATTTTTTTTGTCCTAGTATCTTTCACACTTGTCCAACCGTCTTATTTTTTTAAAAGTTCTGTTGCTTGTAT
TAACACGAAACTAGAGAGAAATAGTTTCTGAAGCCAGTTTATTGTGAAGATCCCCAAGGGGGAGGTTCGGTAGAG
AAAAATAGTAAGCTGGTTTAGAAACTGACGAGGGCAAACAGCCAGGACGCATTGGAGAGGAATTTGCCAAAGATC
TACCCTGAGATAACGCCTGTCCAGTGTCTTCACCACGTGAATAACCAGCGCTCCAAAGTGTTTTTCTGCTTTGAA
AAAAAAAAATTCCACAAGCTTTTAAAGGTGCATTTAAGAATCCATGTGACTTTAGAATGGAACTGCCGGCCCTGG
CAACTGTCACGTGTGCTAGAAGGTTCGATGCCTCTGGAATGCATGTGATACTCATCTCCATTTTGTTTCCTTGAT
TGCATTTTTGTTCTTTTAGCAGATCTGTCCCTGTGGGTGGTGTCTAAGAAGTCGGACACCTTGGTTTTTGTGTTA

FIGURE 38B

GATTGAGCTGGGCAGCTGCAATCAGCTTCTTTATATGCAAATTAGGCACGACCCATCTGTGGTTCCTGGTTGGTG
GCTAATGAAGTGAGGGGAGGGAGGGATGTCACCCCAAAAGTAGGCCCTCCCATTGGCTTTGGCCAGGCCAGACAC
TTCACATCGTTTACATGGTTCTGTGTAATTTTAAAGTTTATGTGTATAAAGCGAAGCTGTTTCTGTGAAACTGTA
TATTTTGTAAATAAATATATTGCTACTTTGAGGTTCATGATTCAAGGTTCAGGCGATTGCGTTCTGTGCTGAAGG
A

FIGURE 39

MDSDSCAAAFHPEEYSPSCKRRRTVEDFNKFCTFVLAYAGYIPYPKEELPLRSSPSPANSTAGTIDSDGWDAGFS
DIASSVPLPVSDRCFSHLQPTLLQRAKPSNFLLDRKKTDKLKKKKKRKRRDSDAPGKEGYRGGLLKLEAADPYVE
TPTSPTLQDIPQAPSDPCSGWDSDTPSSGSCATVSPDQVKEIKTEGKRTIVRQGKQVVFRDEDSTGNDEDIMVDS
DDDSWDLVTCFCMKPFAGRPMIECNECHTWIHLSCAKIRKSNVPEVFVCQKCRDSKFDIRRSNRSRTGSRKLFLD

FIGURE 40

GACGGCTCCGGGCCGCCAGGGGCCGCTGTGGCGCAGCCGGGCTGGCCCGCGCTGTCCCTGACGCGGATCACTGGC
CCCTCTTGAGCACGGCCTTGCCGGTTTGGCGGGGTGAAAGGTTGCGAAGATGGCGACGGCCTTGAGCGAGGAGGA
GCTGGACAATGAAGACTATTACTCGTTGCTGAACGTGCGCAGGGAGGCCTCTTCTGAAGAGCTGAAAGCTGCCTA
CCGGAGGCTCTGTATGCTCTACCATCCAGACAAGCACAGAGACCCAGAGCTCAAGTCACAGGCGGAACGACTGTT
TAACCTTGTTCACCAGGCTTATGAAGTGCTTAGTGACCCCCAAACCAGGGCCATCTATGATATATATGGGAAGAG
AGGACTGGAAATGGAAGGATGGGAGGTTGTGGAAAGGAGGAGAACCCCTGCTGAAATTCGAGAGGAGTTTGAGCG
GCTGCAGAGAGAGAGAAGAGAGGAGATTGCAGCAGCGAACCAATCCCAAGGGAACGATCAGCGTTGGAGTAGA
TGCCACCGACCTTTTTGATCGCTATGATGAGGAGTATGAAGATGTGTCCGGCAGTAGCTTTCCGCAGATTGAAAT
TAATAAAATGCACATATCCCAGTCCATTGAGGCACCCTTGACAGCGACAGACACAGCCATCCTCTCTGGAAGCCT
CTCAACCCAGAATGGAAATGGAGGAGGTTCCATTAACTTTGCGCTCAGACGAGTAACTTCGGCAAAGGGATGGGG
AGAGTTGGAATTTGGAGCTGGAGACCTACAGGGGCCTTTGTTCGGTCTCAAGCTGTTCCGTAATCTCACACCAAG
ATGCTTTGTGACAACAAACTGTGCTCTGCAGTTTTCATCCCGTGGAATCCGACCCGGCCTGACCACTGTCCTAGC
TCGGAACCTAGACAAGAACACCGTGGGCTACCTGCAGTGGCGATGGGGTATCCAGTCAGCCATGAACACTAGCAT
CGTCCGAGACACTAAAACCAGCCACTTCACTGTGGCCCTGCAGCTGGGAATCCCTCACTCCTTTGCACTGATCAG
CTATCAGCACAAATTCCAAGATGACGATCAGACTCGTGTGAAAGGATCCCTCAAAGCAGGCTTCTTTGGGACGGT
GGTGGAGTACGGAGCTGAGAGGAAGATCTCCAGGCACAGCGTTTTGGGTGCAGCTGTCAGCGTTGGAGTTCCACA
GGGTGTTTCTCTCAAAGTCAAGCTCAACAGGGCCAGTCAGACATACTTCTTCCCTATTCACTTGACGGACCAGCT
TCTGCCCAGCGCCATGTTCTATGCCACCGTGGGGCCTCTAGTGGTCTACTTTGCCATGCACCGTCTGATCATCAA
ACCATACCTCAGGGCTCAGAAAGAGAAGGAATTGGAGAAGCAGAGGGAAAGCGCCGCCACCGATGTGCTGCAGAA
GAAGCAAGAGGCGGAGTCCGCTGTCCGGCTGATGCAGGAATCTGTCCGAAGGATAATTGAGGCAGAAGAGTCCAG
AATGGGCCTCATCATCGTCAATGCCTGGTACGGGAAGTTTGTCAATGACAAGAGCAGGAAGAGCGAGAAGGTGAA
GGTGATTGACGTGACTGTGCCCCTGCAGTGCCTGGTGAAGGACTCGAAGCTCATCCTCACGGAGGCCTCCAAGGC
TGGGCTGCCTGGCTTTTATGACCCGTGTGTGGGGGAAGAGAAGAACCTGAAAGTGCTCTATCAGTTCCGGGGCGT
CCTGCATCAGGTGATGGTGCTGGACAGTGAGGCCCTCCGGATACCAAAGCAGTCCCACAGGATCGATACAGATGG
ATAAACTGCCAAGAACCAGATTTTTAAAAGGCCGCAAAAAATCTTTTCCTGGGAGTCTACAAATTTGGAAATGAA
AAAACCCAGACATCAGATGTTTTTATTTTATATTATTATTATAGAAGGTGGTACCATTATCAATTATGTGAAGGG
ACATGCAGACACCCCAGCTTTTGAGGGTGCTGGGGGGTAGGACTGAGGCAGCCCCACTGGGAACCAGACTGCAGCC
TGGCCCATGGCTGTTTTCCCAAGGATCAGTTCCTGGAGGGAAGGGCTCTGGCCCTGACTCCGCTGTGTCCCGAGC
ACACGTGCTGACCGCAGCCCGCCGCCCTGTAGTTCTTGGCTGGGTCTGGAGGTGTCTGTGGAGCACCCTGCCCTC
ACCACAGGAGCGTGAGCCACTTCTGCAGTCCACGCTGAACATGGGAAACAACCTGAAAAGCAGGCAGGCCTCCCG
GTCAGGGAGCCTCTGCTGTGCTGGCTTCCCATGACCACCTCCTCTTGCTGAAATATTACTGCTTGAATCTGGAGC
AGATTGCGGGTTTATAAAACTGCTTTTTATCTGAGAACAAACGGGTTTGGAAATTAGTCGTCTTTTTTCCCCACT
CCCAGAGCTGCTCAAGTCATTCCACCGGCCCCCTCGGCTTGGGACAGGGTAGTGTAACTCCCGATCCCAGGGCCT
AGCCCTGACACAGGTGGCTTCCCGTATCCCGGTGGGAAAACGCCCTGCCACCAGCGGGCTTGAGCTGGCCTGTGT
CCCTCCACCGCCTGCACCACCCACCTCCAGAGTGCAGTGCTGGGCAAGGGCAGCTCAAGAGGACAGGACCAGGCG
CTTGGCAAGACATCAGACACACCCAACCCAAAGGCGTGGACCCCAGGCCCGGCCCGTGGTACCCAGCAGGTGGCA
CTGCAGCTCCCCGCTCCTGCAGGTCCAGCGTCCTCACAGGAACACCAGGGCCTGTGCTCCGGAGCCTTCCTTCAG
ACCCTTCCTCCACGTGCCCACTTGGGATGCAGAATGCAGCGGAGCTAGGACCCCCTCCACGGCCTGGACCTCGGC
TGCAGTAAAGTTACGTGAGGCCTGTCTCTCGGGGCCTGGAAGTGGCAGCCATCAGTTGCTCTTGCTGACCCCTCG
GAGCAAGCGCCGCACAGGTGGTGGCTGAGACAGCTGGCGCGGGGGGGCCCCAAGCTGCGCCGGCCTCCAGCCCACC
CACAGCTGTTGCTGAAGTCAGGCCTCCCTCCCCAGCACTGGTATCTGAGTAACGGCTAAGAACCTCCTTCCTCTG
GTTTTGAAAAGCAGTTCGGGTTGTCCAATTCTGTAACATTCATCTCCATTTTTTAAAAAGGTTTCTCTGACGGCC
CCACGGCCCGAGCCGCGGTGAGCGTCGTGTTGCATGAGCCTGGGCCCCGGGCTTCCCGTGCGCCTCTGCCGCAGG
TGCTTCTGGGCACCCATCCTCTGCGTTTCATTTGCAGTCGACTGTACAGAAGGCACTCACCACAATAAACCTTTC
CTGAAAGC

FIGURE 41

TGCGAGGCAGAGTGCTAGCGGGAGCGCGAGCCAGCAAGAGGCGCCTGCGCGATGTCCGGGCCCCTGAGCCCGCGG
CGCTGAGCCAGCCGGGACGGACATGCGCGGGAGGGCGCCGCGGGGCAGCCGCCGCTCCTCCGGGGGAATGAAAGC
TACTGGTTGATTTTAAAGTGCCTGGGCCTCACAGGTTTGGAGATGTCCCAGAATAAGGCACAATGTCAATAGCAG
GAGTTGCTGCTCAGGAGATCAGAGTCCCATTAAAAACTGGATTTCTACATAATGGCCGAGCCATGGGGAATATGA
GGAAGACCTACTGGAGCAGTCGCAGTGAGTTTAAAAACAACTTTTTAAATATTGACCCGATAACCATGGCCTACA
GTCTGAACTCTTCTGCTCAGGAGCGCCTAATACCACTTGGGCATGCTTCCAAATCTGCTCCGATGAATGGCCACT
GCTTTGCAGAAAATGGTCCATCTCAAAAGTCCAGCTTGCCCCCTCTTCTTATTCCCCCAAGTGAAAACTTGGGAC
CACATGAAGAGGATCAAGTTGTATGTGGTTTTAAGAAACTCACAGTGAATGGGGTTTGTGCTTCCACCCCTCCAC
TGACACCCATAAAAAACTCCCCTTCCCTTTTCCCCTGTGCCCCTCTTTGTGAACGGGGTTCTAGGCCTCTTCCAC
CGTTGCCAATCTCTGAAGCCCTCTCTCTGGATGACACAGACTGTGAGGTGGAATTCCTAACTAGCTCAGATACAG
ACTTCCTTTTAGAAGACTCTACACTTTCTGATTTCAAATATGATGTTCCTGGCAGGCGAAGCTTCCGTGGGTGTG
GACAAATCAACTATGCATATTTTGATACCCCAGCTGTTTCTGCAGCAGATCTCAGCTATGTGTCTGACCAAAATG
GAGGTGTCCCAGATCCAAATCCTCCTCCACCTCAGACCCACCGAAGATTAAGAAGGTCTCATTCGGGACCAGCTG
GCTCCTTTAACAAGCCAGCCATAAGGATATCCAACTGTTGTATACACAGAGCTTCTCCTAACTCCGATGAAGACA
AACCTGAGGTTCCCCCCAGAGTTCCCATACCTCCTAGACCAGTAAAGCCAGATTATAGAAGATGGTCAGCAGAAG
TTACTTCGAGCACCTATAGTGATGAAGACAGGCCTCCCAAAGTACCGCCAAGAGAACCTTTGTCACCGAGTAACT
CGCGCACACCGAGTCCCAAAAGCCTTCCGTCTTACCTCAATGGGGTCATGCCCCCGACACAGAGCTTTGCCCCTG
ATCCCAAGTATGTCAGCAGCAAAGCACTGCAAAGACAGAACAGCGAAGGATCTGCCAGTAAGGTTCCTTGCATTC
TGCCCATTATTGAAAATGGGAAGAAGGTTAGTTCAACACATTATTACCTACTACCTGAACGACCACCATACCTGG
ACAAATATGAAAAATTTTTTAGGGAAGCAGAAGAAACAAATGGAGGCGCCCAAATCCAGCCATTACCTGCTGACT
GCGGTATATCTTCAGCCACAGAAAAGCCAGACTCAAAAACAAAAATGGATCTGGGTGGCCACGTGAAGCGTAAAC
ATTTATCCTATGTGGTTTCTCCTTAGACCTTGGGGTCATGGTTCAGCAGAGGTTACATAGGAGCAAATGGTTCTC
AATTTTCCAGTTTGATTGAAGTGCAGAGAAAAATCCCTTAGATTGCAAAATAAAATAGTTGAACTCTCTGTCTTC
ATGTGGAAGGTTTAGAGCAGTTGTGAGATGCTGTTATGCTGAGAAACCCTGACTTTGTTAGTGTTGGAAAAAAGT
CTTACAAGTCTATAATTTAAAGATGTGATGGTGGGGAGGGGAGGATGGGGAAGCTTTTTATATATGCATACATTA
CATACCTATATATAAACTTGTGGTATAACCATAGACCATAGCTGCAGGTTAACCAATTAGTTACTATCGTAGAGT
AATATATATTCAGAATAATAAACTCAAGCTGGAGAAATGAGTCCTGATAGACTGAAAATTGAGCAAATGGAAGAA
GATACAGTATTGTTTAGATCAGAATCATTAAAAAATATTTTTGTTTAGTAAGTTTGAAGATTTCTGGCTTTTAGG
CCTTTTCTATTTTGTTCCATTTATTTTTGCAGGCAATCTTTTCCATGGAGGGCAGGGTATCCATTCTTTACCATG
GGTGTACCTGCTTAGGTTAAAAATCATACCAAGGCCTCATACTTCCAGGTTTCATGTTGCGTCTTGTTGAGGGAG
GGAGAGCAGGTTACTTGGCAACCATATTGTCACCTGTACCTGTCACACATCTTGAAAAATAAAACGATAATAGAA
CTAGTGACTAATTTTCCCTTACAGTTCCTGCTTGGTCCCACCCACTGAAGTAGCTCATCGTAGTGCGGGCCGTAT
TAGAAGCAGTGGGGTACGTTAGACTCAGATGGAAAAGTATTCTAGGTGCCAGTGTTAGGATGTCAGTTTTACAAA
ATAATGAAGCAATTAGCTATGTGATTGAGAGTTATTGTTTGGGGATGTGTGTTGTGGTTTTGCTTTTTTTTTTTT
AGACTGTATTAATAAACATACAACACAAGCTGGCCTTGTGTTGCTGGTTCCTATTCAGTATTTCCTGGGGATTGT
TTGCTTTTTAAGTAAAACACTTCTGACCCATAGCTCAGTATGTCTGAATTCCAGAGGTCACATCAGCATCTTTCT
GCTTTGAAAACTCTCACAGCTGTGGCTGCTTCACTTAGATGCAGTGAGACACATAGTTGGTGTTCCGATTTTCAC
ATCCTTCCATGTATTTATCTTGAAGAGATAAGCACAGAAGAGAAGGTGCTCACTAACAGAGGTACATTACTGCAA
TGTTCTCTTAACAGTTAAACAAGCTGTTTACAGTTTAAACTGCTGAATATTATTTGAGCTATTTAAAGCTTATTA
TATTTTAGTATGAACTAAATGAAGGTTAAAACATGCTTAAGAAAAATGCACTGATTTCTGCATTATGTGTACAGT
ATTGGACAAAGGATTTTATTCATTTTGTTGCATTATTTTGAATATTGTCTTTTCATTTTAATAAAGTTATAATAC
TTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 42

GAATTCGGCACGAGATAAAA**ATG**GCTTCCAAAAGAGCTCTGGTCATCCTGGCTAAAGGAGCAGAGGAAATGGAGA
CGGTCATCCCTGTAGATGTCATGAGGCGAGCTGGGATTAAGGTCACCGTTGCAGGCCTGGCTGGAAAAGACCCAG
TACAGTGTAGCCGTGATGTGGTCATTTGTCCTGATGCCAGCCTTGAAGATGCAAAAAAAGAGGGACCATATGATG
TGGTGGTTCTACCAGGAGGTAATCTGGGCGCACAGAATTTATCTGAGTCTGCTGCTGTGAAGGAGATACTGAAGG
AGCAGGAAAACCGGAAGGGCCTGATAGCCGCCATCTGTGCAGGTCCTACTGCTCTGTTGGCTCATGAAATAGGTT
GTGGAAGTAAAGTTACAACACACCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCTACTCTGAGA
ATCGTGTGGAAAAAGACGGCCTGATTCTTACAAGCCGGGGGCCTGGGACCAGCTTCGAGTTTGCGCTTGCAATTG
TTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTCCACTTGTTCTTAAAGAC**TAG**AGCAGCGAAC
TGCGACGATCACTTAGAGAAACAGGCCGTTAGGAATCCATTCTCACTGTGTTCGCTCTAAACAAAACAGTGGTAG
GTTAATGTGTTCAGAAGTCGCTGTCCTTACTACTTTTGCGGAAGTATGGAAGTCACAACTACACAGAGATTTCTC
AGCCTACAAATTGTGTCTATACATTTCTAAGCCTTGTTTGCAGAATAAACAGGGCATTTAGCAAACTAAAAAAAA
AAAAAAAAAAACTCGAG

FIGURE 43

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLEDAKKEGPYDVVVLPGG
NLGAQNLSESAAVKEILKEQENRKGLIAAICAGPTALLAHEIGCGSKVTTHPLAKDKMMNGGHYTYSENRVEKDG
LILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD

FIGURE 44

CTCTAAAGCGCCGCAGCTGCCAAA**ATG**TCTACAGGTCCAACTGCTGCCACTGGCAGTAATCGAAGACTTCAGCAG
ACACAAAATCAAGTAGATGAGGTGGTGGACATAATGCGAGTTAACGTGGACAAGGTTCTGGAAAGAGACCAGAAG
CTCTCTGAGTTAGACGACCGTGCAGACGCACTGCAGGCAGGCGCTTCTCAATTTGAAACGAGCGCAGCCAAGTTG
AAGAGGAAATATTGGTGGAAGAATTGCAAGATGTGGGCAATCGGGATTACTGTTCTGGTTATCTTCATCATCATC
ATCATCGTGTGGGTTGTCTCTTCA**TGA**AGAACCAGCGGAACTCAAAACTGCTGTTCAAGAAACCTCTTCAAGACT
TTTGACTTAGAACCTGCTATATTATCAAGCTTACCTACTGTTATCTCTAAAATTTTTTTTGTGTTAATGTAAAGT
TGAATTTCTAGGAAACGTGCCTTTGTTTTTTAATATGCACTCCAAATTAGAAGGCCGGCCCCGTCCACATTTTGC
ACAGTGCCTTTACAGATTTACGTATGGGCTGATGAAGAGGCCTTCTTAAGTTCCAGAGTGCTATAATCTAGATGT
AATGTTGTCACTAATTAATTGCCATTACTCCCCTTTAG

FIGURE 45

MSTGPTAATGSNRRLQQTQNQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
CKMWAIGITVLVIFIIIIVWVVSS

FIGURE 46

GCTGCGGGTCTTTCCCTCACTCGTCCTCCGCGCGTCGCCGCTCTTCGGTTCTGCTCTGTCCGCCGCCATGGCCCA
AGCTGACATCGCGCTGATCGGATTGGCCGTCATGGGCCAGAACTTAATTCTGAACATGAATGACCACGGCTTTGT
GGTCTGTGCTTTTAATAGGACTGTCTCCAAAGTTGATGATTTCTTGGCCAATGAGGCAAAGGGAACCAAAGTGGT
GGGTGCCCAGTCCCTGAAAGAGATGGTCTCCAAGCTGAAGAAGCCCCGGCGGATCATCCTCCTGGTGAAGGCTGG
GCAAGCTGTGGATGATTTCATCGAGAAATTGGTACCATTGTTGGATACTGGTGACATCATCATTGACGGAGGAAA
TTCTGAATATAGGGACACCACAAGACGGTGCCGAGACCTCAAGGCCAAGGGAATTTTATTTGTGGGGAGCGGAGT
CAGTGGTGGAGAGGAAGGGGCCCGGTATGGCCCATCGCTCATGCCAGGAGGGAACAAAGAAGCGTGGCCCCACAT
CAAGACCATCTTCCAAGGCATTGCTGCAAAAGTGGGAACTGGAGAACCCTGCTGTGACTGGGTGGGAGATGAGGG
AGCAGGCCACTTCGTGAAGATGGTGCACAACGGGATAGAGTATGGGGACATGCAGCTGATCTGTGAGGCATACCA
CCTGATGAAAGACGTGCTGGGCATGGCGCAGGACGAGATGGCCCAGGCCTTTGAGGATTGGAATAAGACAGAGCT
AGACTCATTCCTGATTGAAATCACAGCCAATATTCTCAAGTTCCAAGACACCGATGGCAAACACCTGCTGCCAAA
GATCAGGGACAGCGCGGGGCAGAAGGGCACAGGGAAGTGGACCGCCATCTCCGCCCTGGAATACGGCGTACCCGT
CACCCTCATTGGAGAAGCTGTCTTTGCTCGGTGCTTATCATCTCTGAAGGATGAGAGAATTCAAGCTAGCAAAAA
GCTGAAGGGTCCCCAGAAGTTCCAGTTTGATGGTGATAAGAAATCATTCCTGGAGGACATTCGGAAGGCACTCTA
CGCTTCCAAGATCATCTCTTACGCTCAAGGCTTTATGCTGCTAAGGCAGGCAGCCACCGAGTTTGGCTGGACTCT
CAATTATGGTGGCATCGCCCTGATGTGGAGAGGGGGCTGCATCATTAGAAGTGTATTCCTAGGAAAGATAAAGGA
TGCATTTGATCGAAACCCGGAACTTCAGAACCTCCTACTGGACGACTTCTTTAAGTCAGCTGTTGAAAACTGCCA
GGACTCCTGGCGGCGGGCAGTCAGCACTGGGGTCCAGGCTGGCATTCCCATGCCCTGTTTTACCACTGCCCTCTC
CTTCTATGACGGGTACAGACATGAGATGCTTCCAGCCAGCCTCATCCAGGCTCAGCGGGATTACTTCGGGGCTCA
CACCTATGAACTCTTGGCCAAACCAGGGCAGTTTATCCACACCAACTGGACAGGCCATGGTGGCACCGTGTCATC
CTCGTCATACAATGCCTGATCATGCTGCTCCTGTCACCCTCCACGATTCCACAGACCAGGACATTCCATGTGCCT
CATGGCACTGCCACCTGGCCCTTTGCCCTATTTTCTGTTCAGTTTTTTAAAAGTGTTGTAAGAGACTCCTGAGGA
AGACACACAGTTTATTTGTAAAGTAGCTCTGTGAGAGCCACCATGCCCTCTGCCCTTGCCTCTTGGGACTGACCA
GGAGCTGCTCATGTGCGTGAGAGTGGGAACCATCTCCTTGCGGCAGTGGCTTCCGCGTGCCCCGTGTGCTGGTGC
GGTTCCCATCACGCAGACAGGAAGGGTGTTTGCGCACTCTGATCAACTGGAACCTCTGTATCATGCGGCTGAATT
CCCTTTTTCCTTTACTCAATAAAAGCTACATCAGACTG

FIGURE 47

MAQADIALIGLAVMGQNLILNMNDHGFVVCAFNRTVSKVDDFLANEAKGTKVVGAQSLKEMVSKLKKPRRIILLV
KAGQAVDDFIEKLVPLLDTGDIIIDGGNSEYRDTTRRCRDLKAKGILFVGSGVSGGEEGARYGPSLMPGGNKEAW
PHIKTIFQGIAAKVGTGEPCCDWVGDEGAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGMAQDEMAQAFEDWNK
TELDSFLIEITANILKFQDTDGKHLLPKIRDSAGQKGTGKWTAISALEYGVPVTLIGEAVFARCLSSLKDERIQA
SKKLKGPQKFQFDGDKKSFLEDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGK
IKDAFDRNPELQNLLLDDFFKSAVENCQDSWRRAVSTGVQAGIPMPCFTTALSFYDGYRHEMLPASLIQAQRDYF
GAHTYELLAKPGQFIHTNWTGHGGTVSSSSYNA

FIGURE 48

CGCCGCTCCGGCCTCCCGCGACTTCTCGAAGGTGGGCAGGTCCCACCTTGTGGAGG**ATG**GAGGTGACCGGGGACG
CCGGGGTACCAGAATCTGGCGAGATCCGGACTCTAAAGCCGTGTCTGCTGCGCCGCAACTACAGCCGCGAACAGC
ACGGCGTGGCCGCCTCCTGCCTCGAAGACCTGAGGAGCAAGGCCTGTGACATTCTGGCCATTGATAAGTCCCTGA
CACCAGTCACCCTTGTCCTGGCAGAGGATGGCACCATAGTGGATGATGACGATTACTTTCTGTGTCTACCTTCCA
ATACTAAGTTTGTGGCATTGGCTAGTAATGAGAAATGGGCATACAACAATTCAGATGGAGGTACAGCTTGGATTT
CCCAAGAGTCCTTTGATGTAGATGAAACAGACAGCGGGGCAGGGTTGAAGTGGAAGAATGTGGCCAGGCAGCTGA
AAGAAGATCTGTCCAGCATCATCCTCCTATCAGAGGAGGACCTCCAGATGCTTGTTGACGCTCCCTGCTCAGACC
TGGCTCAGGAACTACGTCAGAGTTGTGCCACCGTCCAGCGGCTGCAGCACACACTCCAACAGGTGCTTGACCAAA
GAGAGGAAGTGCGTCAGTCCAAGCAGCTCCTGCAGCTGTACCTCCAGGCTTTGGAGAAAGAGGGCAGCCTCTTGT
CAAAGCAGGAAGAGTCCAAAGCTGCCTTTGGTGAGGAGGTGGATGCAGTAGACACGGGTATCAGCAGAGAGACCT
CCTCGGACGTTGCGCTGGCGAGCCACATCCTTACTGCACTGAGGGAGAAGCAGGCTCCAGAGCTGAGCTTATCTA
GTCAGGATTTGGAGTTGGTTACCAAGGAAGACCCCAAAGCACTGGCTGTTGCCTTGAACTGGGACATAAAGAAGA
CGGAGACTGTTCAGGAGGCCTGTGAGCGGGAGCTCGCCCTGCGCCTGCAGCAGACGCAGAGCTTGCATTCTCTCC
GGAGCATCTCAGCAAGCAAGGCCTCACCACCTGGTGACCTGCAGAATCCTAAGCGAGCCAGACAGGATCCCACA**T**
AGCAGCAGCGGGAAGTGTGCCAAGGAAGCTCTGTGGCGTTGTGTTATTGGTAGACACCCTCAGCCTCATCATTTG
ACTACCTATGTACTACTCTACCCCCTGCCTTAGAGCACCTTCCAGAGAAGCTATTCCAGGTCTCAACATACGCCG
TTCCACCAATTTTTTTTTAGCCCCACCAGCTTCAGGACTTCTGCCAATTTTGAATGATATAGCTGCACCAACAA
TATCCCGCCTCCTCTAATTACATATGATGTTCTCTGTTCAAAAGTAATTGGCAGTGATTGGCCAGGCGCAGTGGC
TCACGCCTGTAATCCCAGCACTGGGAGGCCGAGGGGGGCGGATCGTGAAGTCAGGAGATCGAGACCATCCTGGCT
AACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAAAAATTAGCCAGCCATGGTGGCGGGCGCCTGTAATCCC
AGCTACTTGGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCAGAGCTTGCAGTGAGCTGAGATTGCGCC
ACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAA

FIGURE 49

MEVTGDAGVPESGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIDKSLTPVTLVLAEDGTIVDDDDY
FLCLPSNTKFVALASNEKWAYNNSDGGTAWISQESFDVDETDSGAGLKWKNVARQLKEDLSSIILLSEEDLQMLV
DAPCSDLAQELRQSCATVQRLQHTLQQVLDQREEVRQSKQLLQLYLQALEKEGSLLSKQEESKAAFGEEVDAVDT
GISRETSSDVALASHILTALREKQAPELSLSSQDLELVTKEDPKALAVALNWDIKKTETVQEACERELALRLQQT
QSLHSLRSISASKASPPGDLQNPKRARQDPT

FIGURE 50

CGGCGGAGCTGGTCCCGTTGTGCTGCGGCGCCGCGCGGCCTGCAGTCCCGGGCCCGCGCCCCGCGCCGCCCCGCCC
GCCCGCC**ATG**GAGCCCGGCCCCGACGGCCCCGCCGCCTCCGGCCCCGCCGCCATCCGCGAGGGCTGGTTCCGCGA
GACCTGCAGCCTGTGGCCCGGCCAGGCCCTGTCGCTGCAGGTGGAGCAGCTGCTCCACCACCGGCGCTCGCGCTA
CCAGGACATCCTCGTCTTCCGCAGTAAGACCTATGGCAACGTGCTGGTGTTGGACGGTGTCATCCAGTGCACGGA
GAGAGACGAGTTCTCCTACCAGGAGATGATCGCCAACCTGCCTCTCTGCAGCCACCCCAACCCGCGAAAGGTGCT
GATCATCGGGGGCGGAGATGGAGGTGTCCTGCGGGAGGTGGTGAAGCACCCCTCCGTGGAGTCCGTGGTCCAGTG
TGAGATCGACGAGGATGTCATCCAAGTCTCCAAGAAGTTCCTGCCAGGCATGGCCATTGGCTACTCTAGCTCGAA
GGTGACCCTACATGTGGGTGACGGTTTTGAGTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGA
CTCCTCAGACCCCATGGGCCCCGCCGAAAGTCTCTTCAAGGAGTCCTATTACCAGCTCATGAAGACAGCCCTCAA
GGAAGATGGTGTCCTCTGCTGCCAGGGCGAGTGCGAGTGGCTGCACCTGGACCTCATCAAGGAGATGCGGCAGTT
CTGCCAGTCCCTGTTCCCCGTGGTGGCCTATGCCTACTGCACCATCCCCACCTACCCCAGCGGCCAGATCGGCTT
CATGCTGTGCAGCAAGAACCCGAGCACGAACTTCCAGGAGCCGGTGCAGCCGCTGACACAGCAGCAGGTGGCGCA
GATGCAGCTGAAGTACTACAACTCCGACGTGCACCGCGCCGCCTTTGTGCTGCCCGAGTTTGCCCGCAAGGCCCT
GAATGATGTGAGC**TGA**GCCCAGGCGCCACCACTGATGCCACCCAGGACCTCGGACCTTGGAGCCTGCGGGGTGCC
TCGGCCCCTCCAGCCCCGGGCCGGACCTCCTGCTGGCTCTCGCCCACCAACCAAGTGTTACAAGCCCCAGAATGC
TGCCCGGCCTGCCCTGCTGGGCGGACTGTCTGTGTGTCTGTCTCTCTGGCGTTCCACCTCCAAGCCTATACCAGC
TGTGTACAGCGCCATCTCTCTGCCTTCTGTTGCCCCCG

FIGURE 51

MEPGPDGPAASGPAAIREGWFRETCSLWPGQALSLQVEQLLHHRRSRYQDILVFRSKTYGNVLVLDGVIQCTERD
EFSYQEMIANLPLCSHPNPRKVLIIGGGDGGVLREVVKHPSVESVVQCEIDEDVIQVSKKFLPGMAIGYSSSKVT
LHVGDGFEFMKQNQDAFDVIITDSSDPMGPAESLFKESYYQLMKTALKEDGVLCCQGECEWLHLDLIKEMRQFCQ
SLFPVVAYAYCTIPTYPSGQIGFMLCSKNPSTNFQEPVQPLTQQQVAQMQLKYYNSDVHRAAFVLPEFARKALND
VS

FIGURE 52

AGGCGCAGGCGCAGGCGAGGGGCTGGGTGGCGGTTGAGACAGCGGCGGTACTGGGAGGCGTAGGTGAGGGTCGCG
AGGCTGCCCGAGCTTCTGAGCGAGCGCGGTGCTTTTGGGAACGCGGGACGGGCGATCTGCGGCGCCAGGAGCTGG
GCCGAGGCGCGGCGGCGCGGCTGCCGGCTGCCCTGTGAATGGGAAGTTACGCGAAGTCCACCCAGCGTTTCTGAG
GCAATCTGAAGGCAAATCCTGTTTAGACCCAGGCGAAGGTTCCCGGTGACCCGGGCTCTCACCAGCCAATTGTCC
CTTGCCGTCCTCCTGAGGGTGCCTGGAGCTTAAGCACTGTGTGCTCTTGGCCTCCACACTGGGG**ATG**CCGCTGAC
TCCCACTGTCCAGGGCTTCCAGTGGATTCTCCGAGGCCCTGATGTAGAAACTTCCCCATTGGGTGCACCAAGAGC
AGCCTCACATGGTGTGGGC**TGA**CATCAAGAGCTGCCAGATCCAACAGGAAGATGGCCAATCTTTCCTAAGCTGCT
CACCTTACAAGAAAACGAATCGTACTGCTAAGAATTCAAACTTCAGCAGTCATGGGGAGCCTTGGAAGGAGCCCG
AATCACTGATGGAATTGGACAGTGCATGGAGATGGTTCAGCAGGACAAGGGTAAGTGCAGGGGCAAGTCCAGGTC
ATACTGAGAGACAACGAGTGGCGCTGACAGAGACAGACAAAGATAAAATCAAAAGTTTGTGCTTCATCTTCAAAA
ACTCAAACTAATAACAAACTTGGCCTT

FIGURE 53

MPLTPTVQGFQWILRGPDVETSPLGAPRAASHGVG

FIGURE 54

CTGCGCCCGCGACGGAGGCGCGCTTCAAAGCGCAGGCGCGGGGAGGGGGTGGGGGAGGAGGGAAAGCGGCGAGTA
AGATGGAAGATGAGGAGGTCGCTGAGAGCTGGGAAGAGGCGGCAGACAGCGGGGAAATCCAAATCTCCTCCCAAA
GTGCCCATTGTGATTCAGGACGATAGCCTTCCCGCGGGGCCCCCTCCACAGATCCGCATCCTCAAGAGGCCCACC
AGCAACGGTGTGGTCAGCAGCCCCAACTCCACCAGCAGGCCCACCCTTCCAGTCAAGTCCCTAGCACAGCGAGAG
GCCGAGTACGCCGAGGCCCGGAAGCGGATCCTGGGCAGCGCCAGCCCCGAGGAGGAGCAGGAGAAACCCATCCTC
GACAGGCCAACCAGGATCTCCCAACCCGAAGACAGCAGGCAGCCCAATAATGTGATCAGACAGCCTTTGGGTCCT
GATGGGTCTCAAGGCTTCAAACAGCGCAGATAAATGCAGGCAAGAAAAGATGCCGCCGTTGCTGCCGTCACCGCC
TCCTGGGTCGTCCGCCACGGGTTGCACTGCCGTGGCAGACAGCTGGACTTGAGCAGAGGGAACGACCTGACTTAC
TTGCACTGTGATCCCCCTTGCTCCGCCCACTGTGACCTTGAACCCCATGCACTGTGACCTCCCCCCTTCTCCCCC
TTCCCACTGTGATTGGCACATCGACAAGGGCTGTCCCAAGTCAATGGAAAGGGAAAGGGTGGGGGTTAGGGGAAG
GTTGGGGGGACCCAGCAAGGACTCAGAGAGTCAGACAGTGCCACTTGGCCACTTGGGGTAAAGCCAGTGCCAGCA
ATAACAGTTTATCATGCTCATTAATTTGGGATTTCAAAACACAAATGAAAACTCACACCCACCCACCCCCAAGTG
CATGTCTCCATCACTTAAAAAGTAAGTTCCATTTGAAAATATCCTTTCTTTTTTTTTTCTTCCTATTTTTGTTTG
TTTATACAAATATCTGATTTGCAAGAAAAAGTGCATGGGAGGGGTTTTAGTGGTTTAATGAATTTTTAATTAAGA
AAGGGTAGTTTGGTAGTCTACTTAAAAATGTTTCTGGGAAATTCACTAGAAACATTAACCAATAGGATTTTGGTG
AGCTTAGCTTCTGTATTCCTACTGCCGCCCAGAAAAGGGGCAGGGCTCTGCAGCCGCCAGGACAGACGAGCACCC
CATGCCTATACCTCCCTCCCCGAGCTAAGTCCCAGGGCATCTGGGCCTTGCCTGGAGACTGGGCTAGCTCTGTAG
GCTCGGAGAGCCTGGGGAGGGTGCCAACCCCACCTCTAGTATTTTGGGAGATAGGGAAAGTGAACCGACTTCCCC
TTCCCATACCCCTCAGGGTGGTTCCCTACCAGCCAGGCTTACTACTTCTAGAAGAAAGCAGAGTGCCAGGGAGTG
AGATTGCATCCCTGGGCTTAGAAGTGACGGAGAGAAGACTTGTTTAGTATTTTGCCATCAGCACAAGGAAAACCA
GGAGAGAGTCTGCCTCCAGGACTCTGAGCCTTCTGCCTCGTATGTTCAGAAGGTGGATAGGTCTTCCCACTCCAG
CATGGCTTGAACTCTTAGGGGTCTGCAGTGCTCCATCTCCATTGGTGGCCCCAGCTCAGTAACTATACCTGGTAC
ATTTCCTGTGTGCAATCAGTACCTTGAAGGCAGAACATTCTGAATAAAGTTGGAAAAAGAACA

FIGURE 55

CCACCTGGCACTGCCCACCACCCTGTAGCAGTGTGCCAGCAGGAGAGTCTGTCCTTTGCAGAGCTGCCCGCCCTG
AAGCCCCCGAGCCCAGTGTGTCTGGACCTTTTCCCTGTTGCCCCAGAGGAGCTTCGGGCTCCTGGCAGCCGCTGG
TCCCTGGGGACCCCTGCCCCTCTCCAAGGGTTGCTATGGCCATTATCCCCAGGAGGCTCAGATACAGAGATCACC
AGCGGGGGGATGCGGCCCAGCAGGGCTGGCAGCTGGCCACACTGTCCTGGTGCCCAGCCCCCAGCTCTGGAGGGA
CCCTGGAGTCCCCGACACACACAGCCACAGCGCCGGGCCAGCCACGGCTCGGAGAAGAAGTCTGCCTGGCGCAAG
ATGCGGGTGTACCAGCGTGAAGAGGTCCCCGGCTGCCCCGAGGCCCACGCTGTCTTCCTAGAGCCTGGCCAGGTA
GTGCAAGAGCAGGCCCTGAGCACAGAGGAGCCCAGGGTGGAGTTGTCTGGGTCCACCCGAGTGAGCCTCGAAGGT
CCTGAGCGGAGGCGCTTCTCGGCATCGGAGCTGATGACCCGGCTGCACTCTTCTCTGCGCCTGGGGCGGAATTCA
GCAGCCCGGGCACTCATCTCTGGGTCAGGCACCGGAGCAGCCCGGGAAGGGAAAGCATCTGGAATGGAGGCTCGA
AGTGTAGAGATGAGCGGGGACCGGGTGTCGCGGCCAGCCCCTGGTGACTCACGAGAGGGCGATTGGTCCGAGCCC
AGGCTAGACACACAGGAAGAGCCGCCTTTGGGGTCCAGGAGCACCAACGAGCGGCGCCAGTCTCGATTCCTCCTT
AACTCCGTCCTCTATCAGGAATACAGCGACGTGGCCAGCGCCCGCGAACTGCGGCGGCAGCAGCGCGAGGAGGAG
GGCCCGGGGGACGAGGCCGAGGGCGCAGAGGAGGGGCCGGGGCCGCCGCGGGCCAACCTCTCCCCCAGCAGCTCC
TTCCGGGCGCAGCGCTCGGCGCGAGGCTCCACCTTCTCGCTGTGGCAGGATATCCCCGACGTACGCGGCAGCGGC
GTCCTGGCCACGCTGAGCCTGCGGGACTGCAAGCTGCAGGAGGCCAAGTTTGAGCTGATCACCTCCGAGGCCTCC
TACATCCACAGCCTGTCGGTGGCTGTGGGCCACTTCTTAGGCTCTGCCGAGCTGAGCGAGTGTCTGGGGGCGCAG
GACAAGCAGTGGCTGTTTTCCAAACTGCCCGAGGTCAAGAGCACCAGCGAGAGGTTCCTGCAGGACCTGGAGCAG
CGGCTGGAGGCAGATGTGCTGCGCTTCAGCGTGTGCGACGTGGTGCTGGACCACTGCCCGGCCTTCCGCAGAGTC
TACCTGCCCTATGTCACCAACCAGGCCTACCAGGAGCGCACCTACCAGCGCCTGCTCCTGGAGAACCCCAGGTTC
CCTGGCATCCTGGCTCGCCTGGAGGAGTCTCCTGTGTGCCAGCGTCTGCCCCTTACCTCCTTCCTTATCCTGCCC
TTCCAGAGGATCACCCGCCTCAAGATGTTGGTGGAGAACATCCTGAAGCGGACAGCACAGGGCTCTGAAGACGAA
GACATGGCCACCAAGGCCTTCAATGCGCTCAAGGAGCTGGTGCAGGAGTGCAATGCTAGTGTACAGTCCATGAAG
AGGACAGAGGAACTCATCCACCTGAGCAAGAAGATCCACTTTGAGGGCAAGATTTTCCCGCTGATCTCTCAGGCC
CGCTGGCTGGTTCGGCATGGAGAGTTGGTAGAGCTGGCACCACTGCCTGCAGCACCCCCTGCCAAGCTGAAGCTG
TCCAGCAAGGCAGTCTACCTCCACCTCTTCAATGACTGCTTGCTGCTCTCTCGGCGGAAGGAGCTAGGGAAGTTT
GCCGTTTTCGTCCATGCCAAGATGGCTGAGCTGCAGGTGCGGGACCTGAGCCTGAAGCTGCAGGGCATCCCCGGC
CACGTGTTCCTCCTCCAGCTCCTCCACGGGCAGCACATGAAGCACCAGTTCCTGCTGCGGGCCCGGACGGAAAGT
GAGAAGCAGCGATGGATCTCAGCCTTGTGCCCCTCCAGCCCCCAGGAGGACAAGGAGGTCATCAGTGAGGGGGAA
GATTGCCCCCAGGTTCAGTGTGTTAGGACATACAAGGCACTGCACCCAGATGAGCTGACCTTGGAGAAGACTGAC
ATCCTGTCAGTGAGGACCTGGACCAGTGACGGCTGGCTGGAAGGGGTCCGCCTGGCAGATGGTGAGAAGGGGTGG
GTGCCCCAGGCCTATGTGGAAGAGATCAGCAGCCTCAGCGCCCGCCTCCGAAACCTCCGGGAGAATAAGCGAGTC
ACAAGTGCCACCAGCAAACTGGGGGAGGCTCCTGTGTGATGGGCAGCCATGGCCTAGGACCCCACCTCCATGCCT
GGCTCCTGGATGGTCCTGGAGGGGCCTGCAGTGTCTCCATTCCCCAAGCTGCTCCTGCTGGCACTTCGCTTCTGT
GGCCTTGGCATTGAGGGCACAGGCTGGACACAGGAATGGGGGCGCCTCCAGAGGGTCTCTCCGTCCTCATGCTCC
TCAGTGTCCACACTTCAAGGCCAAGGATAGTTTCTTCCTCTGACATGGGGACCATAACAGGTGATCACTGATACC
TGGCAAAGACTGGGGCCCTCTCCTTTCTATGTCCTCAATCCTGCCTGACTCTTGGTCCTTCTGGCAGGGACCTGG
CTGGGGAACGTTCTGGTGCTGATGGTGCTGGGACCTATATGTATATTTATATATATCTGGGGTCTTGTCTACCAC
CTCC

FIGURE 56

MDCGPPATLQPHLTGPPGTAHHPVAVCQQESLSFAELPALKPPSPVCLDLFPVAPEELRAPGSRWSLGTPAPLQG
LLWPLSPGGSDTEITSGGMRPSRAGSWPHCPGAQPPALEGPWSPRHTQPQRRASHGSEKKSAWRKMRVYQREEVP
GCPEAHAVFLEPGQVVQEQALSTEEPRVELSGSTRVSLEGPERRRFSASELMTRLHSSLRLGRNSAARALISGSG
TGAAREGKASGMEARSVEMSGDRVSRPAPGDSREGDWSEPRLDTQEEPPLGSRSTNERRQSRFLLNSVLYQEYSD
VASARELRRQQREEEGPGDEAEGAEEGPGPPRANLSPSSSFRAQRSARGSTFSLWQDIPDVRGSGVLATLSLRDC
KLQEAKFELITSEASYIHSLSVAVGHFLGSAELSECLGAQDKQWLFSKLPEVKSTSERFLQDLEQRLEADVLRFS
VCDVVLDHCPAFRRVYLPYVTNQAYQERTYQRLLLENPRFPGILARLEESPVCQRLPLTSFLILPFQRITRLKML
VENILKRTAQGSEDEDMATKAFNALKELVQECNASVQSMKRTEELIHLSKKIHFEGKIFPLISQARWLVRHGELV
ELAPLPAAPPAKLKLSSKAVYLHLFNDCLLLSRRKELGKFAVFVHAKMAELQVRDLSLKLQGIPGHVFLLQLLHG
QHMKHQFLLRARTESEKQRWISALCPSSPQEDKEVISEGEDCPQVQCVRTYKALHPDELTLEKTDILSVRTWTSD
GWLEGVRLADGEKGWVPQAYVEEISSLSARLRNLRENKRVTSATSKLGEAPV

FIGURE 57A

GAAGTTGCGCGCAGGCCGGCGGGCGGGAGCGGACACCGAGGCCGGCGTGCAGGCGTGCGGGTGTGCGGGAGCCGG
GCTCGGGGGGGATCGGACCGAGAGCGAGAAGCGCGGCATGGAGCTCCAGGCAGCCCGCGCCTGCTTCGCCCTGCTG
TGGGGCTGTGCGCTGGCCGCGGCCGCGGCGGCGCAGGGCAAGGAAGTGGTACTGCTGGACTTTGCTGCAGCTGGA
GGGGAGCTCGGCTGGCTCACACACCCGTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGAATGACATGCCG
ATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACTGGCTCCGCACCAACTGGGTGTACCGA
GGAGAGGCTGAGCGTATCTTCATTGAGCTCAAGTTTACTGTACGTGACTGCAACAGCTTCCCTGGTGGCGCCAGC
TCCTGCAAGGAGACTTTCAACCTCTACTATGCCGAGTCGGACCTGGACTACGGCACCAACTTCCAGAAGCGCCTG
TTCACCAAGATTGACACCATTGCGCCCGATGAGATCACCGTCAGCAGCGACTTCGAGGCACGCCACGTGAAGCTG
AACGTGGAGGAGCGCTCCGTGGGGCCGCTCACCCGCAAAGGCTTCTACCTGGCCTTCCAGGATATCGGTGCCTGT
GTGGCGCTGCTCTCCGTCCGTGTCTACTACAAGAAGTGCCCCGAGCTGCTGCAGGGCCTGGCCCACTTCCCTGAG
ACCATCGCCGGCTCTGATGCACCTTCCCTGGCCACTGTGGCCGGCACCTGTGTGGACCATGCCGTGGTGCCACCG
GGGGGTGAAGAGCCCCGTATGCACTGTGCAGTGGATGGCGAGTGGCTGGTGCCCATTGGGCAGTGCCTGTGCCAG
GCAGGCTACGAGAAGGTGGAGGATGCCTGCCAGGCCTGCTCGCCTGGATTTTTTAAGTTTGAGGCATCTGAGAGC
CCCTGCTTGGAGTGCCCTGAGCACACGCTGCCATCCCCTGAGGGTGCCACCTCCTGCGAGTGTGAGGAAGGCTTC
TTCCGGGCACCTCAGGACCCAGCGTCGATGCCTTGCACACGACCCCCCTCCGCCCCACACTACCTCACAGCCGTG
GGCATGGGTGCCAAGGTGGAGCTGCGCTGGACGCCCCCTCAGGACAGCGGGGGCCGCGAGGACATTGTCTACAGC
GTCACCTGCGAACAGTGCTGGCCCGAGTCTGGGGAATGCGGGCCGTGTGAGGCCAGTGTGCGCTACTCGGAGCCT
CCTCACGGACTGACCCGCACCAGTGTGACAGTGAGCGACCTGGAGCCCCACATGAACTACACCTTCACCGTGGAG
GCCCGCAATGGCGTCTCAGGCCTGGTAACCAGCCGCAGCTTCCGTACTGCCAGTGTCAGCATCAACCAGACAGAG
CCCCCCAAGGTGAGGCTGGAGGGCCGCAGCACCACCTCGCTTAGCGTCTCCTGGAGCATCCCCCCGCCGCAGCAG
AGCCGAGTGTGGAAGTACGAGGTCACTTACCGCAAGAAGGGAGACTCCAACAGCTACAATGTGCGCCGCACCGAG
GGTTTCTCCGTGACCCTGGACGACCTGGCCCCAGACACCACCTACCTGGTCCAGGTGCAGGCACTGACGCAGGAG
GGCCAGGGGGCCGGCAGCAAGGTGCACGAATTCCAGACGCTGTCCCCGGAGGGATCTGGCAACTTGGCGGTGATT
GGCGGCGTGGCTGTCGGTGTGGTCCTGCTTCTGGTGCTGGCAGGAGTTGGCTTCTTTATCCACCGCAGGAGGAAG
AACCAGCGTGCCCGCCAGTCCCCGGAGGACGTTTACTTCTCCAAGTCAGAACAACTGAAGCCCCTGAAGACATAC
GTGGACCCCCACACATATGAGGACCCCAACCAGGCTGTGTTGAAGTTCACTACCGAGATCCATCCATCCTGTGTC
ACTCGGCAGAAGGTGATCGGAGCAGGAGAGTTTGGGGAGGTGTACAAGGGCATGCTGAAGACATCCTCGGGGAAG
AAGGAGGTGCCGGTGGCCATCAAGACGCTGAAAGCCGGCTACACAGAGAAGCAGCGAGTGGACTTCCTCGGCGAG
GCCGGCATCATGGGCCAGTTCAGCCACCACAACATCATCCGCCTAGAGGGCGTCATCTCCAAATACAAGCCCATG
ATGATCATCACTGAGTACATGGAGAATGGGGCCCTGGACAAGTTCCTTCGGGAGAAGGATGGCGAGTTCAGCGTG
CTGCAGCTGGTGGGCATGCTGCGGGGCATCGCAGCTGGCATGAAGTACCTGGCCAACATGAACTATGTGCACCGT
GACCTGGCTGCCCGCAACATCCTCGTCAACAGCAACCTGGTCTGCAAGGTGTCTGACTTTGGCCTGTCCCGCGTG
CTGGAGGACGACCCCGAGGCCACCTACACCACCAGTGGCGGCAAGATCCCCATCCGCTGGACCGCCCCGGAGGCC
ATTTCCTACCGGAAGTTCACCTCTGCCAGCGACGTGTGGAGCTTTGGCATTGTCATGTGGGAGGTGATGACCTAT
GGCGAGCGGCCCTACTGGGAGTTGTCCAACCACGAGGTGATGAAAGCCATCAATGATGGCTTCCGGCTCCCCACA
CCCATGGACTGCCCCTCCGCCATCTACCAGCTCATGATGCAGTGCTGGCAGCAGGAGCGTGCCCGCCGCCCCAAG
TTCGCTGACATCGTCAGCATCCTGGACAAGCTCATTCGTGCCCCTGACTCCCTCAAGACCCTGGCTGACTTTGAC
CCCCGCGTGTCTATCCGGCTCCCCAGCACGAGCGGCTCGGAGGGGGTGCCCTTCCGCACGGTGTCCGAGTGGCTG
GAGTCCATCAAGATGCAGCAGTATACGGAGCACTTCATGGCGGCCGGCTACACTGCCATCGAGAAGGTGGTGCAG
ATGACCAACGACGACATCAAGAGGATTGGGGTGCGGCTGCCCGGCCACCAGAAGCGCATCGCCTACAGCCTGCTG
GGACTCAAGGACCAGGTGAACACTGTGGGGATCCCCATCTGAGCCTCGACAGGGCCTGGAGCCCCATCGGCCAAG
AATACTTGAAGAAACAGAGTGGCCTCCCTGCTGTGCCATGCTGGGCCACTGGGGACTTTATTTATTTCTAGTTCT
TTCCTCCCCCTGCAACTTCCGCTGAGGGGTCTCGGATGACACCCTGGCCTGAACTGAGGAGATGACCAGGGATGC
TGGGCTGGGCCCTCTTTCCCTGCGAGACGCACACAGCTGAGCACTTAGCAGGCACCGCCACGTCCCAGCATCCCT
GGAGCAGGAGCCCCGCCACAGCCTTCGGACAGACATATGGGATATTCCCAAGCCGACCTTCCCTCCGCCTTCTCC
CACATGAGGCCATCTCAGGAGATGGAGGGCTTGGCCCAGCGCCAAGTAAACAGGGTACCTCAAGCCCCATTTCCT
CACACTAAGAGGGCAGACTGTGAACTTGACTGGGTGAGACCCAAAGCGGTCCCTGTCCCTCTAGTGCCTTCTTTA
GACCCTCGGGCCCCATCCTCATCCCTGACTGGCCAAACCCTTGCTTTCCTGGGCCTTTGCAAGATGCTTGGTTGT

FIGURE 57B

GTTGAGGTTTTTAAATATATATTTTGTACTTTGTGGAGAGAATGTGTGTGTGTGGCAGGGGGCCCCGCCAGGGCT
GGGGACAGAGGGTGTCAAACATTCGTGAGCTGGGGACTCAGGGACCGGTGCTGCAGGAGTGTCCTGCCCATGCCC
CAGTCGGCCCCATCTCTCATCCTTTTGGATAAGTTTCTATTCTGTCAGTGTTAAAGATTTTGTTTTGTTGGACAT
TTTTTTCGAATCTTAATTTATTATTTTTTTTATATTTATTGTTAGAAAATGACTTATTTCTGCTCTGGAATAAAG
TTGCAGATGATTCAAACCG

FIGURE 58

GGTGGGCTGTAGGAATGAGGAGGAACTTAGGGAGAAACAGCTAGTGGGGAGGTAGGGCCTGGGGGAGCCGCCCCT
TGCCCCAAGAGAAGGAGCCAGAACCCCCGGATCTGCATGCAAGGCCTGCTCCATGCCTCGCTCACAGCAGCCCAT
CCCACAGCCCGCCCCGGTGGGGCAGGCAACATCAAGACCCTAGGAGACGCCTATGAGTTTGCGGTGGACGTGAGA
GACTTCTCACCTGAAGACATCATTGTCACCACCTCCAACAACCACATCGAGGTGCGGGCTGAGAAGCTGGCGGCT
GACGGCACCGTCATGAACACCTTCGCTCACAAGTGCCAGCTGCCGGAGGACGTGGACCCGACGTCGGTGACCTCG
GCTCTGCGGGAGGACGGCAGCCTCACTATCCGGGCACGGCGTCACCCGCATACAGAACACGTCCAGCAGACCTTC
CGGACGGAGATCAAAATCTGAGTGCCTCTCCCTTCCCTTTCCCTGTCCCCCCGCCCCACGCCTGCCAGCAAAGCC
TCGCTAACCCCATTACAACAGCTCCAGGACATCTCAGCCCAGGTTCTAGCCCCCACGCACCCCAGACCCCAGGTG
GACCATCCTCCCAAACTAGGGCCCTCCACTCTATCCAGGGCAGGCCAGGGACTCCCTGGCCTGACACATGATGCC
CAGATTTCAGATTTGGCCTCCGTCACTTAATCCAGAGTACAGGGGCTGGGGTCAGGGAAGGAAGATCTAAAGAAC
CCACTGTGGGTCAGGGGAATGGGACCAGCAGGACATATGGGCAAGCTCTGCAGGACAGACAGGCAGACAAACCCT
CTGATCTATGA

FIGURE 59

GCTCGTGTTAAATCTAGAACCGTAGCCAGACATGGGACTGGAGGACGAGCAAAAGATGCTTACCGAATCCGGAGA
TCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCTAACAACAGTGAGAGAGCAATGCGAGCAGTT
GGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTATGATGAGCATGTATCCTCTCGATCACATACAGAAGA
GGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCAAAGGACCATTGCGTGGCCCACAAACTCTTTAACAACTT
GAAATAAATGTGTGGACTTAATTCACCCCAGCCTTCATCATCTGGGCATCAGAATATTTCCTTATGGTTTCGGAT
GTACCATTTGTTTCTTATTTGTGTAACTGTAAGTTCACATGAACCTCGTGGGTTTTGGCTTAGGCTGGTAGCTTC
TATGTAATTCGCAGTGATTCCATCTAAATAAAAGTTCTGTGATCTGC

FIGURE 60

CTTACAGAACTCCCACGGACACACC**ATG**ATAAGGACGCTGCTGCTGTCCACTTTGGTGGCTGGAGCCCTCAGTTG
TGGGGACCCCACTTACCCACCTTATGTGACTAGGGTGGTTGGCGGTGAAGAAGCGAGGCCCAACAGCTGGCCCTG
GCAGGTCTCCCTGCAGTACAGCTCCAATGGCAAGTGGTACCACACCTGCGGAGGGTCCCTGATAGCCAACAGCTG
GGTCCTGACGGCTGCCCACTGCATCAGCTCCTCCAGGACCTACCGCGTGGGGCTGGGCCGGCACAACCTCTACGT
TGCGGAGTCCGGCTCGCTGGCAGTCAGTGTCTCTAAGATTGTGGTGCACAAGGACTGGAACTCCAACCAAATCTC
CAAAGGGAACGACATTGCCCTGCTCAAACTGGCTAACCCCGTCTCCCTCACCGACAAGATCCAGCTGGCCTGCCT
CCCTCCTGCCGGCACCATTCTACCCAACAACTACCCCTGCTACGTCACGGGCTGGGGAAGGCTGCAGACCAACGG
GGCTGTTCCTGATGTCCTGCAGCAGGGCCGGTTGCTGGTTGTGGACTATGCCACCTGCTCCAGCTCTGCCTGGTG
GGGCAGCAGCGTGAAAACCAGTATGATCTGTGCTGGGGGTGATGGCGTGATCTCCAGCTGCAACGGAGACTCTGG
CGGGCCACTGAACTGTCAGGCGTCTGACGGCCGGTGGCAGGTGCACGGCATCGTCAGCTTCGGGTCTCGCCTCGG
CTGCAACTACTACCACAAGCCCTCCGTCTTCACGCGGGTCTCCAATTACATCGACTGGATCAATTCGGTGATTGC
AAATAAC**TAA**CCAAAAGAAGTCCCTGGGACTGTTTCAGACTTGGAAAGGTCACAGAAGGAAAATAATATAATAAA
GTGACAACTATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 61

MIRTLLLSTLVAGALSCGDPTYPPYVTRVVGGEEARPNSWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCI
SSSRTYRVGLGRHNLYVAESGSLAVSVSKIVVHKDWNSNQISKGNDIALLKLANPVSLTDKIQLACLPPAGTILP
NNYPCYVTGWGRLQTNGAVPDVLQQGRLLVVDYATCSSSAWWGSSVKTSMICAGGDGVISSCNGDSGGPLNCQAS
DGRWQVHGIVSFGSRLGCNYYHKPSVFTRVSNYIDWINSVIANN

FIGURE 62

CGGACGCGTGGGCCCGGCCAAGGCGAGTGCCGCGCGGGCCACC**ATG**GCCACGGACGAGCTGGCCACCAAGCTGAG
CCGGCGGCTGCAGATGGAGGGCGAGGGCGGCGGCGAGACCCCGGAGCAGCCCGGGCTGAACGGGGCAGCGGCGGC
GGCGGCGGGGGCACCCGACGAGGCGGCCGAGGCGCTGGGCAGCGCGGACTGCGAGCTGAGCGCCAAGCTGCTGCG
GCGCGCAGACCTCAACCAGGGCATCGGCGAGCCCCAGTCGCCCAGCCGCCGCGTCTTCAACCCCTACACCGAGTT
CAAGGAGTTCTCCAGGAAGCAGATCAAGGACATGGAGAAGATGTTCAAGCAGTATGATGCCGGGCGGGACGGCTT
CATCGACCTGATGGAGCTAAAACTCATGATGGAGAAACTTGGGGCCCCTCAGACCCACCTGGGCCTGAAAAACAT
GATCAAGGAGGTGGATGAGGACTTTGACAGCAAGCTGAGCTTCCGGGAGTTCCTCCTGATCTTCCGCAAGGCGGC
GGCCGGGGAGCTTCAGGAGGACAGCGGGCTGTGCGTGCTGGCCCGCCTCTCTGAGATCGACGTCTCCAGTGAGGG
TGTCAAGGGGGCCAAGAGCTTCTTTGAGGCCAAGGTCCAGGCCATCAACGTGTCCAGCCGCTTCGAGGAGGAGAT
CAAGGCAGAGCAGGAGGAAAGGAAGAAGCAGGCGGAGGAGATGAAGCAGCGGAAAGCGGCCTTCAAGGAGCTGCA
GTCCACCTTTAAG**TAG**CGGGGGCTGCAGCCGACCGCCCTGCTCCGGCCCCAGTGTGGTGGGCGAGGGTGGCGCAT
GGGAGGCCGAGCCTGAATCCTTGCCTGTGTCTGACGGGACCACTACTAAAAACCTAAAAATATCTGTGAATGGAG
CAAGTTCAGGGGTCTTATGGAGGTGGCCCGGCCCCTCCCCGCTCCCTTCCACTCTGCACGAGGCCGCCACACCGG
CGCTGGCTCCCTGCCCGGCCCGGCCCTCCCTGGCAATCCCTGGGCTCTCTTGCACCCCTAACTGCCCCCTGCCTG
CTCCGGCACTGCCCCAGGCCCAGCTCCTGGCCCTAGGTCCCTCCCAGCCCCATGTGCCTGCCGCCTGCCCTCCAC
ACATCCCTGTCCCCCCAACCCGGGAACCCCTGCCCTCCTCCAGCAGGCCGCACCGCCCCTGGGGCCCCCTGCCAG
CCCCTTCCCAGGCTGGGAGACAGCAGAAGAGATAGAATCAGGGCTGCCCCCACAGAGTGGGACCCAAGGGGCTAA
TTGGAGGCACGAGGGGACCCCTCCCCAGGGCCTTTTCCTCCTCTGCGTCTTCCATCTACTGAAATGGGAGAGGGG
GTGGGGAGCTTCTGTTCTGGTGAAGGGACCCGGGCAGGCCCCCAGCACCCCATGCTGACTTGGAGAACCCCAGAT
CTCTGGGGCCCAGCCAGGCAGGGTGTGGGGGCAGCTGTGCCAATCTACCTCACAGGCCCACCCCCTGCCGGGCAT
GCCGTGGGATCATGGGCAGGGAAGGCTCTGGGGGTCGGAGACACCGCTGCTTAGCACCCCCAGCCAGAACACCCT
GAGGGTCTCGGGGCTCTGGAGAGAGTGGGGCGGGAGGAAGAATTGGCACCTTCCTAGGGAAGGAGACGAGCGCTT
CGCCTTGATTCTCCGAGAAGCCTCCGAGAAGTGCTTTAAGTGTGTTTGCATGCGCCAGGCGGTGGGCAGCGGGGG
CCTGTCCAGCCCTCTCCCGCCATCCTTCCCCAAGTGACGTCCACTGCCTTGTCACCAGCGACCTGCCTGTCATGC
CCACCCCCTGAGGAAGCATGGGGACCCTAACACCCTGGTGCCCTGCACCAGACAGGCCGTGGTCAGGCCCAGGCC
ACCGGCCGGGTTCTGCCACAGCTTCCCACGTGCTTGCTGACATGCGTGTGCCTGTGTGTGGTGTCTGTTGCTGTG
TCGTGAAACTGTGACCATCACTCAGTCCAAACAAGTGAGTGGCCCTCGAGGCCACAGTTATGCAACTTTCAGTGT
GTGTCATAACGACGTCACTGCTTTTTAAACTCGATAACTCTTTATTTTAGTAAAATGCCCAGGAGTCCTGGAAGC
TACGCGGACTTGCAGAGGTTTTATTTTTTGGCCTTAGAATCTGCAGAAATTAGGAGGCACCGAGCCCAGCGCAGC
AGCCTCGGACCCGGATTGCGTTTGCCTTAGCGGATATGTTTATACAGATGAATATAAAATGTTTTTTTCTTTGGG
AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

MATDELATKLSRRLQMEGEGGGETPEQPGLNGAAAAAAGAPDEAAEALGSADCELSAKLLRRADLNQGIGEPQSP
SRRVFNPYTEFKEFSRKQIKDMEKMFKQYDAGRDGFIDLMELKLMMEKLGAPQTHLGLKNMIKEVDEDFDSKLSF
REFLLIFRKAAAGELQEDSGLCVLARLSEIDVSSEGVKGAKSFFEAKVQAINVSSRFEEEIKAEQEERKKQAEEM
KQRKAAFKELQSTFK

FIGURE 64

GCCTCCCACTTGGTTGCTCGTACGCGGCTAGTGGGTCCTCAGTGGATGTAGGCTGGGCGCCGCGATGTTCGACGG
GACACCGGCGGAGAGCGACCTCGGGGTTAAGGGGTGGGGCTGACGTCAGGAGCCAAGATGGCGGCGGTGGTCGCC
CTCTCCTTGAGGCGCCGGTTGCCGGCCACAACCCTTGGCGGAGCCTGCCTGCAGGCCTCCCGAGGAGCCCAGACA
GCTGCAGCCACAGCTCCCCGTATCAAGAAATTTGCCATCTATCGATGGGACCCAGACAAGGCTGGAGACAAACCT
CATATGCAGACTTATGAAGTTGACCTTAATAAATGTGGCCCCATGGTATTGGATGCTTTAATCAAGATTAAGAAT
GAAGTTGACTCTACTTTGACCTTCCGAAGATCATGCAGAGAAGGCATCTGTGGCTCTTGTGCAATGAACATCAAT
GGAGGCAACACTCTAGCTTGCACCCGAAGGATTGACACCAACCTCAATAAGGTCTCAAAAATCTACCCTCTTCCA
CACATGTATGTGATAAAGGATCTTGTTCCCGATTTGAGCAACTTCTATGCACAGTACAAATCCATTGAGCCTTAT
TTGAAGAAGAAGGATGAATCTCAGGAAGGCAAGCAGCAGTATCTGCAGTCCATAGAAGAGCGTGAGAAACTGGAC
GGGCTCTACGAGTGCATTCTCTGTGCCTGCTGTAGCACCAGCTGCCCCAGCTACTGGTGGAACGGAGACAAATAT
CTGGGGCCTGCAGTTCTTATGCAGGCCTATCGCTGGATGATTGACTCCAGAGATGACTTCACAGAGGAGCGCCTG
GCCAAGCTGCAGGACCCATTCTCTCTATACCGCTGCCACACCATCATGAACTGCACAAGGACCTGTCCTAAGGGT
CTGAATCCAGGGAAAGCTATTGCAGAGATCAAGAAAATGATGGCAACCTATAAGGAGAAGAAAGCTTCAGTTTAA
CTGTTTCCATGCTAAACATGATTTATAACCAGCTCAGAGCTGAACATAATTTATATCTAATTTGAGTTCCTTTAA
AGATCTTGGTTTTCCATGAATACAGCATGTATAATAAAAATTTTAAGAAATAAATGTTATTCTACTTTATTAACA
AAAAA

FIGURE 65

MAAVVALSLRRRLPATTLGGACLQASRGAQTAAATAPRIKKFAIYRWDPDKAGDKPHMQTYEVDLNKCGPMVLDA
LIKIKNEVDSTLTFRRSCREGICGSCAMNINGGNTLACTRRIDTNLNKVSKIYPLPHMYVIKDLVPDLSNFYAQY
KSIEPYLKKKDESQEGKQQYLQSIEEREKLDGLYECILCACCSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDD
FTEERLAKLQDPFSLYRCHTIMNCTRTCPKGLNPGKAIAEIKKMMATYKEKKASV

FIGURE 66

AGTGTTGGGGTTGGCGGCCACAGCTAAGTCCAACACCAGCATGTCGCTGCAGAGAATCGTGCGTGTGTCCCTGGA
GCATCCCACCAGCGCGGTGTGTGTGGCTGGCGTGGAGACCCTCGTGGACATTTATGGGTCAGTGCCTGAGGGCAC
AGAAATGTTTGAGGTCTATGGGACGCCTGGCGTGGACATCTACATCTCTCCCAACATGGAGAGGGGCCGGGAGCG
TGCAGACACCAGGCGGTGGCGCTTTGACGCGACTTTGGAGATCATCGTGGTCATGAACTCCCCCAGCAATGACCT
CAACGACAGCCATGTTCAGATTTCCTACCACTCCAGCCATGAGCCTCTGCCCCTGGCCTATGCGGTGCTCTACCT
CACCTGTGTTGACATCTCTCTGGATTGCGACCTGAACTGTGAGGGAAGGCAGGACAGGAACTTTGTAGACAAGCG
GCAGTGGGTCTGGGGGCCCAGTGGGTATGGCGGCATCTTGCTGGTGAACTGTGACCGTGATGATCCGAGCTGTGA
TGTCCAGGACAATTGTGACCAGCACGTGCACTGCCTGCAAGACCTGGAAGACATGTCTGTCATGGTCCTGCGGAC
GCAGGGCCCTGCAGCCCTCTTTGATGACCACAAACTTGTCCTCCATACCTCCAGCTATGATGCCAAACGGGCACA
GGTCTTCCACATCTGCGGTCCTGAGGATGTGTGTGAGGCCTATAGGCATGTGCTGGGCCAAGATAAGGTGTCCTA
TGAGGTACCCCGCTTGCATGGGGATGAGGAGCGCTTCTTCGTGGAAGGCCTGTCCTTCCCTGATGCCGGCTTCAC
AGGACTCATCTCCTTCCATGTCACTCTGCTGGACGACTCCAACGAGGATTTCTCGGCATCCCCTATCTTCACTGA
CACTGTGGTGTTCCGAGTGGCACCCTGGATCATGACGCCCAGCACTCTGCCACCCCTAGAGGTGTATGTGTGCCG
TGTGAGGAACAACACGTGTTTTGTGGATGCGGTGGCAGAGCTGGCCAGGAAGGCCGGCTGCAAGCTGACCATCTG
CCCACAGGCCGAGAACCGCAACGACCGCTGGATCCAGGATGAGATGGAGCTGGGCTACGTTCAGGCGCCGCACAA
GACCCTCCCGGTGGTCTTTGACTCCCCAAGGAATGGGGAACTGCAGGATTTCCCTTACAAAAGAATCCTGGGTCC
AGATTTTGGTTACGTGACTCGGGAACCACGCGACAGGTCTGTGAGTGGCCTGGACTCCTTTGGGAACCTGGAGGT
CAGCCCTCCAGTGGTGGCCAATGGGAAAGAGTACCCCCTGGGGAGGATCCTCATTGGGGGCAACCTGCCTGGGTC
AAGTGGCCGCAGGGTCACCCAGGTGGTGCGGGACTTCCTCCATGCCCAGAAGGTGCAGCCCCCCGTGGAGCTCTT
TGTGGACTGGTTGGCCGTGGGCCATGTGGATGAGTTTCTGAGCTTTGTCCCTGCCCCCGATGGGAAGGGCTTCCG
GATGCTCCTGGCCAGCCCTGGGGCCTGCTTCAAGCTCTTCCAGGAAAAGCAGAAGTGTGGCCACGGGAGGGCCCT
CCTGTTCCAGGGGGTTGTTGATGATGAGCAGGTCAAGACCATCTCCATCAACCAGGTGCTCTCCAATAAAGACCT
CATCAACTACAATAAGTTTGTGCAGAGCTGCATCGACTGGAACCGTGAGGTGCTGAAGCGGGAGCTGGGCCTGGC
AGAGTGTGACATCATTGACATCCCACAGCTCTTCAAGACCGAGAGGAAAAAAGCAACGGCCTTCTTCCCTGACTT
GGTGAACATGCTGGTGCTGGGGAAGCACCTGGGCATCCCCAAGCCCTTTGGGCCCATCATCAATGGCTGCTGCTG
CCTGGAGGAGAAGGTGCGGTCCCTGCTGGAGCCGCTGGGCCTCCACTGCACCTTCATTGATGACTTCACTCCATA
CCACATGCTGCATGGGGAGGTGCACTGTGGCACCAATGTGTGCAGAAAGCCCTTCTCTTTCAAGTGGTGGAACAT
GGTGCCCTGAGACAGCTCCCACCCACCATCCTGTCCCCCTGGGGCGGGCATTGGCCCAGGTGGTGGAGACAGAGA
CAGGCCCCTGAACGATAAGCACCAAGAGACCCCAAGGCTCCAGATGGAACACTGAGGGTGACCGTCCCTCTCAGA
AGCCTTTTCCCTGGAAGTGTCCATGCCTCACCTGCAACCCATGTGGTTCTCAGACTTGAATCTTCTCGGCCCCCC
AAAAAGAAGGACCTCATTTCTTATAGCCTCTCCTGTGATTCAACACAACCCATGGAGATGTCCCCTTCTCACTCT
GAAATCATCCATTTGGGGACAAATCCACATTGGGGTCTAGAAACATCCACGTATCTCATCAGCCATCTTGTCCTG
TGCATCCTAACAGAGGAAGGATCCATGATTCTGCTTTGGTCCAATTGCTTCCTCTCTGCAGAGGAACAACCCTAA
AACCAGACCACTCCACGCAGGACAGGCAGGAGAGATTCTTCCTAAAGCCTCCCCCATAAAAAGGGAGCTGTGGAT
CCACTTAGATCAGGGCGGAACCATCTTTCACCCGGCCAAGCTCCTGCCCAGATGTTGACCCTCACCCAGCGTGAG
CTGTCACATAGTAGGAGCTTCTAGATGCATGTGGAAGCAATGAGAGTTGTCCCTTAGCCTTATAAACTCCCCATG
ATCTGACATGCAGAAATCCAGCCTTGTCCAGAATCCTCCTGGAATTTCTTGGAGACGAAAGTATCTGGGGGATTG
TTGGGTACTAGGGAGACTGGGTACAAGGGTGAAAAGTAGTTCCCATAATACACATGGTTGACTATGGTGATCCAC
CTTGTGATGGTTAATATTAGGTGTCTGGAGAAGGTTGCTTCATTGGCCCTGGGACTTCTCTCTGCAGGAGGAGAG
AACGCTGCCTCTCCTCTGGATTGGTCTCAGGCTCTCTGTTGGCCTTTGGTCAGCGTTTCCACATCCTGCTCTGCT
GCAGGAGAGGGGGCTAAGGGGCTGGATCCACCAAGGCAGCTCACAGCGGGAAAACTCTGGGAATGAACCACTGAA
TTCAGGGGATGGGGGGTGGGGGGGCGGTTCTCGAGGTGTGTGCCAGCTACACGTGTGTTCTGTATGGGTCCAGCTG
CGTTTCCATCACTCGCTAATAAATCAACAGAAACAC

FIGURE 67

AGCCAGAGGGACGAGCTAGCCCGACGATGGCCCAGGGGACATTGATCCGTGTGACCCCAGAGCAGCCCACCCATG
CCGTGTGTGTGCTGGGCACCTTGACTCAGCTTGACATCTGCAGCTCTGCCCCTGAGGACTGCACGTCCTTCAGCA
TCAACGCCTCCCCAGGGGTGGTCGTGGATATTGCCCACGGCCCTCCAGCCAAGAAGAAATCCACAGGTTCCTCCA
CATGGCCCCTGGACCCTGGGGTAGAGGTGACCCTGACGATGAAAGTGGCCAGTGGTAGCACAGGCGACCAGAAGG
TTCAGATTTCATACTACGGACCCAAGACTCCACCAGTCAAAGCTCTACTCTACCTCACCGGGGTGGAAATCTCCC
TGTGCGCAGACATCACCCGCACCGGCAAAGTGAAGCCAACCAGAGCTGTGAAAGATCAGAGGACCTGGACCTGGG
GCCCTTGTGGACAGGGTGCCATCCTGCTGGTGAACTGTGACAGAGACAATCTCGAATCTTCTGCCATGGACTGCG
AGGATGATGAAGTGCTTGACAGCGAAGACCTGCAGGACATGTCGCTGATGACCCTGAGCACGAAGACCCCCAAGG
ACTTCTTCACAAACCATACACTGGTGCTCCACGTGGCCAGGTCTGAGATGGACAAAGTGAGGGTGTTTCAGGCCA
CACGGGGCAAACTGTCCTCCAAGTGCAGCGTAGTCTTGGGTCCCAAGTGGCCCTCTCACTACCTGATGGTCCCCG
GTGGAAAGCACAACATGGACTTCTACGTGGAGGCCCTCGCTTTCCCGGACACCGACTTCCCGGGGCTCATTACCC
TCACCATCTCCCTGCTGGACACGTTCAACCTGGAGCTCCCCGAGGCTGTGGTGTTCCAAGACAGCGTGGTCTTCC
GCGTGGCGCCCTGGATCATGACCCCCAACACCCAGCCCCCGCAGGAGGTGTACGCGTGCAGTATTTTTGAAAATG
AGGACTTCCTGAAGTCAGTGACTACTCTGGCCATGAAAGCCAAGTGCAAGCTGACCATCTGCCCTGAGGAGGAGA
ACATGGATGACCAGTGGATGCAGGATGAAATGGAGATCGGCTACATCCAAGCCCCACACAAAACGCTGCCCGTGG
TCTTCGACTCTCCAAGGAACAGAGGCCTGAAGGAGTTTCCCATCAAACGCGTGATGGGTCCAGATTTTGGCTATG
TAACTCGAGGGCCCCAAACAGGGGGTATCAGTGGACTGGACTCCTTTGGGAACCTGGAAGTGAGCCCCCCAGTCA
CAGTCAGGGGCAAGGAATACCCGCTGGGCAGGATTCTCTTCGGGGACAGCTGTTATCCCAGCAATGACAGCCGGC
AGATGCACCAGGCCCTGCAGGACTTCCTCAGTGCCCAGCAGGTGCAGGCCCCTGTGAAGCTCTATTCTGACTGGC
TGTCCGTGGGCCACGTGGACGAGTTCCTGAGCTTTGTGCCAGCACCCGACAGGAAGGGCTTCCGGCTGCTCCTGG
CCAGCCCCAGGTCCTGCTACAAACTGTTCCAGGAGCAGCAGAATGAGGGCCACGGGGAGGCCCTGCTGTTCGAAG
GGATCAAGAAAAAAAAACAGCAGAAAATAAAGAACATTCTGTCAAACAAGACATTGAGAGAACATAATTCATTTG
TGGAGAGATGCATCGACTGGAACCGCGAGCTGCTGAAGCGGGAGCTGGGCCTGGCCGAGAGTGACATCATTGACA
TCCCGCAGCTCTTCAAGCTCAAAGAGTTCTCTAAGGCGGAAGCTTTTTTCCCCAACATGGTGAACATGCTGGTGC
TAGGGAAGCACCTGGGCATCCCCAAGCCCTTCGGGCCCGTCATCAACGGCCGCTGCTGCCTGGAGGAGAAGGTGT
GTTCCCTGCTGGAGCCACTGGGCCTCCAGTGCACCTTCATCAACGACTTCTTCACCTACCACATCAGGCATGGGG
AGGTGCACTGCGGCACCAACGTGCGCAGAAAGCCCTTCTCCTTCAAGTGGTGGAACATGGTGCCCTGAGCCCATC
TTCCCTGGCGTCCTCTCCCTCCTGGCCAGATGTCGCTGGGTCCTCTGCAGTGTGGCAAGCAAGAGCTCTTGTGAA
TATTGTGGCTCCCTGGGGGCGGCCAGCCCTCCCAGCAGTGGCTTGCTTTCTTCTCCTGTGATGTCCCAGTTTCCC
ACTCTGAAGATCCCAACATGGTCCTAGCACTGCACACTCAGTTCTGCTCTAAGAAGCTGCAATAAAGTTTTTTTA
AGTCACTTTGTAC

FIGURE 68A

GGAAGCTCGTATTTACATTTTAAGTGTATCTGGTGAGTGGGCTGGAGCCCTCGTCTGGGCCGGAAAAAAAAAAGC
CCTCCGATCCGTCTTTTAGTTGCTTCTCTTCCTTTTTTCTCTCCGGTTTCTCATCACTCCAACCAGCCGCGACCA
TGCCCAGGAAGAAGGCGGCGGCGGCGGCCTGGGAGGAGCCGAGCTCGGGCAACGGCACTGCCCGCGCCGGGCCCA
GGAAACGCGGCGGCCCGGCGGGCAGGAAGCGCGAGCGGCCCGAGCGCTGCAGTAGCAGCAGCGGCGGCGGCAGCA
GCGGCGACGAGGACGGCCTGGAGCTCGACGGGGCCCCCGGCGGGGGCAAGCGCGCGGCGCGGCCGGCGACAGCAG
GCAAGGCGGGCGGCGCGGCCGTGGTCATCACCGAACCCGAGCACACCAAGGAGCGCGTCAAACTTGAAGGGTCAA
AGTGCAAAGGGCAGCTTTTGATTTTGGGGCAACCAACTGGGACTTGATTGGTCGAAAAGAAGTGCCTAAACAGC
AAGCTGCTTACCGCAATCTCGGTCAGAATTTGTGGGGGCCCCACAGATATGGGTGCCTGGCGGGGGTCCGGGTGC
GGACAGTGGTCTCGGGCTCGTGTGCTGCACACAGCCTCCTCATCACCACGGAAGGGAAGCTGTGGAGCTGGGGTC
GAAATGAGAAGGGGCAGCTGGGACATGGTGACACCAAGAGAGTAGAAGCCCCTAGACTCATCGAGGGTCTTAGCC
ACGAAGTGATTGTGTCTGCAGCATGTGGGCGGAACCACACCTTGGCCTTGACGGAAACGGGCTCCGTGTTTGCGT
TTGGGGAAAACAAGATGGGGCAGCTGGGCCTTGGCAACCAGACAGACGCTGTTCCCAGCCCCGCGCAGATAATGT
ACAACGGCCAGCCAATTACCAAAATGGCCTGTGGGGCTGAATTCAGTATGATAATGGACTGCAAAGGAAACCTCT
ATTCCTTTGGGTGCCCTGAATATGGTCAGCTGGGACACAACTCAGATGGGAAGTTCATCGCCCGGGCACAGCGGA
TAGAGTACGACTGTGAACTAGTTCCCCGGCGAGTGGCCATCTTCATTGAGAAGACGAAAGATGGACAGATTCTGC
CTGTACCAAACGTGGTTGTACGAGACGTGGCCTGTGGCGCTAACCACACGCTGGTCCTGGACTCCCAGAAGCGAG
TCTTCTCCTGGGGCTTTGGTGGCTATGGCCGGCTGGGCCACGCAGAGCAGAAGGATGAGATGGTCCCCCGCCTGG
TGAAGCTGTTTGACTTCCCTGGGCGTGGGGCTTCCCAGATCTATGCTGGTTACACCTGCTCCTTTGCTGTCAGTG
AAGTGGGTGGTCTGTTTTTCTGGGGGGCCACCAACACCTCCCGTGAATCTACCATGTACCCAAAAGCAGTGCAGG
ACCTCTGCGGCTGGAGAATTCGGAGCCTGGCTTGTGGGAAGAGCAGCATCATTGTGGCCGCCGATGAGAGCACCA
TCAGCTGGGGTCCGTCACCGACCTTTGGGGAACTGGGCTACGGGGACCACAAGCCCAAGTCTTCCACTGCAGCCC
AGGAGGTAAAGACTCTGGATGGCATTTTCTCAGAGCAGGTCGCCATGGGCTACTCACACTCCTTGGTGATAGCAA
GAGATGAAAGTGAGACTGAGAAAGAGAAGATCAAGAAACTGCCAGAATACAACCCCCGAACCCTCTGATGCTCCC
GGAGACTCCTCCGACTCCACACCTCTCGCGGCAGCTGTCATTTCCATGTGCACTGGGACGGGAAGTCAAACGAGG
AATTTAAAAAAGCAAAAGTTGACCGAAGGTGCATTTTTGTTTAGACTCCCTGAGGTTCCGTTTTACACATGATCC
AACGTTAACTACCTTTTTTTCTGTATGCTTTCCAAAGTCCTTTTTTTTCCCTTAATGTTGAATTAAAATACTTGC
TCATAGTTGATTTACCATTCCTACAAAAGAGGCAGAAACTTTGAGCAATCTAGGTTTTTTTTTTTTTTAAGTTTT
TTCTTTCTTCCTTTCCTGAATACACTCCCCAAAACACCCCTTTCCAGTTACAATTAGCATCGTGATCCAAGCAGA
TGCCACATGGAAGAGGAATCGCCATTTACTCAGAAAAAATGTCCCTTACAGGAACCGGCAGCAGCTAGGCAGTCA
CCGGCCCGCCTCCATCCAAAATCACGCTCGCGTGCTTCGGAAGCATCCGGGTCACTCCTTCTCCGCTTTTTCTTG
CAGATGGGCCTAGGCCGGTGTCGGTTCTGTTTCTCCCCTTGGCTGCCTGTACGCCCACAGCCTTCTGGCTGCGAC
ATTATAGAATCGGCCGTGTCCCCCCTGGTGGGGGATTGGGGATCTGTGTTTAGCCATTTATATCTACTTTAGCTG
TTAAAGAGGTCCAAATGAAAATCAGGTGATTGTGGAACCATGGGGACTTGGGGGTGGGGCAGAGGTGGGAACATT
TGTATCAGTTGAGTCAGCTTGGTGGCTCCCTGTGGAGCCAGGGCTGAGCCTTGTCACGCGCACTCGCCAATTAAG
AGATGGACCAGCCAGCAGTCAAGTGCATTCTCCAGTCCTTGCAAGAAGGATCAGCCCTTTCTGTGCCAGCCTCGA
TCGCCTTGTGCTTTGGTCTCTTTTTCTCCCCCCCGCCTGGATCCTGCCTCGCGCGGGCCGTCCTGTTGCTGAGAC
TCGGGGTACCGTTCTGCTGACCCAGCTCCCTTTAGTCACGTTTGCTTGGCTCTGGTACCAAATAGTTGGGATTAC
CGAAGAGTCCCCTTCCTTGCGTGTCAGCACGGATGCTGTGACTGCCACCTGCGTCCTCGTCAAGTGCCCGAGCTC
GCCGCCGTGTGTGCTGCGCTGAGTGAGTTATGAGGTGCCTTTCCCGGAACCCTCCTCTCGCCTGGACCCAAGAGA
GGCGACAGCTGTGGCTGGGGCTCTTGGTTTCCAGAGGGTCTGGACTGGTTTGGGTGCTTTAAAATAGATATTTAG
TTCAGTGGTGCTTATGGGGGAGATGGGACTAGAACTTAAGTGTGAGACTTGGGTGGATGGGAAAGTTAAATATTG
GTCTCTTCAAGTTTTTTTTTCTTTTGCTTTGTTACCACTTGTCACTGTCTCCATGTTAAAATGCCAAAAATGAT
GTAGTTGTTGTTGCTTTTTTCCCTATTTTCCACCCCAGTCGCTCCTTACCGTGACTCCTGCCCTTGGAGGGCATG
TAGCAGTGTCTGTCCTGCCAGTCCCAAGGCCCTGTGGGAGGAGACTGGCCTGCATCTCTCTAAGACTTAGTCTGA
CGCCACGCGCATCTCTTGTTCTGTGTTCAATCAGTAGTCCAGGGGAGAAGCTTCTGCTACTTCAGAGCTTTGCTA
AACTAACCTAATTTGTCCAAATCACCCCAAAACCACCATCTCTGACGTAAGCTTCCATGCGACAGCCTGATCCGT
TTCCCTGGACAGGTCTCTTTCCTGGAATGCAGCCCAGGCACCTGTGCTCCTGGCACCCTTGAGGTCTCTTCTTTG
AGCCGTGGTCACCGAGAGGGTTGAGGACGCAGCACCCGAGGTCCCAGCCTTTGCAGGAGCCTCCCTGGGCTTAGC

FIGURE 68B

TGGACTTAGATCTTCGGTGGCCTCATGTAAACGTGGCAGCCAGCCTCTTCTAGAACCCTAGCCCAGGGACTGGAG
CAGGAAAGGGACCTTCAAAGTGAAGACTGCCTTGTCCCGCAGCTCCTTCTGGCTTAGATTGAAACATGGGCTTCC
TAATGGGTTAAATCCTTTAAAACAAGGAGTTGTGGGGGAAGGGTGTCGTGCACTCCTAGAGAAAGGTACACAGTT
GCCCGGTTGGGAATGTGCTTGGCGCTGACCCTGCGGGCATCTGACTGGTCTTCCAGCTCAGGAAAAAGAATTTGA
AAGAGGCTTAGCGTGAAGGGGAATCAAAGAGGAGGTTGTGATTTGGTCGAAGGTGCCTGGTTTAGTGCTGTAATT
GTCTTATTATTTTTTTATATATATATTTCTTGGAGTAAACATTTTAAAT

FIGURE 69

ATGAGTGATCAGCAGCTGGACTGTGCCTTGGACCTAATGAGGCGCCTGCCTCCCCAGCAAATCGAGAAAAACCTC
AGCGACCTGATCGACCTGGTCCCCAGTCTATGTGAGGATCTCCTGTCTTCTGTTGACCAGCCACTGAAAATTGCC
AGAGACAAGGTGGTGGGAAAGGATTACCTTTTGTGTGACTACAACAGAGATGGGGACTCCTATAGGTCACCATGG
AGTAACAAGTATGACCCTCCCTTGGAGGATGGGGCCATGCCGTCAGCTCGGCTGAGAAAGCTGGAGGTGGAAGCC
AACAATGCCTTTGACCAGTATCGAGACCTGTATTTTGAAGGTGGCGTCTCATCTGTCTACCTCTGGGATCTGGAT
CATGGCTTTGCTGGAGTGATCCTCATAAAGAAGGCTGGAGATGGATCAAAGAAGATCAAAGGCTGCTGGGATTCC
ATCCACGTGGTAGAAGTGCAGGAGAAATCCAGCGGTCGCACCGCCCATTACAAGTTGACCTCCACGGTGATGCTG
TGGCTGCAGACCAACAAATCTGGCTCTGGCACCATGAACCTCGGAGGCAGCCTTACCAGACAGATGGAGAAGGAT
GAAACTGTGAGTGACTGCTCCCCACACATAGCCAACATCGGGCGCCTGGTAGAGGACATGGAAAATAAAATCAGA
AGTACGCTGAACGAGATCTACTTTGGAAAAACAAAGGATATCGTCAATGGGCTGAGGTCTGTGCAGACTTTTGCA
GACAAATCAAAACAAGAAGCTCTGAAGAATGACCTGGTGGAGGCTTTGAAGAGAAAGCAGCAATGC**TAA**ACCTCT
GTTTCATGCTAACCAGACACGCCGTGCACTCGTTAGATTCCTTTCTTAGAAAACTCGTTTTCTGCTCCCTTCCCT
CGTCCCTTCCCTCCCCGACAGGTCACATAACAGCTGCATCATTGACCGCACAGCGCCATCTCTCCCTGAGAATAA
AGCCGATAGCCACCTCCTCCGGCTCCGAGCCTGCTTCTGCCACACCTCGCTCTCAGTCTCTCCACATTTCCATAG
AGACCGTGTGGTTTTTGTTCACCCGGG

FIGURE 70

MSDQQLDCALDLMRRLPPQQIEKNLSDLIDLVPSLCEDLLSSVDQPLKIARDKVVGKDYLLCDYNRDGDSYRSPW
SNKYDPPLEDGAMPSARLRKLEVEANNAFDQYRDLYFEGGVSSVYLWDLDHGFAGVILIKKAGDGSKKIKGCWDS
IHVVEVQEKSSGRTAHYKLTSTVMLWLQTNKSGSGTMNLGGSLTRQMEKDETVSDCSPHIANIGRLVEDMENKIR
STLNEIYFGKTKDIVNGLRSVQTFADKSKQEALKNDLVEALKRKQQC

FIGURE 71

CCGCGTCTCGCGTAGTCTCCCGCGCCGCCGTCCACTGCGCGCTTCGCTCTCCGCCGCCCGAGGCCCGCGCGCTCG
CC**ATG**TCCCGGCCACCGCCACCGCGGGTCGCCTCGGTGCTGGGCACCATGGAGATGGGGCGCCGCATGGACGCGC
CCGCCAGCGCCGCGGCCGTGCGCGCCTTTCTGGAGCGCGGCCACACCGAACTGGACACGGCCTTCATGTACAGCG
ACGGCCAGTCCGAGACCATCCTGGGCGGCCTGGGGCTCGGGCTGGGCGGTGGCGACTGCAGAGTGAAAATTGCCA
CCAAGGCCAACCCTTGGGATGGAAAATCACTAAAGCCTGACAGTGTCCGGTCCCAGCTGGAGACGTCATTGAAGA
GGCTGCAGTGTCCCCAAGTGGACCTCTTCTACCTACACACACCTGACCACGGCACCCCGGTGGAAGAGACGCTGC
ATGCCTGCCAGCGGCTGCACCAGGAGGGCAAGTTCGTGGAGCTTGGCCTCTCCAACTATGCTAGCTGGGAAGTGG
CCGAGATCTGTACCCTCTGCAAGAGCAATGGCTGGATCCTGCCCACTGTGTACCAGGGCATGTACAACGCCACCA
CCCGGCAGGTGGAAACGGAGCTCTTCCCCTGCCTCAGGCACTTTGGACTGAGGTTCTATGCCTACAACCCTCTGG
CTGGGGGCCTGCTGACTGGCAAGTACAAGTATGAGGACAAGGACGGGAAACAGCCTGTGGGCCGCTTCTTTGGGA
ATAGCTGGGCTGAGACCTACAGGAATCGCTTCTGGAAGGAGCACCACTTCGAGGCCATTGCGTTGGTGGAGAAGG
CCCTGCAGGCCGCATATGGCGCCAGCGCCCCCAGTGTGACCTCGGCTGCCCTCCGGTGGATGTACCACCACTCAC
AGCTGCAGGGTGCCCACGGGGACGCGGTCATCCTGGGCATGTCCAGCCTGGAGCAGCTGGAGCAGAACTTGGCAG
CAACAGAGGAAGGGCCCCTGGAGCCGGCTGTCGTGGATGCCTTTAATCAAGCCTGGCATTTGGTTGCTCACGAAT
GTCCCAACTACTTCCGC**TAG**GCCCATCATGGCTCAGGCTGCCCAAGGCTTTTCTGTCACCTCTTTTGTTCTCTCA
CACTGACCAGTCTTGGCCTTAAGCTGACTTAGAAGGGTTTTTCTGAATTGTCTAGATCCATGCATTATTTTTCTA
GCTTCCTGCCTTGCTCCCTATTCACTTTACACTGTGAAAGGTGGGGGGTGAGTCCCACTTGAGCGCTTCCTGTTG
AATAAAGCAGGCACTTGACCTGGCTGTAGCCTAGGTCTTGAGTGAACCCCAAAAAA

FIGURE 72

MSRPPPPRVASVLGTMEMGRRMDAPASAAAVRAFLERGHTELDTAFMYSDGQSETILGGLGLGLGGGDCRVKIAT
KANPWDGKSLKPDSVRSQLETSLKRLQCPQVDLFYLHTPDHGTPVEETLHACQRLHQEGKFVELGLSNYASWEVA
EICTLCKSNGWILPTVYQGMYNATTRQVETELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDGKQPVGRFFGN
SWAETYRNRFWKEHHFEAIALVEKALQAAYGASAPSVTSAALRWMYHHSQLQGAHGDAVILGMSSLEQLEQNLAA
TEEGPLEPAVVDAFNQAWHLVAHECPNYFR

FIGURE 73

ACCGTCTTCCGCCGCACGTGGATTCAGCGCG**ATG**CCCAAATCCAAGCGCGACAAGAAAGTCTCCTTAACCAAAAC
TGCCAAGAAAGGCTTGGAATTGAAACAAAACCTGATAGAAGAGCTTCGGAAATGTGTGGACACCTACAAGTACCT
TTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACATCCGGAACGCCTGGAAGCACAGCCGGAT
GTTCTTTGGCAAAAACAAGGTGATGATGGTGGCCTTGGGTCGGAGCCCATCTGATGAATACAAAGACAACCTGCA
CCAGGTCAGCAAAAGGTTGAGGGGTGAGGTGGGTCTCCTGTTCACCAACCGCACAAAGGAAGAGGTGAATGAGTG
GTTCACGAAATACACAGAAATGGACTACGCCCGAGCTGGTAACAAAGCAGCTTTCACTGTGAGCCTGGATCCAGG
GCCCCTGGAGCAGTTCCCCCACTCCATGGAGCCACAGCTCAGGCAGCTGGGCCTGCCCACCGCCCTCAAGAGAGG
TGTGGTGACTCTGCTGTCTGACTACGAGGTGTGCAAGGAGGGCGATGTGCTGACCCCAGAGCAGGCTCGCGTCCT
GAAGCTTTTTGGGTATGAGATGGCTGAATTCAAGGTGACCATCAAATACATGTGGGATTCACAGTCGGGAAGGTT
CCAGCAGATGGGAGACGACTTGCCAGAGAGCGCATCTGAGTCCACAGAAGAGTCAGACTCAGAAGATGATGAC**TG**
AAAGGGACTCGGGACTGAAGGTCTCCTGGAAGCTTCTGGGTCTCACTGGACCATCAGGACTGCTGCCGCCCCTCT
GGAGAGAGCAGCTTTTTATTTGTCTGTAGACAGGGAACATGATGGGCACTGACCTCCTGTAAAGAATAAAACTGT
GGGCCGGGCGCGGTGGCTCACGCCTGGAATCCCAGCACTTTGGGAAGCCGAGGTGGGCAGATCATAAGGTCAGGA
GATTAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATAGAAAAAAAAAACTAGTTGGGCATAG
TGGCATGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTG
CCGTGAGTTGAGATTGGACCACTGCTCTCCAGCCTGGGCAACAGAGTAAAACTCTGTCCC

FIGURE 74

MPKSKRDKKVSLTKTAKKGLELKQNLIEELRKCVDTYKYLFIFSVANMRNSKLKDIRNAWKHSRMFFGKNKVMMV
ALGRSPSDEYKDNLHQVSKRLRGEVGLLFTNRTKEEVNEWFTKYTEMDYARAGNKAAFTVSLDPGPLEQFPHSME
PQLRQLGLPTALKRGVVTLLSDYEVCKEGDVLTPEQARVLKLFGYEMAEFKVTIKYMWDSQSGRFQQMGDDLPES
ASESTEESDSEDDD

FIGURE 75

ATCGCTGGGCGACTGATTTCGAGTTTCCGGTCAGGTTAGGCCGGGGGGGTGCGGTCCTGGTCGGAAGGAGGTGGA
GAGTCGGGGGTCACCAGGCCTATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCGCCGTCATGGAGAGCGGAG
GGCGGCCCTCGCTGTGCCAGTTCATCCTCCTGGGCACCACCTCTGTGGTCACCGCCGCCCTGTACTCCGTGTACC
GGCAGAAGGCCCGGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAAGTTCATTTGGGTGAAGATTTAAAGAGTATTC
TTTCAGAAGCTCCAGGAAAATGCGTGCCTTATGCTGTTATAGAAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTA
ACAGCCAGTTTGTGGAAAACTGCAAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAAGATGGTGTGGAATC
GAACCACCCACCTTTGGAATGATTGCTCAAAGATCATTCATCAGAGGACCAACACAGTGCCCTTTGACCTGGTGC
CCCACGAGGATGGCGTGGATGTGGCTGTGCGAGTGCTGAAGCCCCTGGACTCAGTGGATCTGGGTCTAGAGACTG
TGTATGAGAAGTTCCACCCCTCGATTCAGTCCTTCACCGATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCA
AAGGCATCCAAGAGACCGAGGAGATGCTGAAGGTGGGGGCCACCCTCACAGGGGTTGGCGAACTGGTCCTGGACA
ACAACTCTGTCCGCCTGCAGCCGCCCAAACAAGGCATGCAGTACTATCTAAGCAGCCAGGACTTCGACAGCCTGC
TGCAGAGGCAGGAGTCGAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTTTTGGCTTTGCCACATGTGCCACCC
TCTTCTTCATTCTCCGGAAGCAGTATCTGCAGCGGCAGGAGCGCCTGCGCCTCAAGCAGATGCAGGAGGAGTTCC
AGGAGCATGAGGCCCAGCTGCTGAGCCGAGCCAAGCCTGAGGACAGGGAGAGTCTGAAGAGCGCCTGTGTAGTGT
GTCTGAGCAGCTTCAAGTCCTGCGTCTTTCTGGAGTGTGGGCACGTTTGTTCCTGCACCGAGTGCTACCGCGCCT
TGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGGCGATCACCCGGGTGATACCCCTGTACAACAGCTAATAGT
TTGGAAGCCGCACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTCAGGGATTTTTATCTCGAGGCCTTTGGAGG
AGCAGTGGTGGGGGTAGCTGTCACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAAACTCTCCAGACCCATGC
CTCCAATGGCAGGATGCTGCCTTTCCCACCTGAGAGGGGACCCTGTCCATGTGCAGCCTCATCAGAGCCTCACCC
TGGGAGGATGCCGTGGCGTCTCCTCCCAGGAGCCAGATCAGTGCGAGTGTGACTGAAAATGCCTCATCACTTAAG
CACCAAAGCCAGTGATCAGCAGCTCTTCTGTTCCTGTGTCTTCTGTTTTTTTCTGGTGAATCGTTGCTTGCTGTG
GACTTGGTGGAGGACTCAGAGGGGAGGAAAGGCTGGGCCCCGAGTACAACGGATGCCTTGGGTGCTGCCTCCGAA
GAGACTCTGCCGCAGCTTTTCTTCTTTTTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAATTGTCAGGCTGGG
CAGGTCAACTTGTGTTCCTTTCCCCTCACCTGCTTGCCTCCTTAACGCCTGCACGTGTGTGTAGAGGACAAAAGA
AAGTGAAGTCAGCACATCCGCTTCTGCCCAGATGGTCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAA
GGGCAGTTGGTCAGGCAGGCCTCCTGGTTTCGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGG
GGTGGTCCCTGGTTTTCCCTCCTGGAGAATGAGGCGCAGAGGCCTCGCCTCCTGAAGGACGCAGTGTGGATGCCA
CTGGCCTAGTGTCCTGGCCTCACAGCTTCCTTGCAAGGCTGTCACAAGGAAAAGCAGCCGGCTGGCACCCTGAGC
ATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCGCAGCTTTGACATCTTGGTGTACTCATGTCGCTTCTCCTT
GTGTTACCCCCTCCCAGTATTACCATTTGCCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGG
CTGTTTTCCCCCACCTCTGAGTAGTTGGAGGTCACATACACAGCTCTTTTTTTATTGCCCTTTTCTGCCTCTGAA
TGTTCATCTCTCGTCCTCCTTTGTGCAGGCGAGGAAGGGGTGCCCTCAGGGGCCGACACTAGTATGATGCAGTGT
CCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC

FIGURE 76A

GCGGCAGAGCTCGGCGGCTGGGACTGGAGGACAGCGGTGGCGGAGGCGACTAGCGGCGGCGGGAGCGGCGCCGAG
AGGCCGTGCGGGACGCGGGCGCCAGGACCGGCCGAACGCAGAGGTTGATTCTTCACCACACTGAAACCATTAGGA
AAAATCCTTGTGGTTAACAGCAGAGGCTTCAGAGTGTAACCTGTACTCGGGCCTAGAAATTATTTAAAATGGCGA
CTGATACGTCTCAAGGTGAACTCGTCCATCCTAAGGCACTCCCACTTATAGTAGGAGCTCAGCTGATCCACGCGG
ACAAGTTAGGTGAGAAGGTAGAAGATAGCACCATGCCGATTCGTCGAACTGTGAATTCTACCCGGGAAACTCCTC
CCAAAAGCAAGCTTGCTGAAGGGGAGGAAGAAAAGCCAGAACCAGACATAAGTTCAGAGGAATCTGTCTCCACTG
TAGAAGAACAAGAGAATGAAACTCCACCTGCTACTTCGAGTGAGGCAGAGCAGCCAAAGGGGGAACCTGAGAATG
AAGAGAAGGAAGAAAATAAGTCTTCTGAGGAAACCAAAAAGGATGAGAAAGATCAGTCTAAAGAAAAGGAGAAGA
AAGTGAAAAAAACAATTCCTTCCTGGGCTACCCTTTCTGCCAGCCAGCTAGCCAGGGCCCAGAAACAAACACCGA
TGGCTTCTTCCCCACGTCCCAAGATGGATGCAATCTTAACTGAGGCCATTAAGGCATGCTTCCAGAAGAGTGGTG
CATCAGTGGTTGCTATTCGAAAATACATCATCCATAAGTATCCTTCTCTGGAGCTGGAGAGAAGGGGTTATCTCC
TTAAACAAGCACTGAAAAGAGAATTAAATAGAGGAGTCATCAAACAGGTTAAAGGAAAAGGTGCTTCTGGAAGTT
TTGTTGTGGTTCAGAAATCAAGAAAAACACCTCAGAAATCCAGAAACAGAAAGAATAGGAGCTCTGCAGTGGATC
CAGAACCACAAGTAAAATTGGAGGATGTCCTCCCACTGGCCTTTACTCGCCTTTGTGAACCTAAAGAAGCTTCCT
ACAGTCTCATCAGGAAATATGTGTCTCAGTATTATCCTAAGCTTAGAGTGGACATCAGGCCTCAGCTGTTGAAGA
ACGCTCTGCAGAGAGCAGTAGAGAGGGGCCAGTTAGAACAGATAACTGGCAAAGGTGCTTCGGGGACATTCCAGC
TGAAGAAATCAGGGGAGAAACCCCTGCTTGGTGGAAGCCTGATGGAATATGCAATCTTGTCTGCCATTGCTGCCA
TGAATGAGCCGAAGACCTGCTCTACCACTGCTCTGAAGAAGTATGTCCTAGAGAATCACCCAGGAACCAATTCTA
ACTATCAAATGCATTTGCTGAAAAAAACCCTGCAGAAATGCGAAAAGAATGGGTGGATGGAACAGATCTCTGGGA
AAGGGTTCAGTGGCACCTTCCAGCTCTGTTTTCCCTATTATCCCAGCCCAGGAGTTCTGTTTCCGAAGAAAGAGC
CAGATGATTCTAGAGATGAGGATGAAGATGAAGATGAGTCATCAGAAGAAGACTCTGAGGATGAAGAGCCGCCAC
CTAAGAGAAGGTTGCAGAAGAAAACCCCAGCCAAGTCCCCAGGGAAGGCCGCATCTGTGAAGCAGAGAGGGTCCA
AACCTGCACCTAAAGTCTCAGCTGCCCAGCGGGGGAAAGCTAGGCCCTTGCCTAAGAAAGCACCTCCTAAGGCCA
AAACGCCTGCCAAGAAGACCAGACCCTCATCCACAGTCATCAAGAAACCTAGTGGTGGCTCCTCAAAGAAGCCTG
CAACCAGTGCAAGAAAGGAAGTAAAATTGCCGGGCAAGGGCAAATCCACCATGAAGAAGTCTTTCAGAGTGAAAA
AGTAAATTTTATAGGAAAAAAGGGTATCATGATGAAATTCAAAATCTTATTTTCTAAGGTCAGTGTGCATTTGTT
TAGTTTTGATGCTTTTCAAATTACATTATTTTCCTCCCCTATGAACATTGTGGGGAGGGACTCTAAATAAACCAG
TTTAGGCATTTGCTAGCTTTAGGTGCTTTTATTGGTGCCTGCCCTTTTCCTTGTTCATTTTAATTTCTGCAATAA
TCCTGGACTTTCCTAAACTATGTAATGTATACTTGTCCTTTTTCTCTGCCTCCCCCAACCCCCTGTTGTTTTTAT
GGTCAGCTTTGCCTTTTTTTTTTCTTCCAATTTTATCTAAACAGTTGCAGAGATTTTTATATTTGTAGAAAGCAT
CAAGAACGGTATGCCAGTCAGGTCCTGGAAGTAAAATGGAGGCACAATATAGCACTGACTGAGTTGTAAAGCCTC
CTGCCTGGAGACTTCAGTTATAGCTGTAATAATTAATCTTATTTATAAAAGCCACTCCACTAACCTTTTCTCTCC
AACTGTAAACACAGAGACAGCTTTGGGAATAAGCCAAAAACAGGGTGATCTCATTAGATTTTGAAGATATATGAC
TCCTTTGGGCTACATTTCATATTGATCAATTTCTAGGTATTTTTCACTGGCCCAAAGTATTGCATTCCCTTAACA
GCAAGCACAAGTTCTCTATATCACTTGTTTTTTGTTGTTGTTGTTGTTGTCGTCGTTGTTTTGAGACGGAGTCTT
GCTCAGGTGCCCCGGAGTGCAGTGGTGCAATCTCAGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCAATTCTC
CTGCTTCAGCCTCCCGAGTAGCTGGGATTACAGGTGTGTACCACCACGCCTGGCAATTTTTTTGTATTTTTAGTA
GAGATGGGGTTTCGCCGTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCGCCTGCCTCGGCCTCC
CAAAGTGCTGGGATTACAGGAGTGAGCCACTGTGCCTGGCCTATCCCACTTGGTTTTTGACTGAAGGGGAAGTGT
AGAAATATATTGATTTGTGATTTCTGGTGTCACCTGTGTTACCAAAAATCAAAACAAATCTTTTTTATTTTTTAT
TATTATTATTATTTTTGAGACAGAGTCTCGCTCTGTCGCCCAGTGTGGAGTGCAGTGGTGTGATCTTGGCTCACT
GCAAACTCCGCCTCCCAGGTTCAAGCGATTCTCCCACCTCAGCCTCCTGAGTTGGGTCCTACAGGCGCACACGAC
CACGCCCAGCTAATTTTTTGTATTTTTAGTAGAGTTGGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCT
GACCTCGTGATCCACTCACCTCAGCCTCCCAAAATCCTGGGGTTACAGATGTGAGCTACCACTCACGGCCCAAAT
CTTCTTGATCATATGTTTAAATATATTTTTTAATATTTGGAGCATGAGTTGTCACTTCTTGTTTGCCTTTTTTAT
AAGGAAATGTTGGAGAGTTACATCATTGCTAATGTAGAAATGTTAAGTGGAAAAATATACAGTTTGGTAAAATAA
ACTAGATTCTACATTTATTTGTGGGTTTTTTTCCCCTCCTTTCTTTCCACAGCACTTTTGATATCAAGCAAGTGG
CTTCCTTTTTGAGATATTAAAAAAAAAAAGAAAAGGAAAAAAGTAAATGAAGCCCAACTACCTAACCCTTTCTTA

FIGURE 76B

TTTGTATTTGTTTTAGTATTGTGAAGTTGTGTTAAATAGTACTAGCTAGAAATACAAATTTCTGGTTATCATTTC
TCTTCCCTGTGGCACTTGACATTTTAATTGTCTTAAAGTTTTTGAAGTACATCTTCTGGCCCCTTGAGTACTGCC
AGAGGCAAAAGATGTTTGTTTCTTATTCATTCCACTTTTGTCTCCTGGGATCCCTTCTGTAGCCTAAAGTATGGC
TGGGAAATGGACTTGAGAAGATTGGCTTGAATTAGATCATAATCATGTGTGATCCCATCATGAATTCATTGGAAT
TTGTGTTGCATGTAAGGCAATCTTTCCTGTTGTAAATCTTCCTTTTTTAATGTACATATATTTTGAAAAATATGA
ATAAACATGAAATTTT

FIGURE 77

GGCGCCGAGTAGCCGGGCCGGGCCGGAGCGCGGGCGGCGGCGGAGGCAGCTGCGCCCGCGCCTCCTGCCCTCCCA
GGCCCCGCGCCCCCGCGCCCGGGCCCCGGCGATGGTGACACATGCGGCGGCGGCGCGCCAGCGGCAGGACCATGGT
TGAGCGCGCCAGCAAGTTCGTGCTGGTGGTGGCGGGCCCGGTGTGCTTCATGCTCATCTTGTACCAGTACGCGGG
CCCAGGACTGAGCCTGGGCGCGCCCGGCGGCGGCGCGCCGCCCGACGACCTGGACCTGTTCCCCACGCCCGACCC
CCACTACGAGAAGAAGCACTACTTCCCGGTCCGCGAGCTGGAGCGCTCGCTGCGCTTCGACATGAAGGGCGACGA
CGTGATCGTCTTCCTGCACATCCAGAAGACGGGCGGCACCACCTTCGGCCGCCACCTCGTGCAGAACGTACGCCT
CGAGGTGCCGTGCGACTGCCGGCCCGGCCAGAAGAAGTGCACCTGCTACCGGCCCAACCGCCGCGAGACTTGGCT
CTTCTCCCGCTTCTCCACCGGCTGGAGCTGCGGGCTGCACGCCGACTGGACCGAGCTCACCAACTGCGTGCCCGG
CGTGCTGGACCGCCGCGACTCCGCCGCGCTGCGCACGCCCAGGAAGTTCTACTACATCACCCTGCTACGAGACCC
CGTGTCCCGCTACCTGAGCGAGTGGCGGCATGTGCAGAGGGGTGCCACGTGGAAGACGTCGTTGCACATGTGTGA
TGGGCGCACGCCCACGCCTGAGGGGCTGCCGCCCTGCTACGAGGGCACGGACTGGTCGGGCTGCACGCTACAGGA
GTTCATGGACTGCCCGTACAACCTGGCCAACAACCGCCAGGTGCGCATGCTGGCCGACCTGAGCCTGGTGGGCTG
CTACAACCTGTCCTTCATCCCCGAGGGCAAGCGGGCCCAGCTGCTGCTCGAGAGCGCCAAGAAGAACCTGCGGGG
CATGGCCTTCTTCGGCCTGACCGAGTTCCAGCGCAAGACGCAGTACCTGTTCGAGCGGACGTTCAACCTCAAGTT
CATCCGGCCCTTCATGCAGTACAACAGCACGCGGGCGGGCGGCGTGGAGGTGGATGAGGACACCATCCGGCGCAT
CGAGGAGCTCAACGACCTGGACATGCAGCTGTATGACTACGCCAAGGACCTCTTCCAGCAGCACTACCAGTACAA
GCGGCAGCTGGAGCGCAGGGAGCAGCGCCTGAGGAGCCGCGAGGAGCGTCTGCTGCACCGGGCCAAGGAGGCGCT
GCCGCGGGAGGACGCCGACGAGCCGGGCCGCGTGCCCACCGAGGACTACATGAGCCACATCATTGAGAAGTGGTA
GTGGCGGTGGTGGCCACGGGGAGGCCTCTTGGGGTGTGTGGGGGATAAAACAGGACAGACGACAGGTCCACCCAA
GACTGTCAAGGGATGAGCATCCCAAACCTGCTCCACAGAGGTAGCTGCGTCCTGAAAAAAAACACAGCAGGGACA
TAGTGGGGCTGGGCAGGGATGGGGCTTGAGAAATCAACAGGTGCAGCCCAGTGGGTCAGAGGAAAGCGTGCTCGA
AGGATGCCATGGTCAGGGCAGAGCCTCCAGAGCAGGTGTTGTGCCTGGAGCTGCTCTCCTGGCCTCCTTGGATTT
ATCGCAAAAACTGAAGGTTTGCGTGAGAGACGAGGACAGCGGAAAGTGGACCTGCCAGGCCGGGAGTGTGTCCCT
CACCAACTATGCACACAGCACTCGCTCTTAGCTCCTCTGTCCGGGCTACTAGGAGTGAGACCAGCTTCTGGCAAC
TGCCCCAGCTCCAGGCCATCCCATAGCTCCTCCTCTTCTGGCTGCCCCCAATGCCCCGAGGCCTGGGGAGCCCCC
AGCTCACCCATCTGTAGCTCCCTCAAAGTCAGGGCCCACCCCATCTGAGGCAGAGAAGACTCGAGTCCAGCCCCC
AGGAAGCCTGCTCCCCTCTCTGGCCCATGGTCCTGCTTCATGCTTTGGGTCAGGAGGCCAAAGCTGATGTTCAGG
CCCCACCCACTCCCTACAGTCCTCAGACC

FIGURE 78

AGAAACTCCCGGTGTGGCAGCTGAGATGGCCCAGGAAAGAACTATATTACCTTCAAAAAGAGAGGTACATGCGAT
GTTTGAGGTGGCATGAAGCTCAGTGGTGTTATATTGGAATGAGTGAGTGACCATCCTGGAGCCTTCCTGAAAGAG
GATTGGAACATCAGTTAACATCTGACCACTGCCAGCCCACCCCCTCCCACCCACGTCGATTGCATCTCTGGGCTC
CAGGGATAAAGCAGGTCTTGGGGTGCACCATGATTTCACCATTCTTAGTACTGGCCATTGGCACCTGCCTTACTA
ACTCCTTAGTGCCAGAGAAAGAGAAAGACCCCAAGTACTGGCGAGACCAAGCGCAAGAGACACTGAAATATGCCC
TGGAGCTTCAGAAGCTCAACACCAACGTGGCTAAGAATGTCATCATGTTCCTGGGAGATGGGATGGGTGTCTCCA
CAGTGACGGCTGCCCGCATCCTCAAGGGTCAGCTCCACCACAACCCTGGGGAGGAGACCAGGCTGGAGATGGACA
AGTTCCCCTTCGTGGCCCTCTCCAAGACGTACAACACCAATGCCCAGGTCCCTGACAGTGCCGGCACCGCCACCG
CCTACCTGTGTGGGGTGAAGGCCAATGAGGGCACCGTGGGGGTAAGCGCAGCCACTGAGCGTTCCCGGTGCAACA
CCACCCAGGGGAACGAGGTCACCTCCATCCTGCGCTGGGCCAAGGACGCTGGGAAATCTGTGGGCATTGTGACCA
CCACGAGAGTGAACCATGCCACCCCCAGCGCCGCCTACGCCCACTCGGCTGACCGGGACTGGTACTCAGACAACG
AGATGCCCCCTGAGGCCTTGAGCCAGGGCTGTAAGGACATCGCCTACCAGCTCATGCATAACATCAGGGACATTG
ACGTGATCATGGGGGGTGGCCGGAAATACATGTACCCCAAGAATAAAACTGATGTGGAGTATGAGAGTGACGAGA
AAGCCAGGGGCACGAGGCTGGACGGCCTGGACCTCGTTGACACCTGGAAGAGCTTCAAACCGAGATACAAGCACT
CCCACTTCATCTGGAACCGCACGGAACTCCTGACCCTTGACCCCCACAATGTGGACTACCTATTGGGTCTCTTCG
AGCCAGGGGACATGCAGTACGAGCTGAACAGGAACAACGTGACGGACCCGTCACTCTCCGAGATGGTGGTGGTGG
CCATCCAGATCCTGCGGAAGAACCCCAAAGGCTTCTTCTTGCTGGTGGAAGGAGGCAGAATTGACCACGGGCACC
ATGAAGGAAAAGCCAAGCAGGCCCTGCATGAGGCGGTGGAGATGGACCGGGCCATCGGGCAGGCAGGCAGCTTGA
CCTCCTCGGAAGACACTCTGACCGTGGTCACTGCGGACCATTCCCACGTCTTCACATTTGGTGGATACACCCCCC
GTGGCAACTCTATCTTTGGTCTGGCCCCCATGCTGAGTGACACAGACAAGAAGCCCTTCACTGCCATCCTGTATG
GCAATGGGCCTGGCTACAAGGTGGTGGGCGGTGAACGAGAGAATGTCTCCATGGTGGACTATGCTCACAACAACT
ACCAGGCGCAGTCTGCTGTGCCCCTGCGCCACGAGACCCACGGCGGGGAGGACGTGGCCGTCTTCTCCAAGGGCC
CCATGGCGCACCTGCTGCACGGCGTCCACGAGCAGAACTACGTCCCCCACGTGATGGCGTATGCAGCCTGCATCG
GGGCCAACCTCGGCCACTGTGCTCCTGCCAGCTCGGCAGGCAGCCTTGCTGCAGGCCCCCTGCTGCTCGCGCTGG
CCCTCTACCCCCTGAGCGTCCTGTTCTGAGGGCCCAGGGCCCGGGCACCCACAAGCCCGTGACAGATGCCAACTT
CCCACACGGCAGCCCCCCCCTCAAGGGGCAGGGAGGTGGGGGCCTCCTCAGCCTCTGCAACTGCAAGAAAGGGGA
CCCAAGAAACCAAAGTCTGCCGCCCACCTCGCTCCCCTCTGGAATCTTCCCCAAGGGCCAAACCCACTTCTGGCC
TCCAGCCTTTGCTCCCTCCCCGCTGCCCTTTGGCCAACAGGGTAGATTTCTCTTGGGCAGGCAGAGAGTACAGAC
TGCAGACATTCTCAAAGCCTCTTATTTTTCTAGCGAACGTATTTCTCCAGACCCAGAGGCCCTGAAGCCTCCGTG
GAACATTCTGGATCTGACCCTCCCAGTCTCATCTCCTGACCCTCCCACTCCCATCTCCTTACCTCTGGAACCCCC
CAGGCCCTACAATGCTCATGTCCCTGTCCCCAGGCCCAGCCCTCCTTCAGGGGAGTTGAGGTCTTTCTCCTCAGG
ACAAGGCCTTGCTCACTCACTCACTCCAAGACCACCAGGGTCCCAGGAAGCCGGTGCCTGGGTGGCCATCCTACC
CAGCGTGGCCCAGGCCGGGAAGAGCCACCTGGCAGGGCTCACACTCCTGGGCTCTGAACACACACGCCAGCTCCT
CTCTGAAGCGACTCTCCTGTTTGGAACGGCAAAAAAAAATTTTTTTTCTCTTTTTGGTGGTGGTTAAAAGGGAA
CACAAAACATTTAAATAAAACTTTCCAAATATTTCCGAGG

FIGURE 79

GAACCGCCATCTTCCAGTAATTCGCCAAA**ATG**ACGAACACAAAGGGAAAGAGGAGAGGCACCCAATAGATGTTCT
CCAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCACGTATATGCGAATCTATAAGAAAGGTGATATTGTAG
ACATCAAGGGAATGGGTACTGTTCAAAAAGGAACGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACA
ATGTTATCCAGTATGCTGCTAGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATG
TGCGTATTGAGCACATTAAGCACTCTGAGAGCCGAGATAGCTTCCTGAAACGCGTGAAGGAGAATGATCAGAAAA
AGAGAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGCAAAGCACACTTTG
TGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCTCTATGAATTCACGGCA**TAA**TAGGTATTTAAAA
AAAAAAAAAGACCTCTGGGCTGT

FIGURE 80

DRTQRERGEAPNRMFSRPFRKHGVVPLATYMRIYKKGDIVDIKGMGTVQKGTPHKCYHGKTGRVYNVIQYAASIV
VNKQVKGKILAKRINVRIEHIKHSESRDSFLKRVKENDQKKREAKEKGTWVQLKRQPAPPSKAHFVRTNGKEPEL
LEPILYEFTA

FIGURE 81

GGCAGCCGAGGAGACCCCGCGCAGTGCTGCCAACGCCCCGGTGGAGAAGCTGAGGTCATCATCAGATTTGAAATA
TTTAAAGTGGATACAAAATTATTTCAGCA**ATG**CAGACAATTAAGTGTGTTGTTGTGGGCGATGGTGCTGTTGGTA
AAACATGTCTCCTGATATCCTACACAACAAACAAATTTCCATCGGAATATGTACCGACTGTTTTTGACAACTATG
CAGTCACAGTTATGATTGGTGGAGAACCATATACTCTTGGACTTTTTGATACTGCAGGGCAAGAGGATTATGACA
GATTACGACCGCTGAGTTATCCACAAACAGATGTATTTCTAGTCTGTTTTTCAGTGGTCTCTCCATCTTCATTTG
AAAACGTGAAAGAAAAGTGGGTGCCTGAGATAACTCACCACTGTCCAAAGACTCCTTTCTTGCTTGTTGGGACTC
AAATTGATCTCAGAGATGACCCCTCTACTATTGAGAAACTTGCCAAGAACAAACAGAAGCCTATCACTCCAGAGA
CTGCTGAAAAGCTGGCCCGTGACCTGAAGGCTGTCAAGTATGTGGAGTGTTCTGCACTTACACAGAAAGGCCTAA
AGAATGTATTTGACGAAGCAATATTGGCTGCCCTGGAGCCTCCAGAACCGAAGAAGAGCCGCAGGTGTGTGCTGC
TA**TGA**ACATCTCTCCAGAGCCCTTTCTGCACAGCTGGTGTCGGCATCATACTAAAAGCAATGTTTAAATCAAACT
AAAGATTAAAAATTAAAATTCGTTTTTGCAATAATGACAAATGCCCTGCACCTACCCACATGCACTCGTGTGAGA
CAAGGCCCATAGGTATGGCCCCCCCCTTCCCCCTCCCAGTACTAGTTAATTTTGAGTAATTGTATTGTCAGAAAA
GTGATTAGTACTATTTTTTTTTGTTGTTTCAAAAAAAAAATTTTTGTGTGTCTGTTTTTTTTTTTTTTTTTTTT
GTTGTTTAAAAGGAAGGCATGCTTGTGGATGACTCTGTAACAGACTAATTGGAATTGTTGAAGCTGCTCCCTGGT
TCCACTCTGGAGAGTAATCTGGGACATCTTAGTGTTTTGTTTTGTTTTTTTCCCTCCTCTTTTTTTTGGGGGGGA
GTGTGTGTGGGGTTTGTTTTTTAGTCTTGTTTTTTTTAATTCATTAACCAGTGGTTAGCCCTTAAGGGGAGGAGGA
CGGATTGATTCCACATTCCACTTCCTAGATCTAGTTTAGAAAACATGTTCCCCATCTGGTGCTCTTAGGAAGGAG
TATAGTAAATGCCTCATTTAATAACATACTCCTTTTTGAAAGTTGCCTTTTCTCTCCACCCTTGAGTAGATCCAG
TATTTGATGAAACTCATGAAAGTGGGTGGAGCCCATCTTGCCCCTCCTCTTTTCTAGGACGCACTATATGTGACT
GTGACTTTCAAGGACATTTGTTTGCCATTTGCTGATTTTTTTGGGAAGTTAATTTCTAACTTCTTTCACTGATAA
ATGAAGAAAAGTATTGCACCTTTGAAATGCACCAAATGAATTGAGTTTGTAATTAAAAAAATTTTTTTCCCTTTC
AGTCATTGTCTTATATGCTTAGCATAGATTTGCAGCTCAGTAGTATATGGTGTTCCTAGAATGCAGCTGAAGACC
TGTTATGTAGAGGAAATACGAGGGGTGGTGCTAGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTA
GGAGGATGGAGGCCTGCTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACATGGGGAC
CAGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGAGGCTCTCTAGTTTA
ATAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTTAATAGGGATTTTTTCAGCTTATTTTGGTT
GCAGTTTCCAATTTTTAAAAATGTTGAGGTAATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGT
GTTGAACCAATGCTTTCTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACC
CTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAA

FIGURE 82

MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQT
DVFLVCFSVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLARDLK
AVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

FIGURE 83

CGCGCGCGCCATTTCTAGTCGTTTTCAAAGCGCCTCGCGCTGATTCTCACGGGCCCGGCTGCCGGCCCCCGCTCT
GCCCTGCATAATAAA**ATG**GCTAATCAGGTGAATGGTAATGCGGTACAGTTAAAAGAAGAGGAAGAACCAATGGAT
ACTTCCAGTGTAACTCACACAGAACACTACAAGACACTGATAGAGGCAGGCCTCCCACAGAAGGTGGCAGAAAGA
CTTGATGAAATATTTCAGACAGGATTGGTAGCTTATGTCGATCTTGATGAAAGAGCAATTGATGCTCTCAGGGAA
TTTAATGAAGAAGGAGCTCTGTCTGTACTACAGCAGTTCAAGGAAAGTGACTTATCACATGTTCAGAACAAAAGT
GCATTTTTATGTGGAGTTATGAAGACCTACAGGCAGAGAGAGAAACAGGGGAGCAAGGTGCAAGAGTCCACAAAG
GGACCTGATGAAGCGAAGATCAAGGCCTTGCTTGAGAGAACTGGTTATACTCTGGATGTAACCACAGGACAGAGG
AAGTATGGTGGTCCTCCACCAGACAGTGTGTACTCTGGCGTGCAACCTGGAATTGGAACGGAGGTATTTGTAGGC
AAAATACCAAGGGATTTATATGAGGATGAGTTGGTGCCCCTTTTTGAGAAGGCCGGACCCATTTGGGATCTACGT
CTTATGATGGATCCACTGTCCGGTCAGAATAGAGGGTATGCATTTATCACCTTCTGTGGAAAGGAAGCTGCACAG
GAAGCCGTGAAACTGTGTGACAGCTATGAAATTCGCCCTGGTAAACACCTTGGAGTGTGCATTTCTGTGGCAAAC
AACAGACTTTTTGTTGGATCCATTCCGAAGAATAAGACTAAAGAAAACATTTTGGAAGAATTCAGTAAAGTCACA
GAGGGTTTGGTGGACGTTATTCTCTATCATCAACCCGATGACAAAAAGAAGAATCGGGGGTTCTGCTTCCTTGAA
TATGAGGATCACAAGTCAGCAGCACAAGCCAGACGCCGGCTGATGAGTGGAAAAGTAAAAGTGTGGGGAAATGTA
GTTACAGTTGAATGGGCTGACCCTGTGGAAGAACCAGATCCAGAAGTCATGGCTAAGGTAAAAGTTTTGTTTGTG
AGAAACTTGGCTACTACGGTGACAGAAGAAATATTGGAAAAGTCATTTTCTGAATTTGGAAAACTCGAAAGAGTA
AAGAAGTTGAAAGATTATGCATTTGTTCATTTTGAAGACAGAGGAGCAGCTGTTAAGGCTATGGATGAAATGAAT
GGCAAAGAAATAGAAGGGGAAGAAATTGAAATAGTCTTAGCCAAGCCACCAGACAAGAAAAGGAAAGAGCGCCAA
GCTGCTAGACAGGCCTCCAGAAGCACTGCGTATGAAGATTATTACTACCACCCTCCTCCTCGCATGCCACCTCCA
ATTAGAGGTCGGGGTCGTGGTGGGGGGAGAGGTGGATATGGCTACCCTCCAGATTACTACGGCTATGAAGATTAC
TATGATGATTACTATGGTTATGATTATCACGACTATCGTGGAGGCTATGAAGATCCCTACTACGGCTATGATGAT
GGCTATGCAGTAAGAGGAAGAGGAGGAGGAAGGGGAGGGCGAGGTGCTCCACCACCACCAAGGGGGAGGGGAGCA
CCACCTCCAAGAGGTAGAGCTGGCTATTCACAGAGGGGGGCACCTTTGGGACCACCAAGAGGCTCTAGGGGTGGC
AGAGGGGGTCCTGCTCAACAGCAGAGAGGCCGTGGTTCCCGTGGATCTCGGGGCAATCGTGGGGGCAATGTAGGA
GGCAAGAGAAAGGCAGATGGGTACAACCAGCCTGATTCCAAGCGTCGTCAGACCAACAACCAACAGAACTGGGGT
TCCCAACCCATCGCTCAGCAGCCGCTTCAGCAAGGTGGTGACTATTCTGGTAACTATGGTTACAATAATGACAAC
CAGGAATTTTATCAGGATACTTATGGGCAACAGTGGAAG**TAG**ACAAGTAAGGGCTTGAAAATGATACTGGCAAGA
TACGATTGGCTCTAGATCTACATTCTTCAAAAAAAAAAATTGGCTTAACTGTTTCATCTTTAAGTAGCATTTTGC
TGCCATTTGTATTGGGCTGAAGAAATCACTATTGTGTATATACTCAAGTCTTTTTATTTTTCCTCTTTTCATAAA
TGCTCTTGGACATTATTGGGCTTGCAGAGTTCCCTTATTCTGGGGATTACAATGCTTTTATCGTTTCAGGCTTCA
TTTTAGCTTCAAAACAAGCTGGGCACACTGTTAAATCATGATTTTGCAGAACCTTTGGTTTTGGACAGTTTCATT
TTTTTGGATTTGGGATAGATTACATAGGAGTATGGAGTATGCTGTAAATAAAAATACAAGCTAGTGCTTTGTCTT
AGTAGTTTTAAGAAATTAAAGCAAACAAATTTAAGTTTTCTTGTATTGAAAATAACCTATGATTGTATGTTTTGC
ATTCCTAGAAGTAGGTTAACTGTGTTTTTAAATTGTTATAACTTCACACCTTTTTGAAATCTGCCCTACAAAATT
TGTTTGGCTTAAACGTCAAAAGCCGTGACAATTTGTTCTTTGATGTGATTGTATTTCCAATTTCTTGTTCATGTA
AGATTTCAATAAAACTAAAAAATCTATTCAAAACATTA

FIGURE 84

MANQVNGNAVQLKEEEEPMDTSSVTHTEHYKTLIEAGLPQKVAERLDEIFQTGLVAYVDLDERAIDALREFNEEG
ALSVLQQFKESDLSHVQNKSAFLCGVMKTYRQREKQGSKVQESTKGPDEAKIKALLERTGYTLDVTTGQRKYGGP
PPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEKAGPIWDLRLMMDPLSGQNRGYAFITFCGKEAAQEAVKL
CDSYEIRPGKHLGVCISVANNRLFVGSIPKNKTKENILEEFSKVTEGLVDVILYHQPDDKKKNRGFCFLEYEDHK
SAAQARRRLMSGKVKVWGNVVTVEWADPVEEPDPEVMAKVKVLFVRNLATTVTEEILEKSFSEFGKLERVKKLKD
YAFVHFEDRGAAVKAMDEMNGKEIEGEEIEIVLAKPPDKKRKERQAARQASRSTAYEDYYYHPPPRMPPPIRGRG
RGGGRGGYGYPPDYYGYEDYYDDYYGYDYHDYRGGYEDPYYGYDDGYAVRGRGGGRGGRGAPPPPRGRGAPPPRG
RAGYSQRGAPLGPPRGSRGGRGGPAQQQRGRGSRGSRGNRGGNVGGKRKADGYNQPDSKRRQTNNQQNWGSQPIA
QQPLQQGGDYSGNYGYNNDNQEFYQDTYGQQWK

FIGURE 85

CGGACTGGCAGGGGGCAGGGAAGCTCAAAGATCTGGGGTGCTGCCAGGAAAAAGCAAATTCTGGAAGTTAATGGT
TTTGAGTGATTTTTAAATCCTTGCTGGCGGAGAGGCCCGCCTCTCCCCGGTATCAGCGCTTCCTCATTCTTTGAA
TCCGCGGCTCCGCGGTCTTCGGCGTCAGACCAGCCGGAGGAAGCCTGTTTGCAATTTAAGCGGGCTGTGAACGCC
CAGGGCCGGCGGGGGCAGGGCCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGCAGGCTCTATAAGT
GACCGCCGCGGCGAGCGTGCGCGCGTTGCAGGTCACTGTAGCGGGACTTCTTTTGGTTTTCTTTCTCTTTGGGGC
ACCTCTGGACTCACTCCCCAGCATGAAGGCGCTGAGCCCGGTGCGCGGCTGCTACGAGGCGGTGTGCTGCCTGTC
GGAACGCAGTCTGGCCATCGCCCGGGGCCGAGGGAAGGGCCCGGCAGCTGAGGAGCCGCTGAGCTTGCTGGACGA
CATGAACCACTGCTACTCCCGCCTGCGGGAACTGGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGGTGGA
AATCCTACAGCGCGTCATCGACTACATTCTCGACCTGCAGGTAGTCCTGGCCGAGCCAGCCCCTGGACCCCCTGA
TGGCCCCCACCTTCCCATCCAGACAGCCGAGCTCACTCCGGAACTTGTCATCTCCAACGACAAAAGGAGCTTTTG
CCACTGACTCGGCCGTGTCCTGACACCTCCAGGTGAGTATCTCCTCTCTTGGAGAGGGAGGTTTAAACGGCAAGT
CCTGGAGTTGGCAGACGTTTTGAAAAATTGCCACTCACTCGGTTTAGGGAAACTGAGGCCAGAGAGGGACAAGTG
ACTTGCCCATGGTTG

FIGURE 86

MKALSPVRGCYEAVCCLSERSLAIARGRGKGPAAEEPLSLLDDMNHCYSRLRELVPGVPRGTQLSQVEILQRVID
YILDLQVVLAEPAPGPPDGPHLPIQTAELTPELVISNDKRSFCH

FIGURE 87

TTCTCTTCCTGCTCTCCATC**ATG**GCGCAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCA
AACTCTGTCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAGCTCA
CAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATCCGGAGAAATGAAAAGATTG
CTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATCTTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGT
TAAGAAAAAACAACTTCTCAGATACTGGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAAT
ATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCAGACA
AGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGA
AGTATGATGGGATCATCCTTCCTGGCAAA**TAA**ATTCCCGTTTCTATCCAAAAGAGCAATAAAAAGTTTTCAGTGA
AATGTGCAA

FIGURE 88

MAQDQGEKENPMRELRIRKLCLNICVGESGDRLTRAAKVLEQLTGQTPVFSKARYTVRSFGIRRNEKIAVHCTVR
GAKAEEILEKGLKVREYELRKNNFSDTGNFGFGIQEHIDLGIKYDPSIGIYGLDFYVVLGRPGFSIADKKRRTGC
IGAKHRISKEEAMRWFQQKYDGIILPGK

FIGURE 89

GGAAGTTCCGGCGGGGGCGGCCGAGGGGGAAGAGTGTGTCTGCGGGAGAAAGAGGAGAATCGCCCAAGCGGCCTC
GGAAGTCCCAGGGAGTGGAGGCCCCCGCCGTGGAGCCGTGTGGTGT**ATG**TGTGGTAACACCATGTCTGTGCCCCT
GCTCACCGATGCTGCCACCGTGTCTGGAGCTGAGCGGGAAACGGCCGCGGTTATTTTTTTACATGGACTTGGAGA
CACAGGGCACAGCTGGGCTGACGCCCTCTCCACCATCCGGCTCCCTCACGTCAAGTACATCTGTCCCCATGCGCC
TAGGATCCCTGTGACCCTCAACATGAAGATGGTGATGCCCTCCTGGTTTGACCTGATGGGGCTGAGTCCAGATGC
CCCAGAGGACGAGGCTGGCATCAAGAAGGCAGCAGAGAACATCAAGGCCTTGATTGAGCATGAAATGAAGAACGG
GATCCCTGCCAATCGAATCGTCCTGGGAGGCTTTTCACAGGGCGGGGCCCTGTCCCTCTACACGGCCCTCACCTG
CCCCCACCCTCTGGCTGGCATCGTGGCGTTGAGCTGCTGGCTGCCTCTGCACCGGGCCTTCCCCCAGGCAGCTAA
TGGCAGTGCCAAGGACCTGGCCATACTCCAGTGCCATGGGGAGCTGGACCCCATGGTGCCCGTACGGTTTGGGGC
CCTGACGGCTGAGAAGCTCCGGTCTGTTGTCACACCTGCCAGGGTCCAGTTCAAGACATACCCGGGTGTCATGCA
CAGCTCCTGTCCTCAGGAGATGGCAGCTGTGAAGGAATTTCTTGAGAAGCTGCTGCCTCCTGTC**TAA**CTAGTCGC
TGGCCCCAGTGCAGTACCCCAGCTCATGGGGGACTCAGCAAGCAAGCGTGGCACCATCTTGGATCTGAGCCGGTC
GAGCCCCTGTCCCCACCCTTCCTGACCTGTCCTTTTCCCACAGGCCTCTGGGGGCAGGTGGCAAGGCCTGGCCGG
GCCTTCCTTCCTGGCCTTAGCCACCTGGCTCTGTCTGCAGCAGGGGCAGGCTGCTTTCTTATCCATTTCCCTGGA
GGCGGGCCCCCCCTGGCAGCAGTATTGGAGGGGCTACAGGCAGCTGGAGAAAGGGGCCCAGCCGCTGACCCACTCA
CTCAGGACCTCACTCACTAGCCCCGCTTTGGGCCCCCTCCTGTGACCTCAGGGTTTGGCCCATGGGGCCCCCCCA
GGCCCCTGCCCCAACTGATTCTGCCCAGATAATCGTGTCTCCTGCCTCCACTCAGCTGCTTCTCAGTCATGAATG
TGGCCATGGCCCCGGGGTCCCCTTGCTGCTGTGGGCTCCCTGTCCCTGGGCAGGAGTGCTGGTGAGGAGGTGGAG
CCTTTTGAGGGGGGCCTTCCCTCAGCTGTTTCCCCACACTGGGGGGCTGGGCCCTGCCTCCCCGTTACCCTCCTT
CCCTGCAGGCCTGGAGCCTGTAGGGCTGGACTGAGGTTCAGGTCTCCCCCCAGCTGTCTCACCCCCACTTTGTCC
CCACTCTAGAGCAGGGAGGCAGTGGGGGAGGAGTTGTGTCTCGTCTTCTGTCTCCATGTGGTTTTTGGGTGTTTT
TCTTGTTGTGTCCTGGATTCCGATAAAATTAAAGAAATTGCTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 90

MCGNTMSVPLLTDAATVSGAERETAAVIFLHGLGDTGHSWADALSTIRLPHVKYICPHAPRIPVTLNMKMVMPSW
FDLMGLSPDAPEDEAGIKKAAENIKALIEHEMKNGIPANRIVLGGFSQGGALSLYTALTCPHPLAGIVALSCWLP
LHRAFPQAANGSAKDLAILQCHGELDPMVPVRFGALTAEKLRSVVTPARVQFKTYPGVMHSSCPQEMAAVKEFLE
KLLPPV

FIGURE 91

AGAAGGAGAAGGTCGGGTTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGGTGTTCGTGGGCTTTGTCGGTC
CGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCGACGTCGAGAGGGAGCCGCTGCCGCGTTAGTTCCGAGC
TTGAAGTCACTAGGACTTCTCTCAAACTTGTGTGCTGAGGAGACTCAGATGTTGGCCTCAGCTCCTAGGCTGAAC
TCAGCAGATCGGCCCATGAAAACTTCTGTATTGAGACAAAGGAAGGGATCTGTCAGAAAGCAACACTTGTTATCT
TGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAGCAGACTGAAAGGTGACAAAGA
AGCTGAAG**ATG**GGTGGTGGAGAGAGGTATAACATTCCAGCCCCTCAATCTAGAAATGTTAGTAAGAACCAACAAC
AGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTCATAAGAAAAAAGAAAGAGGACATG
GTTATAACTCATCAGCAGCTGCCTGGCAGGCCATGCAAAATGGGGGGAAGAACAAAAATTTTCCAAATAATCAAA
GTTGGAATTCTAGCTTATCAGGTCCCAGGTTACTTTTTAAATCTCAAGCTAATCAGAACTATGCTGGTGCCAAAT
TTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCACCAAGCCACTGGGTCCCTGTTTCCTTTAATCCTTCAG
ATAAGGAAATAATGACATTTCAACTTAAAACCTTACTTAAAGTACAGGTA**TAA**AATAAGACAAATGTTTAAATTT
AGTTATGTTCACGGATAGTTGTCAATTGGTCTGAAACAAATTCGCTAGGGAATCTATTTGTGTAGAACTAATTAA
TGTAAAAAAAACAGACCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGTATCAGTGCAACTTTAATGATTGT
ACTTGATATTAAGTGTTCTCAACTGAGTAACTTTTAAGTGGAAACCAAGTTTAGATTTGGGGAGTGGTAAAGGAA
TCAGCTTTTTCTATTGTTAGGGGAAGACAGTAATTTATCATTCATGGACCAGTAGATTGTTGAAAGTTGGTGAAT
CGGATTATAAGCTTCTAGCTAACACAAGGATTCAGAATTAGGTAAACATCTGAAGGTTTAGTATATTAGAAACAC
CCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGAATTTTTCGTAATAATTGCATTTTAGTG
AATTGTACAGTGGGTGGAAAGGGCATTTGGAGCTCATTAGAATGAGACATAGTACACCCCAATGGCCCTGTTTAT
TAAATGTAGTGGATTAAGTGTCTGTCAACAAATACACCAAAACCATTTTTTATAGAAACAGTATTTAATGGTCAC
TCAATAGCTTTCAAAATACATTTTTGTATTACAGCACTGCACAAGCTATTCTAATAGTGCTCTCGCCTCATCATT
CCTGCAAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTACCTAGGGGAGAAAGAGCCATGTAAATA
TCTGTAATAAACTTGTAGCATATGTAAAGTTTTCTTGGCCTTTATCTTACAAAAATGGAGTATTTTAGTATGAAT
TTGCTGAATGTAAGACCGTGGACTGTTTTTTATAATATGGCCTAATTTTAAAGGTCCAAAATAACTTGTTTTTAA
AGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATTTGGTTGTAAACTATATTTCAAAGTAAA
CCCTAGTGTAATAAGTTTTATAACTAAAAAGGTTTAAGCTGCTAAAACTATTTTTAAGAGATGTGAAATGCAGTA
TGGGACTATCTTTTTTTCCTCCTCTAAGCCCAAAGATTAACTAGAGTCCCTCCAACCTTATAGATTGTTGGCTTT
CACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGTGATGTTTTGTTTTTGTTTGGTCAAGGG
GTAGGTGCAACCCAATGGACCACTTATGCAAAAGATGTAAACTCTTGCATAATACATTGATAACATGTTTTGCCA
ACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGGTCAGCTTAAAAATTTTGATTGTTAATGCC
CTATTTTCTAATTTGGCACCTCTTGATGCCTAAGCAGGTAAGCAGATGCCTAAGCTGTATTTCTCCAAATAAATC
AAGATGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAGTTTATGTAGTACTTAATGTACATGATATG
AATGTGAAGCATAAAATTAAATAAAATTTTTCCCCATTAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGGGERYNIPAPQSRNVSKNQQQLNRQKTKEQNSQMKIVHKKKERGHGYNSSAAAWQAMQNGGKNKNFPNNQSWN
SSLSGPRLLFKSQANQNYAGAKFSEPPSPSVLPKPPSHWVPVSFNPSDKEIMTFQLKTLLKVQV

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FIGURE 93

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
C**ATG**TCCCGCTACCTGCGTCCCCCCAACACGTCTCTGTTCGTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACTATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGACCAAACTGCAGCTGGAATACCCAGTACAGTTC
TGCTTACTACACTTCAAGAAAGATC**TGA**AAGCGGAAAAAGAACCAAAGAAGGGCAGTTCAAGCGACCAAAGGGTG
GGTGGAAGGTGCTGCAGTATGAATACTGTACGAATATTTTGACTCTGGTCTGAAAAGATAAAAGAATGTTATCGA
AAACTACATGGAATAATTGAAGTCCCTTCAAGTTTGAAAGTAAGCATTTTAGGACAAATAAAAGGAAATTCAACT
TTGTACTTGTGGAAACTAATCCCTAAATATGAATAGGTTTATATTGATTCATGGGTAACAGGTCCATAATAAATT
ATTGGAAACTAGGATGTCTGAATATCAAGGAAGACAGCCATAGTCTCTTACAGTGCCTCTGTTGGTCTGTCTCAA
ACTGAATTGGGTGGGAAAAGGTATGGTCCAATATAAAAGTTCCATTTTTGCCATTATTGGCAAATCTTGCCTTTG
TTTATTTTGGTGCCAGTGTTTTCTGCTTAATCATTTGCTTTGTTGGCATCTGTGTTTATTTACTTGTACACCACA
TGCAGTTTACATCTGTCTTAACTACTCCTTCCCAGGTAAATTCCAATTATATTTGACATCCAGCTAAGAGGGCCC
ATCTCTTCTCACCTCTTTCCTAGTCAGTATATTCAGCAAATATTTATTGAGCCCTTACTGTGGGCAAATCATTGT
ACTGGATAATTGAGAAAAATAGATAATTCCCTTATTCAGTAAATGTCTACTGAGCACAATCTAGTGAATCATTAC
AGTATGGCCTCATTGTTTTGTTTGAGGTGTGTTATTCATAACAATATTTTACACCATTCGTATCAATGTAATTAT
AGAACACAATATACGATCAAGGATAAGTAATTGTGTGGTTATCTGCCATTTAAAAGTATCCAGTATTTGATCACA
TTATTATAAATAATGAAAAAATGATTTAATCTGTAATAAACTGGTTTATTGTGCAGTGACTGTAATATACTAGAG
TTATAATAAATTGTTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATTTAACTTTGC
ATTAGGTATAAAGGAGACTGGGTGCTATAATTAGATTATTTTGAGGCAGACAGAGAGCTGTTATCCTAACTGATT
TAGTATGTTCTGTAATTGAGAAAATGTTCACCAAATTATACTTTTTAGTGATTTACATGTACATTTTATAGGGGA
CATGTTCTGTGTATAGCGAATAAATAACTTTTATAGTATCAC

FIGURE 94

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYDDYDRYRRSRSRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRPNCSWNTQYSSAYYTSRKI

FIGURE 95

GTCTGAGGCTCGGCCGCCTGAGCCGCGGACGGTTTGCTGAGCCCGTTAGTGCGCCCGGCCGAGACACGCCGCCGC
C**ATG**TCCCGCTACCTGCGTCCCCCCAACACGTCTCTGTTCGTCAGGAACGTGGCCGACGACACCAGGTCTGAAGA
CTTGCGGCGTGAATTTGGTCGTTATGGTCCTATAGTTGATGTGTATGTTCCACTTGATTTCTACACTCGCCGTCC
AAGAGGATTTGCTTATGTTCAATTTGAGGATGTTCGTGATGCTGAAGACGCTTTACATAATTTGGACAGAAAGTG
GATTTGTGGACGGCAGATTGAAATACAGTTTGCCCAGGGGGATCGAAAGACACCAAATCAGATGAAAGCCAAGGA
AGGGAGGAATGTGTACAGTTCTTCACGCTATGATGATTATGACAGATACAGACGTTCTAGAAGCCGAAGTTATGA
AAGGAGGAGATCAAGAAGTCGGTCTTTTGATTACAACTATAGAAGATCGTATAGTCCTAGAAACAGTAGACCGAC
TGGAAGACCACGGCGTAGCAGAAGCCATTCCGACAATGATAGATTCAAACACCGAAATCGATCTTTTTCAAGATC
TAAATCCAATTCAAGATCACGGTCCAAGTCCCAGCCCAAGAAAGAAATGAAGGCTAAATCACGTTCTAGGTCTGC
ATCTCACACCAAAACTAGAGGCACCTCTAAAACAGATTCCAAAACACATTATAAGTCTGGCTCAAGATATGAAAA
GGAATCAAGGAAAAAAGAACCACCTAGATCCAAATCTCAGTCAAGATCACAGTCTAGGTCTAGGTCAAAATCTAG
ATCAAGGTCTTGGACTAGTCCTAAGTCCAGTGGCCAC**TGA**TAGTATAAACCATGGTCATTTTTAGGCATGTATCA
TTCATTTACTCATAGTTTGGTTTACTTAAATTATCAGGAATACAATGTTGCAATGATGCTTAAAAAACACTTGTT
AGTTTTCCCTGTACCAGGCAATGGTTATAATTAAAATGATATGCTGTTGAGAAGCCACTCTTAAGAGTCCAGTTT
GTTTAATGTTATGGGCAGCTACCAATTTGTGGTGTCTCTGTATATTTTTGTAAAGATTCTCATTTTTTATGCTTG
AAGTATTTGGTGAAAAGATGTTGGTTGACCATAATTTGCAACATTGTCTCATTAAAAATAAACTTTCATATTCAT
ATTTGGTAGAACTGTTAACCTAGAAATGTAGCTTGCTAATAAGATAGAATGATACAAAAGTGAAGTAGTAGCCAC
AGTACAACACTGACTGCTCAGACACATTTAGGTTCAGGGTGGACCTTTATGTCTTGTCAAGATGTCTAGGCCCGG
CTGGGCGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGTT
CGAGACCAGCCTGACCAACACGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTATCCGGGCATGGTGGCACA
TGCCTGTAATCTCAGCTACTCAGGAGGCTGAGGCAAGAGAATCGCTTGAACCTGGGAGGTAGAAGTTGCAGTGAG
CCAAAATCACGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTCCGTCTCAAAAAAAAAAAAAAACCGGATG
TCTAGGCCAATGATAATTATTTTTGATGCAGTGTGGATTAGTTCTTTTGTTAACCCCACTGTCTTGGGGAATGAT
GCCAGCTGGGAAATTGAGTTTTTGACTGAAACATGGAGCCTTCACTGCTTTTTTTCTGGTTCCTATGAAGATTTG
GAACATAGAAAACACAAAAACTCACCTTAAAATTTGAGCAGGTCGTTGATGGCAAAAATAATTTTAAGGAAAAAG
GAATATTCTTATGTAGTTATTCTAAAGTTTAAGGAGCGTTGTTGACCATAATATTGCTTAGTTTTCTTACTGCTG
TTAAGTAAGTAAATTGTTTCAAAGTAGGTTTTGTGTGTGTGTGCCTAGTGTAAAAGAACTGAAATTTTGATGCTT
ACAGCACTTGGCTCGTGCATTTGTATCAAAATTTGCCTGCCTCTTTATGAGGGAGGCCTGCTTTTCACACCTCAG
TTTATTTAATACGAGGCAAGTTGTAAGACAACACTCATTCTAGGTGATTCTGTGGTGCCATGAAATTTAAGGTAA
TTTGGGGAAAAGGATTAGTCAGTTTTAAGCAAGAGTCACATCTTTTGAGCTTTCGATTATCAGTGTAGTACCTGA
CTAAAAATGAAGTAATACCCTTAAACCATTTATAATTTCTAGTATTTCTCTGAAAGATCGTTTTGGGGACAAAAG
TGACTTGACATGTCCAATTTCATTTCAGAATAAAAAGCTAGCATCTTTAAAAATCTCAGATTGCTTGCTTACAGA
TACAAGTACGAATTATGGACAAACGATTCCTTTTAGAGGATTACTTTTTTCAATTTCGGTTTTAGTAATCTAGGC
TTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATTCTAGAACC
TTTGTATATTTGATAGTATTTCTAACTTTCATTTCTTTACTGTTTGCAGTTAATGTTCATGTTCTGCTATGCAAT
CGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCCTGGATGTATAGTTTAAACAACAAAAAGTCTATTTAA
AACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAAACTTTGTATTTTCTTTCTTATAGA
GGCTTCTAAAAAGGTATTTTTATATGTTCTTTTTAACAAATATTGTGTACAACCTTTAAAACATCAATGTTTGGA
TCAAAACAAGACCCAGCTTATTTTCTGCTTGCTGTAAATTAAGCAAACATGCTATAATAAAAACAAAATGAAGG

FIGURE 96

MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLDFYTRRPRGFAYVQFEDVRDAEDALHNLDRKW
ICGRQIEIQFAQGDRKTPNQMKAKEGRNVYSSSRYDDYDRYRRSRSRSYERRRSRSRSFDYNYRRSYSPRNSRPT
GRPRRSRSHSDNDRFKHRNRSFSRSKSNSRSRSKSQPKKEMKAKSRSRSASHTKTRGTSKTDSKTHYKSGSRYEK
ESRKKEPPRSKSQSRSQSRSRSKSRSRSWTSPKSSGH

FIGURE 97

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

FIGURE 98

CAGGAACGAGATGGCGGTTCCCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTCACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGATTATGTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGCCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAATCTTTGAGGAAAAGGTTTGAGAGGAATTATATCT
AAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAATAT
AACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTATTATGATTA
GTACATGATCAAATTTCCATATTTGCCTTGGGAATAATGGACAAAGGGAAATACTCTTAATTCATGAATAAAAAC
TTTGCAGAAAATTAGACAGTGTTTAATTTTCAAAAACTTCCCTCTCTAGTCAGTAGATACCACCTACTGATGGTT
ACATATACTAGGGAAATTTTAAAATTAGGAAATGCTGCTATCTCATATTATAAATTTCTAAATCCTAGGAAGAAA
CGCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCCAGAGACATATCAAAATATTATC
CATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCTAAAACAATCTGTCCACAAATATAAAACTAT
AAGTAATAAATTGTTATTTCCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTATGAAAATAATTTTTTTAA
ATAAAATGTTGTATAAAAAAA

FIGURE 99

AGAGAGAAAGGTTGTG**ATG**GCGGCTATAGCTGCATCCGAGGTGCTGGTGGACAGCGCGGAGGAGGGGTCCCTCGC
TGCGGCGGCGGAGCTGGCCGCTCAGAAGCGCGAACAGAGACTGCGCAAATTCCGGGAGCTGCACCTGATGCGGAA
TGAAGCTCGTAAATTAAATCACCAGGAAGTTGTGGAAGAAGATAAAAGACTAAAATTACCTGCAAATTGGGAAGC
CAAAAAAGCTCGTTTGGAGTGGGAACTAAAGGAAGAGGAAAAGAAAAAGGAATGTGCGGCAAGAGGAGAAGACTA
TGAGAAAGTGAAGTTGCTGGAGATCAGTGCAGAAGATGCAGAAAGATGGGAGAGGAAAAAGAAGAGGAAAAACCC
TGATCTGGGATTTTCAGATTATGCTGCTGCCCAGTTACGCCAGTATCATCGGTTGACCAAGCAGATCAAACCTGA
CATGGAAACATATGAGAGACTGAGAGAAAAACATGGAGAAGAGTTTTTCCCAACATCCAATAGTCTTCTTCATGG
AACACATGTGCCTTCCACAGAGGAAATTGACAGGATGGTCATAGATCTGGAAAAACAGATTGAAAAACGAGACAA
ATATAGCCGGAGACGTCCTTATAATGATGATGCAGATATCGACTACATTAATGAAAGGAATGCCAAATTCAACAA
GAAAGCTGAAAGATTCTATGGGAAATACACAGCTGAAATTAAACAGAATTTGGAAAGAGGAACAGCTGTC**TAA**TC
CCTTCAAGAACTGTTTATAGAAGCTTGAGAATGGGGTAAAAATTTCTGCTAGCAAAATCAAGTTCTTTTTGAAAT
TTTATCAGTAATCCAGAATTTAGTAGTCCATGCCTTCTCACTCAGCATTTAGAAATAAAAATGTGGTTTCTTAAA
CGTATATCCTTTCATGTATATTTCCACATTTTTGTGCTTGGATATAAGATGTATTTCTTGTAGTGAAGTTGTTTT
GTAATCTACTTTGTATACATTCTAATTATATTATTTTTCTATGTATTTTAAATGTATATGGCTGTTTAATCTTTG
AAGCATTTTGGGCTTAAGATTGCCAGCAGCACACATCAGATGCAGTCATTGTTGCTATCAGTGTGGAATTTGATA
GAGTCTAGACTCGGGCCACTTGGAGTTGTGTACTCCAAAGCTAAGGACAGTGATGAGGAAGATGGCAGTGGCCAC
CGGAGGACTGGAGCAGTCCCTCCTCATGGCGGCCTGTGACCAAGGTCGGGGAGGAGTGGAGCTATCCTTCCATGA
TCTGATCATGTACAGTTCCCTTTTTAAAAAGCAATAAATGCTTGGGATTAGAATTTCTAAAAAAAAAAA

FIGURE 100

MAAIAASEVLVDSAEEGSLAAAAELAAQKREQRLRKFRELHLMRNEARKLNHQEVVEEDKRLKLPANWEAKKARL
EWELKEEEKKKECAARGEDYEKVKLLEISAEDAERWERKKKRKNPDLGFSDYAAAQLRQYHRLTKQIKPDMETYE
RLREKHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLEKQIEKRDKYSRRRPYNDDADIDYINERNAKFNKKAERF
YGKYTAEIKQNLERGTAV

FIGURE 101A

GGCGGCCCACTCTGCTCTGTCAGCTTCGGAGCTCCTCCACCCTGGCTGCCGAAAGCCCCTTCCCGCCATCTAATG
ATACACTCTGCATACGCTTCTGTTGAGAATTTGTGGCTAGACATTCCTGTGGGACCGGGAATCCAAATTCTTGGT
AGCTAGAGGAAAAAAAAATAAAACAACAGCCAACCAAGTGAATCCCAACCCAACCCCCTGAAGGGCTGAAAATTC
TCGCCTTCTTCAGAGCGGGGCATGGCATCGAACAGCATCTTCGACTCCTTCCCGACCTACTCGCCGACCTTCATC
CGCGACCCAAGCACCAGCCGCCGCTTCACACCTCCCTCCCCGGCCTTCCCCTGCGGCGGCGGCGGCGGCAAGATG
GGCGAGAACAGCGGCGCGCTGAGCGCGCAGGCGGCCGTGGGGCCCGGAGGGCGCGCCCGGCCCGAGGTGCGCTCG
ATGGTGGACGTGCTGGCGGACCACGCAGGCGAGCTCGTGCGCACCGACAGCCCCAACTTCCTCTGCTCCGTGCTG
CCCTCGCACTGGCGCTGCAACAAGACGCTGCCCGTCGCCTTCAAGGTGGTGGCATTGGGGGACGTGCCGGATGGT
ACGGTGGTGACTGTGATGGCAGGCAATGACGAGAACTACTCCGCTGAGCTGCGCAATGCCTCGGCCGTCATGAAG
AACCAGGTGGCCAGGTTCAACGACCTTCGCTTCGTGGGCCGCAGTGGGCGAGGGAAGAGTTTCACCCTGACCATC
ACTGTGTTCACCAACCCCACCCAAGTGGCGACCTACCACCGAGCCATCAAGGTGACCGTGGACGGACCCCGGGAG
CCCAGACGGCACCGGCAGAAGCTGGAGGACCAGACCAAGCCGTTCCCTGACCGCTTTGGGGACCTGGAACGGCTG
CGCATGCGGGTGACACCGAGCACACCCAGCCCCCGAGGCTCACTCAGCACCACAAGCCACTTCAGCAGCCAGCCC
CAGACCCCAATCCAAGGCACCTCGGAACTGAACCCATTCTCCGACCCCCGCCAGTTTGACCGCTCCTTCCCCACG
CTGCCAACCCTCACGGAGAGCCGCTTCCCAGACCCCAGGATGCATTATCCCGGGGCCATGTCAGCTGCCTTCCCC
TACAGCGCCACGCCCTCGGGCACGAGCATCAGCAGCCTCAGCGTGGCGGGCATGCCGGCCACCAGCCGCTTCCAC
CATACCTACCTCCCGCCACCCTACCCGGGGGCCCCGCAGAACCAGAGCGGGCCCTTCCAGGCCAACCCGTCCCCC
TACCACCTCTACTACGGGACATCCTCTGGCTCCTACCAGTTCTCCATGGTGGCCGGCAGCAGCAGTGGGGGCGAC
CGCTCACCTACCCGCATGCTGGCCTCTTGCACCAGCAGCGCTGCCTCTGTCGCCGCCGGCAACCTCATGAACCCC
AGCCTGGGCGGCCAGAGTGATGGCGTGGAGGCCGACGGCAGCCACAGCAACTCACCCACGGCCCTGAGCACGCCA
GGCCGCATGGATGAGGCCGTGTGGCGGCCCTACTGACCGCCCTGGTGGACTCCTCCCGCTGGAGGCGGGGACCCT
AACAACCTTCAAGACCAGTGATGGGCCGGCTCCGAGGCTCCGGGCGGGAATGGGACCTGCGCTCCAGGGTGGTCT
CGGTCCCAGGGTGGTCCCAGCTGGTGGGAGCCTCTGGCTGCATCTGTGCAGCCACATCCTTGTACAGAGGCATAG
GTTACCACCCCCACCCCGGCCCGGGATACTGCCCCCGGCCCAGATCCTGGCCGTCTCATCCCATACTTCTGTGGG
GAATCAGCCTCCTGCCACCCCCCCGGAAGGACCTCACTGTCTCCAGCTATGCCCAGTGCTGCATGGGACCCATGT
CTCCTGGGACAGAGGCCATCTCTCTTCCAGAGAGAGGCAGCATTGGCCCACAGGATAAGCCTCAGGCCCTGGGAA
ACCTCCCGACCCCTGCACCTTCGTTGGAGCCCCTGCATCCCCTGGGTCCAGCCCCCTCTGCATTTACACAGATTT
GAGTCAGAACTGGAAAGTGTCCCCCACCCCCACCACCCTCGAGCGGGGTTCCCCTCATTGTACAGATGGGGCAGG
ACCCAGCACGCTGCTGGCAGAGATGGTTTGAGAACACATCCAAGCCAGTCCCCCCAGCCCAGCTTCCCCTCCGTT
CCTAACTGTTGGCTTTCCCCCAGCCGCACGGGTCCCAGGCCCCAGAGAAGATGAGTCTATGGCATCAGGTTCTTA
AACCCAGGAAAGCACCTACAGACCGGCTCCTCCATGCACTTTACCAGCTCAACGCATCCACTCTCTGTTCTCTTG
GCAGGGCGGGGGAGGGGGGATAGGAGGTCCCCTTTCCCCTAGGTGGTCTCATAATTCCATTTGTGGAGAGAACAG
GAGGGCCAGATAGATAGGTCCTAGCAGAAGGCATTGAGGTGAGGGATCATTTTGGGTCAGACATCAATGTCCCTG
TCCCCCCTGGGTCCAGCCAAGCTGTGCCCCATCCCCCAAGCCTCCTGGGAGGATCCAGCCAAATCTTGCGACTCC
TGGCACACACCTGTCTGTAACCTGTTTTGTGCTCTGAAAGCAAATAGTCCTGAGCAAAAAAAAAAAAAAAACAAA
AAAACAAAAAAAAAACAAAACAGTTTTTAAAACTGATTTTAGAAAAAGAAGCTTAATCTAACGTTTTCAAACACA
AGGTCTCTTACAGGTATAGTTCCGTGATTATGATAGCTCTGTGATTATAAGCAACATCCCCGCCCCCTCTCCCCC
CCGCGGACCCCCAGCTGCCTCCTGAGGGTGTGGGGTTATTAGGGTCTCAATACTTTCTCAAGGGGCTACACTCCC
CATCAGGCAGCATCCCACCAGCCTGCACCACAGGCTCCCCTGGGAGGACGAGGGAAACGCTGATGAGACGCTGGG
CATCTCTCCTCTGTGGCTCTAGGACATCTGTCCAGGAGGCTGGGCGGAGGTGGGCAGGATGTGAGAGGTGGGGAG
TACTGGCTGTGCGTGGCAGGACAGAAGCACTGTAAAGGGCTCTCCAGCCGCAGCTCAGCTGCACTGCGTTCCGAG
GTGAAGTCTTGCCCCTGAATTTTGCAAAATGGGAAAGTGGGCGCTTGCCCAAGGGCCAGGCTGCATGGATTCTCA
CATCAGAGTTCTCTGGCCCTAGAAAGGCTTAGAAAAGGCGTAAGGGAACTCATAAAGGCTAGCAGCATGCGGTAT
TTTAACTTTCTGCCTCGGCCTCTGTGGATGCAGAAATCTGCCCTACAAAATGCTCTTCATTGGTTGTCTCTGTGA
GAGCACTGTCCCCACCCAACCTGTCACAACGGCCAGAACCATACACCAGAGACACACTGGCAGGTTAGGCAGTCC
TTCTGGTGATCCTATTCCATTCCCTCCTGCTGCGGTTTCTCTTGGCCTGTCCTCACTGGAAAAACAGTCTCCATC
TCCTCAAAATAGTTGCTGACTCCCTGCACCCAAGGGGCCTCTCCATGCCTTCTTAGGAAGCAGCTATGAATCCAT
TGTCCTTGTAGTTTCTTCCCTCCTGTTCTCTGGTTATAGCTGGTCCCAGGTCAGCGTGGGAGGCACCTTTGGGTT

FIGURE 101B

CCCAGTGCCCAGCACTTTGTAGTCTCATCCCAGATTACTAACCCTTCCTGATCCTGGAGAGGCAGGGATAGTAAA
TAAATTGCTCTTCCTACCCCATCCCCCCATCCCCTGACAAAAAGTGACGGCAGCCGTACTGAGTCTGTAAGGCCCA
AAGTGGGTACAGACAGCCTGGGCTGGTAAAAGTAGGTCCTTATTTACAAGGCTGCGTTAAAGTTGTACTAGGCAA
ACACACTGATGTAGGAAGCACGAGGAAAGGAAGACGTTTTGATATAGTGTTACTGTGAGCCTGTCAGTAGTGGGT
ACCAATCTTTTGTGACATATTGTCATGCTGAGGTGTGACACCTGCTGCACTCATCTGATGTAAAACCATCCCAGA
GCTGGCGAGAGGATGGAGCTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTAACGCACAAC
TTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGT

FIGURE 102

CAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTCTGTTGCTGCG
AACTCCAGTGGTCAGACCTGCTCATATCTCAGCATTTCTTCAGGACCGACCTATCCCAGAATGGTGTGGAGTGCA
GCACATACACTTGTCACCGAGCCACCATTCTGGCTCCAAGGCTGCATCTCTCCACTGGACTAGCGAGAGGGTTGT
CAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAATCCTTGCTCTGCGACGGACTATTCCCTGGCTGC
AGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTTACTGACTATGTTCATGGGGATGCCTCGCAGAA
AGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTTGCTGGGCTTTGCTATTTCAACTATCACGATGT
GGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCTTTTTGACTTCCTACTTTGAAGAATTGATGTAT
GCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGGAAGAAATAACAGATAAGTCCATTGGTGGAC
AGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACTTTGAGGAAAAGGTTTGAGAGGAATTATATTTA
AGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTTGCCTCCCAGCTTCTTATAAGACTCACAGTATA
ACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATCTCTTAAAGAGAATCCAGCTTTAGTATGATTAG
CATATGATCAAACTTCCATATTTGCCTTGGGAATAATGGACTAAGGGAAATACTCTTAATTCATGAATAAAAACT
TTGCAGAAAATTAGACAGTGTTTAATTTTCAAAAACTTCCCTCTCTAGTCGGTAGATACCACCTACCGATGGTTA
CATATACTAGGGAAATTTTAAAATTAGGAAATGCTGATATCTCATATTATAAATTTCTAAATCCTAGGAAGAAAC
GCTTGGAGTGCTTCTGAAGATACAGAAGTTCCATTTAAGGGCAAGTTTCCCCATAGACGTATCAAAATATTACCC
ATTGTAAACTGAGATTTAATTCTCAAATGTATTCTACTTGTTCTAAAACAATCTGTCCACAAATATAAAACTATA
AGTAATAAATTGTTATTTTCGCACAATGGGAATCTCTAATGTGAAAATGTATTCTGTGAAAATAAATTTTTAAAT
AAAATGTTGTATAATAA

FIGURE 103

AGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCAAGGAGGCCGAGCTGGCTCCAAGGCT
GCATCTCTCCACTGGACTAGCGAGAGGGTTGTCAGTGTTTTGCTCCCGGGTCTGCTTCCGGCTGCTTATTTGAAT
CCTTGCTCTGCGACGGACTATTCCCTGGCTGCAGCCCTCACTCTTCATGGTCACTGGGGCCTTGGACAAGTTGTT
ACTGACTATGTTCATGGGGATGCCTCGCAGAAAGCTGCCAAGGCAGGGCTTTTGGCATTTTCAGCTTTAACCTTT
GCTGGGCTTTGCTATTTCAACTATCACGATGTGGGCATCTGCAAAGCTGTTGCCATGCTGTGGAAGCTCTGACCT
TTTTGACTTCCTACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAA
GGAAGAAATAACAGATAAGTCCATTGGTGGACAGCCTTCTTCTCTTAATCACAAGATTATTTTCAGAATTTAACT
TTGAGGAAAAGGTTTGAGAGGAATTATATTTAAGTTGTGAGACTGAGTTCTGTATTCTGGTGAGTTAATGGGGTT
GCCTCCCAGCTTCTTATAAGACTCACAGTATAACTAAACATGATATATCAGCTTTTGCCTTTTAATTTCTCAATC
TCTTAAAGAGAATC

FIGURE 104

MAVLRRLSALYGAQGGRALLLRTPVIRPAHISAFLQDRPIPEWCGVQHLHLSPSHHPGSKAASLHWTSERVVSVL
LLGLLPAAYLNPCSAMDYSLAATLTLPGHWGLRQVVTMFMGMPRRKLPRQGFWHFQL

FIGURE 105

AGTGTGGTCAGGCGGCTCGGACTGAGCAGGACTTTCCTTATCCCAGTTGATTGTGCAGAATACACTGCCTATCGC
TTGTCTTCTATTCACC**ATG**GCTTCTTCTGATATCCAGGTGAAAGAACTGGAGAAGCGTGCCTCAGGCCAGGCTTT
TGAGCTGATTCTCAGCCCTCGGTCAAAAGAATCTGTTCCAGAATTCCCCCTTTCCCCTCCAAAGAAGAAGGATCT
TTCCCTGGAGGAAATTCAGAAGAAATTAGAAGCTGCAGAAGAAAGACGCAAGTCCCATGAAGCTGAGGTCTTGAA
GCAGCTGGCTGAGAAACGAGAGCACGAGAAAGAAGTGCTTCAGAAGGCAATAGAAGAGAACAACAACTTCAGTAA
AATGGCAGAAGAGAAACTGACCCACAAAATGGAAGCTAATAAAGAGAACCGAGAGGCACAAATGGCTGCCAAACT
GGAACGTTTGCGAGAGAAGGATAAGCACATTGAAGAAGTGCGGAAGAACAAAGAATCCAAAGACCCTGCTGACGA
GACTGAAGCTGAC**TAA**TTTGTTCTGAGAACTGACTTTCTCCCCATCCCCTTCCTAAATATCCAAAGACTGTACTG
GCCAGTGTCATTTTATTTTTTCCCTCCTGACAAATATTTTAGAAGCTAATGTAGGACTGTATAGGTAGATCCAGA
TCCAGACTGTAAGATGTTGTTTTAGGGGCTAAAGGGGAGAAACTGAAAGTGTTTTACTCTTTTTCTAAAGTGTTG
GTCTTTCTAATGTAGCTATTTTTCTTGTTGCATCTTTTCTACTTCAGTACACTTGGTGTACTGGGTTAATGGCTA
GTACTGTATTGGCTCTGTGAAAACATATTTGTGAAAAGAGTATGTAGTGGCTTCTTTTGAACTGTTAGATGCTGA
ATATCTGTTCACTTTTCAATCCCAATTCTGTCCCAATCTTACCAGATGCTACTGGACTTGAATGGTTAATAAAAC
TGCACAGTGCTGTTGGTGGCAGTGACTTCTTTTGAGTTAGGTTAATAAATCAAGCCATAGAGCCCCTCCTGGTTG
ATACTTGTTCCAGATGGGGCCTTTGGGGCTGGTAGAAATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCG
TTTCTTGCCCCAGTGTGGTTTGCATTGTCTCCTTCCACAATGACTGCTTTGTTTGGATGCCTCAGCCCAGGTCAG
CTGTTACTTTCTTTCAGATGTTTATTTGCAAACAACCATTTTTTGTTCTGTGTCCCTTTTAAAAGGCAGATTAAA
AGCACAAGCGTGTTTCTAGAGAACAGTTGAGAGAGAATCTCAAGATTCTACTTGGTGGTTTGCTTGCTCTACGTT
ACAGGTGGGGCATGTCCTCATCCTTTCCTGCCATAAAAGCTATGACACGAGAATCAGAATATTAATAAAACTTTA
TGTACTGCTGT

FIGURE 106

MASSDIQVKELEKRASGQAFELILSPRSKESVPEFPLSPPKKKDLSLEEIQKKLEAAEERRKSHEAEVLKQLAEK
REHEKEVLQKAIEENNNFSKMAEEKLTHKMEANKENREAQMAAKLERLREKDKHIEEVRKNKESKDPADETEAD

FIGURE 107

GTGCAACGGCCGTTAGAGGAGCTGAGGGAGGGAACCACCGCTCACCGCAGACGTAGTGGCTGCAGTCAGTCTTCC
CGAGTGAGGGATTTCGCCGCCCGCTTTCAGGCCCGTTTGGCTTAAATAACTGTGATTG**ATG**GCCATGCAGGAGAA
ATATCCAACTGAGGGGATCTCTCACGTCACTTCACCGAGTTCCGATGTGATTCAGAAGGGCAGTTCCCTGGGGAC
TGAATGGCAGACCCCAGTTATCTCGGAGCCCTTTCGGAGCCGCTTCAGCCGCTGTTCAAGTGTAGCCGACAGTGG
GGACACAGCCATTGGTACATCATGCTCAGATATTGCGGAGGATTTTTGCAGCTCAAGTGGCAGTCCTCCTTTCCA
GCCCATCAAAAGCCACGTAACCATTCCAACAGCCCATGTGATGCCTTCTACTTTAGGGACCTCTCCTGCCAAGCC
AAATTCTACACCTGTTGGACCCTCTTCCTCTAAACTCCCTTTGTCAGGGTTGGCTGAAAGTGTGGGAATGACAAG
AAATGGAGACCTCGGTGCAATGAAACATTCTCCAGGCCTATCTAGAGATCTCATGTATTTCTCTGGTGCTACTGG
AGAAAATGGAATTGAGCAGTCCTGGTTTCCAGCAGTGGGCCATGAAAGACAAGAAGAGGCGAGGAAGTTTGATAT
TCCTAGCATGGAATCTACCCTCAATCAGTCGGCAATGATGGAGACACTTTATTCAGATCCTCACCACCGAGTCCG
CTTCCACAACCCAAGAACCAGCACAAGTAAGGAGTTGTACAGAGTGTTGCCTGAGGCCAAGAAGGCACCGGGCAG
CGGGGCAGTGTTTGAGCGGAATGGACCACATTCTAATAGCAGTGGGGTCCTCCCTTTGGGACTCCAGCCTGCTCC
CGGGCACTCCAGCCAGCCTCTGCCCTCTCAGGTGTGGCAGCCGAGTCCTGACACTTGGCATCCCCGAGAGCAATC
TTGTGAACTCAGCACTTGTCGGCAGCAGCTGGAATTGATTCGTTTACAGATGGAGCAAATGCAGCTTCAGAATGG
AGCCATCTGCCACCATCCTGCTGCTTTTGGTCCTTCACTGCCCATCTTAGAGCCAGCACAGTGGATCAGCATCTT
GAACAGTAATGAACACCTTCTGAAGGAAAAAGAGCTTCTCATTGACAAGCAGAGGAAACACATCTCTCAGCTGGA
GCAGAAAGTGCGAGAGAGCGAACTGCAAGTCCACAGTGCCCTCTTGGGCCGCCCTGCCCCCTTTGGTGATGTCTG
CTTGCTGAGGCTACAGGAATTGCAGCGAGAAAACACTTTCTTACGTGCACAGTTTGCACAGAAGACAGAAGCCTT
GAGCAGAGAAAAGATTGACCTTGAAAAGAAACTCTCTGCTTCTGAAGTTGAAGTCCAGCTCATCAGAGAGTCGCT
CAAAGTGGCGTTGCAGAAGCATTCTGAGGAAGTGAAGAAACAGGAAGAAAGGGTCAAAGGTCGTGATAAACATAT
CAATAATTTGAAAAAGAAATGCCAGAAGGAATCAGAGCAGAACCGGGAGAAGCAGCAGCGTATTGAGACCTTGGA
GCGCTACCTGGCTGACCTGCCCACACTGGAAGACCATCAGAAGCAGAGCCAGCAGCTTAAGGATTCTGAGTTGAA
GAGCACAGAGCTGCAGGAGAAAGTGACTGAGCTGGAGAGTTTGCTGGAGGAGACCCAGGCAATCTGCAGAGAGAA
GGAGATTCAACTGGAAAGCCTGAGGCAGAGAGAAGCAGAATTCTCCTCCGCTGGACATAGCCTGCAAGATAAACA
GTCTGTGGAGGAGACCAGTGGAGAAGGTCCAGAAGTGGAAATGGAGTCCTGGCAGAAGCGATACGATTCGCTCCA
AAAGATTGTGGAGAAGCAGCAGCAGAAGATGGATCAGTTGCGCTCACAAGTACAGAGCCTAGAGCAGGAAGTGGC
TCAAGAAGAAGGAACAAGCCAGGCCCTGAGAGAGGAGGCCCAGCGAAGGGATTCAGCCCTGCAGCAGCTGCGCAC
AGCCGTGAAGGAGCTTTCAGTGCAAAACCAGGACTTGATTGAGAAGAATCTGACACTCCAGGAACACCTGCGCCA
GGCCCAACCAGGGTCTCCACCTTCACCAGACACGGCCCAGCTGGCACTTGAGCTGCACCAGGAGTTGGCCAGTTG
CCTTCAAGATCTGCAGGCTGTCTGTAGCATTGTGACCCAGAGGGCCCAGGGCCATGACCCCAATCTCTCCCTGCT
CCTGGGCATTCACTCACAGCACCCAGAGACTCAGCTAGATTTGCAGAAGCCAGATGTGATCAAGAGGAAACTAGA
AGAGGTTCAACAGCTGCGTCGTGACATTGAGGACTTAAGGACCACCATGTCAGACAGATATGCCCAGGACATGGG
AGAAAACTGTGTCACACAG**TGA**GGAATTCTGGGGGATTCCCCCAGGGAGGAGCTGGGCTGCTGAGAGCCTAGTCC
AGCAGGTTTCTGCCCTGACATTCTCTTGTCTGCTATTCCCAGAGAGGTCTCAGAGGGGAGGGGAGAGCCTGCATC
TGGGGGCCAAGGGCTGATTAGGGAACTGTGTCCTACCCACACTGGCATGTTGGATTACGTTTGTCCTGTTAATTC
ACTCTCGACGGTGAGTTACTAATTAACTTTTGGCAGGTACAACAGATAAGTCCTCACAAACTGTTCCCAGCCCTA
GGCTGACATGAGAGACGAACAGGCTGTCCACCTTTCTTCTCCATCCAATGGGATGGATCCATGTTCATTCCCACT
TCACACCTTGGTCCTGCTGATTAGAGAGCTCATCAGAGGGGCCTGGAAAGGCTGAGCAAGTACCAGTGACAATGG
CCATTTAAGAATTCTCAGGCCCCATGTGCCAGCCTTCTTGGGAACTGAGCTGGCTTTCTGGGTTTTCTCATGCCT
GGTCTTACTGCTTCTTCCTCAGGGCTCTTGTTCTCCCAGAAGCCTCAGGGTAATGTGTTGGTTAGCACGTAACTA
CTAGGATTGGGGCCCTAGGGATTATAGCCAGGACTCTAATCTGCCTACCATGCCATTTAACAAGAGATCCCACTC
TCCAGCTGCCTTGTGTCCCTAGGGTCCTGGCCATGTGTTTAGTGTGCTAAACTTTCTCCTTTGTTCTCAGGCCTT
CCAGGTAGTCCCCTTCCTGGACTTAAGAGTGCAAACTCTTCTCTGTGGTTCTAGCCTTGGGCAGAATTATATCCC
AGAGACCACAGAGCAACTGTCAAGCTGCTTACCCCCTCACCCAGGGCTACAGCCTGTGCCCAGCCCTCTAATTTG
TGCCTCTCTTGTGTTGGGGGTGGTGGGGGTTATTCCTTTCCCTTTCCTGCTCTGGCCTCCTTGAAAGTTCAGAGT
ACCCAGTACAAGTCAGCCACCATGCTGACGGGTATTTTTCCTCATAAAGTTTATAACCAGTTATTTATATGAATC
TTTGTTATGTCCATTTGTTTGTATTGCGTATTTTGATTATAAAATAAAGTATCTTAACAG

FIGURE 108

MAMQEKYPTEGISHVTSPSSDVIQKGSSLGTEWQTPVISEPFRSRFSRCSSVADSGDTAIGTSCSDIAEDFCSSS
GSPPFQPIKSHVTIPTAHVMPSTLGTSPAKPNSTPVGPSSSKLPLSGLAESVGMTRNGDLGAMKHSPGLSRDLMY
FSGATGENGIEQSWFPAVGHERQEEARKFDIPSMESTLNQSAMMETLYSDPHHRVRFHNPRTSTSKELYRVLPEA
KKAPGSGAVFERNGPHSNSSGVLPLGLQPAPGHSSQPLPSQVWQPSPDTWHPREQSCELSTCRQQLELIRLQMEQ
MQLQNGAICHHPAAFGPSLPILEPAQWISILNSNEHLLKEKELLIDKQRKHISQLEQKVRESELQVHSALLGRPA
PFGDVCLLRLQELQRENTFLRAQFAQKTEALSREKIDLEKKLSASEVEVQLIRESLKVALQKHSEEVKKQEERVK
GRDKHINNLKKKCQKESEQNREKQQRIETLERYLADLPTLEDHQKQSQQLKDSELKSTELQEKVTELESLLEETQ
AICREKEIQLESLRQREAEFSSAGHSLQDKQSVEETSGEGPEVEMESWQKRYDSLQKIVEKQQQKMDQLRSQVQS
LEQEVAQEEGTSQALREEAQRRDSALQQLRTAVKELSVQNQDLIEKNLTLQEHLRQAQPGSPPSPDTAQLALELH
QELASCLQDLQAVCSIVTQRAQGHDPNLSLLLGIHSQHPETQLDLQKPDVIKRKLEEVQQLRRDIEDLRTTMSDR
YAQDMGENCVTQ

FIGURE 109

GTAGCAGCTTCTTCTCCGAACCAACCCTTTGCCTTCGGACTTCTCCGGGGCCAGCAGCCGCCCGACCAGGGGCCC
GGGGCCACGGGCTCAGCCGACGACCATGGGCTCCGTGTCCAACCAGCAGTTTGCAGGTGGCTGCGCCAAGGCGGC
AGAAGAGGCGCCCGAGGAGGCGCCGGAGGACGCGGCCCGGGCGGCGGACGAGCCTCAGCTGCTGCACGGTGCGGG
CATCTGTAAGTGGTTCAACGTGCGCATGGGGTTCGGCTTCCTGTCCATGACCGCCCGCGCCGGGGTCGCGCTCGA
CCCCCCAGTGGATGTCTTTGTGCACCAGAGTAAGCTGCACATGGAAGGGTTCCGGAGCTTGAAGGAGGGTGAGGC
AGTGGAGTTCACCTTTAAGAAGTCAGCCAAGGGTCTGGAATCCATCCGTGTCACCGGACCTGGTGGAGTATTCTG
TATTGGGAGTGAGAGGCGGCCAAAAGGAAAGAGCATGCAGAAGCGCAGATCAAAAGGAGACAGGTGCTACAACTG
TGGAGGTCTAGATCATCATGCCAAGGAATGCAAGCTGCCACCCCAGCCCAAGAAGTGCCACTTCTGCCAGAGCAT
CAGCCATATGGTAGCCTCATGTCCGCTGAAGGCCCAGCAGGGCCCTAGTGCACAGGGAAAGCCAACCTACTTTCG
AGAGGAAGAAGAAGAAATCCACAGCCCTACCCTGCTCCCGGAGGCACAGAATTGAGCCACAATGGGTGGGGGCTA
TTCTTTTGCTATCAGGAAGTTTTGAGGAGCAGGCAGAGTGGAGAAAGTGGGAATAGGGTGCATTGGGGCTAGTTG
GCACTGCCATGTATCTCAGGCTTGGGTTCACACCATCACCCTTTCTTCCCTCTAGGTGGGGGGAAAGGGTGAGTC
AAAGGAACTCCAACCATGCTCTGTCCAAATGCAAGTGAGGGTTCTGGGGGCAACCAGGAGGGGGGAATCACCCTA
CAACCTGCATACTTTGAGTCTCCATCCCCAGAATTTCCAGCTTTTGAAAGTGGCCTGGATAGGGAAGTTGTTTTC
CTTTTAAAGAAGGATATATAATAATTCCCATGCCAGAGTGAAATGATTAAGTATAAGACCAGATTCATGGAGCCA
AGCCACTACATTCTGTGGAAGGAGATCTCTCAGGAGTAAGCATTGTTTTTTTTTCACATCTTGTATCCTCATACC
CACTTTTGGGATAGGGTGCTGGCAGCTGTCCCAAGCAATGGGTAATGATGATGGCAAAAAGGGTGTTTGGGGGAA
CAGCTGCAGACCTGCTGCTCTATGCTCACCCCCGCCCCATTCTGGGCCAATGTGATTTTATTTATTTGCTCCCTT
GGATACTGCACCTTGGGTCCCACTTTCTCCAGGATGCCAACTGCACTAGCTGTGTGCGAATGACGTATCTTGTGC
ATTTTAACTTTTTTTCCTTAATATAAATATTCTGGTTTTGTATTTTTGTATATTTTAATCTAAGGCCCTCATTTC
CTGCACTGTGTTCTCAGGTACATGAGCAATCTCAGGGATAGCCAGCAGCAGCTCCAGGTCTGCGCAGCAGGAATT
ACTTTTTGTTGTTTTTGCCACCGTGGAGAGCAACTATTTGGAGTGCACAGCCTATTGAACTACCTCATTTTTGCC
AATAAGAGCTGGCTTTTCTGCCATAGTGTCCTCTTGAAACCCCCTCTGCCTTGAAAATGTTTTATGGGAGACTAG
GTTTTAACTGGGTGGCCCCATGACTTGATTGCCTTCTACTGGAAGATTGGGAATTAGTCTAAACAGGAAATGGTG
GTACACAGAGGCTAGGAGAGGCTGGGCCCGGTGAAAAGGCCAGAGAGCAAGCCAAGATTAGGTGAGGGTTGTCTA
ATCCTATGGCACAGGACGTGCTTTACATCTCCAGATCTGTTCTTCACCAGATTAGGTTAGGCCTACCATGTGCCA
CAGGGTGTGTGTGTGTTTGTAAAACTAGAGTTGCTAAGGATAAGTTTAAAGACCAATACCCCTGTACTTAATCCT
GTGCTGTCGAGGGATGGATATATGAAGTAAGGTGAGATCCTTAACCTTTCAAAATTTTCGGGTTCCAGGGAGACA
CACAAGCGAGGGTTTTGTGGTGCCTGGAGCCTGTGTCCTGCCCTGCTACAGTAGTGATTAATAGTGTCATGGTAG
CTAAAGGAGAAAAAGGGGGTTTCGTTTACACGCTGTGAGATCACCGCAAACCTACCTTACTGTGTTGAAACGGGA
CAAATGCAATAGAACGCATTGGGTGGTGTGTGTCTGATCCTGGGTTCTTGTCTCCCCTAAATGCTGCCCCCCAAG
TTACTGTATTTGTCTGGGCTTTGTAGGACTTCACTACGTTGATTGCTAGGTGGCCTAGTTTGTGTAAATATAATG
TATTGGTCTTTCTCCGTGTTCTTTGGGGGTTTTGTTTACAAACTTCTTTTTGTATTGAGAGAAAAATAGCCAAAG
CATCTTTGACAGAAGGTTCTGCACCAGGCAAAAAGATCTGAAACATTAGTTTGGGGGGCCCTCTTCTTAAAGTGG
GGATCTTGAACCATCCTTTCTTTTGTATTCCCCTTCCCCTATTACCTATTAGACCAGATCTTCTGTCCTAAAAAC
TTGTCTTCTACCCTGCCCTCTTTTCTGTTCACCCCCAAAAGAAAACTTACACACCCACACACATACACATTTCAT
GCTTGGAGTGTCTCCACAACTCTTAAATGATGTATGCAAAAATACTGAAGCTAGGAAAACCCTCCATCCCTTGTT
CCCAACCTCCTAAGTCAAGACCATTACCATTTCTTTCTTTCTTTTTTTTTTTTTTTTAAAATGGAGTCTCACTGT
GTCACCCAGGCAGAGGTTGCAGTGAGCTGAGATCGCACCACTGCACTCCAGCCTGGTTACAGAGCAAGACTCTGT
CTCAAACAAAACAAAACAAAACAAAAACACACTACTGTATTTTGGATGGATCAAACCTCCTTAATTTTAATTTCT
AATCCTAAAGTAAAGAGATGCAATTGGGGGCCTTCCATGTAGAAAGTGGGGTCAGGAGGCCAAGAAAGGGAATAT
GAATGTATATCCAAGTCACTCAGGAACTTTTATGCAGGTGCTAGAAACTTTATGTCAAAGTGGCCACAAGATTGT
TTAATAGGAGACGAACGAATGTAACTCCATGTTTACTGCTAAAAACCAAAGCTTTGTGTAAAATCTTGAATTTAT
GGGGCGGGAGGGTAGGAAAGCCTGTACCTGTCTGTTTTTTTCCTGATCCTTTTCCCTCATTCCTGAACTGCAGGA
GACTGAGCCCCTTTGGGCTTTGGTGACCCCATCACTGGGGTGTGTTTATTTGATGGTTGATTTTGCTGTACTGGG
TACTTCCTTTCCCATTTTCTAATCATTTTTTAACACAAGCTGACTCTTCCCTTCCCTTCTCCTTTCCCTGGGAAA
ATACAATGAATAAATAAAGACTTATTGGTACGC

FIGURE 110

GAGCAGTGTGAAGAAGAGGCGAGAACGACCCCCGGACCGACCAAAGCCCGCGCGCCGCTGCATCCCGCGTCCAGC
ACCTACGTCCCGCTGCCGTCGCCGCCGCCACC**ATG**CCCAAGAGAAAGGCTGAAGGGGATGCTAAGGGAGATAAAG
CAAAGGTGAAGGACGAACCACAGAGAAGATCCGCGAGGTTGTCTGCTAAACCTGCTCCTCCAAAGCCAGAGCCCA
AGCCTAAAAAGGCCCCTGCAAAGAAGGGAGAGAAGGTACCCAAAGGGAAAAAGGGAAAAGCTGATGCTGGCAAGG
AGGGGAATAACCCTGCAGAAAATGGAGATGCCAAAACAGACCAGGCACAGAAAGCTGAAGGTGCTGGAGATGCCA
AG**TGA**AGTGTGTGCATTTTTGATAACTGTGTACTTCTGGTGACTGTACAGTTTGAAATACTATTTTTTATCAAGT
TTTATAAAAATGCAGAATTTTGTTTTACTTTTTTTTTTTTTTTTAAAAGCTATGTTGTTAGCACACAGAACACTTC
ATTGTTGTTTTTGGGGGAAGGGGCATATGTCACTAATAGAATGTCTCCAAAGCTGGATTGATGTGGAGAAAACAC
CTTTCCCTTCTAGTTTTGAGAGACTTCCTCTTGGCTCCCAGGAGGAGGGATTCCCTGACTTTGACACACATGGCC
ACCTTGGCACAAAAGCCTTGTGGTATAGAAAAACAAATTTGTTTTTATGTCCTCTTCTCCCTTTCCATCTTTCAG
CATAGACTTAACTCCCTTAAGCCCAGACATCTGTTGAGACCTGACCCCTAGTCATTGGTTACCAGTGTGTCAGGC
AATCTGGACTTTCCAGTGATGCCACTGAGATGGCACCTGTCAAAAGAGCAGTGGTTCCATTTCTAGATTGTGGAT
CTTCAGATAAATTCTGCCATTTTCATTTCACTTCCTGAAAGTCAGGGTCGGCTTGTGAAAAGTTGTTAAACAACA
TGCTAAATGTGAAATGTCAACCCTCACTCTAAACTTTCCCTGTTCAGAGCATCAGATGAAGACTTCATTGGGTTT
TATAGTGGCTTTCTGATTTTTGGTAGTCCATTGAAGAAGGGAGTTTGAAAGTTGTTGTATACTGTTAACGATTGT
CTGCCCATGTCCTGCCTGAAATACCATGATTGTTTATGGAAAGTATCTTTAATAAAGCTGGATACAGTTTGGC

FIGURE 111

MPKRKAEGDAKGDKAKVKDEPQRRSARLSAKPAPPKPEPKPKKAPAKKGEKVPKGKKGKADAGKEGNNPAENGDA
KTDQAQKAEGAGDAK

FIGURE 112A

GAAAGCGGAGAGTCACAGCGGGGCCAGGCCCTGGGGAGCGGAGCCTCCACCGCCCCCCTCATTCCCAGGCAAGGG
CTTGGGGGGAATGAGCCGGGAGAGCCGGGTCCCGAGCCTACAGAGCCGGGAGCAGCTGAGCCGCCGGCGCCTCGG
CCGCCGCCGCCGCCTCCTCCTCCTCCGCCGCCGCCAGCCCGGAGCCTGAGCCGGCGGGGCGGGGGGGAGAGGAGC
GAGCGCAGCGCAGCAGCGGAGCCCCGCGAGGCCCGCCCGGGCGGGTGGGGAGGGCAGCCCGGGGGACTGGGCCCC
GGGGCGGGGTGGGAGGGGGGGAGAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTCGAGGCGGCGGCTGCGGCAGCGGC
CGAGCGCGGTGGAAATGAAGGCAGCCGCCGGGCAGGAAAGCGAGGGCCCCGCCGTGGGGCCGCCGCATCCGCTGG
GAAAGGAGCTGCTGGACGGGGCCGAGAGCAATGGGGGTGGCGGCGGCGGCGGAGCCGGCAGCGGCGGCGGGCCCG
GCGCGGAGCCGGACCTGAAGAACTCGAACGGGAACGCGGGCCCTAGGCCCGCCCTGAACAATAACCTCACGGAGC
CGCCCGGCGGCGGCGGTGGCGGCAGCAGCGATGGGGTGGGGGCGCCTCCTCACTCAGCCGCGGCCGCCTTGCCGC
CCCCAGCCTACGGCTTCGGGCAACCCTACGGCCGGAGCCCGTCTGCCGTCGCCGCCGCCGCGGCCGCCGTCTTCC
ACCAACAACATGGCGGACAACAAAGCCCTGGCCTGGCAGCGCTGCAGAGCGGCGGCGGCGGGGGCCTGGAGCCCT
ACGCGGGGCCCCAGCAGAACTCTCACGACCACGGCTTCCCCAACCACCAGTACAACTCCTACTACCCCAACCGCA
GCGCCTACCCCCCGCCCGCCCCGGCCTACGCGCTGAGCTCCCCGAGAGGTGGCACTCCGGGCTCCGGCGCGGCGG
CGGCTGCCGGCTCCAAGCCGCCTCCCTCCTCCAGCGCCTCCGCCTCCTCGTCGTCTTCGTCCTTCGCTCAGCAGC
GCTTCGGGGCCATGGGGGGAGGCGGCCCCTCCGCGGCCGGCGGGGGAACTCCCCAGCCCACCGCCACCCCCACCC
TCAACCAACTGCTCACGTCGCCCAGCTCGGCCCGGGGCTACCAGGGCTACCCCGGGGGCGACTACAGTGGCGGGC
CCCAGGACGGGGGCGCCGGCAAGGGCCCGGCGGACATGGCCTCGCAGTGTTGGGGGGCTGCGGCGGCGGCAGCTG
CGGCGGCGGCCGCCTCGGGAGGGGCCCAACAAAGGAGCCACCACGCGCCCATGAGCCCCGGGAGCAGCGGCGGCG
GGGGGCAGCCGCTCGCCCGGACCCCTCAGCCATCCAGTCCAATGGATCAGATGGGCAAGATGAGACCTCAGCCAT
ATGGCGGGACTAACCCATACTCGCAGCAACAGGGACCTCCGTCAGGACCGCAGCAAGGACATGGGTACCCAGGGC
AGCCATACGGGTCCCAGACCCCGCAGCGGTACCCGATGACCATGCAGGGCCGGGCGCAGAGTGCCATGGGCGGCC
TCTCTTATACACAGCAGATTCCTCCTTATGGACAACAAGGCCCCAGCGGGTATGGTCAACAGGGCCAGACTCCAT
ATTACAACCAGCAAAGTCCTCACCCTCAGCAGCAGCAGCCACCCTACTCCCAGCAACCACCGTCCCAGACCCCTC
ATGCCCAACCTTCGTATCAGCAGCAGCCACAGTCTCAACCACCACAGCTCCAGTCCTCTCAGCCTCCATACTCCC
AGCAGCCATCCCAGCCTCCACATCAGCAGTCCCCGGCTCCATACCCCTCCCAGCAGTCGACGACACAGCAGCACC
CCCAGAGCCAGCCCCCCTACTCACAGCCACAGGCTCAGTCTCCTTACCAGCAGCAGCAACCTCAGCAGCCAGCAC
CCTCGACGCTCTCCCAGCAGGCTGCGTATCCTCAGCCCCAGTCTCAGCAGTCCCAGCAAACTGCCTATTCCCAGC
AGCGCTTCCCTCCACCGCAGGAGCTATCTCAAGATTCATTTGGGTCTCAGGCATCCTCAGCCCCCTCAATGACCT
CCAGTAAGGGAGGGCAAGAAGATATGAACCTGAGCCTTCAGTCAAGACCCTCCAGCTTGCCTGATCTATCTGGTT
CAATAGATGACCTCCCCATGGGGACAGAAGGAGCTCTGAGTCCTGGAGTGAGCACATCAGGGATTTCCAGCAGCC
AAGGAGAGCAGAGTAATCCAGCTCAGTCTCCTTTCTCTCCTCATACCTCCCCTCACCTGCCTGGCATCCGAGGCC
CTTCCCCGTCCCCTGTTGGCTCTCCCGCCAGTGTTGCTCAGTCTCGCTCAGGACCACTCTCGCCTGCTGCAGTGC
CAGGCAACCAGATGCCACCTCGGCCACCCAGTGGCCAGTCGGACAGCATCATGCATCCTTCCATGAACCAATCAA
GCATTGCCCAAGATCGAGGTTATATGCAGAGGAACCCCCAGATGCCCCAGTACAGTTCCCCCCAGCCCGGCTCAG
CCTTATCTCCGCGTCAGCCTTCCGGAGGACAGATACACACAGGCATGGGCTCCTACCAGCAGAACTCCATGGGGA
GCTATGGTCCCCAGGGGGGTCAGTATGGCCCACAAGGTGGCTACCCCAGGCAGCCAAACTATAATGCCTTGCCCA
ATGCCAACTACCCCAGTGCAGGCATGGCTGGAGGCATAAACCCCATGGGTGCCGGAGGTCAAATGCATGGACAGC
CTGGCATCCCACCTTATGGCACACTCCCTCCAGGGAGGATGAGTCACGCCTCCATGGGCAACCGGCCTTATGGCC
CTAACATGGCCAATATGCCACCTCAGGTTGGGTCAGGGATGTGTCCCCCACCAGGGGGCATGAACCGGAAAACCC
AAGAAACTGCTGTCGCCATGCATGTTGCTGCCAACTCTATCCAAAACAGGCCGCCAGGCTACCCCAATATGAATC
AAGGGGGCATGATGGGAACTGGACCTCCTTATGGACAAGGGATTAATAGTATGGCTGGCATGATCAACCCTCAGG
GACCCCCATATTCCATGGGTGGAACCATGGCCAACAATTCTGCAGGGATGGCAGCCAGCCCAGAGATGATGGGCC
TTGGGGATGTAAAGTTAACTCCAGCCACCAAAATGAACAACAAGGCAGATGGGACACCCAAGACAGAATCCAAAT
CCAAGAAATCCAGTTCTTCTACTACAACCAATGAGAAGATCACCAAGTTGTATGAGCTGGGTGGTGAGCCTGAGA
GGAAGATGTGGGTGGACCGTTATCTGGCCTTCACTGAGGAGAAGGCCATGGGCATGACAAATCTGCCTGCTGTGG
GTAGGAAACCTCTGGACCTCTATCGCCTCTATGTGTCTGTGAAGGAGATTGGTGGATTGACTCAGGTCAACAAGA
ACAAAAAATGGCGGGAACTTGCAACCAACCTCAATGTGGGCACATCAAGCAGTGCTGCCAGCTCCTTGAAAAAGC

FIGURE 112B

AGTATATCCAGTGTCTCTATGCCTTTGAATGCAAGATTGAACGGGGAGAAGACCCTCCCCCAGACATCTTTGCAG
CTGCTGATTCCAAGAAGTCCCAGCCCAAGATCCAGCCTCCCTCTCCTGCGGGATCAGGATCTATGCAGGGGCCCC
AGACTCCCCAGTCAACCAGCAGTTCCATGGCAGAAGGAGGAGACTTAAAGCCACCAACTCCAGCATCCACACCAC
ACAGTCAGATCCCCCCATTGCCAGGCATGAGCAGGAGCAATTCAGTTGGGATCCAGGATGCCTTTAATGATGGAA
GTGACTCCACATTCCAGAAGCGGAATTCCATGACTCCAAACCCTGGGTATCAGCCCAGTATGAATACCTCTGACA
TGATGGGGCGCATGTCCTATGAGCCAAATAAGGATCCTTATGGCAGCATGAGGAAAGCTCCAGGGAGTGATCCCT
TCATGTCCTCAGGGCAGGGCCCCAACGGCGGGATGGGTGACCCCTACAGTCGTGCTGCCGGCCCTGGGCTAGGAA
ATGTGGCGATGGGACCACGACAGCACTATCCCTATGGAGGTCCTTATGACAGAGTGAGGACGGAGCCTGGAATAG
GGCCTGAGGGAAACATGAGCACTGGGGCCCCACAGCCGAATCTCATGCCTTCCAACCCAGACTCGGGGATGTATT
CTCCTAGCCGCTACCCCCCGCAGCAGCAGCAGCAGCAGCAGCAACGACATGATTCCTATGGCAATCAGTTCTCCA
CCCAAGGCACCCCTTCTGGCAGCCCCTTCCCCAGCCAGCAGACTACAATGTATCAACAGCAACAGCAGAATTACA
AGCGGCCAATGGATGGCACATATGGCCCTCCTGCCAAGCGGCACGAAGGGGAGATGTACAGCGTGCCATACAGCA
CTGGGCAGGGGCAGCCTCAGCAGCAGCAGTTGCCCCCAGCCCAGCCCCAGCCTGCCAGCCAGCAACAAGCTGCCC
AGCCTTCCCCCTCAGCAAGATGTATACAACCAGTATGGCAATGCCTATCCTGCCACTGCCACAGCTGCTACTGAGC
GCCGACCAGCAGGCGGCCCCCAGAACCAATTTCCATTCCAGTTTGGCCGAGACCGTGTCTCTGCACCCCCTGGCA
CCAATGCCCAGCAAAACATGCCACCACAAATGATGGGCGGCCCCATACAGGCATCAGCTGAGGTTGCTCAGCAAG
GCACCATGTGGCAGGGGCGTAATGACATGACCTATAATTATGCCAACAGGCAGAGCACGGGCTCTGCCCCCCAGG
GCCCCGCCTATCATGGCGTGAACCGAACAGATGAAATGCTGCACACAGATCAGAGGGCCAACCACGAAGGCTCGT
GGCCTTCCCATGGCACACGCCAGCCCCCATATGGTCCCTCTGCCCCTGTGCCCCCCATGACAAGGCCCCCTCCAT
CTAACTACCAGCCCCCACCAAGCATGCAGAATCACATTCCTCAGGTATCCAGCCCTGCTCCCCTGCCCCGGCCAA
TGGAGAACCGCACCTCTCCTAGCAAGTCTCCATTCCTGCACTCTGGGATGAAAATGCAGAAGGCAGGTCCCCCAG
TACCTGCCTCGCACATAGCACCTGCCCCTGTGCAGCCCCCCATGATTCGGCGGGATATCACCTTCCCACCTGGCT
CTGTTGAAGCCACACAGCCTGTGTTGAAGCAGAGGAGGCGGCTCACAATGAAAGACATTGGAACCCCGGAGGCAT
GGCGGGTAATGATGTCCCTCAAGTCTGGTCTCCTGGCAGAGAGCACATGGGCATTAGATACCATCAACATCCTGC
TGTATGATGACAACAGCATCATGACCTTCAACCTCAGTCAGCTCCCAGGGTTGCTAGAGCTCCTTGTAGAATATT
TCCGACGATGCCTGATTGAGATCTTTGGCATTTTAAAGGAGTATGAGGTGGGTGACCCAGGACAGAGAACGCTAC
TGGATCCTGGGAGGTTCAGCAAGGTGTCTAGTCCAGCTCCCATGGAGGGTGGGGAAGAAGAAGAAGAACTTCTAG
GTCCTAAACTAGAAGAGGAAGAAGAAGAGGAAGTAGTTGAAAATGATGAGGAGATAGCCTTTTCAGGCAAGGACA
AGCCAGCTTCAGAGAATAGTGAGGAGAAGCTGATCAGTAAGTTTGACAAGCTTCCAGTAAAGATCGTACAGAAGA
ATGATCCATTTGTGGTGGACTGCTCAGATAAGCTTGGGCGTGTGCAGGAGTTTGACAGTGGCCTGCTGCACTGGC
GGATTGGTGGGGGGGACACCACTGAGCATATCCAGACCCACTTCGAGAGCAAGACAGAGCTGCTGCCTTCCCGGC
CTCACGCACCCTGCCCACCAGCCCCTCGGAAGCATGTGACAACAGCAGAGGGTACACCAGGGACAACAGACCAGG
AGGGGCCCCCACCTGATGGACCTCCAGAAAAACGGATCACAGCCACTATGGATGACATGTTGTCTACTCGGTCTA
GCACCTTGACCGAGGATGGAGCTAAGAGTTCAGAGGCCATCAAGGAGAGCAGCAAGTTTCCATTTGGCATTAGCC
CAGCACAGAGCCACCGGAACATCAAGATCCTAGAGGACGAACCCCACAGTAAGGATGAGACCCCACTGTGTACCC
TTCTGGACTGGCAGGATTCTCTTGCCAAGCGCTGCGTCTGTGTGTCCAATACCATTCGAAGCCTGTCATTTGTGC
CAGGCAATGACTTTGAGATGTCCAAACACCCAGGGCTGCTGCTCATCCTGGGCAAGCTGATCCTGCTGCACCACA
AGCACCCAGAACGGAAGCAGGCACCACTAACTTATGAAAAGGAGGAGGAACAGGACCAAGGGGTGAGCTGCAACA
AAGTGGAGTGGTGGTGGGACTGCTTGGAGATGCTCCGGGAAAACACCTTGGTTACACTCGCCAACATCTCGGGGC
AGTTGGACCTATCTCCATACCCCGAGAGCATTTGCCTGCCTGTCCTGGACGGACTCCTACACTGGGCAGTTTGCC
CTTCAGCTGAAGCCCAGGACCCCTTTTCCACCCTGGGCCCCAATGCCGTCCTTTCCCCGCAGAGACTGGTCTTGG
AAACCCTCAGCAAACTCAGCATCCAGGACAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGG
AGAAGTTGTATAGCACTATGGTGCGCTTCCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTAC
TGCTGGCCAACCTGGCTCAGGGGGACAGCCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACC
TCCTGGGCTTCCTAGAGGACAGCCTTGCCGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGA
ACCCACCCTTTGAGCCAACTAGTGTGGACATGATGCGGCGGGCTGCCCGCGCGCTGCTTGCCTTGGCCAAGGTGG
ACGAGAACCACTCAGAGTTTACTCTGTACGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACTCAT
TGGTTTCACAAGTCATTTGTGATGTACTGTTTTTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCC

FIGURE 112C

GTGTGTGTGTGCGTGTGTGGAGAACTTAGAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCA
GTTTACCCTGTGCTGTCCAGCTTCTCCCTTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCT
CCCTCCATCACCTCACGCCTTTCTGTTCCTTGTCCTCACCTTACTCCCCTCAGGACCCTACCCCACCCTCTTTGA
AAAGACAAAGCTCTGCCTACATAGAAGACTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGG
GAAAAAAAATAAAATAAAAATGGCTTTCCCAGTCCTTGCATCAACGGGATGCCACATTTCATAACTGTTTTTAAT
GGTAAAAAAAAAAAAAA

FIGURE 113

CAACAATGTGGACCTGATTCTGGCCACACCCCCCTTCAGCCGCCTGGAGAAGTTGTATAGCACTATGGTGCGCTT
CCTCAGTGACCGAAAGAACCCGGTGTGCCGGGAGATGGCTGTGGTACTGCTGGCCAACCTGGCTCAGGGGGACAG
CCTGGCAGCTCGTGCCATTGCAGTGCAGAAGGGCAGTATCGGCAACCTCCTGGGCTTCCTAGAGGACAGCCTTGC
CGCCACACAGTTCCAGCAGAGCCAGGCCAGCCTCCTCCACATGCAGAACCCACCCTTTGAGCCAACTAGTGTGGA
CATGATGCGGCGGGCTGCCCGCGCGCTGCTTGCCTTGGCCAAGGTGGACGAGAACCACTCAGAGTTTACTCTGTA
CGAATCACGGCTGTTGGACATCTCGGTATCACCGTTGATGAACTCATTGGTTTCACAAGTCATTTGTGATGTACT
GTTTTTGATTGGCCAGTCATGACAGCCGTGGGACACCTCCCCCCCCCGTGTGTGTGTGCGTGTGTGGAGAACTTA
GAAACTGACTGTTGCCCTTTATTTATGCAAAACCACCTCAGAATCCAGTTTACCCTGTGCTGTCCAGCTTCTCCC
TTGGGAAAAAGTCTCTCCTGTTTCTCTCTCCTCCTTCCACCTCCCCTCCCTCCATCACCTCACGCCTTTCTGTTC
CTTGTCCTCACCTTACTCCCCTCAGGACCCTACCCCACCCTCTTTGAAAAGACAAAGCTCTGCCTACATAGAAGA
CTTTTTTTATTTTAACCAAAGTTACTGTTGTTTACAGTGAGTTTGGGGAAAAAAAATAAAATAAAAATGGCTTTC
CCAGTCCTTGCATCAACGGGATGCCACATTTCATAACTGTTTTTAATGGTAAAAAAAAAAAAAAAAAATACAAAA
AAAAATTCTGAAGGACAAAAAAGGTGACTGCTGAACTGTGTGTGGTTTATTGTTGTACATTCACAATCTTGCAGG
AGCCAAGAAGTTCGCAGTTGTGAACAGACCCTGTTCACTGGAGAGGCCTGTGCAGTAGAGTGTAGACCCTTTCAT
GTACTGTACTGTACACCTGATACTGTAAACATACTGTAATAATAATGTCTCACATGGAAACAGAAAACGCTGGGT
CAGCAGCAAGCTGTAGTTTTTAAAAATGTTTTTAGTTAAACGTTGAGGAGAAAAAAAAAAAAAGGCTTTTCCCCCA
AAGTATCATGTGTGAACCTACAACACCCTGACCTCTTTCTCTCCTCCTTGATTGTATGAATAACCCTGAGATCAC
CTCTTAGAACTGGTTTTAACCTTTAGCTGCAGCGGCTACGCTGCCACGTGTGTATATATATGACGTTGTACATTG
CACATACCCTTGGATCCCCACAGTTTGGTCCTCCTCCCAGCTACCCCTTTATAGTATGACGAGTTAACAAGTTGG
TGACCTGCACAAAGCGAGACACAGCTATTTAATCTCTTGCCAGATATCGCCCCTCTTGGTGCGATGCTGTACAGG
TCTCTGTAAAAAGTCCTTGCTGTCTCAGCAGCCAATCAACTTATAGTTTATTTTTTTCTGGGTTTTTGTTTTGTT
TTGTTTTCTTTCTAATCGAGGTGTGAAAAAGTTCTAGGTTCAGTTGAAGTTCTGATGAAGAAACACAATTGAGAT
TTTTTCAGTGATAAAATCTGCATATTTGTATTTCAACAATGTAGCTAAAACTTGATGTAAATTCCTCCTTTTTTT
CCTTTTTTGGCTTAATGAATATCATTTATTCAGTATGAAATCTTTATACTATATGTTCCACGTGTTAAGAATAAA
TGTACATTAAATCTTGGT

FIGURE 114

ATTGGTCCCAGGCAGCAGTTAGCCCGCCGCCCGCCTGTGTGTCCCCAGAGCCATGGAGAGAGCCAGTCTGATCCA
GAAGGCCAAGCTGGCAGAGCAGGCCGAACGCTATGAGGACATGGCAGCCTTCATGAAAGGCGCCGTGGAGAAGGG
CGAGGAGCTCTCCTGCGAAGAGCGAAACCTGCTCTCAGTAGCCTATAAGAACGTGGTGGGCGGCCAGAGGGCTGC
CTGGAGGGTGCTGTCCAGTATTGAGCAGAAAAGCAACGAGGAGGGCTCGGAGGAGAAGGGGCCCGAGGTGCGTGA
GTACCGGGTCTTCTACCTGAAGATGAAGGGTGACTACTACCGCTACCTGGCCGAGGTGGCCACCGGTGACGACAA
GAAGCGCATCATTGACTCAGCCCGGTCAGCCTACCAGGAGGCCATGGACATCAGCAAGAAGGAGATGCCGCCCAC
CAACCCCATCCGCCTGGGCCTGGCCCTGAACTTTTCCGTCTTCCACTACGAGATCGCCAACAGCCCCGAGGAGGC
CATCTCTCTGGCCAAGACCACTTTCGACGAGGCCATGGCTGATCTGCACACCCTCAGCGAGGACTCCTACAAAGA
CAGCACCCTCATCATGCAGCTGCTGCGAGACAACCTGACACTGTGGACGGCCGACAACGCCGGGGAAGAGGGGGG
CGAGGCTCCCCAGGAGCCCCAGAGCTGAGTGTTGCCCGCCACCGCCCCGCCCTGCCCCCTCCAGTCCCCCACCCT
GCCGAGAGGACTAGTATGGGGTGGGAGGCCCCACCCTTCTCCCCTAGGCGCTGTTCTTGCTCCAAAGGGCTCCGT
GGAGAGGGACTGGCAGAGCTGAGGCCACCTGGGGCTGGGGATCCCACTCTTCTTGCAGCTGTTGAGCGCACCTAA
CCACTGGTCATGCCCCCACCCCTGCTCTCCGCACCCGCTTCCTCCCGACCCCAGGACCAGGCTACTTCTCCCCTC
CTCTTGCCTCCCTCCTGCCCCTGCTGCCTCTGATCGTAGGAATTGAGGAGTGTCCCGCCTTGTGGCTGAGAACTG
GACAGTGGCAGGGGCTGGAGATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGCGCGCGCCAGTGCA
AGACCGAGATTGAGGGAAAGCATGTCTGCTGGGTGTGACCATGTTTCCTCTCAATAAAGTTCCCCTGTGACACTC

FIGURE 115

MERASLIQKAKLAEQAERYEDMAAFMKGAVEKGEELSCEERNLLSVAYKNVVGGQRAAWRVLSSIEQKSNEEGSE
EKGPEVREYREKVETELQGVCDTVLGLLDSHLIKEAGDAESRVFYLKMKGDYYRYLAEVATGDDKKRIIDSARSA
YQEAMDISKKEMPPTNPIRLGLALNFSVFHYEIANSPEEAISLAKTTFDEAMADLHTLSEDSYKDSTLIMQLLRD
NLTLWTADNAGEEGGEAPQEPQS

FIGURE 116

CCGGAAGTCGAGTTAGTCTAGTTAGTATCGGCCTGTTATCTCCTTTTGCGCGACACGGTCTCAGCTGTTCCGCCT
GAGGCGAGTGACGCTGGCCGCCAACGAGGTATACGTACTGGGACCCTCGCCCTCAGTCTCGTCTCCGGCGCGGCT
ACCTGCCCCGTTTTCCCTGTGAGTTGACCTGCTCCGGGCCGCGGGCCGCCA**ATG**GCAGGGGCCGCTCCGACCACG
GCCTTCGGGCAGGCGGTGACCGGCCCGCCGGGCTCAGGGAAGACCACGTACTGCCTGGGCATGAGTGAGTTCCTG
CGCGCGCTGGGCCGGCGCGTGGCGGTGGTGAACCTGGACCCGGCCAACGAGGGGCTGCCGTACGAGTGTGCCGTG
GACGTGGGCGAGCTGGTGGGGCTGGGCGACGTGATGGACGCGCTGCGCCTGGGGCCCAACGGCGGCCTGCTCTAC
TGCATGGAGTACCTGGAAGCCAACCTGGACTGGCTGCGTGCCAAGCTCGACCCCCTCCGCGGCCACTACTTCCTC
TTCGACTGCCCAGGCCAGGTGGAGCTCTGCACGCATCACGGCGCCTTGCGCAGCATCTTCTCCCAAATGGCGCAG
TGGGACCTCAGGCTGACTGCCGTCCACCTCGTGGATTCTCACTACTGCACAGACCCTGCCAAGTTCATTTCAGTA
CTGTGTACCTCCCTGGCCACCATGCTGCACGTGGAACTGCCCCACATCAACCTCCTTTCCAAGATGGACCTCATT
GAGCATTATGGGAAGCTGGCCTTCAACCTGGACTACTACACAGAGGTTCTGGACCTCTCCTACCTGCTTGACCAC
CTGGCTTCTGACCCTTTCTTCCGCCACTACCGCCAGCTCAATGAGAAGCTAGTGCAGCTCATCGAAGACTATAGC
CTTGTCTCCTTTATCCCTCTCAACATCCAGGACAAGGAGAGCATCCAGCGAGTCCTGCAGGCTGTGGATAAAGCC
AATGGATACTGTTTCAGAGCCCAAGAGCAGCGAAGCTTGGAAGCCATGATGTCTGCCGCAATGGGAGCCGACTTC
CATTTCTCTTCCACACTGGGCATCCAGGAGAAGTACCTGGCACCCTCGAACCAGTCAGTGGAGCAGGAAGCCATG
CAGCTG**TAG**CAACAAGGTGGACCCTGGAGAGCAGGATGCATAATCCAGCACTGGGGAAAGTGGAGGCTCCTGATG
CAGGCTGCAGACCCAAGAGCAAGTCCTCCCAGCCAGAGCTGGCGGGCTGGCAAGGGGATATTCAGCTCTGCAAAG
GACTTCTGGCCAAAAAGCCAGACATGGTGCCAAGCAGAACACCCCCCATACTGTCAGTGGTGTCCGTGAGCTCTG
GGCCCTGCCACCAGAAAGTCGAGCACTGGTCCTAGTCAGGCTGTGATGAAATGTGCTACAATACAAGAGTTTATT
TTCT

FIGURE 117

MAGAAPTTAFGQAVTGPPGSGKTTYCLGMSEFLRALGRRVAVVNLDPANEGLPYECAVDVGELVGLGDVMDALRL
GPNGGLLYCMEYLEANLDWLRAKLDPLRGHYFLFDCPGQVELCTHHGALRSIFSQMAQWDLRLTAVHLVDSHYCT
DPAKFISVLCTSLATMLHVELPHINLLSKMDLIEHYGKLAFNLDYYTEVLDLSYLLDHLASDPFFRHYRQLNEKL
VQLIEDYSLVSFIPLNIQDKESIQRVLQAVDKANGYCFRAQEQRSLEAMMSAAMGADFHFSSTLGIQEKYLAPSN
QSVEQEAMQL

FIGURE 118

TAGAGTCGTTGGGCCCGGCGCGACCCGCAGGAGCGTAGAGAGCGCGGGACTAGAGTGCAGAGCTCCGGGACGTGG
ATCGGAGCCGGCGCG**ATG**GGCGGAGAGCAGGAGGAGGAGCGGTTCGACGGCATGTTGCTGGCCATGGCTCAGCAG
CACGAGGGCGGCGTGCAGGAGCTTGTGAACACCTTCTTCAGCTTCCTTCGACGCAAAACAGACTTTTTCATTGGA
GGAGAAGAAGGGATGGCAGAGAAGCTTATCACACAGACTTTCAGCCACCACAATCAGCTGGCACAGAAGACCCGG
CGGGAGAAGAGAGCCCGGCAGGAGGCCGAGCGGCGGGAGAAGGCGGAGCGGGCGGCCAGACTGGCCAAGGAAGCC
AAGTCAGAGACCTCAGGGCCCCAGATCAAGGAGCTAACTGATGAAGAGGCAGAGAGGCTGCAGCTAGAGATTGAC
CAGAAAAAGGATGCAGAGAATCATGAGGCCCAGCTCAAGAACGGCAGCCTTGACTCCCCAGGGAAGCAGGATACT
GAGGAAGATGAGGAGGAAGATGAGAAGGACAAAGGAAAACTGAAGCCCAACCTAGGCAACGGGGCAGACCTGCCC
AATTACCGCTGGACCCAGACCCTGTCGGAGCTGGACCTGGCGGTCCCTTTCTGTGTGAACTTCCGGCTGAAAGGG
AAGGACATGGTGGTGGACATCCAGCGGCGGCACCTCCGGGTGGGGCTCAAGGGGCAGCCAGCGATCATTGATGGG
GAGCTCTACAATGAAGTGAAGGTGGAGGAGAGCTCGTGGCTCATTGAGGACGGCAAGGTGGTGACTGTGCATCTG
GAGAAGATCAATAAGATGGAGTGGTGGAGCCGCTTGGTGTCCAGTGACCCTGAGATCAACACCAAGAAGATTAAC
CCTGAGAATTCCAAGCTGTCAGACCTGGACAGTGAGACTCGCAGCATGGTGGAAAAGATGATGTATGACCAGCGA
CAGAAGTCCATGGGGCTGCCAACTTCAGACGAACAGAAGAAACAGGAGATTCTGAAGAAGTTCATGGATCAACAT
CCGGAGATGGATTTTTCCAAGGCTAAATTCAAC**TAG**CCCCTGTTTTTTCCTCCCTGAACTCTTGGGGCTGAGCTG
CAACCACCCAACTTTCTTTCCCACTCTTCTCTGGGACTTGTGGGCCTCAGGGCTTGGGGCAGGCATGGGACTGGC
CCAGGCACACAGGTCCCGGGGCATCAGGAGAAAGGCTGGGTCTTGGGACCTTGTCCTCCCCAGTTGGCCTACTGT
TACACATTAAAACGATTTGCCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 119

MGGEQEEERFDGMLLAMAQQHEGGVQELVNTFFSFLRRKTDFFIGGEEGMAEKLITQTFSHHNQLAQKTRREKRA
RQEAERREKAERAARLAKEAKSETSGPQIKELTDEEAERLQLEIDQKKDAENHEAQLKNGSLDSPGKQDTEEDEE
EDEKDKGKLKPNLGNGADLPNYRWTQTLSELDLAVPFCVNFRLKGKDMVVDIQRRHLRVGLKGQPAIIDGELYNE
VKVEESSWLIEDGKVVTVHLEKINKMEWWSRLVSSDPEINTKKINPENSKLSDLDSETRSMVEKMMYDQRQKSMG
LPTSDEQKKQEILKKFMDQHPEMDFSKAKFN

FIGURE 120

CCTGGTATGATTCCATCCTGAGCGGCTGTTCTCTTGAGCAGCGTTCATTTATCTCCGTCTGCCTTCTGTCCCACC
TAAGTGTGTGCCGCCACCCAATAGAAGATTCG**ATG**GACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTT
TCGGTTGTGAACTAAAGGCTGACAAAGATGATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTT
TAAGAACGGTCAGTTTAGGGGCTGGTACAAAGGATGAATTGCACATTGTTGAAGCAGAGGCAATGAATTACAAAG
GCAGTCCAATTAAAGTAACACTGGCAACTTTGAAAATGTCTGCACAGCCAACAGTTTCCCTTGGGGGCTTTGAAA
TAACACCACCAGTGGTCTTAAGATTTAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTG
TGGAGGAAGATGCAGAGTCAGAAGATGAAGAGGAGGAGGATGTGAAACTCTTAAGTATATCTGGAAAGCGGTCTG
CCCCTGGAGGTGGTAGCAAGGTTCCACAGAAAAAAGTAAAACTTGCTGTTGATGAAGATGATGATGATGATGATG
ATGATGATGATGATGATTTTGATGATGAGGAAGCTGAAGAAAAAGTGCCAGTGAAGAAAGGACAAGAATCCTTCA
AAACACAGGAAAAAACTCCTAAAACACCAAAAGGATCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAA
GTATAGAAAAAGGGGGTTCTCTTCCCAAAGTGGAAGCCGAGTTCATCAATTTTGTGAAGAATTGCTTCTGGATGA
CTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCCT**TAA**GAAAATAGTTTCAACAATTTGTTAA
AAATTTTCCATCATATTTCATTTCTGTAACAGTTGATATCTGGCTGTCCTTTTTATAATGCAGAGTGAGAACTTT
CCCTACCGTGTTTGATAAATGTTGTCCAGGTTCCATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTAGTTTTT
AAAGATGGAACTCACCCTTTGCTTGGTTTTAAATATGTATGGAATGTTATGATAGGACATAGTAGTAGCGGTGGT
CAGACATGGAAATTGTGGGAAGACAAAAATATGCCTGTGAAATAAAACTCAATATTTTAATAAAGTAAAAAAAAA
AAAAAA

FIGURE 121

MDMDMSPLRPQNYLFGCELKADKDDHFKVDNDENEHQLSLRTVSLGAGTKDELHIVEAEAMNYKGSPIKVTLATL
KMSAQPTVSLGGFEITPPVVLRFKCGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGKRSAPGGGSKVPQK
KVKLAVDEDDDDDDDDDDDDFDDEEAEEKVPVKKGQESFKTQEKTPKTPKGSSSVEDIKAKMQASIEKGGSLPKV
EAEFINFVKNCFWMTDQEAIQDLWQWRKSP

FIGURE 122

AGCTGCTGGCTGGGCTGCCTGTTGAGTCAGCCTTCTTCCCTCACGGCTCTTCTCCCGGTCCCTGAAACTCGGCTG
CCAGGGGAGCTGGAGCCACCTGCGAAGGTGTCCTCCCATACTGGACCCCTACAGGAAGCTCCGTGTGCCCAGCTG
GGGCACAGCCCCAGCTG**ATG**CCCCAGAGGGGCCACCCATCGCAAGAGGGGCTTTGGGCTCTGCCCTCCCTCCCCA
TGGCGCATGGGCCAAAGCCTGAGACTGAAGGACTGTTGGACCTCAGCTTCCTGACAGAGGAGGAGCAGGAGGCCA
TTGCTGGCGTCCTCCAACGAGATGCCCGCCTGCGCCAGCTGGAGGAGGGGCGGGTCAGCAAGCTCCGGGCCTCAG
TGGCAGACCCTGGGCAGCTGAAGATCCTGACAGGGGACTGGTTCCAGGAAGCACGCTCCCAGCGGCACCACAATG
CCCACTTCGGCTCTGACCTTGTCCGAGCGTCTATGCGCAGGAAGAAGAGCACCAGGGGAGACCAGGCTCCAGGCC
ACGACAGGGAGGCTGAGGCTGCTGTGAAAGAGAAGGAAGAGGGGCCAGAGCCCAGGCTCACCATTGATGAGGCCC
CTCAGGAGAGGCTCAGGGAGACTGAGGCTTCAGATCCTGAGGAGGCGTCCCAGGCCCAGGAAGATCCTGGCCAAG
GAGACCAACAGGTCTGTGCCGAGGAGGCTGACCCGGAGCTGGAGCCCGCGTCGGGGGGAGAGCAGGAGCCGCGGC
CCCAGCAAGCCCAGACCAAGGCCGCGTCCCAGATCCTGGAGAATGGGGAGGAGGCCCCGGGGCCCGACCCCTCTC
TCGACCGCATGCTCAGCAGCAGCTCCTCGGTGTCCAGCCTTAACTCCTCCACGCTGAGCGGCAGCCAGATGAGCC
TGTCAGGCGACGCGGAGGCGGTGCAGGTCCGCGGCTCCGTGCACTTCGCGCTGCACTACGAGCCGGGCGCCGCCG
AGCTGCGCGTGCACGTGATCCAGTGCCAGGGCCTGGCCGCCGCCCGGCGCCGCCGCTCGGACCCCTACGTCAAAA
GCTACCTCCTCCCGGATAAGCAGAGCAAGCGCAAGACGGCGGTGAAGAAACGGAATCTGAATCCGGTTTTCAACG
AGACTCTCCGGTACTCCGTCCCGCAGGCCGAGCTTCAGGGCCGCGTGCTGAGCCTGTCTGTGTGGCACCGCGAAA
GCCTGGGTCGCAACATCTTTCTGGGCGAAGTTGAAGTGCCCCTGGACACGTGGGACTGGGGCTCTGAGCCCACCT
GGCTCCCCCTGCAGCCCCGGGTCCCACCCTCTCCCGACGACCTTCCGAGCCGCGGGTTACTCGCCCTGTCCCTCA
AGTACGTCCCCGCCGGCTCCGAGGGCGCAGGACTGCCCCCGAGCGGGGAGCTGCACTTCTGGGTGAAGGAGGCTC
GGGACCTCCTGCCGCTGCGGGCAGGATCCCTGGACACTTACGTACAATGCTTCGTGCTGCCTGATGACAGCCAGG
CCAGCCGCCAGCGTACAAGGGTTGTGCGACGCAGCCTCAGCCCTGTGTTCAATCACACCATGGTGTACGATGGCT
TTGGGCCTGCTGACCTGCGCCAGGCTTGTGCCGAGCTCTCCCTCTGGGACCATGGGGCCCTGGCCAACCGCCAGC
TGGGGGGCACACGCCTCAGCCTGGGCACCGGCAGCAGCTATGGGCTGCAGGTGCCCTGGATGGATTCCACACCTG
AGGAGAAGCAGCTGTGGCAAGCCCTCCTGGAGCAGCCGTGCGAATGGGTGGATGGCCTTCTACCCCTCAGAACCA
ACCTGGCCCCCAGGACG**TAG**CCCCACCAAGCCTCTCTCTCTGGACCCCCATCTCAGGGCCTGCCCTTGGCTAAAG
TCAATAAAGTCTATTCTAAGAGC

FIGURE 123

MPQRGHPSQEGLWALPSLPMAHGPKPETEGLLDLSFLTEEEQEAIAGVLQRDARLRQLEEGRVSKLRASVADPGQ
LKILTGDWFQEARSQRHHNAHFGSDLVRASMRRKKSTRGDQAPGHDREAEAAVKEKEEGPEPRLTIDEAPQERLR
ETEASDPEEASQAQEDPGQGDQQVCAEEADPELEPASGGEQEPRPQQAQTKAASQILENGEEAPGPDPSLDRMLS
SSSSVSSLNSSTLSGSQMSLSGDAEAVQVRGSVHFALHYEPGAAELRVHVIQCQGLAAARRRRSDPYVKSYLLPD
KQSKRKTAVKKRNLNPVFNETLRYSVPQAELQGRVLSLSVWHRESLGRNIFLGEVEVPLDTWDWGSEPTWLPLQP
RVPPSPDDLPSRGLLALSLKYVPAGSEGAGLPPSGELHFWVKEARDLLPLRAGSLDTYVQCFVLPDDSQASRQRT
RVVRRSLSPVFNHTMVYDGFGPADLRQACAELSLWDHGALANRQLGGTRLSLGTGSSYGLQVPWMDSTPEEKQLW
QALLEQPCEWVDGLLPLRTNLAPRT

FIGURE 124

ATGCCGTTAGTAACGAGGAACATCGAGCCAAGGCACCTGTGCCGTCAGACGTTGCCTAGCGTTAGAAGCGAGCTG
GAATGCGTGACCAACATCACCCTGGCAAATGTCATCCGACAGCTGGGCAGCCTGAGTAAATATGCAGAGGACATT
TTTGGAGAGCTCTTTACTCAGGCAAATACCTTTGCCTCTCGGGTAAGCTCCCTTGCTGAGAGGGTCGACCGACTA
CAGGTTAAAGTCACTCAGCTGGATCCCAAGGAAGAAGAAGTGTCACTGCAAGGAATCAACACCCGAAAAGCCTTC
AGAAGTTCCACCATTCAAGACCAGAAGCTTTTTGACAGAAACTCTCTCCCAGTGCCTGTCTTAGAAACATACAAT
ACCTGTGATACTCCTCCCCCTCTCAACAATCTTACCCCTTACAGGGACGATGGAAAAGAGGCACTCAAATTCTAC
ACAGACCCTTCATACTTCTTTGATCTTTGGAAGGAGAAGATGCTGCAGGACACCAAGGATATCATGAAAGAGAAG
AGAAAGCACAGGAAAGAAAAGAAAGATAATCCAAATCGAGGGAATGTAAACCCACGTAAAATCAAGACACGTAAG
GAAGAGTGGGAGAAAATGAAGATGGGGCAAGAATTTGTGGAGTCCAAAGAAAAGCTGGGGACTTCTGGGTATCCA
CCCACTTTGGTGTACCAGAATGGCAGCATTGGCTGTGTTGAAAACGTGGATGCAAGTAGCTATCCGCCACCACCA
CAGTCAGACTCTGCTTCTTCACCTTCTCCTTCCTTCTCCGAGGACAACTTGCCTCCTCCACCAGCAGAATTCAGT
TACCCAGTGGACAACCAAAGAGGATCTGGTTTGGCTGGACCCAAAAGATCCAGTGTGGTCAGCCCAAGCCATCCA
CCACCAGCTCCTCCTCTAGGCTCTCCACCAGGCCCTAAACCCGGGTTTGCTCCACCACCTGCCCCTCCGCCACCT
CCGCCTCCAATGATAGGCATCCCACCTCCACCACCGCCTGTAGGATTTGGGTCTCCAGGGACGCCTCCACCACCC
TCACCCCCATCTTTCCCACCTCACCCTGATTTTGCTGCCCCTCCACCTCCTCCTCCACCACCAGCAGCTGACTAC
CCAACTCTGCCACCACCTCCCTTGTCCCAGCCAACAGGAGGAGCACCTCCTCCTCCCCCTCCTCCTCCTCCTCCG
GGGCCCCCTCCTCCCCCTTTCACTGGTGCAGATGGCCAGCCTGCTATACCACCACCGCTTTCTGATACCACCAAG
CCCAAGTCCTCCTTGCCTGCCGTGAGCGATGCCCGTAGCGACCTGCTTTCAGCCATCCGTCAAGGTTTTCAGCTG
CGCAGGGTTGAGGAGCAGCGGGAACAAGAGAAGCGGGATGTTGTGGGCAATGACGTGGCCACCATCTTGTCTCGT
CGCATTGCTGTTGAGTACAGTGACTCAGAAGATGACTCCTCTGAATTTGATGAGGACGACTGGTCCGAT**TAA**

FIGURE 125

MPLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLSKYAEDIFGELFTQANTFASRVSSLAERVDRL
QVKVTQLDPKEEEVSLQGINTRKAFRSSTIQDQKLFDRNSLPVPVLETYNTCDTPPPLNNLTPYRDDGKEALKFY
TDPSYFFDLWKEKMLQDTKDIMKEKRKHRKEKKDNPNRGNVNPRKIKTRKEEWEKMKMGQEFVESKEKLGTSGYP
PTLVYQNGSIGCVENVDASSYPPPPQSDSASSPSPSFSEDNLPPPPAEFSYPVDNQRGSGLAGPKRSSVVSPSHP
PPAPPLGSPPGPKPGFAPPPAPPPPPPPMIGIPPPPPPVGFGSPGTPPPPSPPSFPPHPDFAAPPPPPPPPAADY
PTLPPPPLSQPTGGAPPPPPPPPPPGPPPPPFTGADGQPAIPPPLSDTTKPKSSLPAVSDARSDLLSAIRQGFQL
RRVEEQREQEKRDVVGNDVATILSRRIAVEYSDSEDDSSEFDEDDWSD

FIGURE 126

GCAGCACCCCAGTTCTCCCCGCACGCCGGCACTCGCGGCTGCTGGAGCCCCGGCTGGCTCACCCCGGGGCCGGGC
AGAATTGGGCTCCAGGTCTCTGACCCCTCCCAAGGATCATGCCGCAGCCCCACTGACCCAGGAGTAGGGGCCTAA
GGGCAGGGAACCTGGAATGGGCTGTGTGTTCTGCAAGAAATTGGAGCCGGTGGCCACGGCCAAGGAGGATGCTGG
CCTGGAAGGGGACTTCAGAAGCTACGGGGCAGCAGACCACTATGGGCCTGACCCCACTAAGGCCCGGCCTGCATC
CTCATTTGCCCACATCCCCAACTACAGCAACTTCTCCTCTCAGGCCATCAACCCTGGCTTCCTTGATAGTGGCAC
CATCAGGGGTGTGTCAGGGATTGGGGTGACCCTGTTCATTGCCCTGTATGACTATGAGGCTCGAACTGAGGATGA
CCTCACCTTCACCAAGGGCGAGAAGTTCCACATCCTGAACAATACTGAAGGTGACTGGTGGGAGGCTCGGTCTCT
CAGCTCCGGAAAAACTGGCTGCATTCCCAGCAACTACGTGGCCCCTGTTGACTCAATCCAAGCTGAAGAGTGGTA
CTTTGGAAAGATTGGGAGAAAGGATGCAGAGAGGCAGCTGCTTTCACCAGGCAACCCCCAGGGGGCCTTTCTCAT
TCGGGAAAGCGAGACCACCAAAGGTGCCTACTCCCTGTCCATCCGGGACTGGGATCAGACCAGAGGCGATCATGT
GAAGCATTACAAGATCCGCAAACTGGACATGGGCGGCTACTACATCACCACACGGGTTCAGTTCAACTCGGTGCA
GGAGCTGGTGCAGCACTACATGGAGGTGAATGACGGGCTGTGCAACCTGCTCATCGCGCCCTGCACCATCATGAA
GCCGCAGACGCTGGGCCTGGCCAAGGACGCCTGGGAGATCAGCCGCAGCTCCATCACGCTGGAGCGCCGGCTGGG
CACCGGCTGCTTCGGGGATGTGTGGCTGGGCACGTGGAACGGCAGCACTAAGGTGGCGGTGAAGACGCTGAAGCC
GGGCACCATGTCCCCGAAGGCCTTCCTGGAGGAGGCGCAGGTCATGAAGCTGCTGCGGCACGACAAGCTGGTGCA
GCTGTACGCCGTGGTGTCGGAGGAGCCCATCTACATCGTGACCGAGTTCATGTGTCACGGCAGCTTGCTGGATTT
TCTCAAGAACCCAGAGGGCCAGGATTTGAGGCTGCCCCAATTGGTGGACATGGCAGCCCAGGTAGCTGAGGGCAT
GGCCTACATGGAACGCATGAACTACATTCACCGCGACCTGAGGGCAGCCAACATCCTGGTTGGGGAGCGGCTGGC
GTGCAAGATCGCAGACTTTGGCTTGGCGCGTCTCATCAAGGACGATGAGTACAACCCCTGCCAAGGTTCCAAGTT
CCCCATCAAGTGGACAGCCCCAGAAGCTGCCCTCTTTGGCAGATTCACCATCAAGTCAGACGTGTGGTCCTTTGG
GATCCTGCTCACTGAGCTCATCACCAAGGGCCGAATCCCCTACCCAGGCATGAATAAACGGGAAGTGTTGGAACA
GGTGGAGCAGGGCTACCACATGCCGTGCCCTCCAGGCTGCCCAGCATCCCTGTACGAGGCCATGGAACAGACCTG
GCGTCTGGACCCGGAGGAGAGGCCTACCTTCGAGTACCTGCAGTCCTTCCTGGAGGACTACTTCACCTCCGCTGA
ACCACAGTACCAGCCCGGGGATCAGACATAGCCTGTCCGGGCATCAACCCTCTCTGGCGGTGGCCACCAGTCCTT
GCCAATCCCCAGAGCTGTTCTTCCAAAGCCCCCAGGCTGGCTTAGAACCCCATAGAGTCCTAGCATCACCGAGGA
CGTGGCTGCTCTGACACCACCTAGGGCAACCTACTTGTTTTACAGATGGGGCAAAAGGAGGCCCAGAGCTGATCT
CTCATCCGCTCTGGCCCCAAGCACTATTTCTTCCTTTTCCACTTAGGCCCCTACATGCCTGTAGCCTTTCTCACT
CCATCCCCACCCAAAGTGCTCAGACCTTGTCTAGTTATTTATAAAACTGTATGTACCTCCCTCACTTCTCTCCTA
TCACTGCTTTCCTACTCTCCTTTTATCTCACTCTAGTCCAGGTGCCAAGAATTTCCCTTCTACCCTCTATTCTCT
TGTGTCTGTAAGTTACAAAGTCAGGAAAAGTCTTGGCTGGACCCCTTTCCTGCTGGGTGGATGCAGTGGTCCAGG
ACTGGGGTCTGGGCCCAGGTTTGAGGGAGAAGGTTGCAGAGCACTTCCCACCTCTCTGAATAGTGTGTATGTGTT
GGTTTATTGATTCTGTAAATAAGTAAAATGACAATATGAATCCTC

FIGURE 127

GGCACGAGGCTTCGTAAAGATGGCCGCGGAGGCTTTTGGAGCCAACTGGGAGCGCAGTACGCGTTTTCTGGAGCA
TGGGCAGAGGAGACAGGAACAAGCGTAGCATCCGTGAGCACCGATTGGCTGAAGCGAGCACCCCGGGAGCTGACT
GGCTCCGCCATTCGCGGGAAGGCGTTTGTGGTGCCAGAGAAAAGTAGCCAGAGCGGCGCAGTGGCGGCCGCGTTC
TGTGGTTTTCCGCTATTCCCCCAGACCCGCACCTTCTCGGCCTCTTTGCGGAGAATCGTGACCAAG**ATG**TGGAAC
AGTGGATTCGAAAGCTATGGCAGCTCCTCATACGGGGGAGCCGGCGGCTACACGCAGTCCCCGGGGGGCTTTGGA
TCGCCCGCACCTTCTCAAGCCGAAAAGAAATCAAGAGCCCGAGCCCAGCACATTGTGCCCTGTACTATATCTCAG
CTGCTTTCTGCCACTTTGGTTGATGAAGTGTTCAGAATTGGGAATGTTGAGATTTCACAGGTCACTATTGTGGGG
ATCATCAGACATGCAGAGAAGGCTCCAACCAACATTGTTTACAAAATAGATGACATGACAGCTGCACCCATGGAC
GTTCGCCAGTGGGTTGACACAGATGACACCAGCAGTGAAAACACTGTGGTTCCTCCAGAAACATATGTGAAAGTG
GCAGGCCACCTGAGATCTTTTCAGAACAAAAAGAGCCTGGTAGCCTTTAAGATCATGCCCCTGGAGGATATGAAT
GAGTTCACCACACATATTCTGGAAGTGATCAATGCACACATGGTACTAAGCAAAGCCAACAGCCAGCCCTCAGCA
GGGAGAGCACCTATCAGCAATCCAGGAATGAGTGAAGCAGGGAACTTTGGTGGGAATAGCTTCATGCCAGCAAAT
GGCCTCACTGTGGCCCAAAACCAGGTGTTGAATTTGATTAAGGCTTGTCCAAGACCTGAAGGGTTGAACTTTCAG
GATCTCAAGAACCAGCTGAAACACATGTCTGTATCCTCAATCAAGCAAGCTGTGGATTTTCTGAGCAATGAGGGG
CACATCTATTCTACTGTGGATGATGACCATTTTAAATCCACAGATGCAGAA**TAA**CTGGATCTAACTGGGTACCTG
AGATATTTTACAGCTGGACCTAGTTTCACAATCTGTTGTCTCCAGCTCTGCATATGTCTGGCCAGGGGGCTTCTA
GGAAGTAGGTTTCATCTATCAAATGTCTCCTCTGACTTCCTTTTGAAACTTACTGCTCTTCTGTTTTATTTTGTT
TTGTTTGAAGCTCAGAGGGAGATGGGCAATTGACAGGGATGCAATCCAGGGTGGGATTTCTTGAGGAAGTTACAA
ATAAGCTTGTTACAACATCAAGATAGATGGAATTGGAAGGATGCTACCAGGAGAGTACTTACATAGTGCTCAGGA
GTTTCTCTTCTTAAAATGTTTACTGCTGAAAGATGAGCAGGACCAGGGCGTTATAGGCAGAGCCCTAGCCGAGAA
ACCTGCTGGCCTCTGCCTGTTTTCATTTCCCACTTTGGTTGTGTGGCATTACTTTCAGAATTGCACTTTCCTGCT
TGTCATGACTTTTTGACACACTTGCCATGACGTGTGTTTCTGTGAACATGAAGTTCTGCGGTAGTGCCTCCAGGG
GCAGAGGAAAAGAAGAAGTGTTACTGCGTTTTGTACAAAATAAATACAGTCATATGTTTAATAAAACAGTTCTAT
TGTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 128

MWNSGFESYGSSSYGGAGGYTQSPGGFGSPAPSQAEKKSRARAQHIVPCTISQLLSATLVDEVFRIGNVEISQVT
IVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLE
DMNEFTTHILEVINAHMVLSKANSQPSAGRAPISNPGMSEAGNFGGNSFMPANGLTVAQNQVLNLIKACPRPEGL
NFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDHFKSTDAE

FIGURE 129

GGAGGGAGACGCAGAGGCGGACAAGATGGCGGCGGCAGCTGTACAGGGCGAGAGAAGCGGTGGTAGCGGAGGCTG
TAGTGGGGCTGGTGGTGCTTCCAACTGCGGGACAGGGAGTGGCCGTAGCGGCTTGTTGGATAAGTGGAAGATAGA
TGATAAGCCTGTAAAAATTGACAAGTGGGATGGATCAGCTGTGAAAAACTCTTTGGATGATTCTGCCAAAAAGGA
GAAGAGCATCTTTCTCGTGGCCCACAGGAAAGATCCTACAGGAATGGATCCTGATGATATTTGGCAGCTGTCCTC
CAGTCTTAAAGGGTTTGATGACAAATACACCTTGAAGCTGACCTTCATCAGTGGGAGAACAAAGCAGCAGCGGGA
AGCCGAGTTCACAAAGTCCATTGCTAAGTTTTTTGACCACAGTGGGACACTGGTCATGGATGCATATGAGCCTGA
AATATCCAGGCTCCATGACAGTCTTGCCATAGAAAGAAAAATAAAGTAGCCAATTCTAAAAGTAGCCCTCTTTCT
CCTGGATCTTGCTGAATTAGTGGCTTGGGGGGTGGGGGAGATAAAAAGAACTTAAAATGGGTAAAGTAAGAAATG
TTAAAAAG

FIGURE 130

CTGGGCCGGGGAAATGGCGGCTTCAGGAGAGAGCGGGACTTCAGGCGGCGGAGGCAGCACCGAGGAAGCATTTAT
GACCTTCTACAGTGAGGTGAAACAAATAGAGAAGAGAGACTCGGTTCTAACTTCGAAAAATCAGATTGAAAGACT
GACCCGTCCTGGTTCCTCTTACTTCAATTTGAACCCATTTGAGGTTCTTCAGATAGATCCTGAAGTTACAGATGA
AGAAATAAAAAAGAGGTTTCGGCAGTTATCCATCTTGGTGCATCCTGACAAAAATCAAGATGATGCTGACAGAGC
ACAAAAGGCTTTTGAAGCTGTGGACAAAGCTTACAAGTTGCTACTGGATCAGGAGCAAAAGAAGAGGGCCCTGGA
TGTAATTCAGGCAGGAAAAGAATACGTGGAACACACTGTGAAAGAGCGAAAAAAACAATTAAAGAAGGAAGGAAA
ACCTACAATTGTAGAGGAGGATGATCCTGAGCTGGAAACGACAAAGGGAAGAAGAGATTGAAGCTCAAGAAAAAG
CCAAACGGGAAAGAGAGTGGCAGAAAAACTTTGAGG

FIGURE 131

TCCAGCACCAAAGCGGCCGTTCTCGGATTCCGGAGCGTTCTGGAGCCCCGAGAGACGCCCCGGGGTTCTAGAAGC
TCCCCGGCGGCGCCCAGTCCCGGCTTCATTCGGGCGTCCCTCCGAAACCCACTCGGGTGCACGGGTCGTCGGCGA
GCCGCGACCGGGTCCTGGCGCGCACC**ATG**ATCGTGGCGGACTCCGAGTGCCGCGCAGAGCTCAAGGACTACCTGC
GGTTCGCCCCGGGCGGCGTCGGCGACTCGGGCCCCGGAGAGGAGCAGAGGGAGAGCCGGGCTCGGCGAGGCCCTC
GAGGGCCCAGCGCCTTCATCCCCGTGGAGGAGGTCCTTCGGGAGGGGGCTGAGAGCCTCGAGCAGCACCTGGGGC
TGGAGGCACTGATGTCCTCTGGGCGAGTAGACAACCTGGCAGTGGTGATGGGCCTGCACCCTGACTACTTTACCA
GCTTCTGGCGCCTGCACTACCTGCTGCTGCACACGGATGGTCCCTTGGCCAGCTCCTGGCGCCACTACATTGCCA
TCATGGCTGCCGCCCGCCATCAGTGTTCTTACCTGGTAGGCTCCCACATGGCCGAGTTTCTGCAGACTGGTGGTG
ACCCTGAGTGGCTGCTGGGCCTCCACCGGGCCCCCGAGAAGCTGCGCAAACTCAGCGAGATCAACAAGTTGCTGG
CGCATCGGCCATGGCTCATCACCAAGGAACACATCCAGGCCTTGCTGAAGACCGGCGAGCACACTTGGTCCCTGG
CCGAGCTCATTCAGGCTCTGGTCCTGCTCACCCACTGCCACTCGCTCTCCTCCTTCGTGTTTGGCTGTGGCATCC
TCCCTGAGGGGGATGCAGATGGCAGCCCTGCCCCCCAGGCACCTACACCCCCTAGTGAACAGAGCAGCCCCCCAA
GCAGGGACCCGTTGAACAACTCTGGGGGCTTTGAGTCTGCCCGCGACGTGGAGGCGCTGATGGAGCGCATGCAGC
AGCTGCAGGAGAGCCTGCTGCGGGATGAGGGGACGTCCCAGGAGGAGATGGAGAGCCGCTTTGAGCTGGAGAAGT
CAGAGAGCCTGCTGGTGACCCCCTCAGCTGACATCCTGGAGCCCTCTCCACACCCAGACATGCTGTGCTTTGTGG
AAGACCCTACTTTCGGATATGAGGACTTCACTCGGAGAGGGGCTCAGGCACCCCCTACCTTCCGGGCCCAGGATT
ATACCTGGGAAGACCATGGCTACTCGCTGATCCAGCGGCTTTACCCTGAGGGTGGGCAGCTGCTGGATGAGAAGT
TCCAGGCAGCCTATAGCCTCACCTACAATACCATCGCCATGCACAGTGGTGTGGACACCTCCGTGCTCCGCAGGG
CCATCTGGAACTATATCCACTGCGTCTTTGGCATCAGATATGATGACTATGATTATGGGGAGGTGAACCAGCTCC
TGGAGCGGAACCTCAAGGTCTATATCAAGACAGTGGCCTGCTACCCAGAGAAGACCACCCGAAGAATGTACAACC
TCTTCTGGAGGCACTTCCGCCACTCAGAGAAGGTCCACGTGAACTTGCTGCTCCTGGAGGCGCGCATGCAAGCCG
CTCTGCTGTACGCCCTCCGTGCCATCACCCGCTACATGACC**TGA**CTCCTGAGCAGGACCTGGGCCCGGTTCAGCT
CCCCACAAGGACTTCTCTGTCTGGAGACAGCCCCAGACCCTTTTGTGTCCCATGCCCACCCTCCCCACGCTGCAG
TGGGCTTGTGTGTGATGTGCAGTCCCGAAGCCACACCCTCCCTTTTCCTCACTGGAATGGACAGTTCATTGCACT
GACTCTGGGATCTCAGCCCTGCTCCTGGGAGCTGGAAGAGCACTTGGAGATCCTAAGGGACCACACCCTTCCTCC
TTCCCCTGCCCACAGAGGCAGAGGGCACAGGAAAGAAGCCGGGCCAAGCTCGGAATTAATGTGCCACAAGTGTTG
TGGCCTTCCTGAACTGGGAAGTCCCTGGCTGGCCCCCGGGGGAGAGGGGCAAATGCCTCCGGGACTGACACTCCA
GGCAGCTTTGCCTTCTCTCCCCTGTCATTTCCAGATTTCATTACCTCCTACTTGCCATTCACCCATCAATGTGAA
AGTCAGGGTCACAGCTGGTCTGTGTGTCCAGTTCCCTAAAAGCCTGTTCTGTTGGGCAGCCTGAGGCTGTTGCCC
GAATCCTAGTTCAGTTTTTTGACTTCCTTTGCCCTTTTTCCCTTTTCTCCATGCTTAATGGTGTGAGGCGTCAGG
AGAGAGGCCAAGTACATAAAAAAAAAAAAAAGCAGATTATCTCTAGAGAGTTTGAGCCTTTGCTGGTCACATTGC
CTTCTGAAGAGGAGGGAGTATTAGATTATAAATCCTCTTTATTTTGGTCCTTTATGCTTGAGGTTCCAACCTGGA
GCCACAGTGTGTGAGAGGAGGAGGAGAGGGAGAATTCTGTTCTCCCAGAGCTGCACCTGCCTCGCAGAGGCCAGC
ACCCCACTCTCCTGCCTCCAGTGGCCCTGCCGCAGATGTCTCCCAAAAAGTTGAGCCTTTCTAGATGGCTTAGGT
GGCACCATGGCTCAGCAGGAGGGGCGGGAGGCACCAGGGTTCTTGTTTGGACCCTGCCCCTGGGCCATGGCCAGG
TGACCATGGCTACATTGCCAAACCTCTGACTGCCACAGCTGCAGACTGAGAGGGTGGGTCTGAGTCCCCACAATG
TCTGAAGCTGCCCCTGGGATTCTCAGGCCAACCTGCCAACAGCAAGCGGATTTTCTTGCAAGATCAGGGACCCCA
TTTCTGCAGCCAGTGTCTCCTGGGTGCCTTCTGAGGACTCCCACCCCCATCCCAGTATCTCATCTGTCCCCTCTC
CTGGGGCTTAAGTGGGTTGCTTCCAGGCAGAAGCAGCCAAGGACCGATTCCAGGCACTTTCTGTAGCAAATGACT
GTGAATTACGACTTCTCTTGCCCTTCTTCTAGCAGTCTGTGCCTCCTCTCTGACCAGTTTGGAGGGCACTGAAGA
AAGGCAAGGGCCGTGCTGCTGCTGGGCGGGGCAGGAGAGGAGCCTGGCCAGTGTGCCACATTAAATACCCGTGCA
GGCGCGGAGAAGCAACCGGCACCCCCTTCCGGCCTGAAAGCCCTCCCTGCAAGAAGGTGTGCAGGAGAGAAGAGG
CCCCGGCATGGGGATCTGGGTTCTAGAGGGCATGTGATGACTGTAAATGTTCACTGGGTGGGTAGGGAGTGGTAT
CCAGTGTTCAAGTGCAGAAATCTTTGGCTTTGCTACCAGTTCCATATGATGAGAAATAAACGTTCGCTGAGGTTT
TGTTTCATAAAAAAAAAAAAAAAAAA

FIGURE 132

MIVADSECRAELKDYLRFAPGGVGDSGPGEEQRESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGR
VDNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAAARHQCSYLVGSHMAEFLQTGGDPEWLLGLH
RAPEKLRKLSEINKLLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLSSFVFGCGILPEGDADGS
PAPQAPTPPSEQSSPPSRDPLNNSGGFESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLLVTPS
ADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQDYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTY
NTIAMHSGVDTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTVACYPEKTTRRMYNLFWRHFRHS
EKVHVNLLLLEARMQAALLYALRAITRYMT

FIGURE 133

GAGACGTCGGCTTCCGACCGGAAGTGAGAAGAGGAGGAAGTTGGCTGGTTGCACCGATCTGGGGGCTTCCCGGGC
TCGGGTAACCGGAGTGCTGGTATCTAATCGTCGCTCAAAAGCTCCTAGGTATATCCCGTGCCTTACCTGACTGGG
GGCTCTGAGTCCAGTTGTGTTGTCTTCAACTTAGACACCATGGAGGCACCTCCAGTCACCATGATGCCTGTCACT
GGGGGCACCATTAACATGATGGAGTACCTGTTGCAGGGAAGTGTTTTAGATCACAGTTTGGAAAGCCTCATCCAC
CGCCTTCGTGGTTTGTGTGACAACATGGAACCTGAGACTTTCCTTGACCATGAGATGGTATTCCTCCTTAAGGGC
CAGCAAGCCAGCCCATTTGTTCTCAGGGCCCGACGCTCTATGGACAGGGCAGGGGCACCCTGGCATCTGCGCTAC
CTGGGACAGCCAGAAATGGGAGACAAGAACCGCCATGCCCTGGTGCGAAACTGCGTGGACATTGCCACATCTGAG
AACCTCACCGACTTCTTGATGGAAATGGGCTTCCGCATGGACCATGAGTTTGTTGCTAAGGGACATTTGTTCCGT
AAGGGCATCATGAAGATTATGGTGTACAAGATTTTCCGCATCCTGGTGCCAGGGAACACAGACAGCACTGAGGCC
TTGTCACTCTCCTATCTCGTGGAATTAAGTGTGGTAGCACCCGCTGGGCAGGACATGGTCTCTGATGACATGAAG
AACTTCGCAGAACAGCTAAAACCTCTGGTTCACCTAGAGAAAATAGACCCCAAGAGGCTCATGTGACTAAGAGGA
TCTGTCCACATTTGGGGCCTATCCTTACTTGTTTGAAAAAATATGTTTGCTTTTTTTGGTTTTTGTTTTGTTTTG
TTTTTGAGACAGAGTCTCGCTTTGTTTCCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTGC
CTCCTGGGTTCAAGCAATTCTCCCACCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACATGCCACCATGCTCAG
CTAATTTTTGTATTTTTAGTAGAAATGGGGATTCACCATGTTGGTCAGGCTATTCTCGAACTCCTGACCTCGTGA
TCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACGCCTGGCCAAAAAAATATGTTTT
AAATGTCCCATTTCACCATTGCCAGGCAGGCATTCTTCCTTCAGGGAGAGGATGGTGAGAATTAATTGGTTCTTT
GCACTGTTCTCCTCATGTGGCGATTTCACTTTCATGACAGCCTTTCTATATTAAAGGCTCAGGATGTCACGGAGA
ATCTATCTAATCCCACTGTATTAAGAGGGGAAACCGGGCCAAGCGCAGTGGCTCACACCTCTAATCCCAGCACTT
TGGGAGGCTGAGGTAGGTGGATCACCCAAGGTCAGGAGTTTGAGACCAGCCTGGCCAAATGGTGAAACCCCATCT
CTACGAAAAATACAAAATTTAGCCGGGCATGGTAGCAGGCGCTTGTAATCCCAGCTACTTGGGAGGCTGAGGCTG
GAGAATCGCTTGAACCCAGGAGGTGAAGGTTGCAGTGACCAGAGATGACGCCATTGCACTCCAGCCTGGGTGAGA
AGAGCGAAACTCCGTCTCAAAAAAAAAATAAAAATGAAGAGGGGAAACCAGAATAAATTATCTTTTGGAAAGGACA
ATTTCTTGTTTGGCCATTTGTGTATAAGGTTGGTAACATTAGAGGCTGTGAGCTTGTGTTACATGGTAATAAAGC
CAATGAAGAG

FIGURE 134

GGCCGGCCTCTCCCTTCCCGGGGTTCTTCGCGCCGGGCCCCTTCCGCGTGGGTGAGTGAATGTGAGAGTCAGCGC
TCGCGCCGCGCGCGCCGCCCGCCTCCGCTGTTCGGCGCTCTGCTTTAGGCGGTGGGGGGCGGGCGCGCGCGTAAA
AGCATAGAGACGGGCATTGAGCTCTTGGGCTAGAGCGTCGCCGAGTCGGAGCCGGAGCCTGAGCCGCGCGCTGTG
TCTCCGCTGCGTCCGCCGAGGCCCCCGAGTGTCAGGGACAAAAGCCTCCGCCTGCTCCCGCAGACGGGGCTCATC
TGCCGCCGCCGCCGCGCTGAGGAGAGTTCGCCGCCGTCGCCGCCCGTGAGGATCTGAGAGCCATGTCGGCCAGCA
GCCTCTTGGAGCAGAGACCAAAAGGTCAAGGAAACAAAGTACAAAATGGATCTGTACATCAAAAGGATGGATTAA
ACGATGATGATTTTGAACCTTACTTGAGTCCACAGGCAAGGCCCAATAATGCATATACTGCCATGTCAGATTCCT
ACTTACCCAGTTACTACAGTCCCTCCATTGGCTTCTCCTATTCTTTGGGTGAAGCTGCTTGGTCTACGGGGGGTG
ACACAGCCATGCCCTACTTAACTTCTTATGGACAGCTGAGCAACGGAGAGCCCCACTTCCTACCAGATGCAATGT
TTGGGCAACCAGGAGCCCTAGGTAGCACTCCATTTCTTGGTCAGCATGGTTTTAATTTCTTTCCCAGTGGGATTG
ACTTCTCAGCATGGGGAAATAACAGTTCTCAGGGACAGTCTACTCAGAGCTCTGGATATAGTAGCAATTATGCTT
ATGCACCTAGCTCCTTAGGTGGAGCCATGATTGATGGACAGTCAGCTTTTGCCAATGAGACCCTCAATAAGGCTC
CTGGCATGAATACTATAGACCAAGGGATGGCAGCACTGAAGTTGGGTAGCACAGAAGTTGCAAGCAATGTTCCAA
AAGTTGTAGGTTCTGCTGTTGGTAGCGGGTCCATTACTAGTAACATCGTGGCTTCCAATAGTTTGCCTCCAGCCA
CCATTGCTCCTCCAAAACCAGCATCTTGGGCTGATATTGCTAGCAAGCCTGCAAAACAGCAACCTAAACTGAAGA
CCAAGAATGGCATTGCAGGGTCAAGTCTTCCGCCACCCCCGATAAAGCATAACATGGATATTGGAACTTGGGATA
ACAAGGGTCCCGTTGCAAAAGCCCCCTCACAGGCTTTGGTTCAGAATATAGGTCAGCCAACCCAGGGGTCTCCTC
AGCCTGTAGGTCAGCAGGCTAACAATAGCCCACCAGTGGCTCAGGCATCAGTAGGGCAACAGACACAGCCATTGC
CTCCACCTCCACCACAGCCTGCCCAGCTTTCAGTCCAGCAACAGGCAGCTCAGCCAACCCGCTGGGTAGCACCTC
GGAACCGTGGCAGTGGGTTCGGTCATAATGGGGTGGATGGTAATGGAGTAGGACAGTCTCAGGCTGGTTCTGGAT
CTACTCCTTCAGAACCCCACCCAGTGTTGGAGAAGCTTCGGTCCATTAATAACTATAACCCCAAAGATTTTGACT
GGAATCTGAAACATGGCCGGGTTTTCATCATTAAGAGCTACTCTGAGGACGATATTCACCGTTCCATTAAGTATA
ATATTTGGTGCAGCACAGAGCATGGTAACAAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAAGGCCCCG
TTTACTTACTTTTCAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAAATCTGCTGTGGACTACA
ACACATGTGCAGGTGTGTGGTCCCAGGACAAATGGAAGGGTCGTTTTGATGTCAGGTGGATTTTTGTGAAGGACG
TTCCCAATAGCCAACTGCGACACATTCGCCTAGAGAACAACGAGAATAAACCAGTGACCAACTCTAGGGACACTC
AGGAAGTGCCTCTGGAAAAGGCTAAGCAGGTGTTGAAAATTATAGCCAGCTACAAGCACACCACTTCCATTTTTG
ATGACTTCTCACACTATGAGAAACGCCAAGAGGAAGAAGAAAGTGTTAAAAAGGAACGTCAAGGTCGTGGGAAAT
AAAAGGCAGTTCTACACAGACTGCAGCAACGGTTGCATCTGCATATCCTAAGAGGAAAAAATGACCTTCAAGAGA
ATTAGGACTTTTTTCTTAATTTCACTGACTTCAGAGACGATTGCAGACTTGCAGTTTAAGTATTGGAATTTCACA
AAAGACATAGGACTTAACTGGAAAATGAAAAAAAAAAGAAAAAGAAAAAACTAAACAAAAAATCCCTCTAGGTAG
TTTAGGTGAAAAATGTCCCTTTTATTTTGGCTTTGGTTGTGATTTCAGAGCATAATGCTATGTTTTTTTGTCTTT
TTACTATGTTTTTCGGATTTTTAAGTCCGTAAGTGCATACAGTTTTCTCTAATTTTTAAACCCTTTCCTCCTCCC
ATTTTGACATTTGCACTTGGAGAACACTTGAGTTGTGAAGGTTTTGGGCATCCACCCCAGAAAGTGGGAATTTGA
TTTTATCCTTCCGAACTGGAAGAACATTTTTATGAAGAATTTTTGTCTAGGAGAATATAACAGTGTTACCCAAGG
TTGTGTCTTTAAGGGTGGTTCATTTTCTCTGACCTTTTGTTACTCAAAGTAAAGTACTAGGAGTCCTAAGAAATG
TTCTGTTCTTGTACATTATACTGATTAAGTCAGGATTAATTTGATTTCAAAGCTGAGAACAGTGGTAAAAACTCG
TTTACAGAAATGCATTTTGGAAGAGAAAAATACTGTAAAACGTGTCGTGAATGTTTCTTCAGTTTCTTGTTCAGC
CAATGAGGAAAGGGCATTGCCTTTCTTTTTACCATTAATCACTTCTCAATAAACGTGAGATCCTGTTGAGCATC

FIGURE 135

GTACGTCGCCGGGGTTCGGCTGCGTCCGTCCCGCCGCCCGCCCGTTGCCGCCGCCGCCGCTGCCGCCGTGCTCTC
GCTTTGCCCGCCGCCGCCTAAGGGGGGCTGGGGCCGGGGCCAGCCATCACTGCCGTTGCCGGGATGCCGCGGGTG
TACATCGGCCGCCTGAGCTACCAGGCCCGGGAGCGCGATGTGGAGCGCTTCTTTAAGGGCTACGGGAAGATCCTG
GAGGTGGATCTGAAGAACGGATATGGTTTTGTGGAGTTTGATGATCTGCGTGATGCAGATGATGCTGTTTATGAA
CTGAATGGCAAAGACCTTTGTGGTGAGCGAGTAATTGTTGAGCATGCCCGCGGCCCACGGCGAGATGGCAGTTAC
GGTTCTGGACGCAGTGGATATGGTTATAGAAGAAGTGGCCGAGATAAATATGGCCCTCCTACTCGCACAGAGTAC
AGACTTATTGTGGAGAATTTGTCAAGTCGGTGCAGCTGGCAAGACCTAAAGGATTATATGCGTCAGGCAGGAGAA
GTGACTTATGCAGATGCTCACAAGGGACGCAAAAATGAAGGGGTGATTGAATTTGTATCTTATTCTGATATGAAA
AGAGCTTTGGAAAAGTTGGATGGAACTGAAGTCAATGGGAGAAAAATCAGATTAGTTGAAGACAAGCCAGGTTCC
AGACGACGCCGGTCCTACTCCAGAAGCCGGAGTCATTCAAGGTCTCGCTCTCGAAGCAGACATTCCCGTAAGAGC
AGAAGCCGAAGTGGCAGCAGCAAAAGCAGTCATTCTAAGAGTAGATCTCGGTCCAGGTCGGGCTCCCGCTCCCGG
AGCAAGAGCCGGAGCCGGAGCCAGAGTCGGAGCCGGAGCAAGAAAGAGAAAAGCAGGAGCCCCAGCAAGGAAAAG
AGCCGCAGCCGCAGCCATAGCGCTGGCAAGAGCCGCAGCAAGAGCAAAGACCAAGCTGAAGAGAAGATCCAAAAC
AATGACAATGTCGGGAAACCCAAGAGCCGGAGTCCTAGCAGGCATAAAAGTAAGAGCAAAAGTCGGAGCAGGAGT
CAGGAGAGGAGAGTGGAGGAGGAGAAGCGAGGGAGTGTGAGCAGGGGCAGGAGCCAGGAGAAGAGCCTCCGCCAG
AGTCGGAGCCGGAGCAGGAGCAAAGGGGGCAGCAGGAGCCGGAGCAGGAGCCGCAGCAAGAGCAAGGACAAGAGG
AAGGGCAGGAAGAGAAGCAGAGAGGAGAGCCGCAGTCGCAGTCGCAGCCGCAGCAAGAGTGAGAGGAGCAGAAAG
CGAGGCAGCAAGCGAGACAGCAAGGCGGGCAGCAGCAAGAAGAAGAAGAAGGAAGACACTGACCGCTCCCAGTCC
AGATCTCCATCCCGCTCCGTGTCAAAGGAGCGGGAACATGCCAAGTCTGAATCCAGCCAGAGGGAAGGTCGAGGA
GAGAGTGAGAATGCTGGCACCAATCAGGAGACCCGGTCCAGGTCGAGATCCAATTCCAAATCGAAACCAAACCTT
CCATCAGAATCACGCTCCAGATCAAAGTCAGCTTCAAAAACCCGATCTCGGTCCAAGTCTAGATCCAGGTCTGCT
TCCAGATCGCCCTCCCGATCTAGATCTAGGTCCCACTCAAGGTCCTAACTGGCTATGGCCACAGCTGGAACTACC
CGAGAAGTCTTTTGTACATGTTTGGTAGCCGTAGCACAAGTGATTGGAGTAGAACATGTCACTGCTGTACATTTT
TAACTCCCCTAATGGTGTGTCTATAATTGTTAAATCTAAGTGCTTCCTCTCAGTAAAGCCTCCTGGCACCAGGCC
TTCCTGCTCGACTGAAAAAAATTTTCTCTTTGAAAATCCCCTTTTACTCATGGCCCACAGTAGAATATCCAAAAC
GCCTTGGCTTTCAGGCCTGGCCTTTCCTACAGGGAGCTCAGTAACCTGGACGGCTCTAAGGCTGGAATGACCACA
TAGGTAGGTATGGTGAGTTCAACCATTTTTGCTCTTGAATTGATGCCCTTCGATGTATGCCATTTAGTGAAAGTG
CTAAGTCTTAAGTTTCCTACCACTTTGGTTTCATATTTTTGGACTTAACAAAGTTGTGAATAGCACAGTCGAGGA
AAATTGATACCTGCAGTAACCCATAGGAAATAAACTGTAGAGTTCCATATTCTGGTATTGTGATTATATTGTTTT
ATATT

FIGURE 136

AGGGTTCTCTCCCCTTGCCACCATGAGCGAGTCATTTGACTGTGCAAAATGCAACGAGTCCCTGTATGGACGCAA
GTACATCCAGACAGACAGCGGCCCCTACTGTGTGCCCTGCTATGACAATACCTTTGCCAACACCTGTGCTGAGTG
CCAGCAGCTTATCGGGCATGACTCGAGGGAGCTGTTCTATGAAGACCGCCATTTCCACGAGGGCTGCTTCCGCTG
CTGCCGCTGCCAGCGCTCACTAGCCGATGAACCCTTCACCTGCCAGGACAGTGAGCTGCTCTGCAATGACTGCTA
CTGCAGTGCGTTTTCCTCGCAGTGCTCCGCTTGTGGGGAGACTGTCATGCCTGGGTCCCGGAAGCTGGAATATGG
AGGCCAGACATGGCATGAGCACTGCTTCCTGTGCAGTGGCTGTGAACAGCCACTGGGCTCCCGTTCTTTTGTGCC
CGACAAGGGTGCTCACTACTGCGTGCCCTGCTATGAGAACAAGTTTGCTCCTCGCTGCGCCCGCTGCAGCAAGAC
GCTGACACAGGGTGGAGTGACATACCGTGATCAGCCGTGGCATCGAGAATGTCTGGTCTGTACCGGATGCCAGAC
GCCCCTGGCAGGGCAGCAGTTCACCTCCCGGGATGAAGATCCCTACTGTGTGGCCTGTTTTGGAGAACTCTTTGC
ACCTAAGTGCAGCAGCTGCAAGCGCCCCATCGTAGGACTCGGTGGAGGCAAGTATGTGTCCTTTGAAGACCGACA
CTGGCACCACAACTGCTTCTCCTGCGCCCGCTGCTCTACCTCCCTGGTGGGCCAGGGCTTCGTACCGGATGGAGA
CCAAGTGCTCTGCCAGGGCTGTAGCCAGGCAGGGCCCTAAGCCAGGGCTCCTGGACCCAGGCTTTCCCATACCAC
GGGCCCAGGACTGTGGCTCCTTTTCTAAACCACCTCTGGGACTCAGCTCCCCCCGCCAAAAAAAATGGGTCTCCT
TCTGGGCTCCAGGATTGTCTCCCCACTCCAGCATCCCCAAACTGGTACTCCCTGACCCAGGGCCCCAAACCTGGG
CTCTTACAGAGCCTCCATGAGTCAAGCCCCCTCCCCACACCTGGACTCCAGAATTCACCCTCTCCCCTGCAGTCT
GGGTTCCCAGACTGAGTCCTCTCCCCAAATCAGGGCTCTAGACCCGAGCCCTCCAAACCTGGACTCTGGGACTTA
GGCCCCCTTAAATCTAGACTTCTCTTTATAGGTTTCAGGTCTCCTATGGGTGCCTGGGAAGTCCTTGAAAGTGGA
CTGTTCTCAGGCTTGACCTGCCCCACCCCATCCCCGCGGTTGAGGCTGTGGGGGCAGCAGATCAGGAGCCCACTG
ATAAGGGGCCCTAGGGTACAGGGTGCTGCCCAGCAGGTCGCCACCGAGTGTCTTCTCATTTTATTTCAGCTCCAT
TTTGCCCATAGATGGGCAGAGGGGTGAGATTGGCTCATCCCCCTTCCAGATTCTGCAATAAAGCGGTGTGAGG

FIGURE 137

CTACAGATACTGCCGTGTGAGAGTACCTGAGGGGCTCCTGAAAGACCTACTGCCAGGACCAGTGACCCTGGTGATG
GGAACGCTCGGAGGAGCTCAACAAGGACCTAAACCCTTTTACGCCTCTTGTAGGCATTCGGATTCCTGATCATGC
TTTTATGCAAGACTTGGCTCAGATGTTTGAGGGTCCGCTTGCTCTCACTAGTGCCAACCTCAGCTCCCAGGCCAG
TTCTCTGAATGTCGAGGAGTTCCAGGATCTCTGGCCTCAGTTGTCCTTGGTTATTGATGGGGGACAAATTGGGGA
TGGCCAGAGCCCCGAGTGTCGCCTTGGCTCAACTGTGGTTGATTTGTCTGTGCCCGGAAAGTTTGGCATCATTCG
TCCAGGCTGTGCCCTGGAAAGTACTACAGCCATCCTCCAACAGAAGTACGGACTGCTCCCCTCACATGCGTCCTA
CCTGTGAAACTCTGGGAAGCAGGAAGGCCCAAGACCTGGTGCTGGATACTATGTGTCTGTCCACTGACGACTGTC
AAGGCCTCATTTGCAGAGGCCACCGGAGCTAGGGCACTAGCCTGACTTTTAAGGCAGTGTGTCTTTCTGAGCACT
GTAGACCAAGCCCTTGGAGCTGCTGGTTTAGCCTTGCACCTGGGGAAAGGATGTATTTATTTGTATTTTCATATA
TCAGCCAAAAGCTGAATGGAAAAGTTAAGAACATTCCTAGGTGGCCTTATTCTAATAAGTTTCTTCTGTCTGTTT
TGTTTTTCAATTGAAAAGTAATTAAATAACAGATTTAGAATCTAGTGAGAGCCTCCTCTCTGGTGGGTGGTGGCA
TTTAAGGTTCAAACCAGCCAGAAGTGCTGGTGCTGTTTAAAAAGTCTCAGGTGGCTGCGTGTGGTGGCTCATGCC
TGTAATCCCAACATTCTGGGAGGCCCAGGCGGGAGAACTGCTTGAGCCCAGGAGTTCAGAATCAGCCTGGGCAAC
ATAGCAATACTCCGTCTCATAAAAATTAATAAATAAAAAGTCTCAGGTGACCAAAGGCTCCTGAAGCTAGAACCA
GGTTTGGATAAAGATTGAAGAGCCACAGGCCACTCTTCCCTCTGAGCCATTGGGCCTAGTGGTGTCATGTATTGT
AATTGCTCGCAGGGAGAGCAGTCTTTTTGGTGTAATAGTGGGATGTCTGCTTAGTTGGCAGGGGTTCAGTCCAAA
TGGAAGAATATTGGGAAATAAACCTCCACTATCCTTTATAGCCAGGGACTTTTTTCTTATTTATTCATAAAATAA
ATTATAGTTAATTATACCCATAACACCTTTATTTAAATCCAGTGTTCTCCGCAGCCTTTTGTCTATTTATATGTG
TACCAAGTGTTAAACATAATTATTATTGGGCATTTGAACTTTGTTTTTCTTTAAAGAAATGCTGCTATTAAACAT
ATTTGTAAATGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 138

MERSEELNKDLNPFTPLVGIRIPDHAFMQDLAQMFEGPLALTSANLSSQASSLNVEEFQDLWPQLSLVIDGGQIG
DGQSPECRLGSTVVDLSVPGKFGIIRPGCALESTTAILQQKYGLLPSHASYL

FIGURE 139A

AGGCCCAGCGCTGGCGCAGTGAGAACTTCGAGAGACCCGTGGACCTGGAGGGCTCTGGGGATGATGACTCCTTTC
CCGATGATGAACTGGATGACCTCTACTCGGGGTCGGGCTCGGGCTGTAAGTACCCCCCTCCCTACCTCTGCCTGG
GGGCAGTGACCAGTCTGTATCCAGCCTCAACTCTGAGAAGCCCACGGGGGGCTTGCTTCAGTGAGGCAGGGGGCA
TTCACTGCCTGGGTCAGGCAAGTTCTTCTTGCTCTGGATCCCCAGAACAAGAAGGGCAGAACATCCTTCTGGGGA
TAGAACAAGACCTGGGAGGACCTCAGGGCCCAGAATGTCCAGGTCTCCAGGGTCCCACGTCTGCATCTTTGTGTG
TGCTATGTGGCTTTCTCTGCAGACCTTGCTTGGTTCCGGTGGTCCCGTCAGGTGCAATAAGCTGTGGCCAATGGT
GGGGTTAGGGCAGTGATGACACAGGGCAGGTGCTTCAAGTGGTGCCTGGGATGGCCCCGCCCTGGGGAAGGGGAG
CCAGGTCAGCTGGGTCTAGCAGAATCTCGGGAGAGAAGGGCACCGCGAACCCCACTCTGCCATGTAGCAACTGTG
TGCCCCTCGGTGCTCCCCCTCCCTGAATCCCTGTATTTTCACCTGTGGATGGTGAGAAATACGACTTCTTCTCAG
TGCCTCTAGGAGGGTTTGGGATAGGAAGCTGGGGTCTGGCACAGAGGAGGAGCTCTCAAAATGGTAGCAAAAAGA
AGGCAGCTGAGACTGGGCCCAGTGAGGGCACGGGCTGGCATCTGAGGAGATGGTACGGGGTCTGCACGCCACAGA
GCTGGCTCCCCACAGCCCTCGCCTCTGGTCTCCCCTCCTTAGCCAAGTCCTTTGAGCCTCTTTCAAATTAATCTT
TGTAAAACCCGTTTATATTGGGTCACATCTCTATTCGCAAAGTTCCCTGGCTCCCCTCCCTCCTGCCTGGTTCCG
AGCCCAGGAGCTGGCTGTGGCTTCTCCCTCCCCCATCCCCTACTCCCCATCTCATTTCCTCCCAAGTTCCTTCAC
TGTCCCGGCTTTGCGTCAGCCAGATTGCTCAAGCAGTTCCCCTGCCTCAAGGGCTTCTTTTCCCTTTTACCCTCC
GCCTCTGCCTCTGGGGGAAGCCCTTAGTGTACCACCCCTGCCTTGAGCTTGTGGTAGGGGTGCCTTTGGGGTCTG
ACTCTTCCCAGAATGCCACTCCTGTGTTCCCCTGCAAGCCCCAGCAAGTTTTGCAGCCAGTAGCGCCTCAGTTGC
TGCTGCCTGGATTCAACCTCATAGAAACTGTAGGCTGGGTGGGCAGGAATAGTCAAGGAAGGCTTCCCGGGAGAG
GCGGCCCCCAGAATTTTTGACTTGGCAGAGAGAAGTTGGGGAACATCAGCAACTGACCACCTTTAGCTGGGCTGT
GCCTTCCTCCTTTCTCTCATCTTTTCTGGGAAAATTGGGTAAAGAGAGGGGGTTGGGAGACCTAATCTTGATGGC
CATTGCTTACCTGGGATCCTCATGCCCCTCACAACCACCCAGCTCCCTAGCTCTCTCCCTCTCCCCCACCCCCTC
AGACTTCGAGCAGGAGTCGGGCATTGAGACAGCCATGCGCTTCAGCCCAGATGTAGCCCTGGCGGTGTCCACCAC
ACCTGCGGTGCTGCCCACCACGAACATCCAGCCTGTGGGCACACCATTTGAAGAGCTCCCCTCTGAGCGCCCCAC
CCTGGAGCCAGCCACCAGCCCCCTGGTGGTGACAGAAGTCCCGGAAGAGCCCAGCCAGAGAGCCACCACCGTCTC
CACTACCATGGCTACCACTGCTGCCACAAGCACAGGGGACCCGACTGTGGCCACAGTGCCTGCCACAGTGGCCAC
CGCCACCCCCAGCACCCCTGCAGCACCCCCTTTTACGGCCACCACTGCTGTTATAAGGACCACTGGCGTACGGAG
GCTTCTGCCTCTCCCACTGACCACAGTGGCTACGGCACGGGCCACTACCCCCGAGGCGCCCTCCCCGCCCACCAC
GGCGGCTGTCTTGGACACCGAGGCCCCAACACCCAGGCTGGTCAGCACAGCTACCTCCCGGCCAAGAGCCCTTCC
CAGGCCGGCCACCACCCAGGAGCCTGACATCCCTGAGAGGAGCACCCTGCCCCTGGGGACCACTGCCCCTGGACC
CACAGAGGTGGCTCAGACCCCAACTCCAGAGACCTTCCTGACCACAATCCGGGATGAGCCAGAGGTTCCGGTGAG
TGGGGGGCCCAGTGGAGACTTCGAGCTGCCAGAAGAAGAGACCACACAACCAGACACAGCCAATGAGGTGGTAGC
TGTGGGAGGGGCTGCGGCCAAGGCATCATCTCCACCTGGGACACTGCCCAAGGGTGCCCGCCCGGGCCCTGGCCT
CCTGGACAATGCCATCGACTCGGGCAGCTCAGCTGCTCAGCTGCCTCAGAAGAGTATCCTGGAGCGGAAGGAGGT
GCTCGTAGCTGTGATTGTGGGCGGGGTGGTGGGCGCCCTCTTTGCTGCCTTCTTGGTCACACTGCTCATCTATCG
TATGAAGAAAAAGGATGAGGGCAGCTACACGCTGGAGGAACCCAAGCAGGCGAGCGTCACATACCAGAAGCCTGA
CAAGCAGGAGGAGTTCTATGCCTAGTGGAGCCACAGTGCCTCCCTGCAGCCTCAACACCACCCTGCTGTCCAGTC
CCCAGCCTGGCCCCACCAGCCCAAGCCTGGGACTGGGCCTGGAACCTGGCCCCAGTTCTTCTCTGCCCTCTCTCC
CAAGGTCTGCCCAGGCTGCCAGCCTCACACAGATCTTCCCCGAGGAAGAGGGGCTGCTGCCATCTGCCCCAGACT
GTGCCCTTACGAGCTCATCTCTTGTTCCCCTCATCCCTGCCACCAGTCTGGGGCTTCAGGACCTCATGTCAGATG
GATGGGAGGAAGAAAGCTCCTGATTGGCTGGTGGTGGAAGAAAGGGTGGGGCTTGAGATGAGCCTGAGCCCTGAC
TTGGCACCCACAGTGCTCACTGAGATCTCCTTTTTGGGGCAGAGAGGCACTCAGGCTGGTTTCCAGGACAAACAT
TTGGTAAACACAGCCCTTGAAATCATCTAGACACTGCAACCTCTTGCTCGTATCCCAGGGCCTCTCTCTAGCTGG
GTGAGAGGGTGTCCCTTGTCACCAGCCTGTTTTGTCCTGGTCTCTCTGGGGTTGTTGAATCTCTCCTCTTGCCTG
CCAAGTACACATGTACCCAGACTTCATTTCTTTCTGCATCTTCCCCCAAGAAACAGCTTCCTGAGGGTGCTGGGG
CAGCCACTGGTGAGGAGGGGCTGCTCTGATGTCCCTCCTATGAGGGGACTCTGCACAGACACCATTGCCCACACT
ATCACCATATTTTCACTCAGTCACACACAAGACAAAAGCATGCAATGACAAAACCATACGCAATCCTGACCGCCC
AGCCAATCAAGACATATCACAGAACACACGCGTCCTTCCAAGAATGTTTATCCTCATGCATCACTTACACACCCC
CAGACACGTACTGCAATGCAAGTCACTAGTCATGGTCACATGACAGTGACAGTGTGGCCTCCTCCTACCCCAAAT

FIGURE 139B

ACACCCACACTCTGGCACCACACACATTGTCTCCAGCTTTCAGGCTTACTGGGGAGGGTGGAATCGAGCCAGAAC
AATCAGCCCATATTGGGTCCCCCTAAGTTGCCCCGTCATACTCAGTCCCATGCCATGGTGCCCACACCAACCATG
CAGCCGCCAACCCCAGCCAGTGTCAGACACAATCCCATGTGGATGCACAGTCTCACTCCACATGACCTGCTCTCA
ATGCTGGAGGGAAACAGGCAGGCCCTTGCCTTTCTCGGAAAAAGTGTGGGGCCACAGCCCTTTTAGGGCATTGCA
TGCAGGTGGGCCTGGCTTCACCCCTACCTGCTTCCTCCCCACCGCAGCTGGCAGAGGGGGAGGTTTGGGGCCAGA
CCCCCACTAGCTGGGAGCCTGGGGGCTCCTCTAAGGCTGAGGAAGGAAATTTGGCCCCAGGTTGTTGGGGGGTCT
TGGGTCTCCCAGGACGGAAGGCCCAGGGCAGGGAGGGGGCATGTGGTTGGGCTCCTTTATCTCCCTGTGTCCCCT
TCCTGCTTTGAGCTAGGGGGCTGACTCTGCCTCCCAGGACACAAGTCTCCAAAGTGCCTGTGAGGGCGGGCCCTC
CGCACCCTCTGCCCTCTGCCTGGCAGGCCAACCTCAGCCCACCTGCCCAGAGGCCCTCCCTGTGGACACCCCCTC
ACCTATTTGGCCAAACAATTCTGGCTGCAGCTTCAGGGGCCATGGCTGGAAGCAGCCCCTGCAGATCCCTCAGGC
CCCGAGGTCAGGGTTTGAGGGATGAGACCAGGTGATAGTGGGGGAGGGGTTACTTCCTTTGTTACCTAGCAAGTA
GGGCTATTTCCATCGGTATTTTAAATGTGGGGTCACAGATCTTTTGGGGAGGGTGTGCTTGGCAGGGGGCCTCTT
GGAGCCAAAGGGATGTGGTGTGAGTTGCGATTGGCTGGCACTCACACCCCCACCCCTCACCCACATCCCAGATTC
AAGTCAGGAAGGCAGGTTTTATTTCAGGGCCCTTTTCAAGATGCCCTGGCAGCAGATTTCTGCAGGATGAGGGGT
AGCGGTGTGTAGGCAGTGAGGGGGAGGTTCCAGGGGCTGTCCCACAGCCTGTCTTTTCCAGGCTGGGCTCCATCT
TCCAGTCCCAAAACCCTCCTTCACAGGGCCCAGAGGCTTGTGAGGAAGCCAGGTGGACCCAGCCTTAGAAGAGTG
GGCATGGGGGGCCCCTGATATCTGGAGGGGGCGGGTTGGCCTCAGTCATCTTTGGAGCAGAAGGGCTGGGTCCTG
GGGCCACAGACCACAAGGCTCAGCCTCCCTACCCTGCTCCCTGGGGTGCTGCTGTCTTGGAGAGCACAGCTCTGG
TGAGACGGCCTGGGCAGGCCGAGGCTGAGAAACCAGGGAGGATAGAGGAGAAAAGGGCTTGGGCCCCCAGCCCCA
GAAGATGCTGGACCCCAGGTGGGAGACCCAACAGTGGGTGCAGTTTCTCAGTAGGGCTGGAGCCAATGGTGGGGG
TGGCCCCGGCAGGCCTGGCTCCTCACATCCCAGGGGTTGGCTTCTGATTTGGGGCTTGGGCTCCAGGCACTGGCT
TCTCTTCTCTGTGTCCTTAGCATTTGAGAGAAGAGGCCAGGGGCCTTGTTCATGGATCCCTGGACCCAAGGCAGA
TGTCCAGGCTTTATCCTCCTGAGGATGAGGAGTCTGACCAGCCCAAATCTGCCCTGGCCGGCCTGACCGGGGCAA
GGCAGTCCAAGAGAGTTCAGTGAGGACCAGCTAGGCTCTCCCAGGTGCAATGTGGGTGCAGGGCCCTCATGTCCC
CCTACCCCTGCCTGTGATGGAGTGTTCTGAGGGGCTTTGGCATTTGCTGGAAGCACAGGGAGTTCCAAATGAGAG
GGAGCTTCTGTGGCTTGAGAGCCTCTGGGGCCTTGGCTGCCAGAGCACGAGGCAGGCCAGGACCTGGAGAGCCCA
GACCCTGTCTCCAGGAGGCCAGGAGGCCAGATGGGGGCCTTGCCTGAAAGACTGGTCCCCTTGATCGCTGGAGGC
ATGTGGGTGGCAACCAGGGCTGGGCAGGGCTTAGGGTGTGTGGGCCAAACCCCCCTGGGGTTGGCAAAGCCGCCT
GTCAGGCCTCCTGGTGGGGGCCCCTGGACACAGGGAGCAGACCCTCTGCCTCATGGGGTAGGAGTGGCTGCCTCC
TGTGTTCTCTGGATTTCTTCTCCCAACAACTACAACCCTGGACTTGCCTCCCCAGGCCTCTTGCCTGTAAATAGA
AGCCCGCAAACTGTACAGATTTACAGAGGCATCGAGACTGGGCCCTGGGAGTTGCCATCTGAGAGCCGATGGCCC
CAGCATCCCCCAGGTGCCTGCCTGGCACCACAGTGACCCTGGCCTCAGCGTGGCAAATGCATGTAAATATTTTTC
GTAGGCAGCGTGGCTCCAGAGAGCCCCCTGAAGACAGTGTCCCTCCCTCCTGTGAGTCCTTTCTCCTGTACAGAA
CCTGCCTGGGGTGGGTGGGGGTCTGCCATTCCCTCCCCCAGGCCTTCCCTGCCCCTTCTCTCCCCTGTAACCTGT
TTATTAACCATACCTGTCCTGAGTTCATGGCCAAAACCTTAAATAAGAAAAACAAAAGAAAAAGACAGTGGAAAA
AAGAGACCAAGGCGCCTGCCCCACTGCGGGTACTCTCCTGTTCCAGCCTTGTGAAGGAACTGGTTTTGTTTTTGT
TTTTTTTTTTTTTTTTTTTTTTTTGTTTGTTTGTTTTTTTAACACTTCCTGTGCTGTGCCCATTTATAAGAGGAA
ATAAAATTAAGCTGAAATG

FIGURE 140

AGCCATGCCTTTCTTGGACATCCAGAAAAGGTTCGGCCTTAACATAGATCGATGGTTGACAATCCAGAGTGGTGA
ACAGCCCTACAAGATGGCTGGTCGATGCCATGCTTTTGAAAAAGAATGGATAGAATGTGCACATGGAATCGGTTA
TACTCGGGCAGAGAAAGAGTGCAAGATAGAATATGATGATTTCGTAGAGTGTTTGCTTCGGCAGAAAACGATGAG
ACGTGCAGGTACCATCAGGAAGCAGCGGGATAAGCTGATAAAGGAAGGAAAGTACACCCCTCCACCTCACCACAT
TGGCAAGGGGGAGCCTCGGCCCTGAACAGAGCAGCTGCTGATGTCTGGAGGCTGATTTTCCTGTTCTCTGTTCTC
CACTGGAAAGGTTGTTTACGACAAACCTCCTTGTCAAAGTGTGTAAAAATAAAGGATTGCTCCATCCT

FIGURE 141

GCTGAGCGGGCTTTGGACACCATGAACTTTGATGTGATTAAGGGAAAGCCAATCCGCATCATGTGGTCTCAGAGG
GATCCCTCTTTGAGAAAATCTGGTGTGGGAAACGTCTTCATCAAGAACCTGGACAAATCTATAGATAACAAGGCA
CTTTATGATACTTTTTCTGCTTTTGGAAACATACTGTCCTGCAAGGTGGTGTGTGATGAGAACGGCTCTAAGGGT
TATGCCTTTGTCCACTTCGAGACCCAAGAGGCTGCCGACAAGGCCATCGAGAAGATGAATGGCATGCTCCTCAAT
GACCGCAAAGTATTTGTGGGCAGATTCAAGTCTCGCAAAGAGCGGGAAGCTGAGCTTGGAGCCAAAGCCAAGGAA
TTCACCAATGTTTATATCAAAAACTTTGGGGAAGAGGTGGATGATGAGAGTCTGAAAGAGCTATTCAGTCAGTTT
GGTAAGACCCTAAGTGTCAAGGTGATGAGAGATCCCAATGGGAAATCCAAAGGCTTTGGCTTTGTGAGTTACGAA
AAACACGAGGATGCCAATAAGGCTGTGGAAGAGATGAATGGAAAAGAAATAAGTGGTAAAATCATATTTGTAGGC
CGTGCACAAAAGAAAGTAGAACGGCAGGCAGAGTTAAAACGGAAATTTGAACAGTTGAAACAGGAGAGAATTAGT
CGATATCAGGGGGTGAATCTCTACATTAAGAACTTGGATGACACTATTGATGATGAGAAATTAAGGAAAGAATTT
TCTCCTTTTGGATCAATTACCAGTGCTAAGGTAATGCTGGAGGATGGAAGAAGCAAAGGGTTTGGCTTCGTCTGC
TTCTCATCTCCTGAAGAAGCAACCAAAGCAGTCACTGAGATGAATGGACGCATTGTGGGCTCCAAGCCACTATAT
GTTGCCCTGGCCCAGAGGAAGGAAGAGAGAAAGGCTCACCTGACCAACCAGTATATGCAACGAGTGGCTGGAATG
AGAGCACTTCCTGCCAATGCCATCTTAAATCAGTTCCAGCCTGCAGCGGGTGGCTACTTTGTGCCAGCAGTCCCA
CAGGCTCAGGGAAGGCCTCCATATTATACACCTAACCAGTTAGCACAGATGAGGCCTAATCCACGCTGGCAGCAA
GGTGGGAGACCTCAAGGCTTCCAAGGAATGCCAAGTGCTATACGCCAGTCTGGGCCTCGTCCAACTCTTCGCCAT
CTGGCTCCAACTGGTAATGCTCCGGCCTCTCGTGGCCTCCCTACTACCACTCAGAGAGTCGGGTCTGAGTGCCCG
GACCGCTTGGCTATGGACTTTGGTGGGGCTGGTGCCGCCCAGCAAGGGCTGACTGACAGCTGCCAGTCTGGAGGC
GTTCCCACAGCTGTGCAGAACTTAGCGCCACGCGCTGCTGTTGCTGCTGCTGCTCCCCGGGCTGTTGCCCCCTAC
AAATACGCCTCCAGTGTCCGCAGCCCTCATCCTGCCATACAGCCTCTGCAGGCACCCCAGCCTGCGGTCCATGTG
CAGGGGCAGGAGCCACTGACTGCCTCCATGCTGGCTGCAGCACCCCCCCAGGAACAGAAGCAGATGCTGGGAGAA
CGCTTGTTCCCACTCATCCAAACAATGCATTCAAATCTGGCTGGGAAGATCACGGGAATGCTGCTGGAGATAGAC
AACTCTGAGCTGCTGCACATGTTAGAGTCCCCCGAGTCTCTCCGCTCCAAGGTGGATGAAGCTGTAGCAGTTCTA
CAGGCTCATCATGCCAAGAAAGAAGCTGCCCAGAAGGATTCAAAAGCCAAATAACCCCTTATGGAATTCAACTCA
AGGTTTGAAGACTTCCTAGCTTGTCCTATGGACCTCAACACCAAGGATTACAAATTGCAAATTTAATAGGTCATT
TTGTATCAAAAGGTCAATTATGAAGCACCTAGAATTTTTCAATTATACGAATATGTTCTTTGGGTTCTGCTGTGG
CCCAGACAGTGTTAACTTTTTTTTTATTGTGGGTTTTGATTTTTTCCCCCAGAAATTGGTTTTATTTGATGTACC
CAAGTCTTACGTTTCCCAATAAAGAAAAAAAATCTCCAT

FIGURE 142

ACCAGGCAGCCTGCGTTCGCC**ATG**AAGCGACCCAAGGAGCCGAGCGGCTCCGACGGGGAGTCCGACGGACCCATC
GACGTGGGCCAAGAGGGCCAGCTGAGCCAGATGGCCAGGCCGCTGTCCACCCCCAGCTCTTCGCAGATGCAAGCC
AGGAAGAAACGCAGAGGGATCATAGAGAAACGGCGTCGAGACCGCATCAACAGTAGCCTTTCTGAATTGCGACGC
TTGGTCCCCACTGCCTTTGAGAAACAGGGCTCTTCCAAGCTGGAGAAAGCCGAGGTCTTGCAGATGACGGTGGAT
CACTTGAAAATGCTCCATGCCACTGGTGGGACAGGATTCTTTGATGCCCGAGCCCTGGCAGTTGACTTCCGGAGC
ATTGGTTTTCGGGAGTGCCTCACTGAGGTCATCAGGTACCTGGGGGTCCTTGAAGGGCCCAGCAGCCGTGCAGAC
CCCGTCCGGATTCGCCTTCTCTCCCACCTCAACAGCTACGCAGCCGAGATGGAGCCTTCGCCCACGCCCACTGGC
CCTTTGGCCTTCCCTGCCTGGCCCTGGTCTTTCTTCCATAGCTGTCCAGGGCTGCCAGCCCTGAGCAACCAGCTC
GCCATCCTGGGAAGAGTGCCCAGCCCTGTCCTCCCCGGTGTCTCCTCTCCTGCTTACCCCATCCCAGCCCTCCGA
ACCGCTCCCCTTCGCAGAGCCACAGGCATCATCCTGCCAGCCCGGAGGAATGTGCTGCCCAGTCGAGGGGCATCT
TCCACCCGGAGGGCCCGCCCCCTAGAGAGGCCAGCGACCCCTGTGCCTGTCGCCCCCAGCAGCAGGGCTGCCAGG
AGCAGCCACATCGCTCCCCTCCTGCAGTCTTCCTCCCCAACACCCCCTGGTCCTACAGGGTCGGCTGCTTACGTG
GCTGTTCCCACCCCCAACTCATCCTCCCCAGGGCCAGCTGGGAGGCCAGCGGGAGCCATGCTCTACCACTCCTGG
GTCTCTGAAATCACTGAAATCGGGGCTTTC**TGA**GCTGCCCCTTCACCACCCCGCCCCAAGGAATAAGGAAGGTTC
TTTTACCAGGAGCCCAAAAAAGGGCACTGCCTTTTCTGCTTTGCTTCGTGGACTGGCTCATATGTGAAGGCACGT
TCTCCAGCCATCAGAGGCCCCCTCCTCCTCCAACCCATCTCTCCTTCTCACTGTTATCCCAGCTTATCCACCCAG
CTCTCCTGGAGCTGTTCTGGTCTCAGAGGCTTGGTTCCATTTCTCACCTGAACAGATGAGTCCTGGGAGAGACCC
TCAGAGATCCGCCCAGACCCCTCTCCTGCCCTCTGCACACCAGCAGCAGGCATGAACCTTGGGTCTGGGAAAAAG
CTTTAACCTGCAGGGCACCAGGACCCAAGGCAGGCTGTTCCTTGGGGCGGTCAGACCCCAGTCAGGAGCAATGAC
TGACTGGCTGCAGCCTTCCCACGCCAAGAGGCTGGAACATAGTGTCTGCCTCGCTTCCTGGAGATAGTAACTGAG
CAGGGGCTACAAAGAGGTCTCCTGGGAACCCTGTCTGCCCCTTCCCACCTGTCCTTGGGCCACACCATCACACTG
AACCACAGGACAGACCCTTTCTCCACCACAGCCAAGGCCTGGAGACTGGGGGCCCAGCAGAGCCTGCTCCCACCC
TCCTCCCAGCAGCAGACACCCACCCTCTCACTGACTAACAGGTCCCTGCACACAGCTGGCCTGGTAAACCCAGCT
GGGAGGTTTCTAGGCAGCAGCAAAACTCTGTGACAGGGTGTCCTCACACCAGGCCTTGGACAGCTCTCCCAGACA
GGAGCCAGGGTTGAGCAATGGAGAGCCCAGCCCCCACGTCTTACAGTCGCCATCCTCCAGGCGTGTGGTCCCTCC
CCATTGGGTGCACAGTGCAGAGGGGCCGTGGCCCCATGTGATGGTGCGCAGAGAGGAACCTCTTGGGATTCAGCA
CCAGACGTCTGTGCTGCCTGGTTTGCATCCGGCTCACAGAGCCCAGACTGCTGGAACAGCCAAGGACTGTCAGGC
TGGACAAAAATAACTGCAAGGAGGGGCAAGAGAAAGGATGATTCGAGGCACCTTGGCCCTTCAAGGTCATGCAGT
GGGTCGAGCGCCTGAGATCCTGTTCACCAGGACTCCACAGAGCTGGCTCTGCTCAGAAGCCATTTCATTCCCCGG
CTCCACCCTAGGCCACTTTTTCTAACAGAGGAAACAAATGGTCCAGCAGTCGTTCCCAGCAGAACAGCGGAGCCT
GGACTGACACCCAGTGGGACCAGTGTTGCCACACCAGTTGATAAAATGCAGAAACCCTTCTGTACTCGTTGGTAA
ATATCTACTCCCCCAAGTGACTCCAGGTGCCCCCCACCGCCTGGCACTTCCCCCAGGACTCCTACGATCTGGTTA
CTGCCTGGCCGATCCAAGGCTGTGGAGTCCCAGAGCCAGCAGTTCACTGGTGCTCATTCCACACTGGTTAGATAC
TTCAGTTGTCACCCCTGGGAAGATTCTCCCACCTCCTCCCTTTGATGGAACCACCCTCCCCAGAGGCTGCATTGA
GGAGACTCCACAGACTGAAAAGTGAGTTTGCAGAAACCTTGGGGAAAAGGGCCCTTTCAAAGAAGTGGATAAGAG
GGAGGAGATCATTGAGTGACCCAGAAAGCTCTTTTGAAAAGACAGACTCCTCAAGGAGAGATAAAGAGGAAAGCA
CCTCTTTCATTTTTTAGTGTGAGCTAATTCCATCAGACTGCTGTCCTCCTGGACCCATCTGAGATGTGCAGTAGC
AAGGAGAGGGGGGATCATTTTAGAGAGTGGGTCATTGGCAGGGAGTGCTCCGGAGGGAGGCAGAGGGGAGACTGT
GGTAGAAGGAAGACAGAACTCACACATGCTCCCAGGATTGGGGACAGGGACAGAGGAGGTAACAGAAGGCAAAGG
CCAGTTTCCCCGTTATCATGAAGGGGCCCACTCAGGACAGGAACAAGGACAACTCCTCCTCCTCCTCCTCCTCTC
CTGCTGCTCCTGGGATACCAGGTCAGTGATGTAGTCTTGCAGTTTGGCAACTTCCTAGCCTGAGAATCCCTAGTG
GGGCTGTGGGAAACACATTTCCACGTTGCAAGCATGCAACTCCAAAGAATCTGTGATGCCACTGAAATGAGATGG
GAATGATCCAGCTCTTTCAGCATCTTGGTTGAACTTGCTTTCATTGTCCCTGGGATATTGTGGAAGGAAAGGTGA
CTGTGTGATCTGATTCTGTGGTCAAGGACTTGCATCTTGTGTTTCTATCCCCAAGCCTTCCTGGTGTCTCCAACT
CCTACCCCATTGCATGGGTTGTTGCGGACATCCAATAAAGATTTTTTTAGTGCTTCTGGAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACC

FIGURE 143

MKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQMQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFE
KQGSSKLEKAEVLQMTVDHLKMLHATGGTGFFDARALAVDFRSIGFRECLTEVIRYLGVLEGPSSRADPVRIRLL
SHLNSYAAEMEPSPTPTGPLAFPAWPWSFFHSCPGLPALSNQLAILGRVPSPVLPGVSSPAYPIPALRTAPLRRA
TGIILPARRNVLPSRGASSTRRARPLERPATPVPVAPSSRAARSSHIAPLLQSSSPTPPGPTGSAAYVAVPTPNS
SSPGPAGRPAGAMLYHSWVSEITEIGAF

FIGURE 144

GATCCTAAATTGCAGCAAGGCTACAATGCTATGGGATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAG
AGATGCCCTTCACCTCCCATGATCAATCTGATCTCGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGA
TGCCCAGGAGAGAGCTCTCACATCTGTGACTTCATCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTT
CAGGAACGCCTCGTGCAAGCCGAATACTGGCATGACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTC
TTGGCAGATATAAATCAGGAGCGGGGTATCAATGAGTCCTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTG
ATGGTGAAATTCCTCAATGATTCCATTGTGGACCCTGTAGATTCGGAGTGGTTTGGATTTTACAGAAGTGGCCAA
GCCAAGGAAACCATTCCCTTACAGGAGACCTCCCTGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAAT
GCAGGACAGCTAGTGTTTCTGGCTACAGAAGGGGACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCCACATC
ATACCATTCCTTGGATGAAACCCGTATAGTTCACAATAGAGCTCAGGGAGCCCCTAACTCTTCCAAACCACATGG
GAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCAGATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCC
TACTTGGAAAGATCTAAGATCTGAATCTTATCCTTTGCCATCTTCTGTTACCATATGGTGTTGAATGCAAGTTTA
ATTACCATGGAGATTGTTTTACAAACTTTTGATGTGGTCAAGTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATC
AGTGCCAGAACTGTGCCCAGGCCCAAAGGAGACAACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTT
TTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTGCCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGG
TGATTTAACCAGTGCTTGGAAAAATCTTGCTTGGCTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAG
TACGTTGCCCTCTGTGCTATCATCTTATCATCAATTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCA
GCACCCACTTTGTCTCCTCAGGTAGTGATGAATTAGTTGCTGTCACAAAAGGAGGGAAGTAGCACCCAAATTAAG
TTGCTTAAGAGAGGAAATGTACATCTTGTATAACTTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGA
GGCAGCTAGTTCTTCCTATTCCATTCTCGACCAACCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAG
TCAACTTACTCTGTTGCTGGCTTTAGCAGAGAATAGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCA
TCCCCAAAACACATTTACCAGCATACTCCAAACTGTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAA
AAGCTTGGAAAATACTACACACTCCCTTTCTCCTTCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGA
GAATTCCTGTTACAGTAAACAAAACTAACGTAATCTACCATTTCCTACACTATTTGAGCATGGAAATCATAGTCC
CCACTCTGTGAAAACTTAACGCTTTTTGGAAGACATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGC
CTTGATGAAAGAACCGTGTTGGTGCTGCTAAGTTTAGCCATTATGGTTTTTCCTTTCTCTCTCTTAAGCCTTATT
CTTCAACTAAAAGATGAGGATTAAGAGCAAGAAGTTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAA
T

FIGURE 145

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTCAGCTGTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCAGGTCCTCCTCCCCCTCCACCATGCCCCCCTCCTCCCCCAGTCTCTACCAGTTCATGCT
CATATGAGTCTGCTTCCCGCTCAGCACTGTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACCAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAAATTAACTCCATTACAGTAG
ATAACTGTAAGAAACTTGGCCTGGTATTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCCTCTACCTTTTTGCTCTTAAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAACTGCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTCACACTGGTTAATCTTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCCTGAATCCTTCTTCCCTGCCAGGTGCCTGTCACCTGTCTTCACTGCC
TCCTTTTCCCTGTCATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGCACAGCACTGCTAATGTAAATTTCAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

FIGURE 146

GGCTTCGGTCGCTACCGCTCCCGCTCTGCCACCCCCGCCAACCGCCGCTCGGGCCTCCGTCGCTGCCGCGTCGCT
TTCTCGCTCCTTGGATCGCACATCCTCCCAG**ATG**CAGCGCCGGGACGACCCCGCCGCGCGCATGAGCCGGTCTTC
GGGCCGTAGCGGCTCCATGGACCCCTCCGGTGCCCACCCCTCGGTGCGTCAGACGCCGTCTCGGCAGCCGCCGCT
GCCTCACCGGTCCCGGGGAGGCGGAGGGGGATCCCGCGGGGGCGCCCGGGCCTCGCCCGCCACGCAGCCGCCACC
GCTGCTGCCGCCCTCGGCCACGGGTCCCGACGCGACAGTGGGCGGGCCAGCGCCGACCCCGCTGCTGCCCCCCTC
GGCCACAGCCTCGGTCAAGATGGAGCCAGAGAACAAGTACCTGCCCGAACTCATGGCCGAGAAGGACTCGCTCGA
CCCGTCCTTCACTCACGCCATGCAGCTGCTGACGGCAGAAATTGAGAAGATTCAGAAAGGAGACTCAAAAAAGGA
TGATGAGGAGAATTACTTGGATTTATTTTCTCATAAGAACATGAAACTGAAAGAGCGAGTGCTGATACCTGTCAA
GCAGTATCCCAAGTTCAATTTTGTGGGGAAGATTCTTGGACCACAAGGGAATACAATCAAAAGACTGCAGGAAGA
GACTGGTGCAAAGATCTCTGTATTGGGAAAGGGCTCAATGAGAGACAAAGCCAAGGAGGAAGAGCTGCGCAAAGG
TGGAGACCCCAAATATGCCCACTTGAATATGGATCTGCATGTCTTCATTGAAGTCTTTGGACCCCCATGTGAGGC
TTATGCTCTTATGGCCCATGCCATGGAGGAAGTCAAGAAATTTCTAGTACCGGATATGATGGATGATATCTGTCA
GGAGCAATTTCTAGAGCTGTCCTACTTGAATGGAGTACCTGAACCCTCTCGTGGACGTGGGGTGCCAGTGAGAGG
CCGGGGAGCTGCACCTCCTCCACCACCTGTTCCCAGGGGCCGTGGTGTTGGACCACCTCGGGGGGCTTTGGTACG
TGGTACACCAGTAAGGGGAGCCATCACCAGAGGTGCCACTGTGACTCGAGGCGTGCCACCCCCACCTACTGTGAG
GGGTGCTCCAGCACCAAGAGCACGGACAGCGGGCATCCAGAGGATACCTTTGCCTCCACCTCCTGCACCAGAAAC
ATATGAAGAATATGGATATGATGATACATACGCAGAACAAAGTTACGAAGGCTACGAAGGCTATTACAGCCAGAG
TCAAGGGGACTCAGAATATTATGACTATGGACATGGGGAGGTTCAAGATTCTTATGAAGCTTATGGCCAGGACGA
CTGGAATGGGACCAGGCCGTCGCTGAAGGCCCCTCCTGCTAGGCCAGTGAAGGGAGCATACAGAGAGCACCCATA
TGGACGTTAT**TAA**AAACAAACATGAGGGGAAAATATCAGTTATGAGCAAAGTTGTTACTGATTTCTTGTATCTCC
CAGGATTCCTGTTGCTTTACCCACAACAGACAAGTAATTGTCTAAGTGTTTTTCTTCGTGGTCCCCTTCTTCTCC
CCACCTTATTCCATTCTTAACTCTGCATTCTGGCTTCTGTATGTAGTATTTTAAAATGAGTTAAAATAGATTTAG
GAATATTGAATTAATTTTTTAAGTGTGTAGATGCTTTTTTCTTTGTTGTTTAAATATAAACAGAAGTGTACCTTT
TATAATAAAAAAAAGAAGTTGAGTAAAAAAAAAAAACACACAAACCTGTTAGTTTCAAAAATGACATTGCTTGCT
TAAAGGTTCTGAAGTAAAGGCTTGTTAAGTTTCTCTTAGTTTTGATTTGAGGCATCCCGTAAAGTTGTAGTTGCA
GAATCCCAAACTAGGCTACATTTCAAAATTCAGGGCTGTTTAAGATTTAAAATCACAAACATTAACGGCAGTAGG
CACCACCATGTAAAAGTGAGCTCAGACGTCTCTAAAAAATGTTTCCTTTATAAAAGCACATGGCGGTTGAATCTT
AAGGTTAAATTTTAATATGAAAGATCCTCATGAATTAAATAGTTGATGCAATTTTTAACGTTAATTGATATAAAA
AAAAAAACAACAAAATTAGGCTTGTAAAACTGACTTTTTCATTACGTGGGTTTTGAAATCTAGCCCCAGACATAC
TGTGTTGAGAGATACTTAGAGGGAGGGAGTAGGTTTTGAAGAGGTTGATGGTGGTGGGGAGGGAAGGCCTCCTGA
ATTGAGTTTGATGCAGAGCTTTTTAGCCATGAAGAATCTTTCAGTCATAGTACTAATAATTAAATTTTCAGTATT
TAAAAAGACAAAGTATTTTGTCCATTTGAGATTCTGCACTCCATGAAAAGTTCACTTGGACGCTGGGGCCAAAAG
CTGTTGATTTTCTTAAGTTGACGGTTGTCAATATATCGAACTGTTCCCAAGTTAGTCAAGTATGTCTCAACACTA
GCATGATATAAAAAGGGACACTGCAGCTGAATGAAAAAGGAATCAAAATCCACTTTGTACATAAGTTAAAGTCCT
AATTGGATTTGTACCGTCCTCCCATTTTGTTCTCGGAAGATTAAATGCTACATGTGTAAGTCTGCCTAAATAGGT
AGCTTAAACTTATGTCAAAATGTCTGCAGCAGTTTGTCAATAAAGTTTAGTCCTTTTTTA

FIGURE 147

MQRRDDPAARMSRSSGRSGSMDPSGAHPSVRQTPSRQPPLPHRSRGGGGGSRGGARASPATQPPPLLPPSATGPD
ATVGGPAPTPLLPPSATASVKMEPENKYLPELMAEKDSLDPSFTHAMQLLTAEIEKIQKGDSKKDDEENYLDLFS
HKNMKLKERVLIPVKQYPKFNFVGKILGPQGNTIKRLQEETGAKISVLGKGSMRDKAKEEELRKGGDPKYAHLNM
DLHVFIEVFGPPCEAYALMAHAMEEVKKFLVPDMMDDICQEQFLELSYLNGVPEPSRGRGVPVRGRGAAPPPPPV
PRGRGVGPPRGALVRGTPVRGAITRGATVTRGVPPPPTVRGAPAPRARTAGIQRIPLPPPPAPETYEEYGYDDTY
AEQSYEGYEGYYSQSQGDSEYYDYGHGEVQDSYEAYGQDDWNGTRPSLKAPPARPVKGAYREHPYGRY

FIGURE 148

CTCGCGTCACAGCCGGG**ATG**AAGCCGATCCTACTGCAGGGCCATGAGCGGTCCATTACGCAGATTAAGTATAACC
GCGAAGGAGACCTCCTCTTTACTGTGGCCAAGGACCCTATCGTCAATGTATGGTACTCTGTGAATGGTGAGAGGC
TGGGCACCTACATGGGCCATACCGGAGCTGTGTGGTGTGTGGACGCTGACTGGGACACCAAGCATGTCCTCACTG
GCTCAGCTGACAACAGCTGTCGTCTCTGGGACTGTGAAACAGGAAAGCAGCTGGCCCTTCTCAAGACCAATTCGG
CTGTCCGGACCTGCGGTTTTGACTTTGGGGGCAACATCATCATGTTCTCCACGGACAAGCAGATGGGCTACCAGT
GCTTTGTGAGCTTTTTTGACCTGCGGGATCCGAGCCAGATTGACAACAATGAGCCCTACATGAAGATCCCTTGCA
ATGACTCTAAAATCACCAGTGCTGTTTGGGGACCCCTGGGGGAGTGCATCATCGCTGGCCATGAGAGTGGAGAGC
TCAACCAGTATAGTGCCAAGTCTGGAGAGGTGTTGGTGAATGTTAAGGAGCACTCCCGGCAGATCAACGACATCC
AGTTATCCAGGGACATGACCATGTTTGTGACCGCGTCCAAGGACAACACAGCCAAGCTTTTTGACTCCACAACTC
TTGAACATCAGAAGACTTTCCGGACAGAACGTCCTGTCAACTCAGCTGCCCTCTCCCCCAACTATGACCATGTGG
TCCTGGGCGGTGGTCAGGAAGCCATGGATGTAACCACAACCTCCACCAGGATTGGCAAGTTTGAGGCCAGGTTCT
TCCATTTGGCCTTTGAAGAAGAGTTTGGAAGAGTCAAGGGTCACTTTGGACCTATCAACAGTGTTGCCTTCCATC
CTGATGGCAAGAGCTACAGCAGCGGCGGCGAAGATGGTTACGTCCGTATCCATTACTTCGACCCACAGTACTTTG
AATTTGAGTTTGAGGCT**TAA**GAAGCTGGATCTCCTGCCGGGCGTGGTTGGCTCATGCCTGTAATCCCACCACTTT
TTTTTTAAGGCAGGCGGATCACCTGAGGTCAGGAGTTTAAGACCAGCCTGACCAACATGGAGAAACCTCGTCTCT
ACTAAAAATACAAAAATTAGCCAGGCATGGTGGCACACGCCTATAGTCCCAGCTACTCAGGAGGCTGAGGCAGGA
GAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCACGTCATTGCACTCCATCCTGAGCCACAAG
AGCAAAACTCCGTCTCAAAAAAAAAAAAAGAAGAAGGTGGATCTCCAACCAGGCCAGAGAAGATTCTCACAGAAGG
TTTTGAACTCTAAGAAATAAATTGGTTTGGTAATAAATGGCTTCTGGTCAGA

FIGURE 149

MKPILLQGHERSITQIKYNREGDLLFTVAKDPIVNVWYSVNGERLGTYMGHTGAVWCVDADWDTKHVLTGSADNS
CRLWDCETGKQLALLKTNSAVRTCGFDFGGNIIMFSTDKQMGYQCFVSFFDLRDPSQIDNNEPYMKIPCNDSKIT
SAVWGPLGECIIAGHESGELNQYSAKSGEVLVNVKEHSRQINDIQLSRDMTMFVTASKDNTAKLFDSTTLEHQKT
FRTERPVNSAALSPNYDHVVLGGGQEAMDVTTTSTRIGKFEARFFHLAFEEEFGRVKGHFGPINSVAFHPDGKSY
SSGGEDGYVRIHYFDPQYFEFEFEA

FIGURE 150

GAGCGGAGCCGCGGGCGGGAGGGCGGACGGACCGACTGACGGTAGGGACGGGAGGCGAGCAAG**ATG**GCGCAGACG
CAGGGCACCCGGAGGAAAGTCTGTTACTACTACGACGGGGATGTTGGAAATTACTATTATGGACAAGGCCACCCA
ATGAAGCCTCACCGAATCCGCATGACTCATAATTTGCTGCTCAACTATGGTCTCTACCGAAAAATGGAAATCTAT
CGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCACAGCGATGACTACATTAAATTCTTGCGCTCCATC
CGTCCAGATAACATGTCGGAGTACAGCAAGCAGATGCAGAGATTCAACGTTGGTGAGGACTGTCCAGTATTCGAT
GGCCTGTTTGAGTTCTGTCAGTTGTCTACTGGTGGTTCTGTGGCAAGTGCTGTGAAACTTAATAAGCAGCAGACG
GACATCGCTGTGAATTGGGCTGGGGGCCTGCACCATGCAAAGAAGTCCGAGGCATCTGGCTTCTGTTACGTCAAT
GATATCGTCTTGGCCATCCTGGAACTGCTAAAGTATCACCAGAGGGTGCTGTACATTGACATTGATATTCACCAT
GGTGACGGCGTGGAAGAGGCCTTCTACACCACGGACCGGGTCATGACTGTGTCCTTTCATAAGTATGGAGAGTAC
TTCCCAGGAACTGGGGACCTACGGGATATCGGGGCTGGCAAAGGCAAGTATTATGCTGTTAACTACCCGCTCCGA
GACGGGATTGATGACGAGTCCTATGAGGCCATTTTCAAGCCGGTCATGTCCAAAGTAATGGAGATGTTCCAGCCT
AGTGCGGTGGTCTTACAGTGTGGCTCAGACTCCCTATCTGGGGATCGGTTAGGTTGCTTCAATCTAACTATCAAA
GGACACGCCAAGTGTGTGGAATTTGTCAAGAGCTTTAACCTGCCTATGCTGATGCTGGGAGGCGGTGGTTACACC
ATTCGTAACGTTGCCCCGGTGCTGGACATATGAGACAGCTGTGGCCCTGGATACGGAGATCCCTAATGAGCTTCCA
TACAATGACTACTTTGAATACTTTGGACCAGATTTCAAGCTCCACATCAGTCCTTCCAATATGACTAACCAGAAC
ACGAATGAGTACCTGGAGAAGATCAAACAGCGACTGTTTGAGAACCTTAGAATGCTGCCGCACGCACCTGGGGTC
CAAATGCAGGCGATTCCTGAGGACGCCATCCCTGAGGAGAGTGGCGATGAGGACGAAGACGACCCTGACAAGCGC
ATCTCGATCTGCTCCTCTGACAAACGAATTGCCTGTGAGGAAGAGTTCTCCGATTCTGAAGAGGAGGGAGAGGGG
GGCCGCAAGAACTCTTCCAACTTCAAAAAAGCCAAGAGAGTCAAAACAGAGGATGAAAAAGAGAAAGACCCAGAG
GAGAAGAAAGAAGTCACCGAAGAGGAGAAAACCAAGGAGGAGAAGCCAGAAGCCAAAGGGGTCAAGGAGGAGGTC
AAGTTGGCC**TGA**ATGGACCTCTCCAGCTCTGGCTTCCTGCTGAGTCCCTCACGTTTCTTCCCCAACCCCTCAGAT
TTTATATTTTCTATTTCTCTGTGTATTTATATAAAAATTTATTAAATATAAATATCCCCAGGGACAGAAACCAAG
GCCCCGAGCTCAGGGCAGCTGTGCTGGGTGAGCTCTTCCAGGAGCCACCTTGCCACCCATTCTTCCCGTTCTTAA
CTTTGAACCATAAAGGGTGCCAGGTCTGGGTGAAAGGGATACTTTTATGCAACCATAAGACAAACTCCTGAAATG
CCAAGTGCCTGCTTAGTAGCTTTGGAAAGGTGCCCTTATTGAACATTCTAGAAGGGGTGGCTGGGTCTTCAAGGA
TCTCCTGTTTTTTTCAGGCTCCTAAAGTAACATCAGCCATTTTTAGATTGGTTCTGTTTTCGTACCTTCCCACTG
GCCTCAAGTGAGCCAAGAAACACTGCCTGCCCTCTGTCTGTCTTCTCCTAATTCTGCAGGTGGAGGTTGCTAGTC
TAGTTTCCTTTTTGAGATACTATTTTCATTTTTGTGAGCCTCTTTGTAATAAAATGGTACATTTCT

FIGURE 151

MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKF
LRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDIAVNWAGGLHHAKKSEASGF
CYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVN
YPLRDGIDDESYEAIFKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG
GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQRLFENLRMLPH
APGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEEGEGGRKNSSNFKKAKRVKTEDEKE
KDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA

FIGURE 152

GGCACGAGGGCGCGGAGCGGAGCGGCGGCGGGCGCAGCTAGCGGGTCGGCCGCGGAGCGGAGGTGCAGCTCGGCT
TCCCCCGGCACCCCTCCCCCTCGGGCGCCAGCCCCACCCCTCCGCCGGCCGGGCCGACCCCGCCGTACTATCCCC
TGCGGCGCGAGCCCGGGGCGGCTCCAAGCGCCCCCCAGCAGACCCCCATC**ATG**GGCAGCCAGAGCTCCAAGGCTC
CCCGGGGCGACGTGACCGCCGAGGAGGCAGCAGGCGCTTCCCCCGCGAAGGCCAACGGCCAGGAGAATGGCCACG
TGAAAAGCAATGGAGACTTATCCCCCAAGGGTGAAGGGGAGTCGCCCCCTGTGAACGGAACAGATGAGGCAGCCG
GGGCCACTGGCGATGCCATCGAGCCAGCACCCCCTAGCCAGGGTGCTGAGGCCAAGGGGGAGGTCCCCCCCAAGG
AGACCCCCAAGAAGAAGAAGAAATTCTCTTTCAAGAAGCCTTTCAAATTGAGCGGCCTGTCCTTCAAGAGAAATC
GGAAGGAGGGTGGGGGTGATTCTTCTGCCTCCTCACCCACAGAGGAAGAGCAGGAGCAGGGGGAGATCGGTGCCT
GCAGCGACGAGGGCACTGCTCAGGAAGGGAAGGCCGCAGCCACCCCTGAGAGCCAGGAACCCCAGGCCAAGGGGG
CAGAGGCTAGTGCAGCCTCAGAAGAAGAGGCAGGGCCCCAGGCTACAGAGCCATCCACTCCCTCGGGGCCGGAGA
GTGGCCCTACACCAGCCAGCGCTGAGCAGAATGAG**TAG**CTAGGTAGGGGCAGGTGGGTGATCTCTAAGCTGCAAA
AACTGTGCTGTCCTTGTGAGGTCACTGCCTGGACCTGGTGCCCTGGCTGCCTTCCTGTGCCCAGAAAGGAAGGGG
CTATTGCCTCCTCCCAGCCACGTTCCCTTTCCTCCTCTCCCTCCTGTGGATTCTCCCATCAGCCATCTGGTTCTC
CTCTTAAGGCCAGTTGAAGATGGTCCCTTACAGCTTCCCAAGTTAGGTTAGTGATGTGAAATGCTCCTGTCCCTG
GCCCTACCTCCTTCCCTGTCCCCACCCCTGCATAAGGCAGTTGTTGGTTTTCTTCCCCAATTCTTTTCCAAGTAG
GTTTTGTTTACCCTACTCCCCAAATCCCTGAGCCAGAAGTGGGGTGCTTATACTCCCAAACCTTGAGTGTCCAGC
CTTCCCCTGTTGTTTTTAGTCTCTTGTGCTGTGCCTAGTGGCACCTGGGCTGGGGAGGACACTGCCCCGTCTAGG
TTTTTATAAATGTCTTACTCAAGTTCAAACCTCCAGCCTGTGAATCAACTGTGTCTCTTTTTTGACTTGGTAAGC
AAGTATTAGGCTTTGGGGTGGGGGGAGGTCTGTAATGTGAAACAACTTCTTGTCTTTTTTTCTCCCACTGTTGTA
AATAACTTTTAATGGCCAAACCCCAGATTTGTACTTTTTTTTTTTTCTAACTGCTAAAACCATTCTCTTCCACCT
GGTTTTACTGTAACATTTGGAAAAGGAATAAATGTCGTCCCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MGSQSSKAPRGDVTAEEAAGASPAKANGQENGHVKSNGDLSPKGEGESPPVNGTDEAAGATGDAIEPAPPSQGAE
AKGEVPPKETPKKKKKFSFKKPFKLSGLSFKRNRKEGGGDSSASSPTEEEQEQGEIGACSDEGTAQEGKAAATPE
SQEPQAKGAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE

FIGURE 154

GCTCCCATTGGCTGATGTTGGCGCGAAGGTGCGCGAGTCAGCCCTCGCGCTGGGGGCGCAGGAAACAATAGAGGC
CGCGCGCACAGAGCGAGCTCTTGCAGCCTCCCCGCCCCTCCCGCAACGCTCGACCCCAGGATTCCCCCGGCTCGC
CTGCCCGCCATGGCCGACAAGGAAGCAGCCTTCGACGACGCAGTGGAAGAACGAGTGATCAACGAGGAATACAAA
ATATGGAAAAAGAACACCCCTTTTCTTTATGATTTGGTGATGACCCATGCTCTGGAGTGGCCCAGCCTAACTGCC
CAGTGGCTTCCAGATGTAACCAGAATTTGGAGGTTTTGGTTCAGTTAGTGGAAAAATTGAAATAGAAATCAAGAT
CAACCATGAAGGAGAAGTAAACAGGGCCCGTTATATGCCCCAGAACCCTTGTATCATCGCAACAAAGACTCCTTC
CAGTGATGTTCTTGTTTTTGACTATACAAAACATCCTTCTAAACCAGATCCTTCTGGAGAGTGCAACCCAGACTT
GCGTCTCCGTGGACATCAGAAGGAAGGCTATGGGCTTTCTTGGAACCCAAATCTCAGTGGGCACTTACTTAGTGC
TTCAGATGACCATACCATCTGCCTGTGGGACATCAGTGCCGTTCCAAAGGAGGGAAAAGTGGTAGATGCGAAGAC
CATCTTTACAGGGCATACGGCAGTAGTAGAAGATGTTTCCTGGCATCTACTCCATGAGTCTCTGTTTGGGTCAGT
TGCTGATGATCAGAAACTTATGATTTGGGATACTCGTTCAAACAATACTTCCAAACCAAGCCACTCAGTTGATGC
TCACACTGCTGAAGTGAACTGCCTTTCTTTCAATCCTTATAGTGAGTTCATTCTTGCCACAGGATCAGCTGACAA
GACTGTTGCCTTGTGGGATCTGAGAAATCTGAAACTTAAGTTGCATTCCTTTGAGTCACATAAGGATGAAATATT
CCAGGTTCAGTGGTCACCTCACAATGAGACTATTTTAGCTTCCAGTGGTACTGATCGCAGACTGAATGTCTGGGA
TTTAAGTAAAATTGGAGAGGAACAATCCCCAGAAGATGCAGAAGACGGGCCACCAGAGTTGTTGTTTATTCATGG
TGGTCATACTGCCAAGATATCTGATTTCTCCTGGAATCCCAATGAACCTTGGGTGATTTGTTCTGTATCAGAAGA
CAATATCATGCAAGTGTGGCAAATGGAGTTAGTCCTTGACCACTAGTTTGATGCCATCTCCATTTTGGGTGACCT
GTTTCACCAGCAGGCCTGTTACTCTCCATGACTAACTGTGTAAGTGCTTAAAATGGAATAAATTGCTTTTCTACA
TAA

FIGURE 155A

GGCTCGCATCCCCATAGTGCTGGGTTACAGTGAAGGTACGCCCCGCGCTCTGCTCTGGAGAGGCAGGGTGGGATA
GGGAACGTCTCGAGTGGCGCCCGCAGTC**ATG**GTGGTGTTCGTTGGCCGCCGCCTCCCGGCGCTCCTAGGGCTGTT
TAAGAAGAAGGGCTCTGCCAAGGCTGAGAATGACAAACATCTAAGTGTAGGGCCTGGCCAGGGGCCAGGGTCTGC
AGTGGATGAGCACCAGGACAACGTCTTCTTTCCCAGTGGGCGACCCCCCCACCTGGAAGAGCTGCACACTCAGGC
CCAGGAGGGGCTCCGCTCCCTACAACACCAAGAGAAACAGAAACTGAACAAGGGTGGCTGGGACCATGGAGACAC
CCAGAGTATCCAGTCCTCCCGGACGGGGCCGGATGAAGACAACATCTCCTTCTGCAGTCAGACCACATCCTACGT
GGCTGAGAGCTCCACAGCAGAGGACGCGCTCTCCATCCGCTCGGAGATGATCCAGCGCAAAGGCTCCACCTTCCG
ACCCCATGACTCATTTCCCAAATCTGGAAAGTCAGGGCGGCGTCGGCGGGAGCGGCGGAGCACTGTGCTGGGACT
CCCGCAGCATGTGCAGAAGGAGCTTGGCCTGAGGAATGAGCGTGAGGCACCAGGCACGCCCCGGGCTCCTGGTGC
ACGGGATGCCGTACGCATCCCCACAGTGGACGGCCGCCCCCGAGGCACCTCAGGGATGGGGGCCCGGGTGTCCCT
GCAGGCGCTGGAGGCGGAGGCGGAGGCTGGCGCTGAGACAGAGGCCATGCTGCAGCGCCACATTGACCGTGTCTA
CCGGGATGACACCTTTGTTGGCCGGTCCACGGGTACCCGGGCCCCACCATTGACCCGGCCCATGTCCCTAGCAGT
GCCTGGATTGACAGGAGGGGCAGGGCCTGCAGAGCCCCTGAGCCCGGCCATGTCCATCTCCCCCCAGGCCACCTA
CCTGTCGAAGTTGATTCCACATGCTGTGCTGCCGCCTACAGTGGACGTGGTGGCCCTAGGCCGCTGCAGCCTGCG
CACACTAAGCCGCTGCAGCCTGCACTCGGCCAGCCCAGCCTCAGTCCGCTCGCTGGGGCGCTTCTCCTCCGTCTC
CAGCCCACAGCCCCGCAGCCGCCACCCATCCTCCTCCAGTGACACCTGGAGCCACTCTCAATCCTCCGACACCAT
TGTGTCTGACGGTTCCACCCTCTCCTCTAAGGGTGGCTCTGAGGGCCAGCCGGAGAGCTCTACGGCTAGCAATAG
CGTGGTACCCCCTCCCCAGGGAGGCAGTGGGAGGGGCTCTCCCAGTGGGGGCAGCACTGCTGAGGCCTCAGACAC
ACTCAGCATTCGGAGCAGTGGGCAGTTGTCTGGCCGGAGTGTGTCCCTGCGTAAGCTGAAGCGGCCTCCACCCCC
TCCCCGCCGGACCCACTCCCTCCATCAGCGGGGCTTAGCAGTGCCTGATGGGCCATTAGGGTTGCCCCCTAAGCC
TGAGCGTAAGCAGCAGCCCCAGCTGCCTCGGCCACCCACCACTGGTGGCTCAGAAGGGGCGGGGGCAGCACCCTG
TCCACCCAACCCAGCCAACAGCTGGGTACCTGGCTTGTCTCCGGGTGGTTCCCGGCGCCCCCCACGGTCCCCAGA
ACGGACACTTTCGCCCTCCAGTGGATACTCGAGCCAAAGTGGTACTCCCACCCTCCCTCCCAAGGGCCTGGCAGG
TCCCCCTGCTTCCCCAGGCAAGGCCCAGCCCCCTAAACCAGAGCGTGTCACGTCTCTTCGCTCCCCTGGGGCCTC
CGTCTCCTCTTCCCTCACGTCTTTATGTTCCTCCTCCTCTGACCCAGCCCCCTCAGACCGCTCTGGGCCACAGAT
ATTGACCCCCCTGGGTGACAGGTTTGTCATACCTCCTCACCCCAAGGTGCCTGCCCCCTTCTCCCCACCTCCCTC
CAAGCCCAGGAGCCCTAACCCAGCTGCCCCTGCTCTAGCCGCCCCTGCTGTGGTTCCTGGGCCTGTTTCTACCAC
TGACGCCAGTCCTCAGTCCCCTCCCACTCCCCAGACAACCTTGACTCCACTGCAGGAGTCTCCTGTCATCTCCAA
AGACCAGTCACCCCCACCTTCCCCACCCCCATCTTATCATCCACCCCCACCACCCACTAAGAAGCCAGAGGTGGT
TGTGGAGGCACCATCTGCCTCAGAGACTGCTGAGGAGCCCCTCCAAGATCCCAACTGGCCCCCTCCCCCACCCCC
TGCCCCTGAGGAGCAGGACCTGTCCATGGCTGACTTCCCCCCACCAGAGGAGGCTTTTTTCTCTGTGGCCAGCCC
TGAGCCTGCAGGCCCTTCAGGCTCCCCAGAGCTTGTCAGCTCCCCGGCTGCTTCGTCCTCCTCAGCTACTGCTTT
GCAGATTCAGCCCCCGGGTAGCCCAGACCCTCCTCCAGCTCCGCCAGCCCCAGCTCCTGCTAGTTCCGCCCCAGG
GCATGTGGCCAAGCTCCCTCAGAAGGAACCGGTGGGCTGTAGCAAGGGTGGTGGGCCTCCCAGGGAGGACGTAGG
TGCGCCCCTGGTCACGCCCTCGCTCCTGCAGATGGTGCGGCTGCGCTCCGTGGGTGCTCCAGGAGGGGCTCCCAC
CCCAGCACTGGGGCCATCGGCCCCCCAGAAACCACTGCGAAGGGCCCTGTCAGGGCGGGCCAGCCCAGTGCCTGC
CCCCTCCTCAGGGCTCCATGCTGCGGTCCGACTCAAGGCCTGCAGCCTGGCCGCCAGTGAAGGCCTCTCAAGTGC
TCAGCCCAACGGACCGCCTGAGGCAGAGCCACGGCCTCCCCAGTCCCCTGCCTCAACGGCCAGTTTCATCTTCTC
CAAGGGCTCTAGGAAGCTGCAGCTGGAGCGGCCCGTGTCCCCTGAGACCCAGGCTGACCTCCAGCGGAATCTGGT
GGCAGAACTCCGGAGCATCTCAGAGCAGCGGCCACCCCAGGCCCCAAAGAAGTCACCTAAGGCTCCCCCACCTGT
GGCCCGCAAGCCGTCTGTGGGAGTCCCCCCACCCGCCTCCCCCAGTTACCCTCGAGCTGAGCCCCTTACTGCTCC
TCCCACCAATGGGCTCCCTCACACCCAGGACAGGACTAAGAGGGAGCTGGCGGAGAATGGAGGTGTCCTGCAGCT
GGTGGGCCCAGAGGAGAAGATGGGCCTCCCGGGCTCAGACTCACAGAAAGAGCTGGCC**TGA**CCACCAGGCACCTC
ACTGGCACTGCTGACCCATCCCAGAAACACAATCTCAGGGACCCGAGCAGCTCCAAGGACGAGAGGATACAGCAG
ACACAACCTAATAGAGAGGGCGCCTGCAGCCTTAACCTCCACGGCCTTCGATACTTATGCAAGCCTGGTGTTGCT
CCTGTCCTCAGAGTCATCCTGCGCTCATGCCTTTTCCCGAATGGGTTCACCTCTGGCAGTTGCCGCTTCAGTCTT
GGCCTTAGCCTCATCTTGAAGTGGGTAGCTGGCGGGAGAGGGTGGCTGCGCCCCCTGCTGGCCCTGAGGCTGCAG
AGTTGGGAGCAGGACACCTCACCTGAGTTTCATTTTTTTTCATGTCCAAACCATGCACATACTATAGTCCAGAAT

FIGURE 155B

CAAAGCACTTTTGAAAAGTGGCTGCATGGCCATCCTCCAGGGCCCAGGAAGTTGCATTCCAAGGGCCTGTTTACA
TGGCAGCAGAATCCATCCCCGGCAGTCAGCCCATAGCTTGGGACCAGTCTGTGCCCTCCTGCCCAGTCCAGTTTA
CTCCTCTTGGTTCCTGAAGGTGGCCAAGTCATTGTGTTCCCACAGGCTTCTCTAGGCTGGGGGCAGGTGTGGGGC
TGTGGAATTCCAAAGCACAAAAGGTGCAGAGGGGATTGGCCTTCCTGTGCCTCAACTCACCAACCACCCTCCTGC
CTTCCAGTTCTGCCAGGTGCTCCATGCTGGGGACAAGTAGGAGACTGCCAGGGCCCAAAGAAATGGGTGAGCAGT
AGAGTCATCTCGGGGCACTTGGCAGTGTCAAGCACCTGCCCCTTGCCTCCTTGACCACACTGGGGTGGGTGGGCC
CCCAGCACTTCAGAGGCAGGAGCCTTTGGGCTGAGCAAGCACTGAGGAGGTGGATGGAAGGGAGCATCTGGAGGG
GGGGAGCTTCCTTGAGCAGTGGGCCCAGGCCTGGCCCTCCACACTTCATTCTCTGACCTTTCTCTCTCCTCATTT
CGGTGCATGTCCTTTCTGCAGCTGCCTTTCAGCACAGGTGGTTCCACTGGGGGCAGCTAACGCTGAGTGACAAGG
ATGGGAAGCCACAGGTGCATTTTACTCAAGTCTTCTCTAGTCAATGAGGGGCACCCAGTGCTTCTAGGGCAGGCT
GGGTGGTGGTCCCCTAGGTATCAGCCTCTCTTACTGTACTCTCCGGGAATGTTAACCTTTCTATTTTCAGCCTGT
GCCACCTGTCTAGGCAAGCTGGCTTCCCCATTGGCCCCTGTGGGTCCACAGCAGCGTGGCTGCCCCCCAGGGCCA
CCGCTTCTTTCTTGATCCTCTTTCCTTAACAGTGACTTGGGCTTGAGTCTGGCAAGGAACCTTGCTTTTAGCTTC
ACCACCAAGGAGAGAGGTTGACATGACCTCCCCGCCCCCTCACCAAGGCTGGGAACAGAGGGGATGTGGTGAGAG
CCAGGTTCCTCTGGCCCTCTCCAGGGTGTTTTCCACTAGTCACTACTGTCTTCTCCTTGTAGCTAATCAATCAAT
ATTCTTCCCTTGCCTGTGGGCAGTGGAGAGTGCTGCTGGGTGTACGCTGCACCTGCCCACTGAGTTGGGGAAAGA
GGATAATCAGTGAGCACTGTTCTGCTCAGAGCTCCTGATCTACCCCACCCCCTAGGATCCAGGACTGGGTCAAAG
CTGCATGAAACCAGGCCCTGGCAGCAACCTGGGAATGGCTGGAGGTGGGAGAGAACCTGACTTCTCTTTCCCTCT
CCCTCCTCCAACATTACTGGAACTCTATCCTGTTAGGATCTTCTGAGCTTGTTTCCCTGCTGGGTGGGACAGAGG
ACAAAGGAGAAGGGAGGGTCTAGAAGAGGCAGCCCTTCTTTGTCCTCTGGGGTAAATGAGCTTGACCTAGAGTAA
ATGGAGAGACCAAAAGCCTCTGATTTTTAATTTCCATAAAATGTTAGAAGTATATATATACATATATATATTTCT
TTAAATTTTTGAGTCTTTGATATGTCTAAAAATCCATTCCCTCTGCCCTGAAGCCTGAGTGAGACACATGAAGAA
AACTGTGTTTCATTTAAAGATGTTAATTAAATGATTGAAACTTG

FIGURE 156

MVVFVGRRLPALLGLFKKKGSAKAENDKHLSVGPGQGPGSAVDEHQDNVFFPSGRPPHLEELHTQAQEGLRSLQH
QEKQKLNKGGWDHGDTQSIQSSRTGPDEDNISFCSQTTSYVAESSTAEDALSIRSEMIQRKGSTFRPHDSFPKSG
KSGRRRRERRSTVLGLPQHVQKELGLRNEREAPGTPRAPGARDAVRIPTVDGRPRGTSGMGARVSLQALEAEAEA
GAETEAMLQRHIDRVYRDDTFVGRSTGTRAPPLTRPMSLAVPGLTGGAGPAEPLSPAMSISPQATYLSKLIPHAV
LPPTVDVVALGRCSLRTLSRCSLHSASPASVRSLGRFSSVSSPQPRSRHPSSSSDTWSHSQSSDTIVSDGSTLSS
KGGSEGQPESSTASNSVVPPPQGGSGRGSPSGGSTAEASDTLSIRSSGQLSGRSVSLRKLKRPPPPPRRTHSLHQ
RGLAVPDGPLGLPPKPERKQQPQLPRPPTTGGSEGAGAAPCPPNPANSWVPGLSPGGSRRPPRSPERTLSPSSGY
SSQSGTPTLPPKGLAGPPASPGKAQPPKPERVTSLRSPGASVSSSLTSLCSSSSDPAPSDRSGPQILTPLGDRFV
IPPHPKVPAPFSPPPSKPRSPNPAAPALAAPAVVPGPVSTTDASPQSPPTPQTTLTPLQESPVISKDQSPPPSPP
PSYHPPPPPTKKPEVVVEAPSASETAEEPLQDPNWPPPPPAPEEQDLSMADFPPPEEAFFSVASPEPAGPSGSP
ELVSSPAASSSSATALQIQPPGSPDPPPAPPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLL
QMVRLRSVGAPGGAPTPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAE
PRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVARKPSVGVP
PPASPSYPRAEPLTAPPTNGLPHTQDRTKRELAENGGVLQLVGPEEKMGLPGSDSQKELA

FIGURE 157

ATGGGGGACGCTCCCAGCCCTGAAGAGAAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACTTAAAATTTACTGGGGAACGGCAACCACGGGCAAACCACATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGCGGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACTTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCCTCCGTGGTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCCTTTGCTGAGTGGCCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAGATTTTCACCTTTGCAGAGAAGTACCTCCCT
GCACTTGGCTATTCAAAACGGGTCCATCTGATGAATCCTATGGTTCCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAACTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAATGGGGTTCTGTCCTTCATCAAGCATGTCCTTTTTCCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAACTGGCCAGCGCTGCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACCAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAACTGCAGGACAGGCTGGTAGTGGTGCTGTGCAAC
CTGAAACCCCAGAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAAATTTCTGAGGAG
TGCATCGCACAGTGGAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTTCCTGTAAATCGCTGAAAGGGGGG
AACATTAGC**TAG**CCAGCCCAGCATCTTCCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

FIGURE 158

MGDAPSPEEKLHLITRNLQEVLGEEKLKEILKERELKIYWGTATTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVVKQVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEEESKIDLLDRKEDVKKKLKKAFCEPGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKTYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAKGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHPDADSLYVEKIDVGEAEPRTVVSGLVQFVPKEELQDRLVVVLCNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHVFVKGYEKGQPDEELKPKKKVFEKLQADFKISEECIAQWKQTNFMTKLGSISCKSLKGG
NIS

FIGURE 159

GCGCGAGCAAG**ATG**GCCACCACCAAGCGCGTCTTGTACGTGGGTGGACTGGCAGAGGAAGTGGACGACAAAGTTC
TTCATGCTGCGTTCATTCCTTTTGGAGACATCACAGATATTCAGATTCCTCTGGATTATGAAACAGAAAAGCACC
GAGGATTTGCTTTTGTTGAATTTGAGTTGGCAGAGGATGCTGCAGCAGCTATCGACAACATGAATGAATCTGAGC
TTTTTGGACGTACAATTCGTGTCAATTTGGCCAAACCAATGAGAATTAAGGAAGGCTCTTCCAGGCCAGTTTGGT
CAGATGATGACTGGTTGAAGAAGTTTTCTGGGAAGACGCTTGAAGAGAATAAAGAGGAAGAAGGGTCAGAGCCTC
CCAAAGCAGAGACCCAGGAGGGAGAGCCCATTGCTAAAAAGGCCCGCTCAAATCCTCAGGTGTACATGGACATCA
AGATTGGGAACAAGCCGGCTGGCCGCATCCAGATGCTCCTGCGTTCTGATGTCGTGCCCATGACAGCAGAGAATT
TCCGCTGCCTGTGCACTCATGAAAAGGGCTTTGGCTTTAAGGGAAGCAGCTTCCACCGCATCATCCCCCAGTTCA
TGTGCCAGGGCGGTGATTTCACAAACCACAATGGCACTGGGGGCAAGTCCATCTATGGGAAGAAGTTCGATGATG
AAAACTTTATCCTCAAGCATACGGGACCAGGTCTACTATCCATGGCCAACTCTGGCCCAAACACCAATGGCTCTC
AGTTCTTCCTGACATGTGACAAGACAGACTGGCTGGATGGCAAGCATGTGGTGTTTGGAGAGGTCACCGAAGGCC
TAGATGTCTTGCGGCAAATTGAGGCCCAGGGCAGCAAGGACGGGAAGCCAAAGCAGAAGGTGATCATCGCCGACT
GTGGGGAGTACGTG**TGA**GGCGGCACTCTCTCTGCTTCCCCCTCCGCTCTTGACCCTGCATATCCAGGAAGGAACT
GCCAGCCTCAGAGGAGGCAGCACCGAGGGTGCCTGTTTGAAGCAAGCAGCATTTGGGATATGTGCCCTTCCTCAG
GGTCTGCTTGGAGCAGCTCCTCTGCAGGCACAGCCTGGACTATTCCCAGGCACAGCTGTGGGCCCAGGAGCCAGC
TCAGGTGCTCCCCTCCACCATGGGCAGGCTGTGCAAAAAAGCCACTGGCTTTTCTCAGCATTTGCTGCTGGGCCT
CTCCTGGGACTACCAGTGTGGCTCTTACGTGTTTTCTTTGCTAAAATAAACCCTAGTTCTTATATTAAAAAAAAA
AAAAAAAAAA

FIGURE 160

MATTKRVLYVGGLAEEVDDKVLHAAFIPFGDITDIQIPLDYETEKHRGFAFVEFELAEDAAAAIDNMNESELFGR
TIRVNLAKPMRIKEGSSRPVWSDDDWLKKFSGKTLEENKEEEGSEPPKAETQEGEPIAKKARSNPQVYMDIKIGN
KPAGRIQMLLRSDVVPMTAENFRCLCTHEKGFGFKGSSFHRIIPQFMCQGGDFTNHNGTGGKSIYGKKFDDENFI
LKHTGPGLLSMANSGPNTNGSQFFLTCDKTDWLDGKHVVFGEVTEGLDVLRQIEAQGSKDGKPKQKVIIADCGEY
V

FIGURE 161

TCAAAGCACCTGCAGCCCCAATTTGTGATCCAGCAGCAGCCACAGCCACAACAGCAGCAGCCGCCGCCCCAGCAG
TCACGGCCTGTGCTCCAAGCTGAGCCCCACCCCCAGCTCGCCTCAGTCTCTCCAAGCGTGGCCCTCCAGCCCAGC
TCAGAGGCCCATGCC**ATG**CCACTAGGCCCGGTTACACCCGCCCTGCCACTCCAGTGTCCCACTGCCAACCTGCAC
AAGCCTGGCGGCAGTCAGCAGTGTCACCCTCCCACACCTGATACTGGGCCTCAGAATGGACATCCCGAGGGCGTG
CCCCACACCCCTCAACGCAGGTTCCAGCACACTTCAGCTGTCATCTTACAACTGCAGCCTGCTTCACCAGTGCCC
CAGCAGTGTGTCCCTGATGACTGGAAAGAAGTGGCACCAGGGGAGAAAAGTGTGCCTGAGACGCGGTCTGGCCCA
TCACCACATCAGCAGGCTATTGTCACTGCCATGCCTGGTGGCCTGCCTGTACCCACGAGCCCTAACATCCAGCCG
TCCCCAGCTCACGAGACAGGGCAGGGCATTGTTCATGCACTGACCGACCTCAGCAGCCCCGGCATGACCTCAGGG
AACGGAAACTCTGCCTCCAGCATCGCCGGCACTGCCCCCCAGAATGGTGAGAATAAACCACCACAGGCCATTGTG
AAACCCCAAATCCTGACGCATGTTATCGAAGGGTTTGTGATCCAGGAGGGGGCGGAGCCTTTCCCGGTGGGACGC
TCGTCCCTGCTGGTGGGGAATCTCAAGAAGAAGTATGCACAGGGGTTCCTGCCTGAGAAACTTCCACAGCAGGAT
CACACCACCACCACTGACTCGGAGATGGAGGAGCCCTATCTGCAAGAATCCAAAGAGGAGGGTGCTCCCCTCAAA
CTCAAGTGTGAGCTCTGTGGCCGGGTGGACTTTGCCTATAAGTTCAAGCGTTCCAAGCGCTTCTGTTCCATGGCT
TGTGCAAAGAGGTACAACGTGGGATGCACCAAACGGGTGGGACTTTTCCACTCAGACCGGAGCAAGCTGCAGAAG
GCAGGAGCTGCGACCCACAACCGCCGTCGGGCCAGCAAAGCCAGTCTGCCACCACTTACCAAGGATACCAAGAAG
CAGCCAACAGGCACTGTGCCCCTTTCGGTTACTGCTGCTTTGCAGCTAACACACAGCCAGGAAGACTCCAGCCGT
TGCTCAGATAACTCAAGCTATGAGGAACCCTTGTCACCCATCTCAGCCAGCTCATCTACTTCCCGCCGGCGACAA
GGCCAGCGGGACCTGGAGCTCCCCGACATGCATATGCGGGACCTGGTGGGCATGGGACACCACTTCCTGCCAAGT
GAGCCCACCAAGTGGAATGTAGAAGACGTCTACGAATTCATCCGCTCTCTGCCAGGCTGCCAGGAGATAGCAGAG
GAATTCCGTGCCCAGGAAATCGACGGGCAAGCCCTGCTGCTGCTCAAGGAGGACCACCTGATGAGCGCCATGAAC
ATCAAGCTGGGGCCCGCCCTGAAGATCTACGCCCGCATCAGCATGCTCAAGGACTCC**TAG**GGCTGGTGGCAGCCA
GGATTCTGGCCCAGGGCGCCTCCTCCCGACTGAGCAGAGCCAGACAGACATTCCTGAGGGGCCCAGAAATGGGGC
CGGTTGGAGGGCAGGGGCTCTCCCTAGGGGCATAGCTGGTGAGGAGGTCTGGGCACCTCCTCCATGGCTCTCAGG
CGCCTTTCATTTCTGTGGGAGGGGCAGAGAGGTAGGTGGCACAGAAGATGGGGCTTTATGCTTGTAAATATTGAT
AGCACTGGCTTCCTCCAAAGTCCCAATACTCTAGCCCCGCTCTCTTCCCCTCTTTCTGTCCCCCATTTTCCAGGG
GGTATATGGTCAGGGCTCCCCAACCTGAGTTGGGTTACTTCAAGGGCAGCCAGCAGGCCTGGATGGAGGCCTAGA
AAGCCCTTGCCTTCCTTCCTCCCACTTCTTTCTCCAGGCCTGGTTAACTCTTCCGTTGTCAGCTTCTCCCCCTTC
AGCCTGTTTCTGCAGCAGCCAGGGTTCTCCCCCCTACACCCTCTGCAGGTGGAGAGAGAGAAGCTGGGCCCAGCC
GGGCCGTGCCTGCTGGCACAGACGCCTTAACGCTGTGTGTATGACTGTGTGACTGTGTGGGAGCCTGGACTGACA
GATAGGCCAAGGGCTACTCTCTGGCATCTCCAGGTGTTTTGTAGCAAACAGCCACTTAGTGCTTTGTCCTGGACT
CCACTCAGCCTCAGGATGGGGAATAGCCAAGAATGGCAGCCTCAGCGCAGAGGCAAGGTCAGAAAGAGACGGCGC
TTCAGAGTTTCCTTTCCAGACACCCCTCCCCGCACTGTGAAGTTCCCCTGACCGCCCTCCTGGTTCACAAAGAGC
ATTAAGAAAGCTGCGGTGGTCTGAGCAACATAGCCCAAAGGGCTGAGCCTCCTGGCCTGCCTGCCCGCCCACCCT
GGGAGTCCCAGTGGTGAGGCTCAGAGAACTGCTAAGGGGAAAGAACAGCTGGAGTTTCTGTTGATGTGAAGAAGG
CAGCTCTTGGCCTCCCACTCCCACACTTCTTTGCCTATAAATCTTCCTAGCAGCAATTTGAGCTACCTGAGGAGG
AGGCAGGGCAGAAAGGGCGAGGGCCTGCCTCTGACCTGCCGTGTCCTTTGCAGGAAGGAGGTAGGCACCTTTCTG
AGCTTATTCTATTCCCCACCCACACCCCCAGGCAGGGTTGGAAATGAAGGACTTTTTTAACCTTTGTTTTGTTTT
TTAAAAATAAATCTGTAAAATCTG

FIGURE 162

MPLGPVTPALPLQCPTANLHKPGGSQQCHPPTPDTGPQNGHPEGVPHTPQRRFQHTSAVILQLQPASPVPQQCVP
DDWKEVAPGEKSVPETRSGPSPHQQAIVTAMPGGLPVPTSPNIQPSPAHETGQGIVHALTDLSSPGMTSGNGNSA
SSIAGTAPQNGENKPPQAIVKPQILTHVIEGFVIQEGAEPFPVGRSSLLVGNLKKKYAQGFLPEKLPQQDHTTTT
DSEMEEPYLQESKEEGAPLKLKCELCGRVDFAYKFKRSKRFCSMACAKRYNVGCTKRVGLFHSDRSKLQKAGAAT
HNRRRASKASLPPLTKDTKKQPTGTVPLSVTAALQLTHSQEDSSRCSDNSSYEEPLSPISASSSTSRRRQGQRDL
ELPDMHMRDLVGMGHHFLPSEPTKWNVEDVYEFIRSLPGCQEIAEEFRAQEIDGQALLLLKEDHLMSAMNIKLGP
ALKIYARISMLKDS

FIGURE 163

AGACAAGGCAAATTTAAGTAGGCTC**ATG**GCTTTTCCAGTTGGGTTGGAAAGTTCCTCTCCGATGACTGTTATATT
CTCAAAGAAATATGAGGAGAGGGGCAGGGCATGGTGGCTCACATCCGTAATCCTAGCAAATCATAGTGGCCTACA
GCCAACGCCTTCTTCGCTCACTGGCCAACTGGAAACTTCAGTCCCCCCATGCCTCCCGCCTCTCACCCAGGGGCC
AATAGGAATGATCAGAGGTTCGCAACTTAGTGTCATCAAGCATAGTAATTGCAATTGGCTATTGGAGCTGTCGAT
CGTGGAG**TAG**GCGGGGCCGTGCCAGCTGGCCTATATAAGACGAGGACAAAGGCGGCGCGCCGCCTGTGTCATCCG
CCATTTTGTGAGAAGCAAGGTGGCCTCCACGTTTCCTGAGCGTCTTCTTCGCTTTTGCCTCGACCGCCCCTTGAC
CACAGACATGTCTCGGGATCGGTTCCGGAGTCGTGGCGGTGGCGGTGGTGGCTTCCACAGGCGTGGAGGAGGCGG
CGGCCGCGGCGGCCTCCACGACTTCCGTTCTCCGCCGCCCGGCATGGGCCTCAATCAGAATCGCGGCCAGGCCCG
ACTCCGACCCCGCCGCCTGCAGTCACCTCGGCCCCTCCCGGGGCGCCGCCACCCACCCCGCCAAGCAGCGGGGTC
CCTACCACACCTCCTCAGGCCGGAGGCCCGCCGCCTCCGCCCGCGGCAGTCCCGGGCCCGGGTCCAGGGCCTAAG
CAGGGCCCAGGTCCGGGTGGTCCCAAAGGCGGCAAAATGCCTGGCGGGCCGAAGCCAGGTGGCGGCCCGGGCCTA
AGTACGCCTGGCGGCCACCCCAAGCCGCCGCATCGAGGCGGCGGGGAGCCCCGCGGGGGCCGCCAGCACCACCCG
CCCTACCACCAGCAGCATCACCAGGGGCCCCCGCCCGGCGGGCCCGGCGGCCGCAGCGAGGAGAAGATCTCGGAC
TCGGAG

FIGURE 164

MAFPVGLESSSPMTVIFSKKYEERGRAWWLTSVILANHSGLQPTPSSLTGQLETSVPPCLPPLTQGPIGMIRGSQ
LSVIKHSNCNWLLELSIVE

FIGURE 165

GGCGAGCAGTCTGCGCGCGG**ATG**GCCGCAGCGGCGATGGCGGCAGCGGCAGGTGGAGGGGCTGGCGCGGCCCGCT
CCCTCTCGCGCTTCCGAGGCTGCCTGGCTGGTGCGCTGCTCGGGGACTGCGTGGGCTCCTTCTACGAGGCCCACG
ACACCGTCGACCTGACGTCAGTCCTGCGTCATGTCCAGAGTCTGGAGCCGGACCCCGGCACGCCCGGGAGTGAGC
GGACAGAAGCCTTGTACTACACAGATGACACAGCCATGGCCAGGGCCCTGGTGCAGTCCCTGCTAGCCAAGGAGG
CCTTTGACGAGGTGGACATGGCTCACAGATTTGCTCAGGAGTACAAGAAAGACCCTGACAGGGGCTATGGTGCTG
GAGTAGTCACTGTCTTCAAGAAGCTCCTGAACCCCAAATGTCGCGATGTCTTTGAGCCTGCCCGGGCCCAGTTTA
ACGGGAAAGGCTCCTATGGCAATGGAGGTGCCATGCGGGTGGCTGGCATCTCCCTGGCCTATAGCAGTGTCCAGG
ATGTGCAGAAGTTTGCCCGGCTCTCGGCCCAGCTGACACACGCCTCCTCCCTGGGTTACAATGGCGCCATCCTGC
AGGCCCTGGCTGTGCACCTGGCCTTGCAGGGCGAGTCTTCCAGCGAGCACTTTCTCAAGCAACTCCTGGGCCACA
TGGAGGATCTGGAGGGTGATGCCCAGTCCGTCTTGGATGCCAGGGAGTTGGGCATGGAGGAGCGTCCATACTCCA
GCCGCCTGAAGAAGATTGGAGAGCTTCTAGACCAGGCATCGGTGACCAGGGAGGAAGTGGTGTCTGAGCTAGGGA
ATGGCATTGCTGCCTTTGAGTCGGTACCCACCGCCATCTACTGCTTCCTACGCTGCATGGAGCCAGACCCTGAGA
TCCCTTCTGCCTTCAATAGCCTCCAAAGGACTCTCATTTATTCCATCTCACTTGGTGGGGACACAGACACCATTG
CCACCATGGCTGGGGCCATTGCTGGTGCCTACTATGGGATGGATCAGGTGCCAGAGAGCTGGCAGCAAAGCTGTG
AAGGCTACGAGGAGACAGACATCCTGGCCCAAAGCCTGCACCGTGTCTTCCAGAAGAGT**TGA**TGAGGGCTACAGC
TGTTGGGGCTCTGCCAGGTCCCCTGGGACCAACTACAGCTCCAATCAGAAACCCTGCGCTTCCTTGAGTGTGGCT
TCCCACTTTTCCTGCATTGTGGAGCTGACTGAGTACACCGGTGAGGCTGGGGTCTCTGCAGGGGAGGTCACTGGA
ACAGCGAGCAAGGGACTGGTGCCTCGCTGGTGCTGGGTCTCTGGTTTGCTGCAGAGCCGTAGGACACTCCTGGCT
CCTCAGTAGGACAGACAGACGCAGGCGGGTTTATTTTGGAGGGGTACTTGTGGCATTTTCCTGTATTGTCTTGGA
CATGGGATGTGGGGAGGTGGAAATGATGAGCAGTAGCATCATTTCTCCCTGTTGGGTTTTAGCCAGTTTGCCAGC
AAGCGCATCCTAGCAGGGTCCCCGAGCAGCAGGTTGTGTGGATGAAGGGACAGGCACTTGCATCCAGCTGATCTA
GGTCACACCTGGCTCTTGGCTGCCATGTGGCTTATTAACAGCTTCCAGTGGAAGTCGCAATAAACAGTTTTTGGT
AAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDTVDLTSVLRHVQSLEPDPGTPGSERTEALYY
TDDTAMARALVQSLLAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCRDVFEPARAQFNGKGSYG
NGGAMRVAGISLAYSSVQDVQKFARLSAQLTHASSLGYNGAILQALAVHLALQGESSSEHFLKQLLGHMEDLEGD
AQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVSELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNS
LQRTLIYSISLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILAQSLHRVFQKS

FIGURE 167

CCGTGGCTAGGCGAGTGGGGCGGGGCGGCCGGCACC**ATG**TCGAGGCAGGCGAACCGTGGCACCGAGAGCAAGAAA
ATGAGCTCTGAGCTCTTCACCCTGACCTATGGTGCCCTGGTCACCCAGCTATGTAAGGACTATGAAAATGATGAA
GATGTGAATAAACAGCTGGACAAAATGGGCTTTAACATTGGAGTCCGGCTGATTGAAGATTTCTTGGCTCGGTCA
AATGTTGGGAGGTGCCATGACTTTCGGGAAACTGCGGATGTCATTGCCAAGGTGGCGTTCAAGATGTACTTGGGC
ATCACTCCAAGCATTACTAATTGGAGCCCAGCTGGTGATGAATTCTCCCTCATTTTGGAAAATAACCCCTTGGTG
GACTTTGTGGAACTTCCTGATAACCACTCATCCCTTATTTATTCCAATCTCTTGTGTGGGGTGTTGCGGGGAGCT
TTGGAGATGGTCCAGATGGCTGTGGAGGCCAAGTTTGTCCAGGACACCCTGAAAGGAGACGGTGTGACAGAAATC
CGGATGAGATTCATCAGGCGGATTGAGGACAATCTTCCAGCTGGAGAGGAA**TAA**CCATCCCTACAACTCGAGGAT
AGCCATCAGGAGCACTGTTGGAATCAGCAGGCCTCTGTGCTCCCTCTGCCCTCCAGAACTCAGTGACTCTTGAAC
ATGGATGTTATATATTCTTATAACCTGTTTCCATTCTCCATTCAAATAAAGAGCAGACTGCGATATAGTCCATTT
ACCCCATGTGTGCACATTCAGGAGCGACAGTCTCTGCCCCCATTCCCTTGAGAGGGGCTGGATGTAATCACCTTT
GGTTGGACTAGAAAGAGCTCAAACCATTTTACATTCCTGTTTGAATTTTCCAAAGCAAAACTCACTTTGACCCCA
TTAAGAGGCAAGCCTGGCACATCTATCCCTGGGCCTTTAGAAAGCCATTTGCCTCAAATGGCTATAGGGTTGTGG
GGTGGAGGGAGGAAGGGCTGGGAGGGAGTGGGGAGGAATTGCTAGCTGTAGTGTGACACATTGTAGTGTTTGCCA
GGAAAGGAGCCAGTCATGCCGGAAACACTGACTTCTGGGAAGCCACCCAGGTCTCATTCCTCCCTGCTGTTGGAG
GCAACATCTCCTCTTTTTACAGAGGGTACATCCTTTTTTCTTACAAATTCTTCAATAAAGACACATTCTTGAGTG
AAATCCCTAAAAAAAAA

FIGURE 168

MSRQANRGTESKKMSSELFTLTYGALVTQLCKDYENDEDVNKQLDKMGFNIGVRLIEDFLARSNVGRCHDFRETA
DVIAKVAFKMYLGITPSITNWSPAGDEFSLILENNPLVDFVELPDNHSSLIYSNLLCGVLRGALEMVQMAVEAKF
VQDTLKGDGVTEIRMRFIRRIEDNLPAGEE

FIGURE 169A

ACTTACTATTGGAGGCAGTGGGCAGCGCAGGACAGGCCCAGGGCCGCCGACCCTGGCAATGACTGTCACCAGCTG
GAGGGAAGAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCAGGGCCAAGGCTCT
AGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCATCCTTGGTCCCCGTCTGGGCAACTCACC
GGTGCCAAGCATAGTGCAGTGTTTGGCGAGGAAAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCT
GGAGGAGAGGGGGGACCAAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTC
ACTGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACCGCACCTGTGAAAT
CGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGCGCATCTGCCTCGTCCTGGACTGCCTCTG
TGCTCATGACTTCAGCGATAAGACCGCTGACCTCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAG
CGAGAGGGAGACTGTGGTAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCA
CAGAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCAACTTCTGCCTCGG
GAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGAGCCCTGCCTACATCAGTCCCGACGTGCT
CAGCGGCCGGCCGTACCGTGGCAAGCCCAGTGACATGTGGGCCCTGGGCGTGGTGCTCTTCACCATGCTGTATGG
CCAGTTCCCCTTCTACGACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGA
GGATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCCTTGACCCCCAGCAGCGCCTGGC
CGCCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGCAGTCCCTGTCATCTCTGAGTGGGCCTTT
GCAAGTGGTTCCTGACATTGATGACCAAATGAGCAATGCGGATAGCTCCCAGGAGGTGAGTTGGGGAGGGCAGAT
GGGCCATTACCCAGCCCCAAGGGACAGGCTTCTGGGGGCAGGCAGGGCAAGGGCAGAGGTGGCAGCTACCCGCAG
GCCACAGAGTTTCCTTGGTCTTCTTCCCCAGCCTTGGGGTGGGAAAGGGAGACTTCAGTCCTCAGCCTGAGCTGC
CTGGGGCCTGCCTTGGGCTTGGTGTAGCTGGAGATCTTTGGCCAGAGAGACCTGTGAGACAGCCGAGCTGGAGCC
AGTGCCCAAGTGGCCCAGGCCAGCCCTCTCAGCTTCCTCCTGCTGCCCAAGTCACATTTCTCTGCCCCCTGACTC
AGAGTTCTCTCTCACCCTTCCTGCTTTTCATTTTTCAGATGATTCATTTCTCCCTATTTCTTTCCTCCCCATTCC
CTGCACTGGAGAAAGTGTTGGGCCTAGGGTGGGGGCAGAGACTTGGGCACCAGGCAGCAGAGGGCAGGTGATCTT
AGGGTGCCCCCTGGAGGGCAGGGCTTGGCCGAGCAACAGCATTGCTGGGCCCTGGATATTGGAAGGACCTTCCCT
CCCTGGCCCACCTTGGAGCTCCACAGTGAGCAGTGTGCAGGTAGGACCAGGAGGGGCCGTGCCTGGGAGAGCCTC
CCAGAGCCTCCTGGCCCCCGAGGAAAGAGAGTTCCAATCCCTACCCACCTCCAGCTTCCACCCTTTAGCTGTTTG
GCTAAAATCATCATCACTAGCCCGCAGTGAGTGCCTACCCCGAGGGCACCTCATTCAGCCCTCACTGCGGGCCTG
CGTGGCCTGTGTTCTTAGCCCCATGTTACAGAAGAGGAAACAGGGTTAGAGAGGACTTTCCCAAAGCCACACAGC
TTAGAAGTAGTGGAGCTAAGCCTTGAACCCAAGTCTCATCCGGAAGCCCTGCTGTCTCCTGTGGTGACTGGCACG
GGGACACCACTTCAGCTTCTGTTACCATCTGCCTAGACCATCCCAGGGAGCTCAGCATGGGGCCCTGCGTATGTG
GCTCCTCCAGGTGCTGCGCCCCCAGCCCAGGGCTTGCTCGTACCTCTTGACGTGCATTAGCCGCCTCAGGGCTCA
GAGAACCTTTGCGAGGGGCCAGACAGCTAAGGCTTCTGAGGTAAAGTGACCTCTCACGCAGCCAGTGAGTTAGGA
AGCATGAGTCTGCGTCAGTCCCGGGTCCGCAGGGCGGCCTGCAAGGGGAGTTGAGGTTGGCTGGAGGGGGTCAGG
GACCCACCCTCAGCGCCACTCCCACCCCCGGCCTTGAGGCCTGAGGGTGTGGTGCCTGGAAGGGTGACTGCAGGA
GCCAGGCTGCCAGCACTCTTGCCTGCCCTCCTGTCTGCTGCGCTGCCTTCATCTGGGTTTATCTTTGTCTCCTTC
CCACCCTCCCCCGCCTCAAAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTGAGAACTACATGCGTCAGC
AGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACGCCCGGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCG
CACCACCGGTGCGACGGCTGGGCCACGACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCT
ACCTGCGGAAATAACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCGTGG
CTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGCAGGGACAGGGACAGCCCA
GGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTTTGGGATGATTGCTCGATTGTTTGGTTTTTAAAT
CTGAGAAGCCTAGATAACTAATCTGCTTTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTC
TCTGGACTGAGCAAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTGACC
TGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCCAGAGCGAGCTTCCCCTCC
TCCCTGCTCTCCCAGGCCCCTGCCACAGCCTCTTTCCGTCCCTCTCTTTCTGATCCAGGCCCCTCAGTCCAAGCT
TTGGAAAACCTTCACCTCATCTTAAACCGAACTCAAATATATTTATTTTTTTACCATACCAACTTCTCTCCCATC
TCTAGGTGGCTCAGTCCATGGCCACTCCCTGCCCCCAGCCTGGCTGGACAGCAAGGAATCCACAGCCCACACGTG
AGCTCCCTCCTCACCCCCAGGCAGGGAAGCCCCTCCTGCCAGTCCCTGTCCCCTTTCAGCCCACCAGTCCCTCTC
TGCTGCCGGTGATGGGAGGCCTTTCTAGACCTGGCTCTTTCTCTCCCGTCTCAGTGGCTTCTCTGAGGTGCTGTA

FIGURE 169B

CACGCGCGTTAACCTGTTCCCTTCTCTATCCTTCCCCGTGGTACTGAGCTCACGTGGACTCCCAGTGCGAAGGGG
CCCATGGGTTGGGCTGCAGGCCTGGCCGTGAGCGGGGGCTGCCTGCACGCTCCCCTAGCCTACTCTTGTGTTTAG
GGGATGGTGGGAACATATCCCAGTGCCCTTGCCTCATAATAGATGTGGTGACTCTCCCGGTAGACCCTAGCAAGG
GTCCTCCATGGTGGTGAGGGACTCAGGAGAATTGTAGGGATTGGGGGACCCTGCCTGCCTGGCTTGAGAACAGCC
CTGCTGCCCTTTTGAGCCGAGATTTTGAAGTGGATGCCCGTCTTGCCAGAAATGCTGTTCTCACCAGAATGCCCC
CTCCCCTTGCCCTTACTGGACTTGGCCCTGCCTGATGCCAAGCAAAGACCCTTCCCCAGAGGCCTACCCCCCATA
TGTCCTCAGAGAGGCTGAGTGTCCCCTCCAGGCAGTCATGGGCCCTGAGGCCCCTCCTGCCTGGCCCTGCTCCCC
AGTGGGGAGGTGACTGTGTTTCCCAGAGTGTGAGCCGCTCTCCTCCCCCTAAAAAGCTGACTCACTGTGAGTGAC
CTTGGGCAAGTTCCCAAACCTCCTTGTGCCTCAGTTTCCCCATCTGGAAAAAATGGGGCCACCTCTTGCCAGCAG
TAGCAGGGCTGCCCACGCCCCTTTCTCCCCATGCCCCATCCAGCACTTGGGCGACTCATGCCTCTGCCTCAGTGG
GCCTGTGGGAGCCTACTGGAGCCCAGCACTTACTCCCCCTGAGCAGCGAGCCTGCGTCTGTCTCAGCTGTCCAGC
GCTGAGGGCCAGGGTCTTGTGCTGTGGGGCTGGGGGATGCCCTCTTTTCTATATTTATTTCATAGAAAGTCTCCT
GCGGGAGCGGAAATGCAGTCCGGCCTAGGGCTCCCAGCCCTTGACTGTCCTCCTGTGAGGGCCTGAAGCTGGGCC
AGGGCCCGTCGCAGCGGAGCCCCCTCTCAGCAGCCCACCGGGTCCCTCCAGGCTGCTGCCCGTGCGTGGTCTTTC
TCCTCCTTTTCAAAGCAATAGCCGCCGGGTCTGCAAAGCCCTGTCAGACAGACTGGGCCCTTCCAAGGTCAAGCC
ATGTGTCTGATGACATTCCTGGTGAAGCAAAGGAGAGGAGGATGGGTCAGCCCTCACTGGGTGTCACACACTGAG
AGAAGTCCTATTGTAAAGAAACGGAAAAAGTCACAAAAAAGTTTGTATAAAGACATATTTTTGTACTACATGGGG
ACTCTTCCTGCATGTCAGCAATAAAACTTCCTGATCTGG

FIGURE 170

MKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLARKDGTDDFYQLKILTLEERGD
QGIESQEERQGKMLLHTEYSLLSLLHTQDGVVHHHGLFQDRTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFS
DKTADLINLQHYVIKEKRLSERETVVIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFCLGKHLVS
EGDLLKDQRGSPAYISPDVLSGRPYRGKPSDMWALGVVLFTMLYGQFPFYDSIPQELFRKIKAAEYTIPEDGRVS
ENTVCLIRKLLVLDPQQRLAAADVLEALSAIIASWQSLSSLSGPLQVVPDIDDQMSNADSSQEVSWGGQMGHYPA
PRDRLLGAGRARAEVAATRRPQSFLGLLPQPWGGKGRLQSSA

FIGURE 171

ATTGGGACGCTGCGGCCTGGCCTTCAGGCCACTGGCTACCGAACCCCGGGGCTCTTCACCAGTCCAGCTCGTTTC
CAGCACC**ATG**TCGGTGCGGACGCTACCGCTGCTCTTCTTGAACTTGGGCGGGGAGATGCTTTACATCCTCGACCA
ACGGCTGCGGGCCCAGAACATCCCGGGAGACAAGGCCCGCAAAGTTCTGAATGACATCATCTCCACCATGTTCAA
TAGAAAGTTTATGGAGGAATTATTCAAGCCTCAAGAGCTCTACTCCAAGAAGGCCCTGAGGACTGTCTATGAGCG
CCTGGCTCATGCCTCCATTATGAAACTGAACCAGGCCAGCATGGATAAGCTCTATGACCTGATGACCATGGCTTT
CAAATATCAAGTATTGCTGTGTCCCCGACCCAAGGATGTGCTGCTGGTCACTTTCAATCACTTGGATACCATCAA
GGGATTCATCCGAGACTCCCCAACCATCCTGCAGCAAGTGGACGAGACTTTGCGGCAGCTGACAGAAATATATGG
TGGTCTCTCTGCAGGGGAGTTCCAGCTGATCCGGCAGACACTCCTCATCTTCTTCCAAGACCTGCACATCCGAGT
ATCCATGTTTCTAAAGGACAAAGTTCAGAATAATAACGGTCGCTTTGTGTTGCCGGTGTCCGGGCCTGTTCCTTG
GGGAACTGAAGTTCCAGGACTCATCAGAATGTTCAACAACAAAGGTGAAGAAGTGAAGAGGATAGAATTCAAGCA
TGGTGGAAACTATGTCCCTGCACCCAAAGAAGGTTCTTTTGAACTTTATGGAGACCGAGTCCTGAAACTGGGAAC
TAACATGTACAGCGTGAATCAGCCTGTGGAAACTCATGTGTCTGGATCATCAAAGAACTTAGCCTCATGGACCCA
GGAAAGCATTGCTCCAAACCCTCTTGCTAAAGAAGAGCTGAATTTCTTGGCCAGGCTGATGGGAGGGATGGAGAT
TAAGAAACCCAGTGGCCCTGAGCCCAGATTCCGGTTGAATCTCTTTACCACCGATGAAGAAGAGGAACAAGCAGC
GCTAACCAGGCCAGAAGAGTTATCCTATGAAGTTATCAACATACAAGCCACCCAGTCTCTTTTCAGCAATCTGGC
CACCATTCAGGGGGGCCTGACTGGG**TGA**CAGATGAATGGGAAGGTTCTGACCTGTTTTGAGTCCGGCTCCCACCT
TGCTGTCACATATCAGAATGTCACTGCTCTGAGTGTGTCCCAGGGCCTTGGAGGTGGGCCGTGAGGTGCCGAGAA
GCAGCCGCAGCCTCCTCCCTCCACCTATCCCAGAGCGATGCTGGTGATTTCAAACGTATCTGTCCTATCAGTAAA
TAAACAAGATGCAGATCTCTGGT

FIGURE 172

MSVRTLPLLFLNLGGEMLYILDQRLRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALRTVYERLA
HASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVLLVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGL
SAGEFQLIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGTEVPGLIRMFNNKGEEVKRIEFKHGG
NYVPAPKEGSFELYGDRVLKLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNFLARLMGGMEIKK
PSGPEPGFRLNLFTTDEEEEQAALTRPEELSYEVINIQATQSLFSNLATIQGGLTG

FIGURE 173

GAAGCTGGACTGCAGCTGGTTTCAGGAACTTCTCTTGACGAGAAGAGAGACCAAGGAGGCCAAGCAGGGGCTGGG
CCAGAGGTGCCAACATGGGGAAACTGAGGCTCGGCTCGGAAAGGTGAAGTAACTTGTCCAAGATCACAAAGCTGG
TGAACATCAAGTTGGTGCT**ATG**GCAAGGCTGGGAAACTGCAGCCTGACTTGGGCTGCCCTGATCATCCTGCTGCT
CCCCGGAAGTCTGGAGGAGTGCGGGCACATCAGTGTCTCAGCCCCCATCGTCCACCTGGGGGATCCCATCACAGC
CTCCTGCATCATCAAGCAGAACTGCAGCCATCTGGACCCGGAGCCACAGATTCTGTGGAGACTGGGAGCAGAGCT
TCAGCCCGGGGGCAGGCAGCAGCGTCTGTCTGATGGGACCCAGGAATCTATCATCACCCTGCCCCACCTCAACCA
CACTCAGGCCTTTCTCTCCTGCTGCCTGAACTGGGGCAACAGCCTGCAGATCCTGGACCAGGTTGAGCTGCGCGC
AGGCTACCCTCCAGCCATACCCCACAACCTCTCCTGCCTCATGAACCTCACAACCAGCAGCCTCATCTGCCAGTG
GGAGCCAGGACCTGAGACCCACCTACCCACCAGCTTCACTCTGAAGAGTTTCAAGAGCCGGGGCAACTGTCAGAC
CCAAGGGGACTCCATCCTGGACTGCGTGCCCAAGGACGGGCAGAGCCACTGCTGCATCCCACGCAAACACCTGCT
GTTGTACCAGAATATGGGCATCTGGGTGCAGGCAGAGAATGCGCTGGGGACCAGCATGTCCCCACAACTGTGTCT
TGATCCCATGGATGTTGTGAAACTGGAGCCCCCCATGCTGCGGACCATGGACCCCAGCCCTGAAGCGGCCCCTCC
CCAGGCAGGCTGCCTACAGCTGTGCTGGGAGCCATGGCAGCCAGGCCTGCACATAAATCAGAAGTGTGAGCTGCG
CCACAAGCCGCAGCGTGGAGAAGCCAGCTGGGCACTGGTGGGCCCCCTCCCCTTGGAGGCCCTTCAGTATGAGCT
CTGCGGGCTCCTCCCAGCCACGGCCTACACCCTGCAGATACGCTGCATCCGCTGGCCCCTGCCTGGCCACTGGAG
CGACTGGAGCCCCAGCCTGGAGCTGAGAACTACCGAACGGGCCCCCACTGTCAGACTGGACACATGGTGGCGGCA
GAGGCAGCTGGACCCCAGGACAGTGCAGCTGTTCTGGAAGCCAGTGCCCCTGGAGGAAGACAGCGGACGGATCCA
AGGTTATGTGGTTTCTTGGAGACCCTCAGGCCAGGCTGGGGCCATCCTGCCCCTCTGCAACACCACAGAGCTCAG
CTGCACCTTCCACCTGCCTTCAGAAGCCCAGGAGGTGGCCCTTGTGGCCTATAACTCAGCCGGGACCTCTCGCCC
CACCCCGGTGGTCTTCTCAGAAAGCAGAGGCCCAGCTCTGACCAGACTCCATGCCATGGCCCGAGACCCTCACAG
CCTCTGGGTAGGCTGGGAGCCCCCCAATCCATGGCCTCAGGGCTATGTGATTGAGTGGGGCCTGGGCCCCCCCAG
CGCGAGCAATAGCAACAAGACCTGGAGGATGGAACAGAATGGGAGAGCCACGGGGTTTCTGCTGAAGGAGAACAT
CAGGCCCTTTCAGCTCTATGAGATCATCGTGACTCCCTTGTACCAGGACACCATGGGACCCTCCCAGCATGTCTA
TGCCTACTCTCAAGAAATGGCTCCCTCCCATGCCCCAGAGCTGCATCTAAAGCACATTGGCAAGACCTGGGCACA
GCTGGAGTGGGTGCCTGAGCCCCCTGAGCTGGGGAAGAGCCCCCTTACCCACTACACCATCTTCTGGACCAACGC
TCAGAACCAGTCCTTCTCCGCCATCCTGAATGCCTCCTCCCGTGGCTTTGTCCTCCATGGCCTGGAGCCCGCCAG
TCTGTATCACATCCACCTCATGGCTGCCAGCCAGGCTGGGGCCACCAACAGTACAGTCCTCACCCTGATGACCTT
GACCCCAGAGGGGTCGGAGCTACACATCATCCTGGGCCTGTTCGGCCTCCTGCTGTTGCTCACCTGCCTCTGTGG
AACTGCCTGGCTCTGTTGCAGCCCCAACAGGAAGAATCCCCTCTGGCCAAGTGTCCCAGACCCAGCTCACAGCAG
CCTGGGCTCCTGGGTGCCCACAATCATGGAGGAGGATGCCTTCCAGCTGCCCGGCCTTGGCACGCCACCCATCAC
CAAGCTCACAGTGCTGGAGGAGGATGAAAAGAAGCCGGTGCCCTGGGAGTCCCATAACAGCTCAGAGACCTGTGG
CCTCCCCACTCTGGTCCAGACCTATGTGCTCCAGGGGGACCCAAGAGCAGTTTCCACCCAGCCCCAATCCCAGTC
TGGCACCAGCGATCAGGTCCTTTATGGGCAGCTGCTGGGCAGCCCCACAAGCCCAGGGCCAGGGCACTATCTCCG
CTGTGACTCCACTCAGCCCCTCTTGGCGGGCCTCACCCCCAGCCCCAAGTCCTATGAGAACCTCTGGTTCCAGGC
CAGCCCCTTGGGGACCCTGGTAACCCCAGCCCCAAGCCAGGAGGACGACTGTGTCTTTGGGCCACTGCTCAACTT
CCCCCTCCTGCAGGGGATCCGGGTCCATGGGATGGAGGCGCTGGGGAGCTTC**TAG**GGCTTCCTGGGGTTCCCTTC
TTGGGCCTGCCTCTTAAAGGCCTGAGCTAGCTGGAGAAGAGGGGAGGGTCCATAAGCCCATGACTAAAAACTACC
CCAGCCCAGGCTCTCACCATCTCCAGTCACCAGCATCTCCCTCTCCTCCCAATCTCCATAGGCTGGGCCTCCCAG
GCGATCTGCATACTTTAAGGACCAGATCATGCTCCATCCAGCCCCACCCAATGGCCTTTTGTGCTTGTTTCCTAT
AACTTCAGTATTGTAAAC

FIGURE 174

MARLGNCSLTWAALIILLLPGSLEECGHISVSAPIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQ
QRLSDGTQESIITLPHLNHTQAFLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGPET
HLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVV
KLEPPMLRTMDPSPEAAPPQAGCLQLCWEPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYELCGLLPA
TAYTLQIRCIRWPLPGHWSDWSPSLELRTTERAPTVRLDTWWRQRQLDPRTVQLFWKPVPLEEDSGRIQGYVVSW
RPSGQAGAILPLCNTTELSCTFHLPSEAQEVALVAYNSAGTSRPTPVVFSESRGPALTRLHAMARDPHSLWVGWE
PPNPWPQGYVIEWGLGPPSASNSNKTWRMEQNGRATGFLLKENIRPFQLYEIIVTPLYQDTMGPSQHVYAYSQEM
APSHAPELHLKHIGKTWAQLEWVPEPPELGKSPLTHYTIFWTNAQNQSFSAILNASSRGFVLHGLEPASLYHIHL
MAASQAGATNSTVLTLMTLTPEGSELHIILGLFGLLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPAHSSLGSWVP
TIMEEDAFQLPGLGTPPITKLTVLEEDEKKPVPWESHNSSETCGLPTLVQTYVLQGDPRAVSTQPQSQSGTSDQV
LYGQLLGSPTSPGPGHYLRCDSTQPLLAGLTPSPKSYENLWFQASPLGTLVTPAPSQEDDCVFGPLLNFPLLQGI
RVHGMEALGSF

FIGURE 175

GGGTCGCGCGGAGATTGCTGGGCGGTTCTTGCCGGAAGCGGAGAGCGGCTGATCGCAGTCCGGAGGTGAGGCGGA
ACTCTGAGGCAGATATCCTCCCTTTCCTCCTCGGCTGCTGCTCTTACTTTGACAAGCCAGGCTAACATTGAAGGT
GGTCCATTATGGCTGACATGCAAAATCTGGTAGAAAGATTGGAGAGGGCAGTGGGCCGCCTGGAGGCAGTATCTC
ATACCTCTGACATGCACCGTGGGTATGCAGACAGTCCTTCAAAAGCAGGAGCAGCTCCATATGTGCAGGCATTTG
ACTCGCTGCTTGCTGGTCCTGTGGCAGAGTACTTGAAGATCAGTAAAGAGATTGGGGGAGACGTGCAGAAACATG
CGGAGATGGTCCACACAGGTTTGAAGTTGGAGCGAGCTCTGTTGGTTACAGCTTCTCAGTGTCAACAGCCAGCAG
AAAATAAGCTTTCCGATTTGTTGGCACCCATCTCAGAGCAGATCAAAGAAGTGATAACCTTTCGGGAGAAGAACC
GAGGCAGCAAGTTGTTTAATCACCTGTCAGCTGTCAGCGAAAGTATCCAGGCCCTGGGCTGGGTGGCTATGGCTC
CCAAGCCTGGCCCTTATGTGAAAGAAATGAATGATGCCGCCATGTTTTATACAAACCGAGTCCTCAAAGAGTACA
AAGATGTGGATAAGAAGCATGTAGACTGGGTCAAAGCTTATTTAAGTATATGGACAGAGCTGCAGGCTTACATTA
AGGAGTTCCATACCACCGGACTGGCCTGGAGCAAAACGGGGCCTGTGGCAAAAGAACTGAGCGGACTGCCATCTG
GACCCTCTGCCGGATCATGTCCTCCTCCCCCTCCACCATGCCCCCCTCCTCCCCCAGTCTCTACCATTTCATGCT
CATATGAGTCTGCTTCCCGCTCATCACTGTTCGCGCAGATTAATCAGGGGGAGAGCATTACACATGCCCTGAAAC
ATGTATCTGATGACATGAAGACTCACAAGAACCCTGCCCTGAAGGCTCAGAGTGGTCCAGTACGCAGTGGCCCCA
AACCATTCTCTGCACCTAAACCCCAAACCAGCCCATCCCCCAAACGAGCCACAAAGAAGGAGCCAGCTGTACTTG
AACTGGAGGGCAAGAAGTGGAGAGTGGAAAATCAGGAAAATGTTTCCAACCTGGTGATTGAGGACACAGAGCTGA
AACAGGTGGCTTACATATACAAGTGTGTCAACACGACATTGCAAATCAAGGGCAAAATTAACTCCATTACAGTAG
ATAACTGTAAGAAACTTGGCCTGGTATTCGATGACGTGGTGGGCATTGTGGAGATAATCAACAGTAAGGATGTCA
AAGTTCAGGTAATGGGTAAAGTGCCAACCATATCCATCAACAAAACAGATGGCTGCCATGCTTACCTGAGCAAGA
ATTCCCTGGATTGTGAAATAGTCAGTGCCAAATCTTCCGAGATGAATGTCCTCATTCCTACAGAAGGCGGTGACT
TTAATGAATTCCCAGTTCCTGAGCAGTTCAAGACCCTATGGAACGGGCAGAAGTTGGTCACCACAGTGACAGAAA
TTGCTGGATAAGCGAAGTGCCACTGGGTTCTTTGCCCTCCCTTCACACCATGGGATAAATCTGTATCAAGACGGT
TCTTTTCTAGATTTCCTCTACCTTTTTGCTCTTAAAACTGCTTCTCTGCTCTGAGAAGCACAGCTACCTGCCTTC
ACTGAAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAAGGTGCAGCTTT
TCCATATCAGCTCAACCACGCCGCCAGTCCATTCTTAAGGAACTGCCGACTAGGACTGATGATGCATTTTAGCTT
TGAGCTTTTGGGGGTTATTCTACCAACAAACAGTCCATTGGAAAGAAAACAGTCCCTGGAATTAACAGATCAGAA
TGTTCACACTGGTTAATCTTTTTTTAACAATGAGCATGAAGGTAGCAGAAGCTGGTGTGTTTCCAGATGGTTCTT
CTAACCAAACTAATTTTTCACTGTTGACAAGCGAGGCAAGGGTTGCACTGGACCAAAGGCTGAGGCTTGGCCATC
TAGCATTCCATACAAAATTGTTTCCTATAAGCATTCCTTTTATTCTCTATTCTATCCTGGGTCTGCCTCAACCGT
GAGATAGGAGAGTCTCTGGTACTAGCTGCTGTAGCAGTGCCCTTCATCCAGGGCAGTTAATGGAGTCTTGGACCC
TTTCTTTCTCTGGGATCCCTGCCCAGCACCTTCCTATAGAGATGACTTTAAAAGGAAAAAAAAAAAAAAAAAAAC
CCACATGATTTCAAGGAGTCTGGCATTCCTGAATCCTTCTTCCCTGCCAGGTGCCTGTCACCTGTCTTCACTGCC
TCCTTTTCCCTGTCATGCTCATCAGCTTATGGCTTCTGTCTAAGCACCTGAACAGAGGACTGAAACCTCCACTGC
AGGCTGGTTTTAGGTCTTGAATTATGTAAGAATCTTGCACAGCACTGCTAATGTAAATTTCAGTTGTTTTTCCCT
CTAGGACAAACACTTACCAAAATATGCAACTTTTTTTTGGTGGGAAGAGAGATTGTCCTGTGATTTCTACCCATT
TCCTGAGGCCTGTGGAAATAAACCTTTATGTACTTAAAGTTATACAGAAAATAGAATAAAGTTAATACCAAACTT
G

FIGURE 176

CCGGAGTCTCGCGCCCGCGGTCATGTGACACAGCGAAG**ATG**GCGTCGCCCGGCTGCCTGTGGCTCTTGGCTGTGG
CTCTCCTGCCATGGACCTGCGCTTCTCGGGCGCTGCAGCATCTGGACCCGCCGGCGCCGCTGCCGTTGGTGATCT
GGCATGGGATGGGAGACAGCTGTTGCAATCCCTTAAGCATGGGTGCTATTAAAAAAATGGTGGAGAAGAAAATAC
CTGGAATTTACGTCTTATCTTTAGAGATTGGGAAGACCCTGATGGAGGACGTGGAGAACAGCTTCTTCTTGAATG
TCAATTCCCAAGTAACAACAGTGTGTCAGGCACTTGCTAAGGATCCTAAATTGCAGCAAGGCTACAATGCTATGG
GATTCTCCCAGGGAGGCCAATTTCTGAGGGCAGTGGCTCAGAGATGCCCTTCACCTCCCATGATCAATCTGATCT
CGGTTGGGGGACAACATCAAGGTGTTTTTGGACTCCCTCGATGCCCAGGAGAGAGCTCTCACATCTGTGACTTCA
TCCGAAAAACACTGAATGCTGGGGCGTACTCCAAAGTTGTTCAGGAACGCCTCGTGCAAGCCGAATACTGGCATG
ACCCCATAAAGGAGGATGTGTATCGCAACCACAGCATCTTCTTGGCAGATATAAATCAGGAGCGGGGTATCAATG
AGTCCTACAAGAAAAACCTGATGGCCCTGAAGAAGTTTGTGATGGTGAAATTCCTCAATGATTCCATTGTGGACC
CTGTAGATTCGGAGTGGTTTGGATTTTACAGAAGTGGCCAAGCCAAGGAAACCATTCCCTTACAGGAGACCTCCC
TGTACACACAGGACCGCCTGGGGCTAAAGGAAATGGACAATGCAGGACAGCTAGTGTTTCTGGCTACAGAAGGGG
ACCATCTTCAGTTGTCTGAAGAATGGTTTTATGCCCACATCATACCATTCCTTGGA**TGA**AACCCGTATAGTTCAC
AATAGAGCTCAGGGAGCCCCTAACTCTTCCAAACCACATGGGAGACAGTTTCCTTCATGCCCAAGCCTGAGCTCA
GATCCAGCTTGCAACTAATCCTTCTATCATCTAACATGCCCTACTTGGAAAGATCTAAGATCTGAATCTTATCCT
TTGCCATCTTCTGTTACCATATGGTGTTGAATGCAAGTTTAATTACCATGGAGATTGTTTTACAAACTTTTGATG
TGGTCAAGTTCAGTTTTAGAAAAGGGAGTCTGTTCCAGATCAGTGCCAGAACTGTGCCCAGGCCCAAAGGAGACA
ACTAACTAAAGTAGTGAGATAGATTCTAAGGGCAAACATTTTTCCAAGTCTTGCCATATTTCAAGCAAAGAGGTG
CCCAGGCCTGAGGTACTCACATAAATGCTTTGTTTTGCTGGTGATTTAACCAGTGCTTGGAAAAATCTTGCTTGG
CTATTTCTGCATCATTTCTTAAGGCTGCCTTCCTCTCTCAGTACGTTGCCCTCTGTGCTATCATCTTATCATCAA
TTATTAGACAAATCCCACTGGCCTACAGTCTTGCTTCTGCAGCACCCACTTTGTCTCCTCAGGTAGTGATGAATT
AGTTGCTGTCACAAAAGGAGGGAAGTAGCACCCAAATTAAGTTGCTTAAGAGAGGAAATGTACATCTTGTATAAC
TTAGGGAGCGAAGAAAATGTAGGCGCGAAAGTGAAAAGTGAGGCAGCTAGTTCTTCCTATTCCATTCTCGACCAA
CCTGCCCTTTCTTAATATGACTAGTGGTCTTGATGCTAGAGTCAACTTACTCTGTTGCTGGCTTTAGCAGAGAAT
AGGAGGAACCATATGAAAAAGATCAGGCTTTCTGACTTCCATCCCCAAAACACATTTACCAGCATACTCCAAACT
GTTTCTGATGTGTTCCATGAGAAAAGGATTGTTTGCTCAAAAAGCTTGGAAAATACTACACACTCCCTTTCTCCT
TCTGGAGATCAACCCACATTAGAGTGTCTAAGGACTCCTGAGAATTCCTGTTACAGTAAACAAAACTAACGTAAT
CTACCATTTCCTACACTATTTGAGCATGGAAATCATAGTCCCCACTCTGTGAAAACTTAACGCTTTTTGGAAGAC
ATTTCTGTAGCATGTCAGTTTGGAGAAATGATGAGCTACGCCTTGATGAAAGAACCGTGTTGGTGCTGCTAAGTT
TAGCCATTATGGTTTTTCCTTTCTCTCTCTTAAGCCTTATTCTTCAACTAAAAGATGAGGATTAAGAGCAAGAAG
TTGGGGGGGATGTGAAAATAATTTTATGAGGTTGTCTAAAAT

FIGURE 177

MASPGCLWLLAVALLPWTCASRALQHLDPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIYVLSLEIGKT
LMEDVENSFFLNVNSQVTTVCQALAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMINLISVGGQHQGVFGLP
RCPGESSHICDFIRKTLNAGAYSKVVQERLVQAEYWHDPIKEDVYRNHSIFLADINQERGINESYKKNLMALKKF
VMVKFLNDSIVDPVDSEWFGFYRSGQAKETIPLQETSLYTQDRLGLKEMDNAGQLVFLATEGDHLQLSEEWFYAH
IIPFLG

FIGURE 178

CCTTACGGCCAGAAACGCCACCTTCCAGTAATTCGCCAAA**ATG**ACAAACACAAAGGGAAAGAGGAGAGGCACCCG
ATACATGTTCTCTAGGCCTTTTAGAAAACATGGAGTTGTTCCTTTGGCCATGTATATGCGAATCTATAAGAAAGG
TGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGGAATGTCCCACAAGTGTTACCATGGCAAAACTGG
AAGAGTCTACAATGTTCCCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAA
GAGAATTAATGTGTGTATTGAGCACATTAAGCACTCTAAAAGCCGAGATAGCTTCCTGAAACGTGTGAAGGAAAA
TGATCCTCCACCCAGAGAAGCACAGTGTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAAACTATTCCCTA
TGAATTCATGGCA**TAA**TAGGTGTT

FIGURE 179

MTNTKGKRRGTRYMFSRPFRKHGVVPLAMYMRIYKKGDIVDIKGMGTVQKGMSHKCYHGKTGRVYNVPQHAVGIV
VNKQVKGKILAKRINVCIEHIKHSKSRDSFLKRVKENDPPPREAQCVRTNGKEPELLETIPYEFMA

FIGURE 180A

CGGACGCGTGGGCTGCTGCGGAGCCGGCAGCGCAGGCGGGCGGAGCGGAGCTGCCCCCGTGGTGGCGGGCGATGC
CCCCGTGAGCCTCCCTCGCCGCCCCTCCCCGCCCCGCGTGCCTATCCACTCGGAGTCCGCGCCAGCCTGGGGCCG
GGCCGCGCCTACTGCCGGGTTCGCGGGGCGGGGTCCCGGGGCAGCACCTGCCCCGCCTTGCGGAGCCGCCTCGGC
CTGTGGAGGCCCCCTCCCTGTCTGGACCCCGGCCCCACCTCCGGACCCTTTTATCACATCGCCTCCTCTGGGAGC
CTGCCCTGATTGCCTTCACCTCATTTCTTGAAAATTGGTGTTTTGGCAGAAGTCAATTGAAGCCTTGTGCAAATG
CCCTAGGGGTGTGCTGTTGGGAGGCAGCCCCCTGTGATGCGGAACACCAGGCTCAGATTCATCAGTTCGAGCTGC
CTGAGGCCCTGCCACCCCGGGGACC**ATG**TTTAACGGGGAGCCAGGTCCTGCCTCATCTGGGGCCTCCAGGAATGT
GGTGCGGAGCTCCAGCATTGGCGGTGAAATCTGCGGATCCCAGCAAGCCGGGGGCGGGGCTGGGACCACCACCGC
CAAGAAGCGGCGGAGCAGCCTGGGTGCCAAGATGGTGGCCATCGTGGGCCTGACTCAGTGGAGCAAGAGCACACT
CCAGCTTCCGCAGCCTGAAGGGGCCACCAAGAAGCTGCGCAGCAACATCCGCCGGAGCACGGAGACAGGCATCGC
GGTGGAGATGCGGAGCCGGGTCACACGCCAGGGCAGCCGGGAGTCCACCGATGGGAGCACCAACAGCAACAGCTC
CGACGGCACGTTCATCTTCCCCACTACCCGGCTAGGGGCTGAAAGCCAGTTCAGCGATTTCCTGGATGGGCTGGG
ACCAGCTCAGATTGTGGGGCGACAGACACTGGCAACACCACCCATGGGAGATGTGCACATTGCCATCATGGACCG
GAGTGGCCAGCTGGAGGTGGAAGTGATTGAAGCTCGGGGCCTGACCCCCAAACCAGGCTCCAAATCCCTCCCAGC
CACCTATATCAAGGTTTACCTGCTGGAGAATGGGGCCTGCTTGGCCAAGAAGAAGACAAAGATGACCAAGAAGAC
CTGTGATCCCCTGTACCAGCAGGCTCTGCTCTTTGACGAGGGACCCCAGGGCAAGGTGCTGCAGGTGATCGTCTG
GGGAGACTATGGCCGCATGGACCACAAGTGCTTCATGGGCATGGCCCAGATCATGCTGGACGAGCTGGACCTCAG
CGCCGCGGTCACCGGCTGGTACAAACTCTTCCCCACCTCCTCAGTGGCAGACTCCACACTCGGATCCCTCACCAG
GCGCCTGTCCCAGTCTTCCCTGGAGAGTGCCACCAGCCCCTCATGCTCT**TAA**GGATGTCAGGAAGAGGCCAGGAT
GGTGGTGTGGGGAGGGGTGCCTGCTGGCCCCATGTCCTCCCCTGTACATAGTCTTCGTGTCTTTCTGGACCCCTT
GTCCTGCTGCATGCCTGTTGGCTACTGGGCTCATCCCAGCTGGCAGTGGAGACTGTAGTGTGTGCGTGTGTGCGT
GCGTGTGTGTGTGTGTGTACGTGACCACGTTCTATCTGTTCATTTGTCTGGGTATAGTCACTCCTGGTGATGATA
TGGGCTGAAATGTCTCCACGTCTCTTTGTGTCTTGTTGAAAAGAAACCCAAAGGAGTGTTGTGTGGACATGACTC
ACCCTGAGGAGTCTCCAGGGATGGAGGTGGGGCATGCGGCCACTGGTCGGTGCTGCCTGGTCCTGGCCTGGGGCA
GAGCCTGTGTGTTCTTCACCTGTGCCTGCTCCTGGTGGTCTCTGCTTTGTTTTCTGTCTTGTCTTTTGTTCCACT
CTTGACTCTCCCGGCTCTGCCACTGTTTTCTGAGAAATGTAGCATCCGCTGCAGCTGGCCACACTGAGGGCCCTC
TGGGAACCCCACCCCACTGGAGCCGCTCCGGCAGCTCTTCCTGCCACTGAATGCGTTCTGCAGCATGTAGCATGC
CCACCTAGCTCCCTGGCCAGGGCCCTGGGGAGGCAGAGGGTACCCAGGGGACTGAGGGCTTAGAAATGACTTTCT
CTATGAGGCTGGAACCTCCTCCTTCTTCCAGTGAAGCACGAGGTCTTGGTTCCAGGGTTCCTGGCCAGGTGCCCC
CTTAGCATTTGTTCTTCATCTCCTGTCTCTTCAAGCCTCCCCACTCCACCGTGCCGAAGGAGCTCTGCCAGTGGG
CCTGGGCAGGCAGCCACAGAGGGCATGTTATCTGCTAAAGCAAACAGTCCTCCTGAGGCCCTGAGGGTGGCCCTG
ACCCCCTCAGGGCTCATTCCTGGTGGGCATGACTCGGTAAGGAGGTTCTGTGGGTAGGGCTGTTTGCTGGAATAA
GGAGGGCTGAGGCTGAGTTGTTCCCCGCCACTGTTGAGGATCCCATCTGACATTTGGGGATTCACTGCATGAAGT
TGTTCATTTGGGGCTCCAGTTTTTGTGCATTTCCAGACCAGGGTCCCTGTCTGGGAGCTCAGACTTAGCTGGGCT
CCAGCAGCCTGGCTCCGGACTCTCGTCTGCCACCATCACCAGCTCTGTCTAAGCAATACTTACCCCTCCGGGCTT
CCCTGCTTTCCTGTGCCCCACTGCTGCCCTCTGCAGAGCCATCTGCTCCAGGCACCCACCTGCCTCTGCTTGCTT
TCTCACCCATGTCTGGTTGGAGCTTCTCACAGCCACTCAAACCCTGACTTGATTTGACAACTGGGCCCTGTTGGT
GGAGACCAGTGCCTGAACTGGACCCTGTGAAATCTGTCCCGTGGGAATCCTGAAGTCTGACTCAGGAATGCCCAG
ACCTGTCCCTGTCCCTCCTCAGCTCTAGGGTGAAAGGCGAGAGGTTGCACAGGACATGGACAGAGCAGCCCTTGG
GTTTGTATCTGGTAGGGGAGAAAGCAGCAGGACAGTGGAGGTGTGTGGAAGGCACTCTTTCCACCTCTCTCCAGG
CATTATCCCCAGGTGCTGAAATGGCTGTGGCCCCAGCACCTGAGGCAGGGGTACGCTACCTGGGGTAGCAGTAGA
AAGGTCTTGGGGTCTGAATGACTTGGGGCCTCCATTCATAACCAAAGTTGTAGGGGCATGGAGGCAGTGGCGCCT
TATGGATAGGTCATCTCAGCCCAAAGGGCCTCCTTGGCTGGCATGGTTCTGTGTTACGTTGAAGCCAGAGTCTTA
TAACACCTCCCAAGAAAGATAGGGGAAGAAGCCAGAACCCCACCTGGCCTGCCCACAGGACAAGAAGTGGGTAAG
GGCAGGAAGGAAATGAACGGAGTTAGCTCCCAGGCTCCTATCTCTGCCTGAGCCTCTATTCTTATATTATCAGAG
AAAGGGACCATTGGGTGCATAGAGATGGGGAGGAGGCCACTGGGCTGAATTTTCTCTTTAGGCGGAAATGCTCTC
CCCAGGCCCATTGCGTTCGTCAAGTTCTTGGAAATGGACAAAGGGCTCTGTCCTCCTCGACCCTAGTGGGGGATC
AAGAAGGAAACTCCGTTGCAAAAGGGTATTTTAATCTCCTGTTTATGATATATTCACCTCTAGAGCAGTCACTGT

FIGURE 180B

CAGGGTGTTGCGAAAATACTCTACACCTTTGGGATGATAGGGTTGTTAGTGACCCACAGGACAGTATAGATGTTT
GTGGATGTAGCACTGAGTGGTGATACCCAGACCAGCAGTCACCCCAGGAAGTGGGGGCTACCCATACCCTCATTC
CTCTGGTGGGGAGCTGCCTGCAGAGAGGCCTGCCACTGGGGGTTCCAGGCCGTGGTGACCCTTGCCTCTGGGGAA
GGGTTAGCACAGGGGAGGTTCTAGCTGGAGGAGGGGTCTGATGTGCTGGTAACTTGGGCTGACCTACCTACAGTC
CCTGGCTGCCAAAACTGCTCAGCAGTTGGGCCACTCCACTATTCCACCTCTCTAAAAGAAGGTAATTTCCTCCCC
AAATTGACCTTGGGGAATTATTCTTTTAACCCTTTGCACCAAATAAGTTACTCATCCCCACCTGGATTTTACCCC
ATGAGGGTAAAGTTGTGTGAGGCTGACACGTCTGTGTGATGCAGTGTGGCTGCACTTAAGGGTCTGTTTCTCAGC
ATCATGGATGCAGGGGCTTGTCTGAAAAGCCACTCTGGACCTAGCCTGTCCCAGAAGAGGAGAATGCACAAGTGT
AACTCCTGGTTGTTTGCTGGGGTGGGGGAGCATCTGCTGTTTGAGGACGGGGGGTGGGGAAGGAAGGAACATGAT
CCCTCCAGAAGTCTCCCACCCTGGGGCCAACTCACTGCCATGTTCAGTGTCCCGGCTCCAAATGCCCCCTTGCCC
AGATGAAACCCTGCAGTGGTTACAGGAATGGAGCTCTTTGTCATTCCACCTCCTCTGGTCAGGCGAGGTTCACTG
TGCATATGGCAGAGACAGGAGTGGCCCTGCAGTGATGTTGGGTTGTGGGCAGGGACAGTGATGGATGACTCAGAG
CGTCTGTCTTTGTATTTCTGCTCTGTTCATTCTGTCCCACTTTCTTCATAGACTCCTTTTCCCTGCAATGGGTTT
TTGGTATGAAAAAGGCTCCAGTAAATGGAGCCAAGTCTTGGTTTGACAAGGGGAACTTGATCCTTCAGGGAAGAA
TCATCTCCAAAATGACTCCCCATCTGGTTTCTTCTACCACCCAATTCTACTAGGAAAGGAGCACTTAGGAGGCTC
TTGGGATGCAGCAAGTCCCAGGCAATGCCAGCATTTCATGGGGGCTGAGGCAGAACCCAGGAGCTCCAAGAAAGG
CCACCCATAGAGCTCATCCTCTGTGGAATCACTGCCGGTTAGAACACTGAGGTCAAGCCAGTCCTCCCATGGTCA
TGCCACCCACCAGGGAAGCATGCCTGATCTCTTCTTTACTGCCAGCCTTGAGGAGAGCAGAAGCCTCCATTTTTA
AAGACAATAAAGACCTCCAAGGGTACTTCTTTGGAAATGAAATGTAGCACAATCTTAGCCTACGTTACCAGGAGC
CCTGACATGCAACCAGGGTCCCTCTTCCATGCCCTGCTGCCCAGGAGTTGCTGAGCTCCTCTTCCCCTGGGGTTC
CAGCCCTCCTAATACCTCATATTCCCCATCTTCCTCAGCCCAGAAAGCAATGGGGCTTTAGTGATGCTCCTCTTT
TGTGTCTCTCTGGTTGCCTCTAGCACTGTGCAAACTCTGCAAGAAATTGCTGCCTTTGCTTGATGTTGTAGATGA
GTTGCCCTCCACCTGGCTGGAGAGATGGCACATCATTCAGGGCCAGAAGGTTGTCCAGCAGTGTTTCTGCAGTGG
CTGCAGGGAGATGGAAAAGAAGAGCCCTGCTTCCCTGCCTCCTCCTACCTTTCTCTTCCACTCCTCAGAGTTTTC
TTCTCCAGTATCCTGACATGTAAAGAGATTCTTTAAAATGCTGCTTCTTCTACTGGACTGTCTTTCACTGAGTAG
TCAGGGAGGAGATGAAAATGTGGACACATCCCCCCGCCTTCTCCCTCAACCTTTTCACTCACGTCAGAAGAGGTT
GGGGCAAAACAAAACAAGCATGATTGAAGAGCAGGGGAAGCCCACACAATCAGGTGAGCCCTGATGGGGGCTGGA
CTGGCCTGGTCTGGCTGGGAAAGGATTCTTTTAAAAGCGTGCCTGAGCATCTCAGAGCAATGTCAGTGATGCCAA
AGAGAGCAACTTGGCCTCCTTGGGCACCAACTCTGATGGCTGAGTTGCACAAACGTGGCTCAGATGTTGGCATGC
CCGATGGTGGGACCTTGTTCTCTGATAAAGGGCTTAATCTTTCCATGTAGCAAAGCAACTTTCCCTCCCTCCCCT
CCCCCCGAACCCTGAGCTTGGGCTTGTGTGGGCCCAGCATGGCTGTGCCTGTGAGGGAAGCCACATCAGTGAGAG
AAAGTTGCATTCTCTCAGGGGCCTAGATTGGCTTGGGGCAGGTGCTTGTTGAAAAGCATGAGTGTTTCTGCTTTG
GGAAACCCTTCCAGGGCTCTGGTTGGAAACTTGGCCAGTAAGGACAGGGCCTTGGGCCTCCCAAGGAGTTCACAA
TGATGCCAGGAAGGGTCCCTGAGCCTGGGTTCCAGTCAGCTTGGCTAACAGAATGGGGCTTGGGAATTCCAGGGG
CAACTGAGCATCCACCCCATTAGCCAGTGATCTGGACAGGGACAGCTGGCTACAGGGAATCAAAGGCTGTTCTGT
ACAGTTTTACCAGAAACTGTGACCTTGGGTAAGGCTCCTCACTTTTCTGGGCCTCAACTTCCTCATCTGCAAAAT
CAGAGCATTAGCTGCTCTCCCCATGATTCCCTCCCAGTTTTAATTAAAAGTCTCTGATCTGGAGCACATGAGGGT
TGCGAGCCTGGTGCACCTGGTTCCTGTCTCCGTGGGCTGGTTTCCTTCAGCCCCTGATGCCCAGGCTGGGTGCAG
GCTCTCATCTGGTCCATGCCCAGATGCTGCCTCAGACAAGAACTCTGGGAATCCTAACAGACTCTGCTTTCCTCT
CTTCGTGGTTTGTCCTCCCTCTTTTATTCTTGTGTAATGATGAGACATAATTAAGGGTCATCTACAATGGACAAT
TTTCAAGGTGCTGATGTGATGTCACAACCTCCGCTACATCCTGAGTAAGTCAGTGTCCCCAACAGCAGATGAGGC
TGGGTCTTTCCTCATTTCTGCTTCTGGGATGACATCAGTGGGAGAGTTGAAGATCTGAGAATTCTAAAGGAAATG
TTCTCTGATGGGAGGAGAGAGGGAACTTATTTCCCTTCAAAGTAGTTTGCTTCTTAAGACCACTCCTCCCTCCAG
AATGTCTTTAACCAGACATCATTTCAGAAGGTGGGGCAGCTGCTTCCTTAGGAAGAGTGGGCCTGATAGCTCAAC
CAACTCCTTTAGCATGTAAACTCACAGAAGGCAAGAACCCCTTTTTTTAGACTTTCCAAATGCATCCTGCAAAGA
GAGAGATAGCTGATAGGGACTGACAAGCACACTGTTTAGATAAGAAGCAATTACCCTTTTATATCTGTGCTCTAT
ACATTTTCTATGTGCAGCATCTTTCCTAACTTGTTGTGGTTCCCGGGTGGCAGGTGCACAGCTGGGAGGGACTGC
CGGCTGTTTCGTACAACATTCTTGCCAATTCCCTTGAGGAGAAAATTCTTCACATGGCTTCTGCATGTACAGTAT

FIGURE 180C

TTGGGCAGCAAAACATGATTAAAGTCAGTTTGAAAATGG

FIGURE 181

MFNGEPGPASSGASRNVVRSSSIGGEICGSQQAGGGAGTTTAKKRRSSLGAKMVAIVGLTQWSKSTLQLPQPEGA
TKKLRSNIRRSTETGIAVEMRSRVTRQGSRESTDGSTNSNSSDGTFIFPTTRLGAESQFSDFLDGLGPAQIVGRQ
TLATPPMGDVHIAIMDRSGQLEVEVIEARGLTPKPGSKSLPATYIKVYLLENGACLAKKKTKMTKKTCDPLYQQA
LLFDEGPQGKVLQVIVWGDYGRMDHKCFMGMAQIMLDELDLSAAVTGWYKLFPTSSVADSTLGSLTRRLSQSSLE
SATSPSCS

FIGURE 182

AAGCTGCTGACATCCTGGATCTAGGGTTGTAAAGAAGATTACATGAGCTAATGGATGTGAAAACATCTTAAAAAC
TCTCAAATACTTTTCAACTTTGGAGGATTATTATGATTTTCATTCTGTTCAGCGGCTATACTCAGACTTTACTCT
AAAAGTCAAATCTTCTGACATTCTTTGAAGTGAAGCATTCTATGAATGTGAGCTGAAGAAATGAATGAAATGAAA
TAATGCAGCATCTAGTGCTTTTTGCATGGCCCAAAGGGGCTCTGTGCTGCTCCACTACAGAGGAAACTTCAAGAA
ATGCTGGTTTGCTACAGTGTTTTAGCTTGTGAGATTCTCTGGGACCTTCCCTGCTCCATCATGGGGTCACCTCTA
GGTCATTTTACCTGGGACAAATACCTAAAAGAAACATGTTCAGTCCCAGCGCCTGTCCATTGCTTCAAGCAGTCC
TACACACCTCCAAGCAACGAGTTCAAGATCAGTATGAAATTGGAAGCACAGGACCCCAGGAACACCACATCCACC
TGTATTGCCACAGTAGTTGGACTGACAGGTGCCCGCCTTCGCCTGCGCCTTGATGGGAGCGACAACAAAAATGAC
TTCTGGCGGCTGGTTGACTCAGCTGAAATCCAGCCTATTGGGAACTGTGAAAAGAATGGGGGTATGCTACAGCCA
CCTCTTGGATTTCGGCTGAATGCGTCTTCTTGGCCCATGTTCCTTTTGAAGACGCTAAATGGAGCAGAGATGGCT
CCCATCAGGATTTTCCACAAGGAGCCACCATCGCCTTCCCACAACTTCTTCAAAATGGGAATGAAGCTAGAAGCT
GTGGACAGGAAGAACCCTCATTTCATTTGCCCAGCCACTATTGGGGAGGTTCGGGGCTCAGAGGTGCTTGTCACT
TTTGATGGGTGGCGAGGGGCCTTTGACTACTGGTGCCGCTTCGACTCCCGAGACATCTTCCCTGTGGGCTGGTGT
TCCTTGACTGGAGACAACCTGCAGCCTCCTGGCACCAAAGTTGTGATTCCAAAGAATCCCTATCCTGCCTCCGAT
GTGAATACTGAGAAGCCCAGCATCCACAGCAGCACCAAAACTGTCTTGGAACATCAACCAGGGCAGAGGGGGCGT
AAACCAGGAAAGAAGCGGGGCCGGACACCCAAGACCCTAATTTCCCATCCCATCTCTGCCCCATCCAAGACAGCT
GAACCTTTGAAATTCCCAAAGAAGAGAGGTCCCAAACCTGGCAGCAAGAGGAAACCTCGGACTTTGCTGAACCCA
CCACCTGCCTCACCAACAACCAGCACTCCTGAACCGGATACCAGCACTGTACCCCAGGATGCTGCCACCATCCCC
AGCTCAGCCATGCAGGCCCCAACAGTTTGTATCTACTTGAACAAGAATGGCAGCACAGGCCCCCACTTAGATAAG
AAGAAGGTCCAGCAACTCCCTGACCATTTTGGACCAGCCCGTGCCTCTGTGGTGTTGCAGCAGGCTGTCCAGGCC
TGTATCGACTGTGCTTATCACCAGAAAACCGTCTTCAGCTTCCTCAAGCAAGGCCATGGTGGTGAGGTTATCTCA
GCCGTGTTTGACCGGGAACAGCATACCCTCAACCTCCCAGCAGTCAACAGCATCACCTACGTCCTCCGCTTCCTG
GAGAAACTCTGCCACAACCTTCGTAGTGACAATCTGTTTGGCAACCAGCCCTTTACACAGACTCACTTGTCACTC
ACTGCCATAGAGTACAGCCACAGCCACGACAGGTACCTACCAGGTGAAACCTTTGTCCTGGGGAATAGTCTGGCC
CGCTCCTTGGAACCACACTCAGACTCAATGGACTCTGCCTCAAATCCCACCAACCTTGTCAGCACCTCCCAAAGG
CACCGGCCCTTGCTTTCATCCTGTGGCCTCCCACCAAGCACTGCCTCAGCTGTGCGCAGGCTATGCTCCAGGGGA
GTGTTAAAAGGATCAAATGAAAGAAGGGATATGGAATCATTTTGGAAACTAAATCGTTCCCCAGGGTCGGACCGA
TACCTGGAGAGCCGCGATGCCTCTCGACTGAGTGGCCGGGACCCCTCCTCATGGACAGTCGAGGATGTGATGCAG
TTTGTCCGGGAAGCTGATCCTCAGCTTGGACCCCACGCTGACCTGTTTCGCAAACACGAGATCGATGGCAAGGCC
CTGCTGCTGCTGCGCAGTGACATGATGATGAAGTACATGGGCCTGAAGCTGGGGCCTGCACTCAAGCTCTCCTAC
CACATTGACCGGCTGAAGCAGGGCAAGTTCTGAACCAGGAGAGGCAGCCTAGACAACCAAGTGGCAGCAGGTGGG
GGCATTCTTCTAGGAATGAGGGGCATCAGCCCACCCCAGGCACCTCAGTGGGGTTCCGGGCCACCTCAGGACTCC
AAGAGGCTGTGTGGAGCCACCACTCCTAGCCACAGCTGCCATGATAAGTCCTTCCATGAAGGACTGAGGAGGGAG
AGTGGGGGTCCAGGGCTGGTGCTGCTCTTCCCTCAGCTCTGCCGGGGCTCTAAGGTCCCTCTATTTATTTCTCAA
CCCTGGCTGGCCTCTCACCAGGAGTTTAGGCTGAATGCCTTCCACGTGATGGAGGAAAAGGCCAACTCTGTCCTG
GTCTTGCTGTGGCACCCCATCGCCCCACAGCTCGTACCTTCTCACCAGATTCCCCTGAATCCAAACTCGTGGTGC
AAACCTCTACCTTTTTTACAAAAAGATCTTATTGTTAATTTATTGTTTCTGGCACTTGGGCAAACCCTGTAGTTA
ATACTCCTCCCACACTAGACACTGGGTTTCAGGAGGAGGGAGACTGCCCTGCTTTGGTCCCAGAGAGGCCCTCTG
CAGATAGGCGTGGCCCCTCTTCAGAGGACACTACCCTAGGGCACTTTCTCTTTGAGGTGGAGAGACCCATAAAGC
CTTGACCACATCACTCCATATGGGGAGGAGAAGGATCCCTGTCACCTTCTCCTCTCTTCACGGGGCCCTTTTGCA
GCCCTAGGCCTCATCTGTGGGAAGGGAGTCCCTGGCTTATACTGCCCCCACCACAGCTCCTTGCCCTGGCCAGAA
CTGCTGTCGAAGAAAATCAGGCCGGAAGGCCAAGAAGGCGCTAAGGGGGATGGGAGGGCAGGTTTTCCAGGCTGG
AGTCGGTTCCACCCACTCGCCTGTCCACAGGCTTCCTTGTAAGCAAGTCAGCAGCACAGCTACTCACGCTGCCAT
CTGGACTTATTTTATGTCAATCTGTTTATAAATAAAAACCAATATAGAT

FIGURE 183

GCTGCAG**ATG**GCGGAAATGGATCCGGTAGCCGAGTTCCCCCAGCCTCCCGGTGCTGCGCGCTGGGCTGAGGTTAT
GGCTCGCTTCGCGGCCAGGCTGGGCGCGCAGGGCCGGCGGGTGGTGTTGGTTACGTCAGGCGGCACCAAGGTCCC
ACTGGAAGCGCGGCCGGTGCGCTTCCTGGACAACTTCAGCAGCGGGCGGCGCGGTGCAACCTCGGCCGAGGCCTT
CCTAGCCGCCGGCTACGGGGTCCTGTTCTTGTATCGCGCTCGCTCTGCCTTCCCCTATGCCCACCGCTTCCCACC
CCAGACTTGGCTGTCCGCTCTGCGGCCTTCGGGCCCAGCCCTTTCGGGCTTGCTGAGCCTGGAGGCCGAGGAGAA
TGCACTTCCGGGTTTTGCTGAGGCTCTGAGGAGCTACCAGGAGGCTGCGGCTGCAGGCACCTTCCTGGCAGTAGA
GTTCACCACTTTGGCGGACTATTTGCATCTGTTGCAGGCTGCGGCCCAGGCACTCAATCCGCTAGGCCCTTCTGC
GATGTTTTACCTGGCTGCGGCTGTGTCAGATTTCTATGTTCCTGTCTCTGAAATGCCTGAACACAAGATCCAGTC
ATCTGGGGGCCCACTGCAGATAACAATGAAGATGGTGCCAAAACTGCTTTCTCCTTTGGTTAAAGATTGGGCTCC
CAAAGCATTTATAATTTCCTTTAAGTTGGAGACTGACCCCGCCATTGTAATTAATCGAGCTCGGAAGGCTTTGGA
AATTTATCAGCATCAAGTGGTGGTGGCTAATATCCTTGAGTCACGACAGTCCTTTGTGTTTATTGTAACCAAAGA
CTCGGAAACCAAGTTATTGCTATCAAGGAAGAAA**TAG**AAAAAGGCGTAGAGATAGAAGAGAAGATAGTGGATAAT
CTTCAGTCTCGACACACAGCTTTTATAGGTGACAGAAACTGAAGTAAAAAGCCCTTATAGGATTAAAAATTGTTC
AGGGCTCTTAGAGATGGTGAAAACTACAAAAAAAACCATGGCTTTCATATGGACAGAGAAAATGAAAGAAAGGGA
AAAGGCAGTGGTGTGTAGGCAAATATGGTTTGGCATTCGTCTTTTAATGACACCTGATATGATGTCATTTTGATT
TTGAAATTGAACACTAGAACTGTTAATCACCTTTAAAAAGAAGAGCTTATTGGGAATTATATATTCCTTAAAATA
TACATGGGGGCCTGAATGTCAGCCATCTTTATACTATAGAAAAAGGATTATGGATGCATGAATGGTCATGCTTTG
GAGATCAAATATTGGTTGAATGCCTATGTATGTCAGGCCCTGTGCTGAGCCATGAGGATTAAAAAGATGAATAAA
CATATCTTGTTTAGGAAATGGATGTATAAAAAAATCAAGTGCAATAAAGTGTGTGTCCAAAAGCTGACACAATGG
AAAGG

FIGURE 184

MAEMDPVAEFPQPPGAARWAEVMARFAARLGAQGRRVVLVTSGGTKVPLEARPVRFLDNFSSGRRGATSAEAFLA
AGYGVLFLYRARSAFPYAHRFPPQTWLSALRPSGPALSGLLSLEAEENALPGFAEALRSYQEAAAAGTFLAVEFT
TLADYLHLLQAAAQALNPLGPSAMFYLAAAVSDFYVPVSEMPEHKIQSSGGPLQITMKMVPKLLSPLVKDWAPKA
FIISFKLETDPAIVINRARKALEIYQHQVVVANILESRQSFVFIVTKDSETKLLLSRKK

FIGURE 185

CGGGAGCGGAGAGCGGACCCCAGAGAGCCCTGAGCAGCCCCACCGCCGCCGCCGGCCTAGTTACCATCACACCCC
GGGAGGAGCCGCAGCTGCCGCAGCCGGCCCCAGTCACCATCACCGCAACC**ATG**AGCAGCGAGGCCGAGACCCAGC
AGCCGCCCGCCGCCCCCCCCGCCGCCCCCGCCCTCAGCGCCGCCGACACCAAGCCCGGCACTACGGGCAGCGGCG
CAGGGAGCGGTGGCCCGGGCGGCCTCACATCGGCGGCGCCTGCCGGCGGGGACAAGAAGGTCATCGCAACGAAGG
TTTTGGGAACAGTAAAATGGTTCAATGTAAGGAACGGATATGGTTTCATCAACAGGAATGACACCAAGGAAGATG
TATTTGTACACCAGACTGCCATAAAGAAGAATAACCCCAGGAAGTACCTTCGCAGTGTAGGAGATGGAGAGACTG
TGGAGTTTGATGTTGTTGAAGGAGAAAAGGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCCAGTTC
AAGGCAGTAAATATGCAGCAGACCGTAACCATTATAGACGCTATCCACGTCGTAGGGGTCCTCCACGCAATTACC
AGCAAAATTACCAGAATAGTGAGAGTGGGGAAAAGAACGAGGGATCGGAGAGTGCTCCCGAAGGCCAGGCCCAAC
AACGCCGGCCCTACCGCAGGCGAAGGTTCCCACCTTACTACATGCGGAGACCCTATGGGCGTCGACCACAGTATT
CCAACCCTCCTGTGCAGGGAGAAGTGATGGAGGGTGCTGACAACCAGGGTGCAGGAGAACAAGGTAGACCAGTGA
GGCAGAATATGTATCGGGGATATAGACCACGATTCCGCAGGGGCCCTCCTCGCCAAAGACAGCCTAGAGAGGACG
GCAATGAAGAAGATAAAGAAAATCAAGGAGATGAGACCCAAGGTCAGCAGCCACCTCAACGTCGGTACCGCCGCA
ACTTCAATTACCGACGCAGACGCCCAGAAAACCCTAAACCACAAGATGGCAAAGAGACAAAAGCAGCCGATCCAC
CAGCTGAGAATTCGTCCGCTCCCGAGGCTGAGCAGGGCGGGGCTGAG**TAA**ATGCCGGCTTACCATCTCTACCATC
ATCCGGTTTAGTCATCCAACAAGAAGAAATATGAAATTCCAGCAATAAGAAATGAACAAAAGATTGGAGCTGAAG
ACCTAAAGTGCTTGCTTTTTGCCCGTTGACCAGATAAATAGAACTATCTGCATTATCTATGCAGCATGGGGTTTT
TATTATTTTTACCTAAAGACGTCTCTTTTTGGTAATAACAAACGTGTTTTTTAAAAAAGCCTGGTTTTTCTCAAT
ACGCCTTTAAAGG

FIGURE 186

MSSEAETQQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDKKVIATKVLGTVKWFNVRNGYGFI
NRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSKYAADRNHYRRYPR
RRGPPRNYQQNYQNSESGEKNEGSESAPEGQAQQRRPYRRRRFPPYYMRRPYGRRPQYSNPPVQGEVMEGADNQG
AGEQGRPVRQNMYRGYRPRFRRGPPRQRQPREDGNEEDKENQGDETQGQQPPQRRYRRNFNYRRRRPENPKPQDG
KETKAADPPAENSSAPEAEQGGAE

FIGURE 187

GGCGGGTGGCTGGCGGTTCCGTTAGGTCTGAGGGAGCGATGGCGGTACGCGCGTTGAAGCTGCTGACCACACTGC
TGGCTGTCGTGGCCGCTGCCTCCCAAGCCGAGGTCGAGTCCGAGGCAGGATGGGGCATGGTGACGCCTGATCTGC
TCTTCGCCGAGGGGACCGCAGCCTACGCGCGCGGGGACTGGCCCGGGGTGGTCCTGAGCATGGAACGGGCGCTGC
GCTCCCGGGCAGCCCTCCGCGCCCTTCGCCTGCGCTGCCGCACCCAGTGTGCCGCCGACTTCCCGTGGGAGCTGG
ACCCCGACTGGTCCCCCAGCCCGGCCCAGGCCTCGGGCGCCGCCGCCCTGCGCGACCTGAGCTTCTTCGGGGGCC
TTCTGCGTCGCGCTGCCTGCCTGCGCCGCTGCCTCGGGCCGCCGGCCGCCCACTCGCTCAGCGAAGAGATGGAGC
TGGAGTTCCGCAAGCGGAGCCCCTACAACTACCTGCAGGTCGCCTACTTCAAGATCAACAAGTTGGAGAAAGCTG
TTGCTGCAGCACACACCTTCTTCGTGGGCAATCCTGAGCACATGGAAATGCAGCAGAACCTAGACTATTACCAAA
CCATGTCTGGAGTGAAGGAGGCCGACTTCAAGGATCTTGAGACTCAACCCCATATGCAAGAATTTCGACTGGGAG
TGCGACTCTACTCAGAGGAACAGCCACAGGAAGCTGTGCCCCACCTAGAGGCGGCGCTGCAAGAATACTTTGTGG
CCTATGAGGAGTGCCGTGCCCTCTGCGAAGGGCCCTATGACTACGATGGCTACAACTACCTTGAGTACAACGCTG
ACCTCTTCCAGGCCATCACAGATCATTACATCCAGGTCCTCAACTGTAAGCAGAACTGTGTCACGGAGCTTGCTT
CCCACCCAAGTCGAGAGAAGCCCTTTGAAGACTTCCTCCCATCGCATTATAATTATCTGCAGTTTGCCTACTATA
ACATTGGGAATTATACACAGGCTGTTGAATGTGCCAAGACCTATCTTCTCTTCTTCCCCAATGACGAGGTGATGA
ACCAAAATTTGGCCTATTATGCAGCTATGCTTGGAGAAGAACACACCAGATCCATCGGCCCCCGTGAGAGTGCCA
AGGAGTACCGACAGCGAAGCCTACTGGAAAAAGAACTGCTTTTCTTCGCTTATGATGTTTTTGGAATTCCCTTTG
TGGATCCGGATTCATGGACTCCAGAAGAAGTGATTCCCAAGAGATTGCAAGAGAAACAGAAGTCAGAACGGGAAA
CAGCCGTACGCATCTCCCAGGAGATTGGGAACCTTATGAAGGAAATCGAGACCCTTGTGGAAGAGAAGACCAAGG
AGTCACTGGATGTGAGCAGACTGACCCGGGAAGGTGGCCCCCTGCTGTATGAAGGCATCAGTCTCACCATGAACT
CCAAACTCCTGAATGGTTCCCAGCGGGTGGTGATGGACGGCGTAATCTCTGACCACGAGTGTCAGGAGCTGCAGA
GACTGACCAATGTGGCAGCAACCTCAGGAGATGGCTACCGGGGTCAGACCTCCCCACATACTCCCAATGAAAAGT
TCTATGGTGTCACTGTCTTCAAAGCCCTCAAGCTGGGGCAAGAAGGCAAAGTTCCTCTGCAGAGTGCCCACCTGT
ACTACAACGTGACGGAGAAGGTGCGGCGCATCATGGAGTCCTACTTCCGCCTGGATACGCCCCTCTACTTTTCCT
ACTCTCATCTGGTGTGCCGCACTGCCATCGAAGAGGTCCAGGCAGAGAGGAAGGATGATAGTCATCCAGTCCACG
TGGACAACTGCATCCTGAATGCCGAGACCCTCGTGTGTGTCAAAGAGCCCCCAGCCTACACCTTCCGCGACTACA
GCGCCATCCTTTACCTAAATGGGGACTTCGATGGCGGAAACTTTTATTTCACTGAACTGGATGCCAAGACCGTGA
CGGCAGAGGTGCAGCCTCAGTGTGGAAGAGCCGTGGGATTCTCTTCAGGCACTGAAAACCCACATGGAGTGAAGG
CTGTCACCAGGGGGCAGCGCTGTGCCATCGCCCTGTGGTTCACCCTGGACCCTCGACACAGCGAGCGGGTGAGAG
CAGCTCGAGCGGGTGAGAGCAGCTGGTGCTGTGGTGACCCGTTCCCAGAGCGCCCTTGGTTTGCCTTTCTCTTCC
CCAAATCCCATTGCCAGTGGCTGAGACACGAAAGGAGCACTTGGGACACCAGCTCCAACGCCCTGTCATTATGGT
CACATTGCCTTGTCCTCCCTGGGCCTGCTGTGAACGGGATCCAGGTGGGGAAAGAGGTCAAGACAGGGAGCGATG
CTGAGTTCTTGGTTCCCTCCTTGGGCCCCACTTCAGCTGTCCTTTTCCAGAGAGTAGGACCTGCTGGGAAGGAGA
TGAGCCTGGGGCCATTAAGGAACCTTCCTTGTCCCCTGGGAAGTAGCAGCTGAGAGATAGCGAGTGTCTGGAGCG
GAGGCCTCTCTGAATGGGCAGGGGTTTGTCCTTGCAGGACAGGGTGCAGGCAGATGACCTGGTGAAGATGCTCTT
CAGCCCAGAAGAGATGGACCTCTCCCAGGAGCAGCCCCTGGATGCCCAGCAGGGTCCCCCCGAACCTGCACAAGA
GTCTCTCTCAGGCAGTGAATCGAAGCCCAAGGATGAGCTATGACAGCGTCCAGGTCAGACGGATGGGTGACTAGA
CCCATGGAGAGGAACTCTTCTGCACTCTGAGCTGGCCAGCCCCTCGGGGCTGCAGAGCAGTGAGCCTACATCTGC
CACTCAGCCGAGGGGACCCTGCTCACAGCCTTCTACATGGTGCTACTGCTCTTGGAGTGGACATGACCAGACACC
GCACCCCCCTGGATCTGGCTGAGGGCTCAGGACACAGGCCCAGCCACCCCCAGGGGCCTCCACAGGCCGCTGCATG
ACAGCGATACAGTACTTAAGTGTCTGTGTAGACAACCAAAGAATAAATGATTCATGGTTTTTTTT

FIGURE 188

TAGTCGCGGGTCCCCGAGTGAGCACGCCAGGGAGCAGGAGACCAAACGACGGGGGTCGGAGTCAGAGTCGCAGTG
GGAGTCCCCGGACCGGAGCACGAGCCTGAGCGGGAGAGCGCCGCTCGCACGCCCGTCGCCACCCGCGTACCCGGC
GCAGCCAGAGCCACCAGCGCAGCGCTGCC**ATG**GAGCCCAGCAGCAAGAAGCTGACGGGTCGCCTCATGCTGGCTG
TGGGAGGAGCAGTGCTTGGCTCCCTGCAGTTTGGCTACAACACTGGAGTCATCAATGCCCCCCAGAAGGTGATCG
AGGAGTTCTACAACCAGACATGGGTCCACCGCTATGGGGAGAGCATCCTGCCCACCACGCTCACCACGCTCTGGT
CCCTCTCAGTGGCCATCTTTTCTGTTGGGGGCATGATTGGCTCCTTCTCTGTGGGCCTTTTCGTTAACCGCTTTG
GCCGGCGGAATTCAATGCTGATGATGAACCTGCTGGCCTTCGTGTCCGCCGTGCTCATGGGCTTCTCGAAACTGG
GCAAGTCCTTTGAGATGCTGATCCTGGGCCGCTTCATCATCGGTGTGTACTGCGGCCTGACCACAGGCTTCGTGC
CCATGTATGTGGGTGAAGTGTCACCCACAGCCTTTCGTGGGGCCCTGGGCACCCTGCACCAGCTGGGCATCGTCG
TCGGCATCCTCATCGCCCAGGTGTTCGGCCTGGACTCCATCATGGGCAACAAGGACCTGTGGCCCCTGCTGCTGA
GCATCATCTTCATCCCGGCCCTGCTGCAGTGCATCGTGCTGCCCTTCTGCCCCGAGAGTCCCCGCTTCCTGCTCA
TCAACCGCAACGAGGAGAACCGGGCCAAGAGTGTGCTAAAGAAGCTGCGCGGGACAGCTGACGTGACCCATGACC
TGCAGGAGATGAAGGAAGAGAGTCGGCAGATGATGCGGGAGAAGAAGGTCACCATCCTGGAGCTGTTCCGCTCCC
CCGCCTACCGCCAGCCCATCCTCATCGCTGTGGTGCTGCAGCTGTCCCAGCAGCTGTCTGGCATCAACGCTGTCT
TCTATTACTCCACGAGCATCTTCGAGAAGGCGGGGGTGCAGCAGCCTGTGTATGCCACCATTGGCTCCGGTATCG
TCAACACGGCCTTCACTGTCGTGTCGCTGTTTGTGGTGGAGCGAGCAGGCCGGCGGACCCTGCACCTCATAGGCC
TCGCTGGCATGGCGGGTTGTGCCATACTCATGACCATCGCGCTAGCACTGCTGGAGCAGCTACCCTGGATGTCCT
ATCTGAGCATCGTGGCCATCTTTGGCTTTGTGGCCTTCTTTGAAGTGGGTCCTGGCCCCATCCCATGGTTCATCG
TGGCTGAACTCTTCAGCCAGGGTCCACGTCCAGCTGCCATTGCCGTTGCAGGCTTCTCCAACTGGACCTCAAATT
TCATTGTGGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGTCTTCATCATCTTCACTGTGCTCC
TGGTTCTGTTCTTCATCTTCACCTACTTCAAAGTTCCTGAGACTAAAGGCCGGACCTTCGATGAGATCGCTTCCG
GCTTCCGGCAGGGGGGAGCCAGCCAAAGTGATAAGACACCCGAGGAGCTGTTCCATCCCCTGGGGGCTGATTCCC
AAGTG**TGA**GTCGCCCCAGATCACCAGCCCGGCCTGCTCCCAGCAGCCCTAAGGATCTCTCAGGAGCACAGGCAGC
TGGATGAGACTTCCAAACCTGACAGATGTCAGCCGAGCCGGGCCTGGGGCTCCTTTCTCCAGCCAGCAATGATGT
CCAGAAGAATATTCAGGACTTAACGGCTCCAGGATTTTAACAAAAGCAAGACTGTTGCTCAAATCTATTCAGACA
AGCAACAGGTTTTATAATTTTTTTATTACTGATTTTGTTATTTTTATATCAGCCTGAGTCTCCTGTGCCCACATC
CCAGGCTTCACCCTGAATGGTTCCATGCCTGAGGGTGGAGACTAAGCCCTGTCGAGACACTTGCCTTCTTCACCC
AGCTAATCTGTAGGGCTGGACCTATGTCCTAAGGACACACTAATCGAACTATGAACTACAAAGCTTCTATCCCAG
GAGGTGGCTATGGCCACCCGTTCTGCTGGCCTGGATCTCCCCACTCTAGGGGTCAGGCTCCATTAGGATTTGCCC
CTTCCCATCTCTTCCTACCCAACCACTCAAATTAATCTTTCTTTACCTGAGACCAGTTGGGAGCACTGGAGTGCA
GGGAGGAGAGGGGAAGGGCCAGTCTGGGCTGCCGGGTTCTAGTCTCCTTTGCACTGAGGGCCACACTATTACCAT
GAGAAGAGGGCCTGTGGGAGCCTGCAAACTCACTGCTCAAGAAGACATGGAGACTCCTGCCCTGTTGTGTATAGA
TGCAAGATATTTATATATATTTTTGGTTGTCAATATTAAATACAGACACTAAGTTATAGTATATCTGGACAAGCC
AACTTGTAAATACACCACCTCACTCCTGTTACTTACCTAAACAGATATAAATGGCTGGTTTTTAGAAACATGGTT
TTGAAATGCTTGTGGATTGAGGGTAGGAGGTTTGGATGGGAGTGAGACAGAAGTAAGTGGGGTTGCAACCACTGC
AACGGCTTAGACTTCGACTCAGGATCCAGTCCCTTACACGTACCTCTCATCAGTGTCCTCTTGCTCAAAAATCTG
TTTGATCCCTGTTACCCAGAGAATATATACATTCTTTATCTTGACATTCAAGGCATTTCTATCACATATTTGATA
GTTGGTGTTCAAAAAAACACTAGTTTTGTGCCAGCCGTGATGCTCAGGCTTGAAATCGCATTATTTTGAATGTGA
AGGGAA

FIGURE 189

MEPSSKKLTGRLMLAVGGAVLGSLQFGYNTGVINAPQKVIEEFYNQTWVHRYGESILPTTLTTLWSLSVAIFSVG
GMIGSFSVGLFVNRFGRRNSMLMMNLLAFVSAVLMGFSKLGKSFEMLILGRFIIGVYCGLTTGFVPMYVGEVSPT
AFRGALGTLHQLGIVVGILIAQVFGLDSIMGNKDLWPLLLSIIFIPALLQCIVLPFCPESPRFLLINRNEENRAK
SVLKKLRGTADVTHDLQEMKEESRQMMREKKVTILELFRSPAYRQPILIAVVLQLSQQLSGINAVFYYSTSIFEK
AGVQQPVYATIGSGIVNTAFTVVSLFVVERAGRRTLHLIGLAGMAGCAILMTIALALLEQLPWMSYLSIVAIFGF
VAFFEVGPGPIPWFIVAELFSQGPRPAAIAVAGFSNWTSNFIVGMCFQYVEQLCGPYVFIIFTVLLVLFFIFTYF
KVPETKGRTFDEIASGFRQGGASQSDKTPEELFHPLGADSQV

FIGURE 190

CACGTCGTTCACGGCCTTCTTCGGCCCCTCTAGCACGACATTGAGGCCTGGCTTCAGAAGCCCTCGGGAAAACGC
ATCCTGCAACTCTCTGTCTGTGACAAGGGATTCATCGGATTCCGACTCCGAATCCGAGAGCGGGGGAGTGTCCAT
CTCGCCGCACGCACGTCCCACACAGCTACTGCTCAACTTTTGATTGGGACTTCCGCTTCCGGCGGCAAACCATAC
TTCCGGTTTGTCGTTGCTATAGGAACCGCTACGGCGTTTGAAAGTGTCCGGGTTGCTTAGGATCCCTACAGGTAG
CGCCTCTGGATACATGCGTGGTCTGCTGACCCAGAGAGAAACGAAAGCAGAACTGTTTGGCGGGAGATC**ATG**TCA
GCCGTGGTAGCTCAGACGCTGCATGTTTTTGGTCTTCGATCCCACGTGGCCAACAATATCTTCTACTTCGATGAA
CAGATCATTATATTTCCTTCAGGAAATCACTGTGTGAAGTACAATGTGGATCAGAAATGGCAAAAATTCATTCCA
GGCTCAGAGAAGAGTCAGGGCATGTTGGCCTTGTCCATCAGTCCCAATCGGCGGTACCTCGCTATCTCTGAGACT
GTGCAAGAAAAACCTGCCATCACCATTTATGAATTGTCATCCATCCCTTGCCGGAAGCGCAAAGTTCTTAATAAT
TTTGACTTCCAAGTTCAGAAATTTATTAGCATGGCTTTTTCTCCAGACTCCAAATACCTATTGGCTCAGACGTCA
CCTCCAGAGTCAAATCTTGTCTACTGGCTGTGGGAAAAACAGAAAGTAATGGCCATTGTTAGAATCGACACTCAG
AACAACCCTGTCTACCAGGTGAGCTTCAGTCCACAGGATAACACTCAGGTGTGTGTCACTGGAAATGGGATGTTT
AAGCTTCTCCGTTTTGCTGAGGGAACCCTGAAGCAAACCAGCTTTCAGAGGGGAGAACCCCAAAACTATCTAGCC
CACACCTGGGTGGCTGATGACAAGATTGTCGTTGGCACTGACACAGGCAAACTCTTCCTCTTTGAATCTGGAGAT
CAGCGTTGGGAGACCAGCATAATGGTCAAGGAACCTACCGATGGCTCAAAGAGCCTGGATGTCATTCAGGAATCA
GAGAGCCTGATTGAATTTCCACCAGTCAGTTCTCCACTCCCTTCCTATGAACAGATGGTGGCGGCCAGTAGCCAT
AGCCAGATGTCCATGCCCCAGGTGTTTGCCATTGCAGCCTATTCAAAGGGATTTGCCTGTTCTGCTGGGCCAGGG
AGAGTTCTGCTGTTTGAGAAGATGGAAGAAAAGGATTTTTACCGTGAGAGCAGAGAAATCAGGATTCCTGTGGAC
CCGCAGAGCAATGATCCAAGTCAGTCTGACAAACAGGACGTTCTCTGCCTGTGCTTCAGCCCCTCAGAGGAAACT
CTGGTTGCCAGCACCAGTAAGAACCAACTCTACAGCATCACCATGTCCCTGACAGAGATCAGCAAGGGAGCCTGC
TCACTTTGAGTATTTGATGTATCCATTGCACTCAGCACCCATCACCGGTCTAGCTACCTGCATCCGCAAACCCCT
TATAGCCACCTGTTCTCTGGATCGATCCATCCGCCTTTGGAATTATGAAACAAACACCCTGGAACTATTTAAGGA
ATACCAAGAAGAGGCATATTCCATCAGCCTTCATCCATCTGGACACTTCATTGTAGTAGGGTTTGCTGACAAACT
ACGCCTCATGAATCTACTCATTGATGATATACGTTCTTTCAAAGAATACTCTGTTAGAGGATGCGGAGAGTGTTC
CTTTAGCAATGGAGGTCACCTGTTTGCTGCAGTCAATGGAAATGTGATTCACGTTTACACCACCACGAGCCTAGA
GAACATCTCAAGCCTGAAAGGACACACAGGGAAGATTCGCTCAATTGTGTGGAATGCAGA**TGA**TAGCAAACTGAT
TTCTGGTGGCACAGATGGTGCTGTGTATGAATGGAATCTGTCCACAGGAAAGAGAGAGACAGAATGCGTGCTCAA
GTCTTGCAGCTACAACTGTGTTACTGTCTCCCCCGATGCCAAAATTATCTTTGCTGTTGGATCAGACCACACCCT
CAAGGAGATTGCAGATTCCTTGCCTTCGAGAGATATCGGCGTTTGATGTCACCTACACCGCCATTGTCATCTCGC
ATTCTGGACGCATGATGTTTGTGGGCACCTCGGTGGGAACCATTCGTGCCATGAAGTACCCTCTGCCTCTGCAGA
AGGAATTCAATGAGTACCAGGCCCATGCCGGTCCTATCACCAAGGTGAGCAGGGCCCTCTCCCCAGGAACCCAGT
CCCACACCTGCCTGCTACGTGCCTTGTTCATCCCTTCAACCTCCCAATGTCTTTTCTCTCTCCTTCTTCTCTCTT
ATTTATTCATCCATCATTCATTGAATCACCATCTATTGACTATGAATATACTCTTTGTTTAAACTACTTCCAGGA
ATTTAGCCTAGGAAATCATCAGAGATACACCTAAAAATGTATGTACAACGTTTTCACCATAATATTATGCATAAT
AAGGGGCCGTTTGGTGGATGCCGTAGCTGCCGTGAGTGTGGGCTGCACTTGACCACAGCTGCCTCCTCCTCCAGA
GAATGCCCCAGACTGAAAGGAGCCATAGCCCTGAAGATTGGCCCCTACCTCTCCCTGAGGGTACAAAAGGCCACC
CCAGGGGCAATACCATGAGTACACATTTGTAAATTGTCCTTCCATTCACCCTTCTCATAAAGTAGTATCTATGTT
CAACAGTCAAAATGTGGAAGCAACCAAGCATCCATCGACAGACGAATGCATAAGCAAAAGATGGTATATCTATAC
AATGGAACAATACCCTGCCTAAAAAGGAAGGGAATTCTGCAATGTGCTACCACATGGATGAACCTTGAGGATGTT
ATGCTAAATTAAATAAGGCCAACCACAAAAAGATAAGTACAGTGTGATTCCACTTTTAGGAGATACTTGGAGCAG
TCAGAATCACAAAGACAGAGTGGTGGTTGGCAGGGGCTGCAGGAAGGGGGAATGAGGAATGATTGTTTCATAGGT
ATAGAGTTTTGGTTTTACAAGACAAAAGGATTATGGGGGTAGTTGGTGGCAATGGCTGCACAACATTACAAATGT
ATTTAATAACATGAACTGTACACTTGAAAATGGTTAAGATAGCAAATTTTACAGAATATGTATTTTACGACAATT
TTAAAAATGAAATAAAAAAGAATTATCTTGC

FIGURE 191

MSAVVAQTLHVFGLRSHVANNIFYFDEQIIIFPSGNHCVKYNVDQKWQKFIPGSEKSQGMLALSISPNRRYLAIS
ETVQEKPAITIYELSSIPCRKRKVLNNFDFQVQKFISMAFSPDSKYLLAQTSPPESNLVYWLWEKQKVMAIVRID
TQNNPVYQVSFSPQDNTQVCVTGNGMFKLLRFAEGTLKQTSFQRGEPQNYLAHTWVADDKIVVGTDTGKLFLFES
GDQRWETSIMVKEPTNGSKSLDVIQESESLIEFPPVSSPLPSYEQMVAASSHSQMSMPQVFAIAAYSKGFACSAG
PGRVLLFEKMEEKDFYRESREIRIPVDPQSNDPSQSDKQDVLCLCFSPSEETLVASTSKNQLYSITMSLTEISKG
EPAHFEYLMYPLHSAPITGLATCIRKPLIATCSLDRSIRLWNYETNTLELFKEYQEEAYSISLHPSGHFIVVGFA
DKLRLMNLLIDDIRSFKEYSVRGCGECSFSNGGHLFAAVNGNVIHVYTTTSLENISSLKGHTGKSLNCVECR

FIGURE 192

GCGATTCGGTGGCACGTGGAGCCACGGCGTGGGAGTAGGGGGCTGAAGGCAGGCAGCAGCGGCCAGGGCCGCCCT
CTGCTAGCCGCTTGGGTCTCGGGATACCCCGTTTCTTCCTGTAGGTGTGGGACGTGCGTGCGGCGAG**ATG**GACAC
TCCCCCGCTCTCGGATTCGGAGTCGGAATCCGATGAATCCCTTGTCACAGACAGAGAGTTGCAGGATGCGTTTTC
CCGAGGGCTTCTGAAGCCAGGCCTCAATGTCGTGCTAGAGGGGCCGAAGAAGGCCGTGAACGACGTGAATGGCCT
GAAGCAATGTTTGGCAGAATTCAAGCGGGATCTGGAATGGGTTGAAAGGCTCGATGTGACACTGGGTCCGGTACC
GGAGATCGGTGGATCTGAGGCGCCAGCACCTCAGAACAAGGACCAGAAAGCTGTTGATCCAGAAGACGACTTCCA
GCGAGAGATGAGTTTCTATCGCCAAGCCCAGGCCGCAGTGCTTGCAGTCTTACCCCGCCTCCATCAGCTCAAAGT
CCCTACGAAGCGACCCACTGATTATTTTGCGGAAATGGCCAAATCTGATCTGCAGGTGCAGAAGATTCGACAGAA
GCTGCAGACTAAACAGGCTGCCATGGAGAGGTCTGAAAAAGCTAAGCAACTGCGAGCACTTAGGAAATACGGGAA
GAAGGTGCAAACGGAGGTTCTTCAGAAGAGGCAGCAGGAGAAAGCCCATATGATGAATGCTATTAAGAAATATCA
GAAAGGCTTCTCTGATAAACTGGATTTCCTTGAGGGAGATCAGAAACCTCTGGCACAGCGCAAGAAGGCAGGAGC
CAAAGGCCAGCAGATGAGGAAGGGGCCCAGTGCTAAACGACGGTATAAAAACCAGAAGTTTGGTTTTGGTGGAAA
GAAGAAAGGCTCAAAGTGGAACACTCGGGAGAGCTATGATGATGTATCTAGCTTCCGGGCCAAGACAGCTCATGG
CAGAGGCCTCAAGAGGCCTGGCAAGAAAGGGTCAAATAAGAGACCTGGAAAACGAACAAGAGAGAAGATGAAGAA
CAGAACACAC**TAA**ATAGCATCTTTGAATACAAAGAACCAAGAAAAAGGAATGAAGACTCGCAATTTCACGACACA
CTTTGATCCCTTCTGTTGGTGTCATGTTGTAAACATTTCTTTCAATAAACTAAAGAAAAATTATTAAAGGAACAC
ATACCTTTGGTTAAATAGTCTAGACTAAAAGATTGAGAAGTTACTTTCCATTGCTATCTATTGATAATTTAGACA
TTGAGTTCAAATTGCCTTCATTTTATGATAAATAATGATTTAACTGAAAA

FIGURE 193

MDTPPLSDSESESDESLVTDRELQDAFSRGLLKPGLNVVLEGPKKAVNDVNGLKQCLAEFKRDLEWVERLDVTLG
PVPEIGGSEAPAPQNKDQKAVDPEDDFQREMSFYRQAQAAVLAVLPRLHQLKVPTKRPTDYFAEMAKSDLQVQKI
RQKLQTKQAAMERSEKAKQLRALRKYGKKVQTEVLQKRQQEKAHMMNAIKKYQKGFSDKLDFLEGDQKPLAQRKK
AGAKGQQMRKGPSAKRRYKNQKFGFGGKKKGSKWNTRESYDDVSSFRAKTAHGRGLKRPGKKGSNKRPGKRTREK
MKNRTH

FIGURE 194

CCACGCGTCCGGGCGTAAGCCAGGCGTGTTAAAGCCGGTCGGAACTGCTCCGGAGGGCACGGGCTCCGTAGGCAC
CAACTGCAAGGACCCCTCCCCCTGCGGGCGCTCCC**ATG**GCACAGTTCGCGTTCGAGAGTGACCTGCACTCGCTGC
TTCAGCTGGATGCACCCATCCCCAATGCACCCCCTGCGCGCTGGCAGCGCAAAGCCAAGGAAGCCGCAGGCCCGG
CCCCCTCACCCATGCGGGCCGCCAACCGATCCCACAGCGCCGGCAGGACTCCGGGCCGAACTCCTGGCAAATCCA
GTTCCAAGGTTCAGACCACTCCTAGCAAACCTGGCGGTGACCGCTATATCCCCCATCGCAGTGCTGCCCAGATGG
AGGTGGCCAGCTTCCTCCTGAGCAAGGAGAACCAGTCTGAAAACAGCCAGACGCCCACCAAGAAGGAACATCAGA
AAGCCTGGGCTTTGAACCTGAACGGTTTTGATGTAGAGGAAGCCAAGATCCTTCGGCTCAGTGGAAAACCACAAA
ATGCGCCAGAGGGTTATCAGAACAGACTGAAAGTACTCTACAGCCAAAAGGCCACTCCTGGCTCCAGCCGGAAGA
CCTGCCGTTACATTCCTTCCCTGCCAGACCGTATCCTGGATGCGCCTGAAATCCGAAATGACTATTACCTGAACC
TTGTGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCACTGGACAACAGTGTGTACCTGTGGAGTGCAAGCTCTG
GTGACATCCTGCAGCTTTTGCAAATGGAGCAGCCTGGGGAATATATATCCTCTGTGGCCTGGATCAAAGAGGGCA
ACTACTTGGCTGTGGGCACCAGCAGTGCTGAGGTGCAGCTATGGGATGTGCAGCAGCAGAAACGGCTTCGAAATA
TGACCAGTCACTCTGCCCGAGTGGGCTCCCTAAGCTGGAACAGCTATATCCTGTCCAGTGGTTCACGTTCTGGCC
ACATCCACCACCATGATGTTCGGGTAGCAGAACACCATGTGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTG
GGCTGCGCTGGGCCCCAGATGGACGACATTTGGCCAGTGGTGGTAATGATAACTTGGTCAATGTGTGGCCTAGTG
CTCCTGGAGAGGGTGGCTGGGTTCCTCTGCAGACATTCACCCAGCATCAAGGGGCTGTCAAGGCCGTAGCATGGT
GTCCCTGGCAGTCCAATGTCCTGGCAACAGGAGGGGGCACCAGTGATCGACACATTCGCATCTGGAATGTGTGCT
CTGGGGCCTGTCTGAGTGCCGTGGATGCCCATTCCCAGGTGTGCTCCATCCTCTGGTCTCCCCATTACAAGGAGC
TCATCTCAGGCCATGGCTTTGCACAGAACCAGCTAGTTATTTGGAAGTACCCAACCATGGCCAAGGTGGCTGAAC
TCAAAGGTCACACATCCCGGGTCCTGAGTCTGACCATGAGCCCAGATGGGGCCACAGTGGCATCCGCAGCAGCAG
ATGAGACCCTGAGGCTATGGCGCTGTTTTGAGTTGGACCCTGCGCGGCGGCGGGAGCGGGAGAAGGCCAGTGCAG
CCAAAAGCAGCCTCATCCACCAAGGCATCCGC**TGA**AGACCAACCCATCACCTCAGTTGTTTTTTATTTTTCTAAT
AAAGTCATGTCTCCCTTCATGTTTTTTTTTTTTAAAA

FIGURE 195

MAQFAFESDLHSLLQLDAPIPNAPPARWQRKAKEAAGPAPSPMRAANRSHSAGRTPGRTPGKSSSKVQTTPSKPG
GDRYIPHRSAAQMEVASFLLSKENQSENSQTPTKKEHQKAWALNLNGFDVEEAKILRLSGKPQNAPEGYQNRLKV
LYSQKATPGSSRKTCRYIPSLPDRILDAPEIRNDYYLNLVDWSSGNVLAVALDNSVYLWSASSGDILQLLQMEQP
GEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQQKRLRNMTSHSARVGSLSWNSYILSSGSRSGHIHHHDVRVAEH
HVATLSGHSQEVCGLRWAPDGRHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQSNVLATGG
GTSDRHIRIWNVCSGACLSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAELKGHTSRVLSLT
MSPDGATVASAAADETLRLWRCFELDPARRREREKASAAKSSLIHQGIR

FIGURE 196

GGCACGAGGGAACCGTCCGCAGCCGCCGGAGCCGGGAGCCCTGCCCAAGTCGGAGCGGCGTCCCCTGCTGAGCCC
CGAGCGCCGGGCCAGCAGCCGGATGCCCGGGCCCACTGGGCGGGCCAGTGGCCGCCTGCGGG**ATG**AGCAGACTGC
TGGGGGGGACGCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCC
TCTACTTTGACGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGCCCGAGGCCCTGCCCATGCCCTCC
ACCCAGCTGCTAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCC
CTGAGGTCCCCAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTG
CGGGTGCACAGGGAGAACCCAGGCGTGCTCATGGGCGGCCGATACACACCGCCCGACTGCACCCCAGCCCAGACG
GTGGCGGTCATCATCCCCTT**TAG**ACACCGGGAACACCACCTGCGCTACTGGCTCCACTATCTACACCCCATCTTG
AGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCAGCATGGTGAGGACACCTTCAACCGGGCCAAGCTG
CTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGCCTATGACTGCTTCATCTTCAGCGATGTGGACCTG
GTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCAACCCCGCCACTTTGCCATTGCCATGGACAAGTTT
GGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTCAGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAAT
GGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGATGACATCTTCAACCGGATCTCCCTGACTGGGATG
AAGATCTCACGCCCAGACATCCGAATTGGCCGCTACCGCATGATCAAGCACGACCGCGACAAGCATAACGAACCT
AACCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGACCATGAAGCGGGACGGCATTGGGTCAGTGCGGTAC
CAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATATCACAGTGGACATTGGGCGGCCTCCGTCGTGGCCC
CCTCGGGGCTGACACTAATGGACAGAGGCTCTCGGTGCCGAAGATTGCCTGCCAGAGGACTGACCACAGCCTGGC
TGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGGCTCTGTTTTCCAAGGGTCTTCACTAGGCCCCCTA
GCTACACCTGGAAGTTTCAGAACCCACTTTGGGGGGCCTCCTGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTT
GGAGTCAACCCTCCTTCCCGACCCCCTCCCCCTAGCCCAGCCCCAGTCACTGTCAGGGTCGGGCCAGCCCCTGCA
CTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTCTGTGCCTCAGTTTCCCCCCCTTGAGTCCCCTAGG
GCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCT
TGCTCCCAGGGGAGGGGAAACCTTTTTCATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAG
CAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTCGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCA
GGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTT
GTGTTTGTACATTGCACAGAAACTTGTGTGGGTGCTTTAGTAAAAAACGTGAATGGAAAAAAAAAAAAAAAAAA

FIGURE 197

MSRLLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPPCPDSPPGLAGAQGEPRRAHGRPIHTARLHPSPDGGGHHPL

FIGURE 198

CCCAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTGTGGGCAGA
CTGCTGATCGAGTTCACCTCACCCATGCCCCTGGAGCGGGTGCAGAGGGCCTGGAAGGGTGGGAGGTATGTCTAG
GGGGCAGTGTCTCTTCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCTTGCTCCCAGGGGAGGGGAAACCTTTTT
CATTCAACATTGTAGGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGAT
GCTGTGTCGCTGCCTGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGT
TCCCGCCTCCCTGTCTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAAACTTGT
GTGGGTGCTTTAGTAAAAAACGTGAATGG

FIGURE 199

GCCAGCAGCCGGATGCCCGGGCCCACTGGGCGGGCCAGTGGCCGCCTGCGGG**ATG**AGCAGACTGCTGGGGGGGAC
GCTGGAGCGCGTCTGCAAGGCTGTGCTCCTTCTCTGCCTGCTGCACTTCCTCGTGGCCGTCATCCTCTACTTTGA
CGTCTACGCCCAGCACCTGGCCTTCTTCAGCCGCTTCAGTGCCCGAGGCCCTGCCCATGCCCTCCACCCAGCTGC
TAGCAGCAGCAGCAGCAGCAGCAACTGCTCCCGGCCCAACGCCACCGCCTCTAGCTCCGGGCTCCCTGAGGTCCC
CAGTGCCCTGCCCGGTCCCACGGCTCCCACGCTGCCACCCTGTCCTGACTCGCCACCTGGTCTTGTGGGCAGACT
GCTGATCGAGTTCACCTCACCCATGCCCCTGGAGCGGGTGCAGAGGGAGAACCCAGGCGTGCTCATGGGCGGCCG
ATACACACCGCCCGACTGCACCCCAGCCCAGACGGTGGCGGTCATCATCCCCTTTAGACACCGGGAACACCACCT
GCGCTACTGGCTCCACTATCTACACCCCATCTTGAGGCGGCAGCGGCTGCGCTACGGCGTCTATGTCATCAACCA
GCATGGTGAGGACACCTTCAACCGGGCCAAGCTGCTTAACGTGGGCTTCCTAGAGGCGCTGAAGGAGGATGCCGC
CTATGACTGCTTCATCTTCAGCGATGTGGACCTGGTCCCCATGGATGACCGCAACCTATACCGCTGCGGCGACCA
ACCCCGCCACTTTGCCATTGCCATGGACAAGTTTGGCTTCCGGCTTCCCTATGCTGGCTACTTTGGAGGTGTGTC
AGGCCTGAGTAAGGCTCAGTTTCTGAGAATCAATGGCTTCCCCAATGAGTACTGGGGCTGGGGTGGCGAGGATGA
TGACATCTTCAACCGGATCTCCCTGACTGGGATGAAGATCTCACGCCCAGACATCCGAATCGGCCGCTACCGCAT
GATCAAGCACGACCGCGACAAGCATAACGAACCTAACCCTCAGAGGTTTACCAAGATTCAAAACACGAAGCTGAC
CATGAAGCGGGACGGCATTGGGTCAGTGCGGTACCAGGTCTTGGAGGTGTCTCGGCAACCACTCTTCACCAATAT
CACAGTGGACATTGGGCGGCCTCCGTCGTGGCCCCCTCGGGGC**TGA**CACTAATGGACAGAGGCTCTCGGTGCCGA
AGATTGCCTGCCAGAGGACTGACCACAGCCTGGCTGGCAGCTGCTCTGTGGAGGACCTCCAGGACTGAGACTGGG
CTCTGTTTTCCAAGGGTCTTCACTAGGCCCCCTAGCTACACCTGGAAGTTTCAGAACCCACTTTGGGGGGCCTCC
TGCCTGGGCAGGCTCTTCAAGTGTGGCCCTCTTTGGAGTCAACCCTCCTTCCCGACCCCCTCCCCCTAGCCCAGC
CCCAGTCACTGTCAGGGTCGGGCCAGCCCCTGCACTGCCTCGCAGAGTGGCCTGGGCTAGGTCACTCCACCTCTC
TGTGCCTCAGTTTCCCCCCCTTGAGTCCCCTAGGGCCTGGAAGGGTGGGAGGTATGTCTAGGGGGCAGTGTCTCT
TCCAGGGGGAATTCTCAGCTCTTGGGAACCCCCTTGCTCCCAGGGGAGGGGAAACCTTTTTCATTCAACATTGTA
GGGGGCAAGCTTTGGTGCGCCCCCTGCTGAGGAGCAGCCCCAGGAGGGGACCAGAGGGGATGCTGTGTCGCTGCC
TGGGATCTTGGGGTTGGCCTTTGCATGGGAGGCAGGTGGGGCTTGGATCAGTAAGTCTGGTTCCCGCCTCCCTGT
CTGAGAGAGGAGGCAGGAGCCCCAGGGCCGGCTTGTGTTTGTACATTGCACAGAAACTTGTGTGGGTGCTTTAGT
AAAAAACGTGAATGG

FIGURE 200

MSRLLGGTLERVCKAVLLLCLLHFLVAVILYFDVYAQHLAFFSRFSARGPAHALHPAASSSSSSSNCSRPNATAS
SSGLPEVPSALPGPTAPTLPPCPDSPPGLVGRLLIEFTSPMPLERVQRENPGVLMGGRYTPPDCTPAQTVAVIIP
FRHREHHLRYWLHYLHPILRRQRLRYGVYVINQHGEDTFNRAKLLNVGFLEALKEDAAYDCFIFSDVDLVPMDDR
NLYRCGDQPRHFAIAMDKFGFRLPYAGYFGGVSGLSKAQFLRINGFPNEYWGWGGEDDDIFNRISLTGMKISRPD
IRIGRYRMIKHDRDKHNEPNPQRFTKIQNTKLTMKRDGIGSVRYQVLEVSRQPLFTNITVDIGRPPSWPPRG

FIGURE 201

GCGGAGAAACAGTAGTTAGGATGGCTGAAGGGGATACTCACCGGCTGAAGGCCGACTGTGATTCCCCCTACCCCC
ACAAGGCGATTTTGACCCCCTGAGGGCTGCTCTAGAGGACTCAGGCCCCGAAGCTGTCCCAGGGAGGTCCCCGCT
GCATCCCACCACCCAAGCTGTGCCTCATGGAGTCGATGTTTAGCAGCCCTGCCGAGGCGGCGCTGCAGCGAGAGA
CCGGGGTGCCAGGACTGCTTACTCCTCTTCCGGACCTGGACGGAGTGTACGAGCTGGAGCGAGTCGCTGGATTTG
TCCGCGACCTGGGGTGTGAACGAGTTGCCTTGCAGTTCCCTGACCAGCTATTGGGAGATGCTGTGGCTGTGGCTG
CACGACTGGAGGAGACGACAGGGTCAAAGATGTTCATTCTGGGTGACACAGCCTACGGCAGCTGCTGCGTGGATG
TGCTGGGTGCTGAGCAAGCTGGAGCTCAGGCTCTCATACATTTTGGCCCTGCCTGCTTAAGCCCTCCAGCCCGCC
CACTGCCCGTTGCCTTCGTGCTTCGTCAACGTTCTGTGGCCTTGGAGCTCTGTGTCAAGGCCTTTGAGGCCCAGA
ACCCAGACCCCAAAGCGCCTGTGGTGCTGCTGAGTGAGCCGGCCTGTGCCCATGCCCTGGAGGCTTTGGCTACTC
TCCTGCGCCCACGGTACCTGGACCTGCTAGTCTCCAGCCCAGCTTTTCCCCAACCAGTGGGTTCCCTGAGTCCAG
AGCCTATGCCCCTAGAGCGTTTTGGGCGCCGCTTCCCCCTTGCCCCAGGGAGGCGTCTAGAAGAGTATGGTGCCT
TCTATGTAGGGGGCTCTAAGGCCAGCCCTGACCCAGACCTTGACCCAGACCTGAGTCGGCTGCTCTTGGGGTGGG
CACCAGGTCAACCCTTCTCCTCCTGCTGTCCAGATACAGGGAAGACTCAGGATGAGGGTGCCCGGGCTGGACGGC
TAAGGGCACGAAGACGATATCTGGTAGAGAGGGCCAGAGATGCCCGCGTGGTAGGGCTGCTGGCAGGCACACTGG
GTGTAGCCCAACACCGTGAGGCACTGGCCCACTTGCGGAACCTGACTCAGGCTGCTGGCAAGCGTAGCTATGTGT
TGGCCCTGGGGCGGCCCACCCCTGCCAAGCTTGCCAACTTCCCTGAGGTGGATGTCTTTGTGCTATTAGCCTGTC
CTCTGGGTGCTCTAGCCCCCCAGCTTTCTGGTAGCTTCTTCCAGCCTATACTGGCACCATGTGAGCTGGAAGCTG
CCTGCAACCCTGCCTGGCCACCTCCAGGCCTGGCTCCCCACCTCACACATTATGCGGACTTATTGCCTGGCTCTC
CCTTCCACGTGGCTCTCCCACCACCTGAGTCAGAGCTGTGGGAAACCCCAGACGTGTCACTCATTACTGGAGATC
TCCGACCCCCACCTGCCTGGAAGTCATCAAATGATCATGGAAGCTTGGCTCTGACCCCACGGCCCCAGCTGGAGC
TGGCTGAGAGCAGTCCTGCAGCCTCATTCCTTAGTTCCCGGAGCTGGCAAGGGCTGGAGCCCCGCCTGGGTCAGA
CGCCAGTGACAGAAGCTGTGAGTGGAAGACGAGGGATTGCCATCGCCTATGAGGATGAGGGAAGCGGCTGATACC
ATGTGGGGCTGGAGACATAGATGGACTTATGAATGGCTGCTAGGACCTTTAGTGCTCCCTGCACCAACCTCCCAT
CCCCCTGCCAAGATCCTTGAAGGACCCTGGAAGGAGGGAGAGCAGGCAGCCCTTCACAGGATAGGATCCGTCTCT
GTCCTGTCCTGGCACTGGCACAAGCTCAGCCCATGCCCAGTAATGCGTGTTGTTTGGCTGATGGAATAAAGGGCT
TAGGGACTTCCCTGAGGCCTCTGGACCCATCTGTCTTCCTGAGGGCAGCCCAGGACCTTTGGCCAATCCCAGTTC
CCAGGCTGCAGTTGAGGGTCTGTCCTTGTCAAAAGGCAGGTGCTAGACAGTCTAGACCAGGGTTTCTCAAACTCG
TACTTGACATTTGGGGCCAGATAATTCTTTGTTGTGGGGCTGTCTGGTGTATGGTAGGGTGCTCAGCAGCATCCC
TGGCCTCTGCCCACTAGACATCAGAAGCACTCCCCCAGTTGTGACAACCAAAAATATCTCCAGACCTTGGCAAAT
GTTATCTGTGGGGGAAAATTGCCCTCAATTGAGAACCACTGGTCTAGCTAGACCTGCACTGTCCAGTACAGTAGC
CACTAAATACATGTGGCTAAACTTAAATTTAAGTTAATTAAGATTAAAAGCTCAGTTTCTCAGTCACATTAGTCA
TTCAAGTGTTCAGACAGCCACATGAGGGGACAGTGCAGCTACAGGATATGCCATCATGGCAGAAAGTTCTGTTGG
TTGGACAGCGTTGGTCTATACTGACTCTTATTTCTCAGGGAGATCACAGCAACCTAAATAAACCAGATACCTTTT
C

FIGURE 202A

GCCTTCGCCTGCTGGAAAAGCAGTAGGATCGGCCAGTGGCGACAGCAGGAGCTGAGCCTAAGCCCTGGCGGGGCT
TTGGGCTGTAGATTCCTGTCTGACTAAAGGGACCTCAAAAAGGAGGGAAA**ATG**GCTTCTGAGTCTGAAACTCTGA
ATCCCAGTGCTAGGATAATGACCTTTTATCCAACTATGGAAGAGTTCCGAAACTTCAGTAGATACATTGCCTACA
TTGAATCCCAAGGAGCTCATCGGGCAGGGCTAGCCAAGGTTGTTCCTCCAAAAGAGTGGAAGCCACGAGCATCCT
ATGATGACATTGATGATTTGGTCATTCCTGCCCCCATTCAACAGCTGGTGACGGGGCAGTCTGGCCTCTTTACTC
AGTACAACATACAGAAGAAAGCCATGACTGTTCGAGAGTTCCGCAAGATAGCCAATAGCGATAAGTACTGTACCC
CACGCTATAGTGAGTTTGAAGAGCTCGAGCGGAAATACTGGAAAAATCTTACATTCAATCCTCCAATCTATGGTG
CAGATGTGAATGGTACCCTCTATGAAAAGCATGTTGATGAGTGGAATATTGGCCGGCTGAGAACAATCCTGGACT
TGGTGGAAAAGGAGAGTGGGATCACCATTGAGGGTGTGAACACCCCATACCTGTACTTTGGCATGTGGAAGACAT
CCTTTGCTTGGCACACTGAAGACATGGACCTCTACAGCATCAACTACCTGCACTTTGGAGAACCAAAGTCCTGGT
ACTCTGTTCCACCTGAGCATGGAAAGCGGTTGGAACGCCTCGCCAAAGGCTTTTTCCCAGGAAGTGCTCAAAGCT
GTGAGGCATTTCTCCGCCACAAGATGACCCTGATTTCCCCGTTAATGCTGAAGAAATATGGAATTCCCTTTGACA
AGGTGACTCAAGAGGCTGGAGAGTTTATGATCACTTTCCCTTATGGTTACCATGCCGGCTTTAACCATGGTTTTA
ACTGTGCGGAGTCTACCAATTTTGCTACCCGTCGGTGGATTGAGTACGGCAAGCAAGCTGTGCTGTGCTCCTGTA
GAAAGGACATGGTGAAGATCTCCATGGATGTGTTTGTGAGAAAGTTCCAGCCAGAAAGGTACAAACTTTGGAAAG
CTGGGAAGGACAACACAGTTATTGACCATACTCTGCCCACGCCAGAAGCAGCTGAGTTTCTTAAGGAGAGTGAAC
TGCCTCCAAGAGCTGGCAACGAGGAGGAGTGCCCAGAGGAGGACATGGAAGGGGTGGAGGATGGAGAGGAAGGAG
ACCTGAAGACAAGCCTGGCCAAGCACCGAATAGGGACAAAGAGGCACCGAGTTTGTCTTGAAATACCACAGGAGG
TGAGTCAGAGTGAGCTCTTCCCCAAGGAGGATCTGAGTTCTGAGCAGTATGAGATGACGGAGTGCCCGGCAGCCC
TCGCCCCTGTGAGGCCCACCCATAGCTCTGTGCGGCAAGTTGAGGATGGTCTTACCTTCCCAGATTATTCTGACT
CCACTGAAGTCAAATTTGAAGAGCTTAAAAATGTCAAACTAGAAGAGGAGGATGAGGAGGAAGAACAAGAAGCAG
CTGCCTTGGATCTTTCTGTGAATCCTGCGTCTGTAGGGGGACGCCTTGTCTTCTCAGGCTCCAAAAAGAAATCAT
CTTCTAGCCTGGGCTCTGGCTCTTCACGGGATTCTATCTCTTCTGATTCAGAAACTAGTGAGCCTCTCTCCTGCC
GAGCCCAAGGGCAAACGGGAGTTCTCACTGTGCACAGTTATGCCAAAGGGGATGGCAGGGTCACTGTGGGAGAGC
CATGCACGAGGAAGAAAGGAAGCGCCGCTAGAAGTTTCAGTGAGCGGGAGCTGGCAGAGGTTGCAGATGAATACA
TGTTTTCCCTAGAAGAGAATAAGAAGTCCAAGGGACGCCGTCAGCCTTTAAGCAAGCTCCCCCGCCATCACCCAC
TTGTGCTGCAGGAGTGTGTCAGTGATGATGAGACATCTGAACAGCTGACCCCTGAGGAAGAGGCTGAGGAGACAG
AGGCCTGGGCCAAGCCTCTGAGCCAACTGTGGCAGAACCGACCTCCAAACTTTGAGGCTGAGAAGGAATTCAATG
AGACCATGGCCCAACAGGCCCCTCACTGCGCTGTCTGTATGATCTTCCAGACTTATCATCAGGTTGAATTTGGAG
GCTTTAATCAGAACTGTGGAAATGCTTCAGATTTAGCCCCCCAGAAGCAGAGGACCAAGCCATTGATTCCAGAAA
TGTGCTTCACTTCGACTGGCTGCAGCACGGACATCAACCTTTCTACTCCTTATCTTGAGGAGGATGGCACCAGCA
TACTCGTTTCCTGCAAGAAGTGCAGCGTCCGGGTCCATGCCAGTTGCTATGGGGTCCCCCCTGCAAAGGCTTCTG
AAGACTGGATGTGTTCTCGGTGTTCAGCCAATGCCCTAGAGGAGGACTGCTGTTTATGCTCATTACGAGGAGGGG
CCCTGCAGAGAGCAAATGATGACAGGTGGGTCCACGTTTCATGTGCTGTGGCAATTCTGGAAGCAAGGTTTGTCA
ACATTGCAGAAAGAAGTCCGGTGGATGTGAGCAAAATCCCCCTGCCCCGCTTCAAACTGAAATGTATCTTCTGTA
AGAAGCGGAGGAAAAGAACTGCTGGCTGCTGTGTGCAGTGTTCTCACGGCCGCTGCCCAACTGCCTTCCATGTGA
GCTGCGCCCAGGCTGCCGGTGTGATGATGCAGCCTGACGACTGGCCTTTTGTGGTCTTCATTACCTGCTTTCGGC
ACAAGATTCCTAATTTGGAGCGTGCCAAGGGGGCCTTGCAAAGCATCACTGCAGGCCAGAAAGTCATTAGCAAGC
ATAAGAACGGGCGCTTCTACCAGTGTGAAGTGGTCAGGCTCACCACCGAGACCTTCTATGAAGTCAACTTTGATG
ATGGCTCCTTCAGCGACAATCTTTATCCTGAGGACATAGTGAGCCAGGACTGTCTCCAGTTTGGTCCTCCTGCTG
AAGGGGAAGTGGTCCAAGTGAGATGGACAGACGGCCAAGTCTATGGAGCCAAGTTTGTGGCCTCCCACCCTATCC
AAATGTACCAGGTGGAGTTTGAGGATGGCTCACAACTTGTGGTTAAGAGAGATGATGTATACACACTGGATGAAG
AGCTTCCCAAGAGAGTCAAATCTAGACTGTCAGTAGCCTCAGACATGCGCTTCAATGAGATTTTCACAGAGAAAG
AGGTTAAGCAAGAAAAGAAACGGCAACGAGTTATCAACTCAAGATACCGGGAAGATTATATTGAGCCTGCACTAT
ACCGGGCCATCATGGAG**TAG**GTGCTTCCAGGGTCCAAGGGATTCTCAGCCATCCAGGCAAGAGCACTCTGGGTTC
CACAGCACAGCAGACATGGAACGCTGAAGTCTCTGAAAGTGAAGTTGTAAAAAGAAAAGGAATGAAATAACCGAC
CCATCATCTTCTCACCCACCCTCATTGCATTCCGCTGTAGTGAAAGGACGAGCCATTTCTGGGCACGTGGCAGCA
GTCGCTGATCTCCCAGCTGAGGGGCTGAGCACTGGAATGCTGTGGCTGCACTGGCCCCAGTCCATAGAGGGGTCA

FIGURE 202B

ACTATGCTGGCTGGACTGGCTGCCTTGTTCCTGGCCTAGGACTTAGCTTCATAACTATCACCTGCACCGACTAGG
CTGAGGTGCTGGTACTTGCCCCAACCCCTACTTTTGTATTTATATGTGTGTGTGTGTGTGCGTGCGTGCGTGCGT
GCGTGTATGTTTGGTCTGGACCAGCTTCTGCCAGCCCCTGGCCTTTACTTTCTTCCTTGCCTATGCAGGGCAAAC
AAAATGTGAAATTCTGCCCTCAGCTGAGCTGAGTAAGGGCTCCTGGGGGTTGGCTGGAGATGGGTGTGGCATCTG
TCCAGGCCTGGAACCGTCTCAAGACAGTGCTGGCAAAGCTGCAGTATTGAGATGCTAAGGAGCTGATGCCACCTC
TTTGTCTTCCCCTAAAGGAGAACATGGGGATAACATGGGTGTGTGCCCACAACACTCTAGGTGCAGAGCCCCTGT
GGCAAAGTATTACAGGGTGTGGGTGGGGATTACCCTGAATCGGGGATTTTAATGATGGAAGCAGGCAGAGCCTGG
TGGGTGATTCTGTCAACAGAAAATTGCAATCATGCAGGGGCTGGGAGGGTTAGGATGAAAAAACTGGGGCCATTG
GAGGCCCACTGTAGGTGGGAGGGAGCTGATTTTGGGGTGGGGGGTGGGACTAGAGGGCAATACTGAAGGGGTTAA
ACAGGTTTTTGCTCCTCAAGAATTTGTTTGCCTGGGCCCAGGATTGGAGGGCTTCACACCAATACCCTGTGTATA
CAAGAATCAGATTTATAATACTTCCCCTTTTTTGTTACGTATGAACACTATAAACCAAATTATTTTG

FIGURE 203

MASESETLNPSARIMTFYPTMEEFRNFSRYIAYIESQGAHRAGLAKVVPPKEWKPRASYDDIDDLVIPAPIQQLV
TGQSGLFTQYNIQKKAMTVREFRKIANSDKYCTPRYSEFEELERKYWKNLTFNPPIYGADVNGTLYEKHVDEWNI
GRLRTILDLVEKESGITIEGVNTPYLYFGMWKTSFAWHTEDMDLYSINYLHFGEPKSWYSVPPEHGKRLERLAKG
FFPGSAQSCEAFLRHKMTLISPLMLKKYGIPFDKVTQEAGEFMITFPYGYHAGFNHGFNCAESTNFATRRWIEYG
KQAVLCSCRKDMVKISMDVFVRKFQPERYKLWKAGKDNTVIDHTLPTPEAAEFLKESELPPRAGNEEECPEEDME
GVEDGEEGDLKTSLAKHRIGTKRHRVCLEIPQEVSQSELFPKEDLSSEQYEMTECPAALAPVRPTHSSVRQVEDG
LTFPDYSDSTEVKFEELKNVKLEEEDEEEEQEAAALDLSVNPASVGGRLVFSGSKKKSSSSLGSGSSRDSISSDS
ETSEPLSCRAQGQTGVLTVHSYAKGDGRVTVGEPCTRKKGSAARSFSERELAEVADEYMFSLEENKKSKGRRQPL
SKLPRHHPLVLQECVSDDETSEQLTPEEEAEETEAWAKPLSQLWQNRPPNFEAEKEFNETMAQQAPHCAVCMIFQ
TYHQVEFGGFNQNCGNASDLAPQKQRTKPLIPEMCFTSTGCSTDINLSTPYLEEDGTSILVSCKKCSVRVHASCY
GVPPAKASEDWMCSRCSANALEEDCCLCSLRGGALQRANDDRWVHVSCAVAILEARFVNIAERSPVDVSKIPLPR
FKLKCIFCKKRRKRTAGCCVQCSHGRCPTAFHVSCAQAAGVMMQPDDWPFVVFITCFRHKIPNLERAKGALQSIT
AGQKVISKHKNGRFYQCEVVRLTTETFYEVNFDDGSFSDNLYPEDIVSQDCLQFGPPAEGEVVQVRWTDGQVYGA
KFVASHPIQMYQVEFEDGSQLVVKRDDVYTLDEELPKRVKSRLSVASDMRFNEIFTEKEVKQEKKRQRVINSRYR
EDYIEPALYRAIME

FIGURE 204

AGTTACAGACAGCTGACC**ATG**GAAGCGAATGGGTTGGGACCTCAGGGTTTTCCGGAGCTGAAGAATGACACATTC
CTGCGAGCAGCCTGGGGAGAGGAAACAGACTACACTCCCGTTTGGTGCATGCGCCAGGCAGGCCGTTACTTACCA
GAGTTTAGGGAAACCCGGGCTGCCCAGGACTTTTTCAGCACGTGTCGCTCTCCTGAGGCCTGCTGTGAACTGACT
CTGCAGCCACTGCGTCGCTTCCCTCTGGATGCTGCCATCATTTTCTCCGACATCCTTGTTGTACCCCAGGCACTG
GGCATGGAGGTGACCATGGTACCTGGCAAAGGACCCAGCTTCCCAGAGCCATTAAGAGAAGAGCAGGACCTAGAA
CGCCTACGGGATCCAGAAGTGGTAGCCTCTGAGCTAGGCTATGTGTTCCAAGCCATCACCCTTACCCGACAACGA
CTGGCTGGACGTGTGCCGCTGATTGGCTTTGCTGGTGCCCCATGGACCCTGATGACATACATGGTTGAGGGTGGT
GGCTCAAGCACCATGGCTCAGGCCAAGCGCTGGCTCTATCAGAGACCTCAGGCTAGTCACCAGCTGCTTCGCATC
CTCACTGATGCTCTGGTCCCATATCTGGTAGGACAAGTGGTGGCTGGTGCCCAGGCATTGCAGCTGTTTGAGTCC
CATGCAGGGCATCTTGGCCCACAGCTCTTCAACAAGTTTGCACTGCCTTACATCCGTGATGTGGCCAAGCAAGTG
AAGGCCAGGTTGCGGGAGGCAGGCCTGGCACCAGTGCCCATGATCATCTTTGCTAAGGATGGGCATTTTGCCCTG
GAGGAGCTGGCCCAAGCTGGCTATGAGGTGGTTGGGCTTGACTGGACAGTGGCCCCAAAGAAAGCCCGGGAGTGT
GTGGGGAAGACGGTGACATTGCAGGGCAACCTGGACCCCTGTGCCTTGTATGCATCTGAGGAGGAGATCGGGCAG
TTGGTGAAGCAGATGCTGGATGACTTTGGACCACATCGCTACATTGCCAACCTGGGCCATGGGCTTTATCCTGAC
ATGGACCCAGAACATGTGGGCGCCTTTGTGGATGCTGTGCATAAACACTCACGTCTGCTTCGACAGAAC**TGA**GTG
TATACCTTTACCCTCAAGTACCACTAACACAGATGATTGATCGTTTCCAGGACAATAAAAGTTTCGGAGTTGAAC
TATTGTGTAGTTTTGTTTGTGAAAGATTGTGCCCATATCCTCAGTTCTTCTTAGCCTCTGCTCCTTCCCTGGGAA
CCCTCTCTATATCCTCTT

FIGURE 205

MEANGLGPQGFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFFSTCRSPEACCELTLQPLRR
FPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVP
LIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTDALVPYLVGQVVAGAQALQLFESHAGHLG
PQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVT
LQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQN

FIGURE 206

AGCTTTGCGCAGTGGCAGTATCGTAGCCAATGAGGTTTATCCGAGGCGCGATTATTGCTAATTGAAAACTTTTCC
CAATACCCCGCCATGACGACTTGAAATATAGTCGGCATTGGCAATTTTTGACAGTCTCTACGGAGACTGCATGTG
CTGGTGAAGCTCCTGGAAGTG**ATG**GAAGGAATGGACAAGGAGACGTTTGAGTTCAAGTTTGGGAAGGAACTAACA
TTCACCACTGTACTGAGTGACCAACAGGTGGTGGAGCTGATCCCTGGGGGTGCAGGCATCGTCGTGGGATATGGG
GACCGTTCTCGTTTCATCCAACTGGTCCAGAAGGCACGGCTAGAGGAGAGCAAGGAGCAGGTGGCAGCTATGCAG
GCAGGTCTGCTGAAGGTGGTACCACAGGCTGTGCTGGACTTGCTGACCTGGCAAGAGTTGGAGAAGAAAGTGTGT
GGGGATCCAGAGGTCACTGTGGATGCTCTGCGCAAGCTCACCCGGTTTGAGGACTTCGAGCCATCTGACTCGCGG
GTGCAGTATTTCTGGGAGGCACTGAACAACTTCACCAACGAGGACCGGAGCCGCTTCCTGCGCTTTGTCACGGGC
CGCAGTCGCCTGCCAGCACGGATCTACATCTACCCAGACAAGCTGGGCTACGAGACCACAGACGCGCTGCCCGAG
TCTTCCACTTGCTCCAGCACCCTCTTCCTGCCACACTATGCCAGTGCCAAGGTATGCGAGGAGAAGCTCCGCTAT
GCGGCCTACAACTGCGTGGCCATCGACACTGACATGAGCCCTTGGGAGGAG**TGA**GGCGTGCCGCCGGCTGTGGGA
CCAGCAAGACTGCACGTGTCCCTCTTGGCCTTGCCCAGGGCGAAGACACCTTCCCTGCCCTGGTTTGGCTGACGT
GCTCAGCAAAACCCCATGTGCCCTGCTCCTGTGTGCAGTTGGGGTAGGGGCAGCTGGCATGGTCAGGTAACACTA
GTGGCCCAGCCCCGCAGACCCACAAGCCCTACCCGTGCTGGGGCTTGCTTCCCGAGGTATTTCACCTCTTAAGAG
GGAATCTTCCACAAGCCCAGCACAAGCTGCCAGGCCTGAGCTACTTGAAGGGGCCATCTAGGTCCCCAACCCAT
GGACTTTGCCTCCATTTTCAGCTCCGCCTTTTTTCTCCTATTTTCTCTCTGGCTTTCTTCAGCCATGACTCACAA
CTAAAAACATAAAACACTGGAGGTTAGTGGAGGCCCCTCCCCAAGCAGGGAGCCTGGGATGGGCAGGGAGTGATA
GCCAAACTCCTTGGTCACCTGCTCCAAGAAGGAAGCAGTAGCTGAGCACCTGCCCTCACATACTGCTCTTTTCCC
CTCTCCCTCCACACCAGAGATGTGGTGAGCTCTGTTCTTCTACCAACCCAGTCTCAACACACAAAGTGCCACCAC
CTTCCCTGACTCAGAACCCACATCCACTCAATGTGAACTCTACTACCACGACCTCCCCATATTCCTCACTTCTCC
ATCACCTCCAGCCTGACTCCCTGTCTGCCCTTTCACCCCCAAGATTTTGCACAGGTTAAGGCCAGTTATGGCCTT
TTTGAAATCTGTAATAGCTCCCCTTTCCCCAACTCTAAAGCCTAGACCTTAAACCTGTTCCTAGAGCTATGCACA
CCCCTGCCCCAGTTTACCGTTCCTCCCTCAGGGCCTCCGTGACACTCCATGAAAAGAAGTTCTTGCATACCGGAA
AGTTGAATAAATGGATGAATTCAAAAAAAAAAAAAAAAA

FIGURE 207

MEGMDKETFEFKFGKELTFTTVLSDQQVVELIPGGAGIVVGYGDRSRFIQLVQKARLEESKEQVAAMQAGLLKVV
PQAVLDLLTWQELEKKVCGDPEVTVDALRKLTRFEDFEPSDSRVQYFWEALNNFTNEDRSRFLRFVTGRSRLPAR
IYIYPDKLGYETTDALPESSTCSSTLFLPHYASAKVCEEKLRYAAYNCVAIDTDMSPWEE

FIGURE 208

CACAATGGTGCGCATGAATGCCCTGGCAGATGCTCTCAAGAGCATCAACAATGCCGAAAAGAGAGGCAAACGCCA
GGTGCTTCTTAGGCCATGCTCCAAAGTCATCGTCCAGTTTCTCACTGTGATGATGAAGCATGGTTACATTGGCGA
ATTTGAAATCACTGATGATCACAGAGCTGGGAAAATTGTTGTGAACCTCACAGGCAGGCTAAACAAGTGTGGAGC
GATCAGCCCCAGATTTGATGTGCAACTCAAAGATCTGGAAAAATGGCAGAATAATCTGCTTCCATCCCGCCAGTT
TGATTTCATTGTACTGACAACCTCAGCTGGCATCATGGACCATGAAGCAAGACGAAAACACACAGGAGGGAAAAT
CCAGGGATTCTTTTTCTAGGGATGTAATACATATATTTACAAATAAAATGCCTCAAGGAC

FIGURE 209

MVRMNALADALKSINNAEKRGKRQVLLRPCSKVIVQFLTVMMKHGYIGEFEITDDHRAGKIVVNLTGRLNKCGAI
SPRFDVQLKDLEKWQNNLLPSRQFDFIVLTTSAGIMDHEARRKHTGGKIQGFFF

FIGURE 210

CTCTTTCCAGCCAGCGCCGAGCG**ATG**GGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAAACCGGGGGCAAGA
GAAAGCCCTACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCCCGCCGCA
TCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTGGACGTGGGGAATTTCTCCTGGG
GCTCAGAGTGTTGTACTCGTAAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTA
CCAAGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATG
CGCTGCCCCTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTAAACAAAAAACGATCTA
AAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGC
AGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCA
AAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCAAAGGCAAA**TAA**ATCCTTGTTTTGTCTTCACCCATGT
AATAAAGGTGTTTATTGTTTTGTTCCCACA

FIGURE 211

MGISRDNWHKRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGNKKYRALRLDVGNFSWGSECCTRK
TRIIDVVYNASNNELVRTKTLVKNCIVLIDSTPYRQWYESHYALPLGRKKGAKLTPEEEEILNKKRSKKIQKKYD
ERKKNAKISSLLEEQFQQGKLLACIASRPGQCGRADGYVLEGKELEFYLRKIKARKGK

FIGURE 212

ACGCTTGCGCGCGGGATTTAAACTGCGGCGGTTTACGCGGCGTTAAGACTTCGTAGGGTTAGCGAAATTGAGGTT
TCTTGGTATTGCGCGTTTCTCTTCCTTGCTGACTCTCCGAATGGCCATGGACTCGTCGCTTCAGGCCCGCCTGTT
TCCCGGTCTCGCTATCAAGATCCAACGCAGTAATGGTTTAATTCACAGTGCCAATGTAAGGACTGTGAACTTGGA
GAAATCCTGTGTTTCAGTGGAATGGGCAGAAGGAGGTGCCACAAAGGGCAAAGAGATTGATTTTGATGATGTGGC
TGCAATAAACCCAGAACTCTTACAGCTTCTTCCCTTACATCCGAAGGACAATCTGCCCTTGCAGGAAAATGTAAC
AATCCAGAAACAAAAACGGAGATCCGTCAACTCCAAAATTCCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCAC
TCGCATGTCCACTGTCTCAGAGCTTCGCATCACGGCTCAGGAGAATGACATGGAGGTGGAGCTGCCTGCAGCTGC
AAACTCCCGCAAGCAGTTTTCAGTTCCTCCTGCCCCCACTAGGCCTTCCTGCCCTGCAGTGGCTGAAATACCATT
GAGGATGGTCAGCGAGGAGATGGAAGAGCAAGTCCATTCCATCCGAGGCAGCTCTTCTGCAAACCCTGTGAACTC
AGTTCGGAGGAAATCATGTCTTGTGAAGGAAGTGGAAAAAATGAAGAACAAGCGAGAAGAGAAGAAGGCCCAGAA
CTCTGAAATGAGAATGAAGAGAGCTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTGCCCGAATGATTAA
AGAATTTCGGGCTACTTTGGAATGTCATCCACTTACTATGACTGATCCTATCGAAGAGCACAGAATATGTGTCTG
TGTTAGGAAACGCCCACTGAATAAGCAAGAATTGGCCAAGAAAGAAATTGATGTGATTTCCATTCCTAGCAAGTG
TCTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA
CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTCACAGCAAGGCCACTGGTACAGACAATCTT
TGAAGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGGCGGAGACCT
CTCTGGGAAAGCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTTCCTCCTGAAGAATCA
ACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCT
GCTCAACAAGAAGGCCAAGCTGCGCGTGCTGGAGGACGGCAAGCAACAGGTGCAAGTGGTGGGGCTGCAGGAGCA
TCTGGTTAACTCTGCTGATGATGTCATCAAGATGATCGACATGGGCAGCGCCTGCAGAACCTCTGGGCAGACATT
TGCCAACTCCAATTCCTCCCGCTCCCACGCGTGCTTCCAAATTATTCTTCGAGCTAAAGGGAGAATGCATGGCAA
GTTCTCTTTGGTAGATCTGGCAGGGAATGAGCGAGGCGCGGACACTTCCAGTGCTGACCGGCAGACCCGCATGGA
GGGCGCAGAAATCAACAAGAGTCTCTTAGCCCTGAAGGAGTGCATCAGGGCCCTGGGACAGAACAAGGCTCACAC
CCCGTTCCGTGAGAGCAAGCTGACACAGGTGCTGAGGGACTCCTTCATTGGGGAGAACTCTAGGACTTGCAGATT
GCCACGATCTCACCAGGCATAAGCTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAG
CTGAGCCCCCACAGTGGGCCCAGTGGAGAGCAGTTGATTCAAATGGAAACAGAAGAGATGGAAGCCTGCTCTAAC
GGGGCGCTGATTCCAGGCAATTTATCCAAGGAAGAGGAGGAACTGTCTTCCCAGATGTCCAGCTTTAACGAAGCC
ATGACTCAGATCAGGGAGCTGGAGGAGAAGGCTATGGAAGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGG
CTTGAGCTCTCTGAGATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCTG
GCCCAGCAAGCCAAGCATTTCTCAGCCCTGCGAGATGTCATCAAGGCCTTGCGCCTGGCCATGCAGCTGGAAGAG
CAGGCTAGCAGACAAATAAGCAGCAAGAAACGGCCCCAGTGACGACTGCAAATAAAAATCTGTTTGGTTTGACAC
CCAGCCTCTTCCCTGGCCCTCCCCAGAGAACTTTGGGTACCTGGTGGGTCTAGGCAGGGTCTGAGCTGGGACAGG
TTCTGGTAAATGCCAAGTATGGGGGCATCTGGGCCCAGGGCAGCTGGGGAGGGGGTCAGAGTGACATGGGACACT
CCTTTTCTGTTCCTCAGTTGTCGCCCTCACGAGAGGAAGGAGCTCTTAGTTACCCTTTTGTGTTGCCCTTCTTTC
CATCAAGGGGAATGTTCTCAGCATAGAGCTTTCTCCGCAGCATCCTGCCTGCGTGGACTGGCTGCTAATGGAGAG
CTCCCTGGGGTTGTCCTGGCTCTGGGGAGAGAGACGGAGCCTTTAGTACAGCTATCTGCTGGCTCTAAACCTTCT
ACGCCTTTGGGCCGAGCACTGAATGTCTTGTACTTTAAAAAAATGTTTCTGAGACCTCTTTCTACTTTACTGTCT
CCCTAGAGATCCTAGAGGATCCCTACTGTTTTCTGTTTTATGTGTTTATACATTGTATGTAACAATAAAGAGAAA
AAATAAA

FIGURE 213A

TAGGCAGGCGGCTGAGCCGGCGGCGGGTGGCCTGCCCAACGTGTGCTGGGTGGGAGAAGGCGAGGCGTCAGCGAT
GCTGTCTCTTCCGTGAGGAGCGCAGAGGAGGTCGCGGCGCCGGAGGCCCCAGAAGGCTCGAAGGCGCCGCGGGCT
GGGGTCGGTGGCTTAGGGAGCCCGTCCGGCCATGGTGGCCGCGGGTGGTGGTTGGCGCGGCTGCGCTGCGGCCCG
GGGCAGTGCGGAGCCGGGACAGTCGCGGCGCTGACGCCCGCGGGCCCCAGCTGCAGATATGAAGCGGAGCCGCTG
CCGCGACCGACCGCAGCCGCCGCCGCCCGACCGCCGGGAGGATGGAGTTCAGCGGGCAGCGGAGCTGTCTCAGTC
TTTGCCGCCGCGCCGGCGAGCGCCGCCCGGGAGGCAGCGGCTGGAGGAGCGGACGGGCCCCGCGGGGCCCGAGGG
CAAGGAGCAGGATGTAGTAACTGGAGTTAGTCCCCTGCTCTTCAGGAAACTCAGTAATCCTGACATATTTTCATC
CACTGGAAAAGTTAAACTTCAGCGACAACTGAGTCAGGATGATTGTAAGTTATGGAGAGGAAACCTGGCCAGCTC
TCTATCGGGTAAGCAGCTGCTCCCTTTGTCCAGCAGTGTACATAGCAGTGTGGGACAGGTGACTTGGCAGTCGTC
AGGAGAAGCATCAAACCTGGTTCGAATGAGAAACCAGTCCCTTGGACAGTCTGCACCTTCTCTTACTGCTGGCCT
GAAGGAGTTGAGCCTTCCAAGAAGAGGCAGCTTTTGTCGGACAAGTAACCGCAAGAGCTTGATTGTGACCTCTAG
CACATCACCTACACTACCACGGCCACACTCACCACTCCATGGCCACACAGGTAACAGTCCTTTGGACAGCCCCCG
GAATTTCTCTCCAAATGCACCTGCTCACTTTTCTTTTGTTCCTGCCCGTAGGACTGATGGGCGGCGCTGGTCTTT
GGCCTCTTTGCCCTCTTCAGGATATGGAACTAACACTCCTAGCTCCACTGTCTCATCATCATGCTCCTCACAGGA
AAAGCTGCATCAGTTGCCTTTCCAGCCTACAGCTGATGAGCTGCACTTTTTGACGAAGCATTTCAGCACAGAGAG
CGTACCAGATGAGGAAGGACGGCAGTCCCCAGCCATGCGGCCTCGCTCCCGGAGCCTCAGTCCCGGACGATCCCC
AGTATCCTTTGACAGTGAAATAATAATGATGAATCATGTTTACAAAGAAAGATTCCCAAAGGCCACCGCACAAAT
GGAAGAGCGACTAGCAGAGTTTATTTCCTCCAACACTCCAGACAGCGTGCTGCCCTTGGCAGATGGAGCCCTGAG
CTTTATTCATCATCAGGTGATTGAGATGGCCCGAGACTGCCTGGATAAATCTCGGAGTGGCCTCATTACATCACA
ATACTTCTACGAACTTCAAGATAATTTGGAGAAACTTTTACAAGATGCTCATGAGCGCTCAGAGAGCTCAGAAGT
GGCTTTTGTGATGCAGCTGGTGAAAAAGCTGATGATTATCATTGCCCGCCCAGCACGTCTCCTGGAATGCCTGGA
GTTTGACCCTGAAGAGTTCTACCACCTTTTAGAAGCAGCTGAGGGCCACGCCAAAGAGGGACAAGGGATTAAATG
TGACATTCCCCGCTACATCGTTAGCCAGCTGGGCCTCACCCGGGATCCCCTAGAAGAAATGGCCCAGTTGAGCAG
CTGTGACAGTCCTGACACTCCAGAGACAGATGATTCTATTGAGGGCCATGGGGCATCTCTGCCATCTAAAAAGAC
ACCCTCTGAAGAGGACTTCGAGACCATTAAGCTCATCAGCAATGGCGCCTATGGGGCTGTATTTCTGGTGCGGCA
CAAGTCCACCCGGCAGCGCTTTGCCATGAAGAAGATCAACAAGCAGAACCTGATCCTACGGAACCAGATCCAGCA
GGCCTTCGTGGAGCGTGACATACTGACTTTCGCTGAGAACCCCTTTGTGGTCAGCATGTTCTGCTCCTTTGATAC
CAAGCGCCACTTGTGCATGGTGATGGAGTACGTTGAAGGGGGAGACTGTGCCACTCTGCTGAAGAATATTGGGGC
CCTGCCTGTGGACATGGTGCGTCTATACTTTGCGGAAACTGTGCTGGCCCTGGAGTACTTACACAACTATGGCAT
CGTGCACCGTGACCTCAAGCCTGACAACCTCCTAATTACATCCATGGGGCACATCAAGCTCACGGACTTTGGACT
GTCCAAAATTGGCCTCATGAGTCTGACAACGAACTTGTATGAGGGTCATATTGAAAAGGATGCCCGGGAATTCCT
GGACAAGCAGGTATGCGGGACCCCAGAATACATTGCGCCTGAGGTGATCCTGCGCCAGGGCTATGGGAAGCCAGT
GGACTGGTGGGCCATGGGCATTATCCTGTATGAGTTCCTGGTGGGCTGCGTCCCTTTTTTTGGAGATACTCCGGA
GGAGCTCTTTGGGCAGGTGATCAGTGATGAGATTGTGTGGCCTGAGGGTGATGAGGCACTGCCCCCAGACGCCCA
GGACCTCACCTCCAAACTGCTCCACCAGAACCCTCTGGAGAGACTTGGCACAGGCAGTGCCTATGAGGTGAAGCA
GCACCCATTCTTTACTGGTCTGGACTGGACAGGACTTCTCCGCCAGAAGGCTGAATTTATTCCTCAGTTGGAGTC
AGAGGATGATACTAGCTATTTTGACACCCGCTCAGAGCGATACCACCACATGGACTCGGAGGATGAGGAAGAAGT
GAGTGAGGATGGCTGCCTTGAGATCCGCCAGTTCTCTTCCTGCTCTCCAAGGTTCAACAAGGTGTACAGCAGCAT
GGAGCGGCTCTCACTGCTCGAGGAGCGCCGGACACCACCCCCGACCAAGCGCAGCCTGAGTGAGGAGAAGGAGGA
CCATTCAGATGGCCTGGCAGGGCTCAAAGGCCGAGACCGGAGCTGGGTGATTGGCTCCCCTGAGATATTACGGAA
GCGGCTGTCGGTGTCTGAGTCATCCCACACAGAGAGTGACTCAAGCCCTCCAATGACAGTGCGACGCCGCTGCTC
AGGCCTCCTGGATGCGCCTCGGTTCCCGGAGGGCCCTGAGGAGGCCAGCAGCACCCTCAGGAGGCAACCACAGGA
GGGTATATGGGTCCTGACACCCCCATCTGGAGAGGGGGTATCTGGGCCTGTCACTGAACACTCAGGGGAGCAGCG
GCCAAAGCTGGATGAGGAAGCTGTTGGCCGGAGCAGTGGTTCCAGTCCAGCTATGGAGACCCGAGGCCGTGGGAC
CTCACAGCTGGCTGAGGGAGCCACAGCCAAGGCCATCAGTGACCTGGCTGTGCGTAGGGCCCGCCACCGGCTGCT
CTCTGGGGACTCAACAGAGAAGCGCACTGCTCGCCCTGTCAACAAAGTGATCAAGTCCGCCTCAGCCACAGCCCT
CTCACTCCTCATTCCTTCGGAACACCACACCTGCTCCCCGTTGGCCAGCCCCATGTCCCCACATTCTCAGTCGTC
CAACCCATCATCCCGGGACTCTTCTCCAAGCAGGGACTTCTTGCCAGCCCTTGGCAGCATGAGGCCTCCCATCAT

FIGURE 213B

CATCCACCGAGCTGGCAAGAAGTATGGCTTCACCCTGCGGGCCATTCGCGTCTACATGGGTGACTCCGATGTCTA
CACCGTGCACCATATGGTGTGGCACGTGGAGGATGGAGGTCCGGCCAGTGAGGCAGGGCTTCGTCAAGGTGACCT
CATCACCCATGTCAATGGGGAACCTGTGCATGGCCTGGTGCACACGGAGGTGGTAGAGCTGATCCTGAAGAGTGG
AAACAAGGTGGCCATTTCAACAACTCCCCTGGAGAACACATCCATTAAAGTGGGGCCAGCTCGGAAGGGCAGCTA
CAAGGCCAAGATGGCCCGAAGGAGCAAGAGGAGCCGCGGCAAGGATGGGCAAGAAAGCAGAAAAAGGAGCTCCCT
GTTCCGCAAGATCACCAAGCAAGCATCCCTGCTCCACACCAGCCGCAGCCTTTCTTCCCTTAACCGCTCCTTGTC
ATCAGGGGAGAGTGGGCCAGGCTCTCCCACACACAGCCACAGCCTTTCCCCCCGATCTCCCACTCAAGGCTACCG
GGTGACCCCCGATGCTGTGCATTCAGTGGGAGGGAATTCATCACAGAGCAGCTCCCCCAGCTCCAGCGTGCCCAG
TTCCCCAGCCGGCTCTGGGCACACACGGCCCAGCTCCCTCCACGGTCTGGCACCCAAGCTCCAACGCCAGTACCG
CTCTCCACGGCGCAAGTCAGCAGGCAGCATCCCACTGTCACCACTGGCCCACACCCCTTCTCCCCCACCCCCAAC
AGCTTCACCTCAGCGGTCCCCATCGCCCCTGTCTGGCCATGTAGCCCAGGCCTTTCCCACAAAGCTTCACTTGTC
ACCTCCCCTGGGCAGGCAACTCTCACGGCCCAAGAGTGCGGAGCCACCCCGTTCACCACTACTCAAGAGGGTGCA
GTCGGCTGAGAAACTGGCAGCAGCACTTGCCGCCTCTGAGAAGAAGCTAGCCACTTCTCGCAAGCACAGCCTTGA
CCTGCCCCACTCTGAACTAAAGAAGGAACTGCCGCCCAGGGAAGTGAGCCCTCTGGAGGTAGTTGGAGCCAGGAG
TGTGCTGTCTGGCAAGGGGGCCCTGCCAGGGAAGGGGGTGCTGCAGCCTGCTCCCTCACGGGCCCTAGGCACCCT
CCGGCAGGACCGAGCCGAACGACGGGAGTCGCTGCAGAAGCAAGAAGCCATTCGTGAGGTGGACTCCTCAGAGGA
CGACACCGAGGAAGGGCCTGAGAACAGCCAGGGTGCACAGGAGCTGAGCTTGGCACCTCACCCAGAAGTGAGCCA
GAGTGTGGCCCCTAAAGGAGCAGGAGAGAGTGGGGAAGAGGATCCTTTCCCGTCCAGAGACCCTAGGAGCCTGGG
CCCAATGGTCCCAAGCCTATTGACAGGGATCACACTGGGGCCTCCCAGAATGGAAAGTCCCAGTGGTCCCCACAG
GAGGCTCGGGAGCCCACAAGCCATTGAGGAGGCTGCCAGCTCCTCCTCAGCAGGCCCCAACCTAGGTCAGTCTGG
AGCCACAGACCCCATCCCTCCTGAAGGTTGCTGGAAGGCCCAGCACCTCCACACCCAGGCACTAACAGCACTTTC
TCCCAGCACTTCGGGACTCACCCCCACCAGCAGTTGCTCTCCTCCCAGCTCCACCTCTGGGAAGCTGAGCATGTG
GTCCTGGAAATCCCTTATTGAGGGCCCAGACAGGGCATCCCCAAGCAGAAAGGCAACCATGGCAGGTGGGCTAGC
CAACCTCCAGGATTTGGAAAACACAACTCCAGCCCAGCCTAAGAACCTGTCTCCCAGGGAGCAGGGGAAGACACA
GCCACCTAGTGCCCCCAGACTGGCCCATCCATCTTATGAGGATCCCAGCCAGGGCTGGCTATGGGAGTCTGAGTG
TGCACAAGCAGTGAAAGAGGATCCAGCCCTGAGCATCACCCAAGTGCCTGATGCCTCAGGTGACAGAAGGCAGGA
CGTTCCATGCCGAGGCTGCCCCCTCACCCAGAAGTCTGAGCCCAGCCTCAGGAGGGGCCAAGAACCAGGGGGCCA
TCAAAAGCATCGGGATTTGGCATTGGTTCCAGATGAGCTTTTAAAGCAAACATAGCAGTTGTTTGCCATTTCTTG
CACTCAGACCTGTGTAATATATGCTCCTGGAAACC

FIGURE 214

GCAAG**ATG**GTGGGTGAAAAAGTTGAGAAGCCAGATGCTAAAGAGAAGAAACCCAAAGCCAAGAAGGCTGATGTTG
GTGGCAAGGTGAAAAAGGGTAACCTCAAGGCTAAAAAGCCCAAGAAGGGAAAGCCCCATTGCAGCCGCAACCCTG
TCCTTGTCAGAGGAATTGGCAGGTATTGCCGATCTGCCATGTATTCCAGAAAGGCCATGTACAAGAGGAAGTACT
CAGCCGCTAAATCTAAGGTTGAAAAGAAAAAGAAGGAGAAGGTTCTTGCAACTGTTACAAAACCAGTTGGTTGTG
ACAAGAATGGCGGTGCCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAA
AGCTGTTGAGCCATGGCAAAAAATCCTTCAGTCAGCACGTGAGGCCA**TAG**GGGCAAGAAGGTGGTTTTCCTGAAG
CAGCTGGCTAGTGGTTTGTTACTTGTGACTGGACCTCTGGTCCTCAATCGAATTCCTCTACGAAGAACATACCAG
AAATTTGTCATTGCCAC

FIGURE 215

MVGEKVEKPDAKEKKPKAKKADVGGKVKKGNLKAKKPKKGKPHCSRNPVLVRGIGRYCRSAMYSRKAMYKRKYSA
AKSKVEKKKKEKVLATVTKPVGCDKNGGARVVKLRKMPRYYPTEDVPRKLLSHGKKSFSQHVRP

FIGURE 216

AATCTGCCATTTTCTGTCCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTTCTCGCAGGCTCTATTCCGT
TCGCTGGTTCGCCACCTCAGGGGAACG**ATG**GCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGAGCTGGTT
TCTGCCGACAAAATTGAAGATGTTCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGT
GAAGCTAAGAAACTATTGGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTC
CAGGAAGCAGCTAGTCTTTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTTCTAT
GGGAAATCACTTCTGGAGTTGGCAAGAATGGAGAATGGTGTGTTGGGAAACGCCTTGGAAGGTGTGCATGTGGAA
GAGGAAGAAGGAGAAAAAACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAA
GAGTTGAGAGAACAGGTTTATGACGCCATGGGAGAAAAAGAAGAAGCCAAAAAAACAGAAGACAAGTCTTTGGCA
AAGCCTGAAACTGATAAAGAACAGGACAGTGAAATGGAGAAGGGTGGAAGAGAAGATATGGATATAAGTAAATCT
GCAGAGGAGCCACAGGAAAAAGTTGACTTGACTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGA
GCAGCACCAGAAGGACCGAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAA
GAAAAATCAGTTTCTGGAACTGATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTCAGGAGAAGCAGGGAGAGGTA
ATTGTGAGCATAGAGGAGAAGCCAAAAGAAGTTTCAGAAGAGCAGCCTGTGGTGACTCTAGAAAAGCAGGGCACT
GCAGTGGAGGTAGAAGCAGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAG
AAGGTAGTTACCTCTGAAAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCT
GAAGAGTCACCAGAGGTGACAACAGAGGCTGCAGAGGCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAG
CCTGGGCAGGAGGCTCCAGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCT
ATTGAACCACAGACTTCTATAGAAAGACTGACAGAAACAAAAGATGGCTCAGGACTAGAGGAGAAGGTCAGGGCA
AAGCTGGTTCCTAGTCAGGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACC
AAGGTAGCCCAGGGAGCTACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAG
AGAGAAGAACAGATGAAAGAGGGTGAAGAAACTGAAGGCTCAGAAGAGGATGATAAAGAAAATGATAAGACCGAA
GAAATGCCAAATGATTCAGTCCTTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAG
CTTGCCTGGGATATGCTGGATTTAGCAAAGATCATTTTTAAAAGGCAAGAAACAAAAGAAGCACAGCTTTATGCT
GCCCAGGCACATCTTAAACTCGGAGAAGTTAGTGTTGAATCTGAAAACTATGTGCAAGCTGTGGAGGAGTTCCAG
TCCTGCCTTAACCTGCAGGAACAGTACCTGGAAGCCCACGACCGTCTCCTTGCAGAGACCCACTACCAGCTGGGC
TTGGCTTATGGGTACAACTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAAC
AGAATGGCTGTACTAAACGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGCTGAATACAAGAAAGAAATTGAGGAA
CTAAAGGAACTGCTACCCGAAATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCT
GAACTGGCTCTGAAAGCTACTCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTC
TCCATGATTGCCAGTAGAAAGCCAACAGACGGTGCTTCCTCATCAAATTGTGTGACTGATATTTCCCACCTTGTC
AGAAAGAAGAGGAAACCAGAGGAAGAGAGTCCCCGGAAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTG
AACGGAGGCAGTGGGGATGCTGTCCCCAGTGGAAATGAAGTTTCGGAAAACATGGAGGAGGAGGCTGAGAATCAG
GCTGAAAGCCGGGCAGCAGTGGAGGGGACAGTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGT**TAA**GAGGGG
GCACAGCCCTCCTCCCAAGGGAAAGTGTTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATTCTTTTTGTAT
AACTTCAATAAAGATTGTAAGCAAAGGTTGAGGCTTTGATGGTTTTTTTCTTAATTATTGGCTGAATCTGCCTTG
GAGCACTGCTGGTTTTATATATTAGCCAAAGGTTTTGTTCTGGCCTTCTGTACTGATCTGTGTTCCTGATCCTAA
TTCCTATCTGTCTAACGTGGAGGTGATCAAGTGTGGCTGTAGGCCTTTGTTTTCCAATGGTGCTATATTCTGTTT
TCAAACACTTCACTGAACCCAGCTGTCTTGCAAACTTTCAGTGGTGCTGTCCCTGGATGGGGGCTACAAAAACAA
GAATTGGTGAAGATCTTGCTCTTCAGTGCTGAAAATGGATGATGGACTTTGGCTGTGAGCCAGGCCTAGGATGGT
TCTTGTCCTATATCCACCTAGTCTTCACCTGGGGCTATAATTCTGTCCTGGAAAAAGAACTCTGAAAACCTGGGT
CAGGGGAATGATTCCTAAGGAAAACGGTCTGCATTTGAGCTCTGGTTTGAAAGTAGCCAAGGGGACTGATGGTGG
ACACTCCAGATGTGGTTGGAAGCATATGTGGGGAGGCTGGCTGGTTGAGTTTTGTTATTTTCTGTATAGAAAGGT
TGAGATATATCAACACTTGGAATTGTTACCCATCTGCAGAATTGACTTCTCAAATAAAGATGCTAAAAATCT

FIGURE 217

MAMESTATAAVAAELVSADKIEDVPAPSTSADKVESLDVDSEAKKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGVLGNALEGVHVEEEEGEKTEDESLVENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAAPEGPNEA
EVTSGKPEQEVPDAEEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKEVSEEQPVVTLEKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAEESPEVTTEAAEASAVEAGSEVSEKPGQEAPVLP
KDGAVNGPSVVGDQTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDSVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQAHLKLGEVSVESENYVQAVEEFQSCLNLQEQYLEAHDRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSIEVIENRMAVLNEQVKEAEGSSAEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLV
ESSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVP
SGNEVSENMEEEAENQAESRAAVEGTVEAGATVESTAC

FIGURE 218

AGCCAGAAATGTGAAGTGCTAGCTGAAGGATGAGCAGCAGCTAGCCAGGCAAAGGGGGCA**ATG**GCGGCTTCCTGT
GTTCTACTGCACACTGGGCAGAAGATGCCTCTGATTGGTCTGGGTACCTGGAAGAGTGAGCCTGGTCAGGTAAAA
GCAGCTGTTAAGTATGCCCTTAGCGTAGGCTACCGCCACATTGATTGTGCTGCTATCTACGGCAATGAGCCTGAG
ATTGGGGAGGCCCTGAAGGAGGACGTGGGACCAGGCAAGGCGGTGCCTCGGGAGGAGCTGTTTGTGACATCCAAG
CTGTGGAACACCAAGCACCACCCCGAGGATGTGGAGCCTGCCCTCCGGAAGACTCTGGCTGACCTCCAGCTGGAG
TATCTGGACCTGTACCTGATGCACTGGCCTTATGCCTTTGAGCGGGGAGACAACCCCTTCCCCAAGAATGCTGAT
GGGACTATATGCTACGACTCCACCCACTACAAGGAGACTTGGAAGGCTCTGGAGGCACTGGTGGCTAAGGGGCTG
GTGCAGGCGCTGGGCCTGTCCAACTTCAACAGTCGGCAGATTGATGACATACTCAGTGTGGCCTCCGTGCGTCCA
GCTGTCTTGCAGGTGGAATGCCACCCATACTTGGCTCAAAATGAGCTAATTGCCCACTGCCAAGCACGTGGCTTG
GAGGTAACTGCTTATAGCCCTTTGGGCTCCTCTGATCGTGCATGGCGTGATCCTGATGAGCCTGTCCTGCTGGAG
GAACCAGTAGTCCTGGCATTGGCTGAAAAGTATGGCCGATCTCCAGCTCAGATCTTGCTCAGGTGGCAGGTCCAG
CGGAAAGTGATCTGCATCCCCAAAAGTATCACTCCTTCTCGAATCCTTCAGAACATCAAGGTGTTTGACTTCACC
TTTAGCCCAGAAGAGATGAAGCAGCTAAATGCCCTGAACAAAAATTGGAGATATATTGTGCCTATGCTTACGGTG
GATGGGAAGAGAGTCCCAAGGGATGCAGGGCATCCTCTGTACCCCTTTAATGACCCGTAC**TGA**GACCACAGCTTC
TTGGCCTCCCTTCCAGCTCTGCAGCTAATGAGGTCCTGCCACAACGGAAAGAGGGAGTTAATAAAGCCATTGGAG
CATCCAT

FIGURE 219

MAASCVLLHTGQKMPLIGLGTWKSEPGQVKAAVKYALSVGYRHIDCAAIYGNEPEIGEALKEDVGPGKAVPREEL
FVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTICYDSTHYKETWKALEAL
VAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRDPDE
PVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIV
PMLTVDGKRVPRDAGHPLYPFNDPY

FIGURE 220

GTTCTTGCCTGGTGTCGGTGGTTAGTTTCTGCGACTTGTGTTGGGACTGCTGATAGGAAG**ATG**TCTTCAGGAAAT
GCTAAAATTGGGCACCCTGCCCCCAACTTCAAAGCCACAGCTGTTATGCCAGATGGTCAGTTTAAAGATATCAGC
CTGTCTGACTACAAAGGAAAATATGTTGTGTTCTTCTTTTACCCTCTTGACTTCACCTTTGTGTGCCCCACGGAG
ATCATTGCTTTCAGTGATAGGGCAGAAGAATTTAAGAAACTCAACTGCCAAGTGATTGGTGCTTCTGTGGATTCT
CACTTCTGTCATCTAGCATGGGTCAATACACCTAAGAAACAAGGAGGACTGGGACCCATGAACATTCCTTTGGTA
TCAGACCCGAAGCGCACCATTGCTCAGGATTATGGGGTCTTAAAGGCTGATGAAGGCATCTCGTTCAGGGGCCTT
TTTATCATTGATGATAAGGGTATTCTTCGGCAGATCACTGTAAATGACCTCCCTGTTGGCCGCTCTGTGGATGAG
ACTTTGAGACTAGTTCAGGCCTTCCAGTTCACTGACAAACATGGGGAAGTGTGCCCAGCTGGCTGGAAACCTGGC
AGTGATACCATCAAGCCTGATGTCCAAAAGAGCAAAGAATATTTCTCCAAGCAGAAG**TGA**GCGCTGGGCTGTTTT
AGTGCCAGGCTGCGGTGGGCAGCCATGAGAACAAAACCTCTTCTGTATTTTTTTTTTCCATTAGTAAAACACAAG
ACTTCAGATTCAGCCGAATTGTGGTGTCTTACAAGGCAGGCCTTTCCTACAGGGGGTGGAGAGACCAGCCTTTCT
TCCTTTGGTAGGAATGGCCTGAGTTGGCGTTGTGGGCAGGCTACTGGTTTGTATGATGTATTAGTAGAGCAACCC
ATTAATCTTTTGTAGTTTGTATTAAACTTGAACTGAG

FIGURE 221

MSSGNAKIGHPAPNFKATAVMPDGQFKDISLSDYKGKYVVFFFYPLDFTFVCPTEIIAFSDRAEEFKKLNCQVIG
ASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGLFIIDDKGILRQITVNDLPVG
RSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQKSKEYFSKQK

FIGURE 222

GCTCGGCTCACTGAGACCCGGTGGTCCAGACGCTGCTCCTGGCTGGGGTGGCGCTGCAGGGAGAACCGCGAGCTC
TCAGGGGTCGGCGGGTGACTTCTTTCCGGAAGAAAGCGAGGAACGCGCTCTGCGGGGTGAGCCGGACTCCCCAAC
TCCGGACGATCAGCCCAGGACTGAGAGCCCCGAAGTCCCCAACCACAAGTAAGCGGCCCCAGAAGGACAAGTCTA
GGTCGCCGTCCAGAGCGCC**ATG**GCCGCGCCCGCCCTTCGTTTGTGCCACATCGCCTTCCACGTGCCCGCCGGGCA
GCCCCTAGCCCGGAACCTGCAGCGCCTCTTCGGCTTCCAGCCCCTGGCTTCGCGGGAGGTGGACGGCTGGCGGCA
GCTAGCCCTGCGCAGCGGCGACGCGGTCTTTTTGGTGAACGAGGGCGCAGGGTCTGGAGAGCCGCTGTACGGCCT
GGATCCGCGTCACGCCGTGCCCAGCGCCACAAACCTGTGCTTCGACGTGGCGGACGCCGGCGCTGCAACCCGGGA
GCTGGCAGCGCTGGGCTGCAGCGTGCCTGTCCCTCCCGTTCGCGTGCGGGACGCGCAGGGTGCCGCCACTTACGC
CGTGGTCAGCTCGCCTGCCGGCATCCTCAGCCTGACCTTGCTGGAGCGCGCTGGCTACCGCGGACCCTTCCTACC
CGGCTTCAGGCCCGTGTCCTCTGCGCCTGGCCCCGGGTGGGTCAGCCGCGTGGACCACCTGACCTTGGCCTGCAC
CCCCGGCAGCTCCCCCACACTTTTGCGCTGGTTCCACGACTGCCTGGGCTTTTGCCACTTGCCGCTGAGCCCAGG
TGAGGATCCCGAGCTGGGCCTCGAAATGACAGCAGGGTTTGGGCTTGGGGGACTGAGGCTTACAGCCCTGCAGGC
CCAGCCGGGCAGCATTGTCCCCACTCTTGTTCTGGCTGAGTCCCTTCCGGGGGCGACGACACGACAGGACCAGGT
GGAGCAGTTCCTGGCCCGGCACAAGGGGCCAGGCCTGCAGCACGTGGGGCTGTATACGCCTAACATTGTGGAGGC
CACTGAGGGGGTGGCAACTGCTGGAGGCCAGTTCCTGGCTCCCCCTGGGGCATACTACCAGCAGCCAGGAAAGGA
GAGGCAGATCCGAGCTGCAGGGCACGAGCCTCATCTGCTTGCTCGACAGGGGATCCTGCTAGATGGTGATAAAGG
CAAGTTTCTGCTTCAGGTCTTCACCAAGTCCCTTTTTACTGAGGACACTTTCTTCCTGGAGCTGATTCAGAGGCA
GGGGGCCACTGGCTTTGGTCAGGGCAACATCAGAGCTCTGTGGCAGTCCGTACAGGAGCAATCTGCCAGGAGCCA
GGAAGCC**TAA**GGATGCCCAGGGCTGGGTGCAGCCAGCTGTCCTGCAGCTCTGGGGAGACCAGCACAGAACTGAGG
AACATCTGCAGGAGGCCCAACTAGTGAAAGGCTTTGCCTCCGGGGGGCAGGTGTGACTTCCATTTCATCAGTGCC
TGCCAGAAGCTGTGTCTCTCATTGGGCTCCAAAGAGGTGGGATTTTTTAAAACTAAAACATTTCTTATATACAGT
CTATAATAAATATGTAAGATACAAAGAACAATAAAAGAATTACACACTAGGAAAAAAAAAAAAAAAAAAA

FIGURE 223

MAAPALRLCHIAFHVPAGQPLARNLQRLFGFQPLASREVDGWRQLALRSGDAVFLVNEGAGSGEPLYGLDPRHAV
PSATNLCFDVADAGAATRELAALGCSVPVPPVRVRDAQGAATYAVVSSPAGILSLTLLERAGYRGPFLPGFRPVS
SAPGPGWVSRVDHLTLACTPGSSPTLLRWFHDCLGFCHLPLSPGEDPELGLEMTAGFGLGGLRLTALQAQPGSIV
PTLVLAESLPGATTRQDQVEQFLARHKGPGLQHVGLYTPNIVEATEGVATAGGQFLAPPGAYYQQPGKERQIRAA
GHEPHLLARQGILLDGDKGKFLLQVFTKSLFTEDTFFLELIQRQGATGFGQGNIRALWQSVQEQSARSQEA

FIGURE 224

GACCACGATGAGTGTGCCGCACTTCCGGCCAGATCGCCGGATTTCCGCTGAGTGACCCTTACAAGTCCTTCTTGA
TCCTGAACTGGGTTAGGTGCCGCTGTTGCTGCTCGTGTTGAATCTAGAACCGTAGCCAGAC**ATG**GGACTGGAGGA
CGAGCAAAAGATGCTTACCGAATCCGGAGATCCTGAGGAGGAGGAAGAGGAAGAGGAGGAATTAGTGGATCCCCT
AACAACAGTGAGAGAGCAATGCGAGCAGTTGGAGAAATGTGTAAAGGCCCGGGAGCGGCTAGAGCTCTGTGATGA
GCGTGTATCCTCTCGATCACATACAGAAGAGGATTGCACGGAGGAGCTCTTTGACTTCTTGCATGCGAGGGACCA
TTGCGTGGCCCACAAACTCTTTAACAACTTGAAA**TAA**ATGTGTGGACTTAATTCACCCCAGTCTTCATCATCTGG
GCATCAGAATATTTCCTTATGGTTTTGGATGTACCATTTGTTTCTTATTTGTGTAACTGTAAGTTCACATGAACC
TCATGGGTTTGGCTTAGGCTGGTAGCTTCTATGTAATTCGCAATGATTCCATCTAAATAAAAGTTCTATGATCTG
C

FIGURE 225

MGLEDEQKMLTESGDPEEEEEEEEELVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSHTEEDCTEELFDFL
HARDHCVAHKLFNNLK

FIGURE 226

CGCGCCTGAGGAGGAGGAGGAGGCGGGGGCGGCC**ATG**GCTGCTGTGGTGGTGGCGGCTGCGGGTGGCGCGGGACC
GGCGGTCCTGCAGGTGGCCGGTCTCTACCGGGGCCTGTGCGCGGTGCGCAGCCGCGCCCTGGGCCTGGGGCTCGT
GTCACCCGCGCAGCTGCGCGTCTTCCCAGTGCGCCCCGGCTCGGGCCGGCCCGAGGGGGGCGCCGACAGCAGCGG
GGTCGGGGCCGAGGCCGAGCTCCAGGCCAACCCTTTCTACGACCGCTACCGCGACAAGATCCAGCTGCTGCGCAG
GTCAGACCCAGCTGCTTTTGAGTCCCGCCTGGAGAAACGCAGTGAATTTCGGAAGCAGCCAGTGGGGCATTCCAG
GCAAGGTGATTTTATCAAATGTGTGGAACAGAAGACAGATGCCTTGGGGAAACAGTCTGTGAACAGAGGATTCAC
TAAGGACAAGACTCTCAGTTCAATCTTTAACATTGAGATGGTAAAAGAAAAAACTGCAGAAGAAATAAAACAGAT
TTGGCAGCAATATTTTGCAGCAAAAGATACAGTCTACGCAGTTATTCCTGCAGAAAAGTTTGATTTGATCTGGAA
CCGGGCTCAGTCCTGTCCAACATTTCTATGTGCTCTGCCAAGAAGGGAAGGTTATGAGTTTTTTGTAGGACAATG
GACAGGTACTGAACTCCACTTCACTGCACTTATAAATATTCAGACCCGAGGGGAAGCTGCAGCCAGCCAGCTGAT
TTTATATCACTATCCTGAACTTAAGGAAGAAAAGGGCATAGTGCTGATGACTGCAGAAATGGATTCCACATTTCT
GAATGTTGCTGAGGCACAGTGCATCGCCAACCAAGTTCAGCTCTTCTACGCTACTGATCGGAAAGAGACCTACGG
GTTAGTGGAGACCTTTAACCTCAGACCAAATGAGTTCAAATATATGTCTGTCATCGCTGAATTGGAGCAAAGCGG
ACTTGGAGCAGAACTGAAATGTGCCCAGAACCAAAATAAGACT**TAG**AACTGTACAGGTTGGCCCTTCACCTAGTT
GACTCAGCCCTCGATAGTCTAGAGCCCACCCCCTCCTCAGGAACTCAAGAGCTCAGCATTTATAATGAGCAGTTG
GTAATGAGTTGCCCTATGTGCTTGTCGCAAGCAGTCACAGAGATGAGCCCTATTACTTGATATTCAGGAACAAAG
GTACCTGAACATTCTGATAATTATCTCAGCATACTTGAGGTTTCCTTTTTTAAGTGTTCGAGGTTATAACAAGAG
ACAGCCAAGGACCTACAAGACAGTTGACTTGATTTTGCACAGTGTAACAGCGCAGTTGCATTCTGGCCACTTTGA
CCTTATAGCTCCCAAATGATGAGTTTGTCATCTTTATGAACTCATGACAGGATAATAAGCTTGAAGACCTGCTGT
AGTTAGATATGGGCTTTAATCCTTCCCAGGCACCAGTCAGCTGAACAAAAGCATAAGCCAAACATCCTGTTTAAA
CTGTAGAATAACCAGATATTCCCATCAGGTTAAAGACTTCATCTAGATGATGCCCCCCAGAGATGCCTTTAGTGT
AAGTAGCTGGCTTGGGGTATCAGCAAATTTCAGGTATAGTTAGATAAACAGGTACAGGGCCTGCATACTATTAAA
CCATAGTTTGTGGCACCCGCTTTTCTAACTCCACCTGTTAGAAGCTATGTGTTTGAAGGAATGAATCAGTGCAGT
ATAAATAAAATTCTTTTGTAAGGAG

FIGURE 227

MAAVVVAAAGGAGPAVLQVAGLYRGLCAVRSRALGLGLVSPAQLRVFPVRPGSGRPEGGADSSGVGAEAELQANP
FYDRYRDKIQLLRRSDPAAFESRLEKRSEFRKQPVGHSRQGDFIKCVEQKTDALGKQSVNRGFTKDKTLSSIFNI
EMVKEKTAEEIKQIWQQYFAAKDTVYAVIPAEKFDLIWNRAQSCPTFLCALPRREGYEFFVGQWTGTELHFTALI
NIQTRGEAAASQLILYHYPELKEEKGIVLMTAEMDSTFLNVAEAQCIANQVQLFYATDRKETYGLVETFNLRPNE
FKYMSVIAELEQSGLGAELKCAQNQNKT

FIGURE 228

ACCTGCCCTCATCCTGGCCCGCGACTGTAAGACCGGACCCACATCCAGACCAATCTTCCTGTCCGGCTGCTGCGA
CGCGGTCCGCAGGTTGCAGGCGGGCGGCCGGGGCGCCTGAAGGTTACCGAGTGCATGACGGCCTCAGTTCCCGCG
CTGCCCCGCCCGCTGGCCCGCCGACCTCCCCGCCGCTCGCCCGCCAGCCCCTCGGGCCCGGCGGCGGCGGCGGCG
GTGGCGGCGACGGTCGCAGGAGGTGCCGTCTGCCTCCCAGGTGCGCGCTTCGCTCCCGGAGCCGCGGAACTCGGT
CGCGCCATGGCGTCCAACATGGACCGGGAGATGATCCTGGCGGATTTTCAGGCATGTACTGGCATTGAAAACATT
GACGAAGCTATTACATTGCTTGAACAAAATAATTGGGACTTAGTGGCAGCTATCAATGGTGTAATACCACAGGAA
AATGGCATTCTACAAAGTGAATATGGAGGTGAGACCATACCAGGACCTGCATTTAATCCAGCAAGTCATCCAGCT
TCAGCTCCTACTTCCTCTTCTTCTTCAGCGTTTCGACCTGTAATGCCATCCAGGCAGATTGTAGAAAGGCAACCT
CGGATGCTGGACTTCAGGGTTGAATACAGAGACAGAAATGTTGATGTGGTACTTGAAGACACCTGTACTGTTGGA
GAGATTAAACAGATTCTAGAAAATGAACTTCAGATACCTGTGTCCAAAATGCTGTTAAAAGGCTGGAAGACGGGA
GATGTGGAAGACAGTACGGTCCTAAAATCTCTACACTTGCCAAAAAACAACAGTCTTTATGTCCTTACACCAGAT
TTGCCACCACCTTCATCATCTAGTCATGCTGGTGCCCTGCAGGAGTCATTAAATCAAAACTTCATGCTGATCATC
ACCCACCGAGAAGTCCAGCGGGAGTACAACCTGAACTTCTCAGGAAGCAGTACTATTCAAGAGGTAAAGAGAAAT
GTGTATGACCTTACAAGTATCCCCGTTCGCCACCAATTATGGGAGGGCTGGCCAACTTCTGCTACAGACGACTCA
ATGTGTCTTGCTGAATCAGGGCTCTCTTATCCCTGCCATCGACTTACAGTGGGAAGAAGATCTTCACCTGCACAG
ACCCGGGAACAGTCGGAAGAACAAATCACCGATGTTCATATGGTTAGTGATAGCGATGGAGATGACTTTGAAGAT
GCTACAGAATTTGGGGTGGATGATGGAGAAGTATTTGGCATGGCGTCATCTGCCTTGAGAAAATCTCCAATGATG
CCAGAAAACGCAGAAAATGAAGGAGATGCCTTATTACAATTTACAGCAGAGTTTTCTTCAAGATATGGTGATTGC
CATCCTGTATTTTTTATTGGCTCATTAGAAGCTGCTTTTCAAGAGGCCTTCTATGTGAAAGCCCGAGATAGAAAG
CTTCTTGCTATCTACCTCCACCATGATGAAAGTGTGTTAACCAACGTGTTCTGCTCACAAATGCTTTGTGCTGAA
TCCATTGTTTCTTATCTGAGTCAAAATTTTATAACCTGGGCTTGGGATCTGACAAAGGACTCCAACAGAGCAAGA
TTTCTCACTATGTGCAATAGACACTTTGGCAGTGTTGTGGCACAAACCATTCGGACTCAAAAAACGGATCAGTTT
CCGCTTTTCCTGATTATTATGGGAAAGCGATCATCTAATGAAGTGTTGAATGTGATACAAGGGAACACAACAGTA
GATGAGTTAATGATGAGACTCATGGCTGCAATGGAGATCTTCACAGCCCAACAACAGGAAGATATAAAGGACGAG
GATGAACGTGAAGCCAGAGAAAATGTGAAGAGAGAGCAAGATGAGGCCTATCGCCTTTCACTTGAGGCTGACAGA
GCAAAGAGGGAAGCTCACGAGAGAGAGATGGCAGAACAGTTTCGTTTGGAGCAGATTCGCAAAGAACAAGAAGAG
GAACGTGAGGCCATCCGGCTGTCCTTAGAGCAAGCCCTGCCTCCTGAGCCAAAGGAAGAAAATGCTGAGCCTGTG
AGCAAACTGCGGATCCGGACCCCCAGTGGCGAGTTCTTGGAGCGGCGTTTCCTGGCCAGCAACAAGCTCCAGATT
GTCTTTGATTTTGTAGCTTCCAAAGGATTTCCATGGGATGAGTACAAGTTACTGAGCACCTTTCCTAGGAGAGAC
GTAACTCAACTGGACCCAAATAAATCATTATTGGAGGTAAAGTTGTTCCCTCAAGAAACCCTTTTCCTTGAAGCA
AAAGAGTAAACACGGCCCAGCGGTGGAACCAGCCATTCCTTGACAAGCCAGCAGCCTGCGTCAGGAGAAGGGCTC
CTCGCCAACCCACCCACACGCTCGTCTCACTCAATTCAATGTCACACTTCTGCCTCTTGCAAAATTGCTGGAAAA
AGTAATAATAAATATAGCTACTTAAAAAAAAAAAAA

FIGURE 229

CTCTGCCGAGCCTCCTTAAAACTCTGCCGTTAAAATGGGGGCGGGTTTTTCAACTCAAAAAGCGCTCAATTTTTT
TCTTTTCAAAAAAAGCTGATGAGGTCGGAAAAAAGGGAGAAGAAACCGGCACCCTCTCTGAGAGGCAACAGAAGC
AGCAATTGTTTCAGCGAAAAAAGCAGCAAGGGAGGGAGTGAAGGAAAAAAGCAAAAAAGGGGGCGACACGCAAGT
GCCTGTAGGGGTGAAAGGAGCAGGGACCGGCGATCTAGGGGGGGATCAGCTACAAAAGAAACTGTCACTGGGAGC
GGTGCGGCCAAGGAGGAAGCAGTGCTGCCAGGCTCTGCTCCAGGGCACAGCTGGCTGGCGGCTGCCCTGTCCGCA
GCAAAGGGGCACAGGCCGGGGACCGCGAGAGGTGGCAAAGTGGCACCGGGCGCCGAGGCTGCTGAGCGCTCGCCG
AGACGGCGACCGGACTGGCTGCCCCGGAACTGCGGCGACTCTCCCTACTCAGAACTTGGCCTACGTTTCCCAGGA
CTCTCCCCATCTCCAGAGGCCCCCACAAAACCGGGAAAGGAAGGAAAGGACAGCGGCGGCAGCAGCTCAATGAGT
GCCTACAGCAGAAAGCCTGAACGAGCTCGGTCGTAGGCGGGAAGTTCCCGGGGGGGCTGCCCAGTGCAGCCGCAA
TGCTGCCGCGAGCTGCCCCAGCAGTCCGGGCTCCGTAGACGCTTTCCGCATCACTCTCCTTCCTCGGGCTGCCGG
GAGTCCCGGGACCTGGCGGGGCCGGCATGACGGGCTTCTCGGGGGCCCGCCGCACGCCCGGCAGCCTCCGGAGAC
GCGCGCCGAGCCCGGCTCCCACGGCCTCTGAGGCTCGGCGGGGCTGCGGCTGCCTGGCGGGCGGGCTCCGGAGCT
TTCCTGAGCGGCATTAGCCCACGGCTTGGCCCGGACGCGACCAAAGGCTCTTCTGGAGAAGCCCAGAGCACTGGG
CAATCGTTACGACCTGTAACTTGAGGGCCACCGAACTGCTACTCCCGTTCGCCTTTGGCGATCATCTTTTAACCC
TCCGGAGCACGTCAGCATCCAGCCACCGCGGCGCTCTCCCAGCAGCGGAGGACCCAGGACTATCCCTTCGGCGAG
ACGGATGGAAACCGAGCCCCCTGGAGGACCTGCCCCTGCAGTTCTGCCTCACACGGCTCAAGTCACCACCGTGAA
CAAGGGACCCTAAAGA**ATG**GCCGAGCCTTGGGGGAACGAGTTGGCGTCCGCAGCTGCCAGGGGGGACCTAGAGCA
ACTTACTAGTTTGTTGCAAAATAATGTAAACGTCAATGCACAAAATGGATTTGGAAGGACTGCGCTGCAGGTTAT
GAAACTTGGAAATCCCGAGATTGCCAGGAGACTGCTACTTAGAGGTGCTAATCCCGATTTGAAAGACCGAACTGG
TTTCGCTGTCATTCATGATGCGGCCAGAGCAGGTTTCCTGGACACTTTACAGACTTTGCTGGAGTTTCAAGCTGA
TGTTAACATCGAGGATAATGAAGGGAACCTGCCCTTGCACTTGGCTGCCAAAGAAGGCCACCTCCGGGTGGTGGA
GTTCCTGGTGAAGCACACGGCCAGCAATGTGGGGCATCGGAACCATAAGGGGGACACCGCCTGTGATTTGGCCAG
GCTCTATGGGAGGAATGAGGTTGTTAGCCTGATGCAGGCAAACGGGGCTGGGGGAGCCACAAATCTTCAA**TAA**AC
GTGGGGAGGGCTCCCCCACGTTGCCTCTACTTTATCAATTAACTGAGTAGCTCTCCTGACTTTTAATGTCATTTG
TTAAAATACAGTTCTGTCATATGTTAAGCAGCTAAATTTTCTGAAACTGCATAAGTGAAAATCTTACAACAGGCT
TATGAATATATTTAAGCAACATCTTTTTAACCTGCAAAATCTGTTCTAACATGTAATTGCAGATAACTTTGACTT
TCTTCTGAATATTTTATCTTTCCTTGGCTTTTCCCTTGCTTCCCCTTTTGCCAATCTCAACACCCAAGTTGAAGA
CTTTGTTTTTAAAATGGTTTGTCCTGATGCTTTTGTCTAATTAAAACACTTTCAAAACAGGAAAAAAAAAAAAAA
AAAA

FIGURE 230

MAEPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRTGFAVIH
DAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGDTACDLARLYGRN
EVVSLMQANGAGGATNLQ

FIGURE 231

AAAACACCAAATGGTGGATGACACCAGTGCAGCGGGGGGGGGCCCGGAGGCCCTGGG**ATG**GGGAACTGCGGTGGC
TTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCAGCCGTAGACGGGGCCGGGGCCGAGGCCGCGGA
GCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCCGTCACCAAGCTGGGCTGCTTGGTGAAGGACATGAAG
ATCAAGTCCCTGGAGGAGATCTATCTCTTCTCCCTGCCCATTAAGGAATCAGAGATCATTGACTTTTTCCTGGGG
GCCTCTCTCAAGGATGAGGTTTTGAAGATTATGCCAGTGCAGACGCAGACCCGTGCTGGCCAGCGCACCAGGTTC
AAGGCGTTTGTTGCTATCGGGGACTACAATGGCCACGTCGGTCTGGGTGTTAAGTGCTCCAAGGAGGTGGCCACC
GCCATCCATGGGGCCATCATCCTGGCCAAGCTCTCCATTGTCCCCGTGCGCAGAGGCTACTGGGGGAACAAGATT
GGCAAGCCCCACACCGTCCCTTGCAAGGTGACAGGCCGCTGCGGCTCTGCACTGGTGCACCTCATCCCTGTACCC
AGGGGCACTGGCATTGTCTCCGCACCTGTGCCCAAGAAGCTGCTCATGATGGCTGGTATCGATGACTGCTGCACC
TCAGCCTGGGGCTGCACTGCCACCCTGGGCAACTTCGCCAAGGCCACCTTTGATGCCATTTCTAAGACCTACAGC
TACCTGACCCCCGACCTCTGGAAGGAGACTGTATTTACCAAGTCTCCCGATCAGGAATTCACTGACCACCTCATC
AAGGCCCACGCCAGAGTCTCCGTGCAGCGGACCCAGGCTCCAGCTGTGGCTACAACA**TAG**GGTTTTTAGACAAGG
AAAATAAAGCGAATTAAGCGT

FIGURE 232

MGNCGGFRGGFGSGIRGRGRSRRRGRGRGRGARGGKAEDKEWMPVTKLGCLVKDMKIKSLEEIYLFSLPIKESEI
IDFFLGASLKDEVLKIMPVQTQTRAGQRTRFKAFVAIGDYNGHVGLGVKCSKEVATAIHGAIILAKLSIVPVRRG
YWGNKIGKPHTVPCKVTGRCGSALVHLIPVPRGTGIVSAPVPKKLLMMAGIDDCCTSAWGCTATLGNFAKATFDA
ISKTYSYLTPDLWKETVFTKSPDQEFTDHLIKAHARVSVQRTQAPAVATT

FIGURE 233

ATGTCTAAGTCAGAATCTCTTAAAGAGCCCGAACAGCTGCAGAAACTCCTCACTGGAGGGTTGAGCATTGAAGCA
ACCAATGAGAGCCTGAGGAGCCATTTTGAGCAATGGGGAACGCTCACGGACTGTGTGGTCCTGAGAGATCCAAAC
ACTAAGTGCTCCAGGGGCTTTGGGTTTGTCACATATGCCACTGTGGAGGAGGTGGATGCAGCCACAAATGCAAGG
CCACACAAGGTGGATGGAAGAGTTGTGGAAACAAAGAGAGCTGTCTCAAGAGAAGATTCCCAAAGACCAGGTGCT
CACTTAACTGTGAAAAAGTTTGGAAAAATGGAAGTGATTGAAATCATGACTGACCATGGCAGTGGCAAGAAAAGG
GACTTTGCCTTTGTAACCTTTGATGACCATGACTCCGTGGATAAGACTGTCATTCAGAAATACCATATTGTGAAT
GGCCACAACTGTGAAGTTAGGAAAGCCCTGTCAAAGCAAGAGATGGCTAGTGCTTCATCCAGCCAAAGAGGTCGA
ACAGGCTCCTTGATGCCTAAAGCCCAATGTCTGGCATTCGAGCCCTCCATGACAGGTTCCCAGCTTTCCTGCAAG
GCCATGCTCCTCACGGCCTATGACTGCCTCCTGTTCTGCGCCTGTCAGGTCTTCCACCTCACCCCTCTTCTCAGC
CTATCCAAGCCCATTCAGTCTTCAGGCGAGCTC**TAG**

FIGURE 234

MSKSESLKEPEQLQKLLTGGLSIEATNESLRSHFEQWGTLTDCVVLRDPNTKCSRGFGFVTYATVEEVDAATNAR
PHKVDGRVVETKRAVSREDSQRPGAHLTVKKFGKMEVIEIMTDHGSGKKRDFAFVTFDDHDSVDKTVIQKYHIVN
GHNCEVRKALSKQEMASASSSQRGRTGSLMPKAQCLAFEPSMTGSQLSCKAMLLTAYDCLLFCACQVFHLTPLLS
LSKPIQSSGEL

FIGURE 235

CGGTCCCGCACTGGTGCAGCC**ATG**TCCTCTTCCCCGTGGGAGCCTGCGACCCTGCGCCGGGTGTTCGTGGTGGGG
GTTGGCATGACCAAGTTTGTGAAGCCTGGAGCTGAGAATTCAAGAGACTACCCTGACTTGGCAGAAGAAGCAGGC
AAGAAGGCTTTAGCTGATGCACAGATCCCTTATTCAGCAGTGGACCAGGCATGTGTTGGCTATGTTTTTGGTGAC
TCTACCTGTGGGCAGAGGGCTATCTATCACAGTTTGGGAATGACTGGAATTCCTATAATCAATGTCAACAATAAC
TGTGCTACTGGTTCTACTGCTTTGTTTATGGCCCGCCAGCTGATTCAGGGTGGTGTGGCAGAATGTGTCTTGGCT
CTTGGGTTTGAGAAGATGAGTAAGGGAAGCCTTGGAATAAAATTTTCAGATAGAACCATTCCCACTGATAAGCAT
GTTGACCTCCTGATCAATAAGTATGGATTGTCTGCTCACCCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAA
GAACATATGGAAAAATATGGAACAAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTT
AATAACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAGTTTTTGATTTT
TTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAGCAGCAATTTTGGCCAGTGAAGCATTTGTACAG
AAGTATGGCCTGCAATCCAAAGCTGTGGAAATTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAA
GAAAAAAGCATTATTAAAATGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAATCTGGC
CTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACTCCTGACTTATGAAGCA
CTCGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAGATAATACATATGGAGGAAAGTGGGTC
ATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTC
TGCTGGCAGCTGAGAGGGGAAGCCGGAAAGAGGCAAGTTCCTGGTGCAAAGGTGGCTCTGCAGCATAATTTAGGC
ATTGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGGTTTTCCGGAAGCCGCCAGTTCTTTTAGAACTCATCAA
ATTGAAGCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAAGGCAAATCTTGTTTTTAAGGAGATTGAGAAGAAA
CTTGAAGAGGAAGGGGAACAGTTTGTGAAGAAAATCGGTGGTATTTTTGCCTTCAAGGTGAAAGATGGCCCTGGG
GGTAAAGAGGCCACCTGGGTGGTGGATGTGAAGAATGGCAAAGGATCAGTGCTTCCTAACTCAGATAAGAAGGCT
GACTGCACAATCACAATGGCTGACTCAGACTTCCTGGCTTTAATGACTGGTAAAATGAATCCTCAGTCGGCCTTC
TTTCAAGGCAAATTGAAAATCACTGGCAACATGGGTCTCGCTATGAAGTTACAAAATCTTCAGCTTCAGCCAGGC
AACGCTAAGCTC**TGA**AGAACTCCCTTTGGCTACTTTTGAAAATCAAGATGAGATATATAGATATATATCCATACA
TTTTATTGTCAGAATTTAGACTGAAACTACACATTGGCAAATAGCGTGGATAGGATTTGTTTCTTAATGGGTGTG
ACCAATCCTGTTTTTCCTATGCTCTGGGTGAATAGAGCCTGATGGTATACTACTGCTTTGCGGAATTGCATACAA
CTGTGCATTACAAAGTTAATATGGTAATTATGGTCTGGGGTAAAATTGAGTTTCAGAATAAAATTAGGAACAGTA
AAATCCAAAGAACTATGTAAACAAAAAAGCTTTTGTTTTGCTTACAAAGTATATTTAAGGATTATTCTGCTGAAG
ATTCAGTTTAAGAGTTTTCCTTGGGAGAACTAAGTAAGAAACACAATGCCAACAGCTGGCCAGTAATTAGTGTTG
TGCACTTCATGTCATTAATCAATTTCTCAATAGTTCTTAAAATTAGTGAGATTAAAAATCTAAAAATTTTGCATT
TCATGCTATCAGAAACAGTATTTTCTTCCCAAATCAAAATAAAAGAAATATGATCAGAGCTTGAACACAGGCTTA
TTTTTAAAATAAAAATATTTTTAACATGGGTTTCCTTATTGAAAAATCAGTGTATTAGTCATAAAACACCATCAT
TAAGAATAATTGAACAATAAAGTTTGCTTTCAGATGCAGTTTTCAAATTATAATCTCATTTCAATTTATAACGTT
CTCAGTCCTTTGTTATAATTTTCCTTTTTCATGTAAGTTTAATTATCTGCATTTATCTTTTTTCCTAGTTTTTCT
AATACTAATGTTATTTCTTAAAATTCAGTGAGATATAGGATAAAATAATGCTTTGAGAAGAATGTTTAATAGAAA
ATTAAAATAACTTTTTCTGGCA

FIGURE 236

MSSSPWEPATLRRVFVVGVGMTKFVKPGAENSRDYPDLAEEAGKKALADAQIPYSAVDQACVGYVFGDSTCGQRA
IYHSLGMTGIPIINVNNNCATGSTALFMARQLIQGGVAECVLALGFEKMSKGSLGIKFSDRTIPTDKHVDLLINK
YGLSAHPVAPQMFGYAGKEHMEKYGTKIEHFAKIGWKNHKHSVNNPYSQFQDEYSLDEVMASKEVFDFLTILQCC
PTSDGAAAAILASEAFVQKYGLQSKAVEILAQEMMTDLPSSFEEKSIIKMVGFDMSKEAARKCYEKSGLTPNDID
VIELHDCFSTNELLTYEALGLCPEGQGATLVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGE
AGKRQVPGAKVALQHNLGIGGAVVVTLYKMGFPEAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEGEQ
FVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLALMTGKMNPQSAFFQGKLKI
TGNMGLAMKLQNLQLQPGNAKL

FIGURE 237

GGCCCTGCGCGCGGCAACATGGCGGGGTCCAGGTGGAGGTCTTGAGGCTATCAGATCGGT**ATG**GCATTGGCGTCC
GGGCCCGCAAGGCGGGCGCTAGCTGGCTCCGGGCAGCTCGGCCTTGGGGGCTTCGGGGCCCCGAGACGCGGGGCG
TATGAGTGGGGCGTGCGCTCCACGCGGAAGTCGGAGCCTCCTCCCCTGGATAGGGTGTACGAGATCCCTGGACTG
GAGCCCATCACCTTTGCGGGGAAGATGCACTTCGTGCCCTGGCTGGCGCGGCCGATCTTTCCGCCCTGGGACCGC
GGCTACAAGGACCCAAGGTTCTACCGCTCGCCCCCTCTTCACGAGCATCCGCTGTACAAAGACCAGGCCTGCTAT
ATCTTTCACCACCGTTGCCGCCTTCTCGAGGGTGTAAAGCAGGCCCTCTGGCTCACCAAGACCAAGTTAATAGAA
GGCCTTCCCGAGAAAGTGCTTAGCCTTGTTGATGATCCAAGGAACCACATAGAGAACCAAGACGAGTGCGTTCTG
AATGTGATCTCTCACGCCCGTCTCTGGCAGACCACTGAGGAAATCCCCAAGAGAGAGACCTACTGCCCGGTCATC
GTGGACAACCTAATACAGCTGTGTAAATCTCAGATTCTCAAGCATCCTTCTCTGGCCAGGAGGATCTGTGTCCAA
AACTCCACGTTTTCTGCTACCTGGAACCGAGAGTCTCTTCTCCTTCAAGTCCGTGGTTCTGGTGGAGCCCGACTG
AGCACTAAGGATCCTCTGCCCACCATCGCCTCCAGAGAGGAGATTGAAGCTACTAAGAATCATGTTCTAGAGACC
TTCTACCCCATATCACCCATCATCGATCTTCATGAATGCAATATTTATGATGTGAAAAATGACACAGGATTCCAG
GAAGGCTATCCTTACCCCTATCCCCATACCCTGTACTTACTGGACAAAGCCAATTTACGACCACACCGCCTTCAA
CCAGATCAGCTGCGGGCCAAGATGATCCTGTTTGCTTTTGGCAGTGCCCTGGCTCAGGCCCGGCTCCTCTATGGG
AATGATGCCAAGGTCTTGGAGCAGCCCGTGGTGGTGCAGAGCGTGGGCACGGATGGACGTGTCTTCCATTTCCTA
GTGTTTCAACTGAATACCACAGACCTGGACTGTAACGAGGGTGTCAAGAATTTGGCCTGGGTGGACTCAGACCAG
CTCCTCTATCAGCATTTTTGGTGTCTCCCAGTGATCAAAAAGAGAGTGGTTGTGGAACCTGTTGGGCCAGTTGGT
TTCAAGCCAGAGACATTCAGAAAGTTTTTAGCTCTATATTTGCATGGTGCTGCG**TGA**GCGGAGGACCCCTCTGAA
TCCTGAAACCCCTCTTGCCTCTCTTCCACGGAAGAGGGCCTGGGCCCCGTGGAGCCTCAGTGCCCGTTTGGCCTG
CTGCTCTCGCTGACAATAAAGAGCCCTTGCGTTGC

FIGURE 238

MALASGPARRALAGSGQLGLGGFGAPRRGAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAGKMHFVPWLARPIF
PPWDRGYKDPRFYRSPPLHEHPLYKDQACYIFHHRCRLLEGVKQALWLTKTKLIEGLPEKVLSLVDDPRNHIENQ
DECVLNVISHARLWQTTEEIPKRETYCPVIVDNLIQLCKSQILKHPSLARRICVQNSTFSATWNRESLLLQVRGS
GGARLSTKDPLPTIASREEIEATKNHVLETFYPISPIIDLHECNIYDVKNDTGFQEGYPYPYPHTLYLLDKANLR
PHRLQPDQLRAKMILFAFGSALAQARLLYGNDAKVLEQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGVKNLAW
VDSDQLLYQHFWCLPVIKKRVVVEPVGPVGFKPETFRKFLALYLHGAA

FIGURE 239

CCGCGGCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGAGCGCG
GCGAGGAGAGCGCCAGCGAGCGAGAGAGCGAGCGAGCGCCGGGGAGGGGGCCGGGAGCGAGGGGCAGCTCGGGAG
AGCCGGAGCGGTAGCGGCGGCGGCGGCGGCGGCGGCGAGGCTCGGCGCCCTCTTCCCTGCAAACC**ATG**TTTGCCA
AAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAAAGTTAGCTTTATACGTCTACGAATATTTAC
TGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTCGATGGGAAAAAAACATCACGTTGGGAG
AACCGCCTGGGTTTTTGCACTCGTGGTGGTGTGTATTTTGGGACCTTTACTGTGCAGCTCCTGAAAGGAGAGACA
CTTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATTATAGTGCAGCAGCTGCCCCGAGCCCCGTGCTTGGCA
ACATTCCCCCCAACGATGGGATGCCGGGAGGCCCCATCCCGCCAGGTTTCTTTCAGGGTCCTCCGGGGTCACAGC
CCTCGCCGCACGCACAGCCTCCACCTCACAATCCTAGCAGCATGATGGGACCCCACAGTCAGCCTCCGGGAGGAG
TTCCTGGGACACAGCCATTGCTGCCCAATTCTATGGATCCCACACGACAACAAGGCCACCCCAACATGGGAGGAT
CAATGCAGAGAATGAACCCTCCCCGAGGCATGGGGCCCATGGGTCCCGGCCCACAGAATTACGGCAGCGGCATGA
GACCACCACCCAACTCCCTCGGCCCCGCCATGCCCGGGATTAACATGGGCCCGGGAGCTGGCAGACCCTGGCCCA
ATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCCTGGTGGTGGCG
GTCCTCCAGGAACACCCATTATGCCCAGTCCCGCAGATTCAACAAATTCCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACTTCCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGGCATGG
GTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCCAAAAAATTCTCCTA
ACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAGGGAACTTCCTCCACT
CCTTTCAGAACGACAATTATTCTCCAAGCATGACGATGAGTGTG**TGA**TCCCCCCTTCTCCGAGACGCTGAGAGAG
CAGGCATTGCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGTCATTATCCAGGAGCTGGTGGGGAGG
GCATCTCCCTGCTCCCCTCAACCCCCTCCCACCCCATCCACGCCCCCTACCTTTCCCAATTTTAGTTTCATGCAA
TAAAAAGGCCAAACTTTTTATTCCATAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA.

FIGURE 240

MFAKGKGSAVPSDGQAREKLALYVYEYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWWCVFWDLYCAAPE
RRDTCEHSSEAKAFHDYSAAAAPSPVLGNIPPNDGMPGGPIPPGFFQGPPGSQPSPHAQPPPHNPSSMMGPHSQP
PGGVPGTQPLLPNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNSLGPAMPGINMGPGAGR
PWPNPNSANSIPYSSSSPGTYVGPPGGGGPPGTPIMPSPADSTNSSDNIYTMINPVPPGGSRSNFPMGPGSDGPM
GGMGGMEPHHMNGSLGSGDIDGLPKNSPNNISGISNPPGTPRDDGELGGNFLHSFQNDNYSPSMTMSV

FIGURE 241

ATGTACGCCTTTGTGCGGTTCCTGGAGGACAACGTCTGCTACGCGCTGCCCGTGTCGTGCGTGCGCGACTTCAGC
CCCCGCTCGCGGCTGGATTTTGACAACCAGAAGGTGTACGCCGTGTACCGGGGCCCGGAGGAATTGGGCGCCGGG
CCCGAGAGCCCCCCGCGCGCCCCCCGCGACTGGGGCGCGCTGTTGCTCCACAAGGCCCAGATCCTGGCGCTGGCA
GAAGACAAATCTGACCTTGAAAACAGTGTGATGCAGAAGAAAATAAAAATCCCCAAGCTTTCTCTTAATCATGTA
GAAGAAGATGGAGAGGTTAAAGATTATGGGGAAGAAGATTTACAGCTTAGACACATCAAGGATTGTCTGGGGAAA
TATTGATCTGCAGTCCAAGAAAATCCCAGCTGCCCTTGCCTGAACTGATTCTCGTTGTCCTACACAGAGACCTGA
GGGGCGGAAGCCGAGCGAAGTGGCGCACAAGAGCATCGAGGCAGTGGTGGCTCGGCTAGAGAAGCAGAACGGCCT
GAGCCTGGGCCATAGCACGTGTCCGGAAGAGGTCTTCGTGGAGGCCTCGCCAGGCACAGAGGAC**ATG**GACAGTCT
AGAAGATGCTGTGGTGCCCCGGGCTCTGTATGAGGAGCTGCTGCGCAACTACCAGCAGCAACAGGAAGAGATGCG
CCACCTCCAGCAGGAGCTGGAGCGGACTCGGAGGCAGCTGGTACAACAGGCCAAGAAGCTCAAGGAGTACGGGGC
ACTTGTGTCTGAAATGAAGGAGCTCCGTGACCTTAACCGGAGGCTCCAGGACGTGCTGCTCCTGAGGCTTGGCAG
CGGTCCCGCCATTGATCTGGAAAAAGTAAAGTCAGAATGTCTCGAGCCCGAGCCGGAGTTACGGAGCACTTTCAG
TGAGGAAGCAAATACGTCGTCCTATTACCCCGCTCCTGCGCCTGTCATGGACAAGTATATCCTAGACAATGGCAA
GGTCCATCTGGGAAGCGGGATTTGGGTTGATGAGGAGAAATGGCACCAGCTACAAGTAACCCAAGGAGATTCCAA
GTACACGAAGAACTTGGCAGTTATGATTTGGGGAACAGATGTTCTGAAAAACAGAAGCGTCACAGGCGTCGCCAC
AAAAAAAAAGAAAGATGCAGTCCCTAAACCACCCCTCTCGCCTCGCAAACTAAGCATCGTCAGAGAGTGTTTGTA
TGACAGAATAGCACAAGAAACTGTGGATGAAACTGAAATTGCACAGAGACTCTCCAAAGTCAACAAGTACATCTG
TGAAAAAATCATGGATATCAATAAATCCTGTAAAAATGAAGAACGAAGGGAAGCAAAATACAATTTGCAA**TAA**AC
TTTGGATTTTTCAT

FIGURE 242

MDSLEDAVVPRALYEELLRNYQQQQEEMRHLQQELERTRRQLVQQAKKLKEYGALVSEMKELRDLNRRLQDVLLL
RLGSGPAIDLEKVKSECLEPEPELRSTFSEEANTSSYYPAPAPVMDKYILDNGKVHLGSGIWVDEEKWHQLQVTQ
GDSKYTKNLAVMIWGTDVLKNRSVTGVATKKKKDAVPKPPLSPRKLSIVRECLYDRIAQETVDETEIAQRLSKVN
KYICEKIMDINKSCKNEERREAKYNLQ

FIGURE 243

CCTTTCGTTGCCTGATCGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTAC
CCTATCGACGCAGCTTCCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCA
AGAAGGGCCTTACTCCTTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGA
CAGGCAATCTCTACCATTTAATTAAGAAAGCAGTTGCTGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGA
TGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATTCACCGTTTG

FIGURE 244

CGCCGCCATCATGGGTCGTATGCGTGCTCCTGAGAAGGGCCTGTCCCAGTCGGCTTTACCCTATCGACGCAGCTT
CCCCACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGATTTACAAACTGGCCAAGAAGGGCCTTACTCC
TTCACAGATCGGTGTAATCGTGAGAGAATCACATGGTGTTGCACAAGTACGTTTTGTGACAGGCAATAAAATTTT
AAGAATTCTTAAGTCTAAGGGACTTGCTCCTGATCTTCCTGAAGATCTCTACCATTTAATTAAGAAAGCAGTTGC
TGTTCAAAGCATCTTGAGAGGAACAGAAAGGATAAGGATGCTAAATTCCATCTGATTCTGATAGAGAGCCAGATT
CACCGTTTGGCTCAATATTATAAGACCAAGCGAGTCCTCCCTCCCAGTTGGAAATATGAATCATCTACAGCCTCT
GCCCTGGTCGCATAAATTTGTCTGTGTACTCAAGCAATAAAATGATTGTTTAACTAAAATAAAACAAAAACAAAA
ACAAAAAAA

FIGURE 245

AGAAG**ATG**CTTCAAATTCAACCCGAGAAGGATATCATTGTAGAGTTTATCAAAAATGGAGATTTCAAGTATGTCC
GCATGCTGGGGGCACTTTACATGAGGCTGACAGGCACTGCAATTGATTGCTACAAGTACTTGGAACCTTTGTACA
ATGACTATCGAAAAATCAAGAGCCAGAACCGAAATGGGGAGTTTGAATTGATGCATGTTGATGAGTTTATTGATG
AACTATTGCACAGTGAGAGAGTCTGTGATATCATTCTGCCCCGACTACAGAAACGCTATGTATTAGAGGAAGCTG
AGCAACTGGAGCCTCGAGTTAGTGCTCTGGAAGAGGACATGGATGATGTGGAGTCCAGTGAAGAGGAAGAAGAGG
AGGATGAGAAGTTGGAAAGAGTGCCATCACCTGATCACCGCCGGAGAAGCTACCGAGACTTGGACAAGCCCCGTC
GCTCTCCCACACTGCGCTACAGGAGGAGTAGGAGCCGGTCTCCCAGAAGGCGGAGTCGATCTCCCAAAAGGAGAA
GCCCCTCCCCTCGCCGAGAAAGGCATCGGAGCAAGAGTCCAAGACGTCACCGCAGCAGGTCCCGAGATCGGCGGC
ACAGATCCCGTTCCAAGTCCCCAGGTCATCACCGTAGTCACAGACACAGGAGCCACTCAAAGTCTCCCGAAAGGT
CTAAGAAGAGCCACAAGAAGAGCCGGAGAGGGAATGAG**TAA**TGGACTCAGTTTGGTTTTAGTCCACATGGCCTCC
TGTGGATATAAGGATATCTGTATGTGGAAGGATTAAGATCTCCCCCAGGCAGCTATAAGAATATTTTAGTTTTTT
TCTTATCAAGTTTCTCAACCTTTATTTTTAATGAAGGAGGTGCTGAGTTTTGTATCTTTTTAATCATAATCAACA
TCAGTTTTTGACCCAACTAACCTTGACTGTATTCAAACTTATGAGAGTATAAAGGATCTGGAGGTTGGGGATATG
ACTGACAAGGAAAGGCTGTGGCCACCTGATGACCCTTTCCCTTTTTATTAAACCGGACACACCTGTTTCCCATTT
CGCTGTAGTTTAGTTTTTGGTTTGTTGTGGTTGGAACTGCTTTGAGAATCCTGGGATTTGTGCTGCTGCTGTTAT
TCAAAGATCAAAGGAGTAAAACATAGTTGCTCCTAACTTTTTTCCAGCAGCAGCAAGTGGTAATAAACATGAAAA
CTGGTTTGTAGCAGTTTTGAAAGAATAGAATGCATTCAAATGTAAGGCTGCTTCTGGATCATTAAAGCCAGTTTC
ATCAAACAGTTCAACAGAGAGCAGCACTTAATACCCTTTATACAGCCCATTTTTTCATAGTTTCATTTGTTCTTG
CCCACAAGCTTGAAATCCAGGTTAAGGTATCCAGCCTTTATCATATAAGCATTGACATTATCCAGGCCTAGTCAG
TAGCAGTAGGGTAACGGGATTGAAAAAGATTTGATGGAGAGGAAAGTATCTAATATTAGTCATGGTTTTGACCTA
AATTGCTAGACAGTCGTGCCATTCACAAAGTCAGAAAATACAGCAGGAAGAGACAGCTTTTAGAGGGGCAGAGAA
TTAGAGGATGGTGGTAGTAATGAAAAAGATGCATTCAGTTTAACAAGTTTAATTTGAGACAGCTATGGTATAGCT
AAAAACAAAAGCCCATAAAGTTGGAGATAGGGACCAGAGTTTAACATAGCGATCTAGGCCAGAATTGACAATGTT
TAAGTAATGGTGGAATCTGTCAATAAGACTTCCCAGAGTGTTAATATATATCAGAAATGCACACAACAGAACCAT
AGGCAACACCAACACAGGAAGAAATAGAAGTCACCTATTGAAAACTGGAATGGCCCATTCAGAAAGACAGGAGAA
TTAGGAGAGAGTGAGTGAAAGAAGCCAAGGGTCAAGAATGCAGAAGCAAAGGAAGGACTAAAAAGCCTCCACGGA
CATCGATAATCAAGAGATTATTAAGATCTTTGCTAGAAGAGTTCCTTTACCTGTACTTAACTCCCTTAAAAAGAG
AAAAGTGATGGAATGACTTCTGCAACTGTAGTCCCAGCAGGAACTGTGAAGACCAGCTGCCCTGCAGGATCCAGT
TTTTCTTGGGAGGTTGTATCTGGTCATAAGGTAAACATTCTATATATTCTATGCCTGCTCTAGAATTGAAAGACT
TCAGCAGTATTAAAGCATTTTTTAATCTT

FIGURE 246

MLQIQPEKDIIVEFIKNGDFKYVRMLGALYMRLTGTAIDCYKYLEPLYNDYRKIKSQNRNGEFELMHVDEFIDEL
LHSERVCDIILPRLQKRYVLEEAEQLEPRVSALEEDMDDVESSEEEEEEDEKLERVPSPDHRRRSYRDLDKPRRS
PTLRYRRSRSRSPRRRSRSPKRRSPSPRRERHRSKSPRRHRSRSRDRRHRSRSKSPGHHRSHRHRSHSKSPERSK
KSHKKSRRGNE

FIGURE 247

GTTCGGGCCAG**ATG**GCGTCCATCATGGAAGGGCCGCTGAGCAAATGGACTAACGTGATGAAGGGCTGGCAGTACC
GTTGGTTCGTGCTGGACTACAATGCAGGACTGCTCTCCTACTACACGTCCAAGGACAAAATGATGAGAGGCTCTC
GCAGAGGATGTGTTAGACTCAGAGGAGCTGTGATTGGTATAGACGATGAGGACGACAGCACCTTCACAATAACTG
TTGATCAGAAAACCTTCCATTTCCAGGCCCGTGATGCTGATGAGCGAGAGAAGTGGATCCATGCCTTAGAAGAAA
CAATTCTTCGACATACTCTCCAGCTTCAAGGTTTGGATTCAGGATTTGTTCCTAGTGTCCAAGATTTTGATAAGA
AACTTACAGAAGCTGATGCTTACCTACAAATCTTGATTGAACAATTAAAGCTTTTTGATGACAAGCTTCAAAACT
GCAAAGAAGATGAACAGAGAAAGAAAATTGAAACTCTCAAAGAGACAACAAATAGCATGGTAGAATCAATTAAAC
ACTGCATTGTGTTGCTGCAGATTGCCAAAGACCAGAGTAATGCGGAGAAGCACGCAGATGGAATGATAAGTACTA
TTAATCCCGTAGATGCAATATATCAACCTAGTCCTTTGGAACCTGTGATCAGCACAATGCCTTCCCAGACTGTGT
TACCTCCAGAACCTGTTCAGTTGTGTAAGTCAGAGCAGCGTCCATCTTCCCTACCAGTTGGACCTGTGTTGGCTA
CCTTGGGACATCATCAGACTCCTACACCAAATAGTACAGGCAGTGGCCATTCACCACCGAGTAGCAGTCTCACTT
CTCCAAGCCACGTGAACTTGTCTCCAAATACAGTCCCAGAGTTCTCTTACTCCAGCAGTGAAGATGAATTTTATG
ATGCTGATGAATTCCATCAAAGTGGCTCATCCCCAAAGCGCTTAATAGATTCTTCTGGATCTGCCTCAGTCCTGA
CACACAGCAGCTCGGGAAATAGTCTAAAACGCCCAGATACCACAGAATCACTTAATTCTTCCTTGTCCAATGGAA
CAAGTGATGCTGACCTGTTTGATTCACATGATGACAGAGATGATGATGCGGAGGCAGGGTCTGTGGAGGAGCACA
AGAGCGTTATCATGCATCTCTTGTCGCAGGTTAGACTTGGAATGGATCTTACTAAGGTAGTTCTTCCAACGTTTA
TTCTTGAAAGAAGATCTCTTTTAGAAATGTATGCAGACTTTTTTGCACATCCGGACCTGTTTGTGAGCATTAGTG
ACCAGAAGGATCCCAAGGATCGAATGGTTCAGGTTGTGAAATGGTACCTCTCAGCCTTTCATGCGGGAAGGAAAG
GATCAGTTGCCAAAAAGCCATACAATCCCATTTTGGGCGAGATTTTTCAGTGTCATTGGACATTACCAAATGATA
CTGAAGAGAACACAGAACTAGTTTCAGAAGGACCAGTTCCCTGGGTTTCCAAAAACAGTGTAACATTTGTGGCTG
AGCAGGTTTCCCATCATCCACCCATTTCAGCCTTTTATGCTGAGTGTTTTAACAAGAAGATACAATTCAATGCTC
ATATCTGGACCAAATCAAAATTCCTTGGGATGTCAATTGGGGTGCACAACATAGGGCAGGGCTGTGTCTCATGTC
TAGACTATGATGAACATTACATTCTCACATTCCCCAATGGCTATGGAAGGTCTATCCTCACAGTGCCCTGGGTGG
AATTAGGAGGAGAATGCAATATTAATTGTTCCAAAACAGGCTATAGTGCAAATATCATCTTCCACACTAAACCCT
TCTATGGGGGCAAGAAGCACAGAATTACTGCCGAGATTTTTTCTCCAAATGACAAGAAGTCTTTTTGCTCAATTG
AAGGGGAATGGAATGGTGTGATGTATGCAAAATATGCAACAGGGGAAAATACAGTCTTTGTAGATACCAAGAAGT
TGCCTATAATCAAGAAGAAAGTGAGGAAGTTGGAAGATCAGAACGAGTATGAATCCCGCAGCCTTTGGAAGGATG
TCACTTTCAACTTAAAAATCAGAGACATTGATGCAGCAACTGAAGCAAAGCACAGGCTTGAAGAAAGACAAAGAG
CAGAAGCCCGAGAAAGGAAGGAGAAGGAAATTCAGTGGGAGACAAGGTTATTTCATGAAGATGGAGAATGCTGGG
TTTATGATGAACCATTACTGAAACGTCTTGGTGCTGCCAAGCAT**TAG**GTTGGAAGATGCAAAGTTTATACCTGAT
GATCAGGGCAGTAGGCATAATTCAGCAACAAACAATCTTCCTTTGGGAGAAACCTGTTCATTCCAATCTTCTAAT
TACAGTGGTTCCTATCTCAGGGATACTGGACTTTCTGACGCAGATGAACAATTAAGGGGAAAAGCTTCCCTTTTC
CCTCTGTGGCAGTTACGATTTTGACTTCAGTCCTGAGAAAAACTTCAGGTTTTGAAAATCAGATGATGTCTTCTC
CTTTTCCAAACACCACACGTTGAAAGCATTTATAAATCCAAGTCTGAAACTCTGCGCTCTAGTACTGCTGTTAAG
ATACACAACTTGTTTCTTAGTTCATATAATCTCGGGATACACACACACACACACATATATATACACACACATACG
TATACACACACATACATATATATAAATATACCTGATGCCAGATTTTTTTCATAAATATTCTGCCTACTGTAAATA
TGGGTTCCTCTGAGTTGTTTTAGAAAATTAGCGCAATGTATTAAAATCAAGTGTTAGGAAATTTCATGGTCTTAC
CTACAATAACTTTTATTTTGGAATTGAACTATTATTAAATTGTATCTAATCCTGGATTACAGTTTAATTAATTAT
TCTTAGTGCTTAAGGCTTCATAAAGTAATTTTTCCAACCTTTTTTTTTAAAAAAAAAAAAAA

FIGURE 248

MASIMEGPLSKWTNVMKGWQYRWFVLDYNAGLLSYYTSKDKMMRGSRRGCVRLRGAVIGIDDEDDSTFTITVDQK
TFHFQARDADEREKWIHALEETILRHTLQLQGLDSGFVPSVQDFDKKLTEADAYLQILIEQLKLFDDKLQNCKED
EQRKKIETLKETTNSMVESIKHCIVLLQIAKDQSNAEKHADGMISTINPVDAIYQPSPLEPVISTMPSQTVLPPE
PVQLCKSEQRPSSLPVGPVLATLGHHQTPTPNSTGSGHSPPSSSLTSPSHVNLSPNTVPEFSYSSSEDEFYDADE
FHQSGSSPKRLIDSSGSASVLTHSSSGNSLKRPDTTESLNSSLSNGTSDADLFDSHDDRDDDAEAGSVEEHKSVI
MHLLSQVRLGMDLTKVVLPTFILERRSLLEMYADFFAHPDLFVSISDQKDPKDRMVQVVKWYLSAFHAGRKGSVA
KKPYNPILGEIFQCHWTLPNDTEENTELVSEGPVPWVSKNSVTFVAEQVSHHPPISAFYAECFNKKIQFNAHIWT
KSKFLGMSIGVHNIGQGCVSCLDYDEHYILTFPNGYGRSILTVPWVELGGECNINCSKTGYSANIIFHTKPFYGG
KKHRITAEIFSPNDKKSFCSIEGEWNGVMYAKYATGENTVFVDTKKLPIIKKKVRKLEDQNEYESRSLWKDVTFN
LKIRDIDAATEAKHRLEERQRAEARERKEKEIQWETRLFHEDGECWVYDEPLLKRLGAAKH

FIGURE 249A

CCCGGGCTGTGGGCTACAGGCGCAGAGCGGGCCAGGCGCGGAGCTGGCGGCAGTGACAGGAGGCGCGAACCCGCA
GCGCTTACCGCGCGGCGCCGCACCATGGAGCCCGCCGTGTCGCTGGCCGTGTGCGCGCTGCTCTTCCTGCTGTGG
GTGCGCCTGAAGGGGCTGGAGTTCGTGCTCATCCACCAGCGCTGGGTGTTCGTGTGCCTCTTCCTCCTGCCGCTC
TCGCTTATCTTCGATATCTACTACTACGTGCGCGCCTGGGTGGTGTTCAAGCTCAGCAGCGCTCCGCGCCTGCAC
GAGCAGCGCGTGCGGGACATCCAGAAGCAGGTGCGGGAATGGAAGGAGCAGGGTAGCAAGACCTTCATGTGCACG
GGGCGCCCTGGCTGGCTCACTGTCTCACTACGTGTCGGGAAGTACAAGAAGACACACAAAAACATCATGATCAAC
CTGATGGACATTCTGGAAGTGGACACCAAGAAACAGATTGTCCGTGTGGAGCCCTTGGTGACCATGGGCCAGGTG
ACTGCCCTGCTGACCTCCATTGGCTGGACTCTCCCCGTGTTGCCTGAGCTTGATGACCTCACAGTGGGGGGCTTG
ATCATGGGCACAGGCATCGAGTCATCATCCCACAAGTACGGCCTGTTCCAACACATCTGCACTGCTTACGAGCTG
GTCCTGGCTGATGGCAGCTTTGTGCGATGCACTCCGTCCGAAAACTCAGACCTGTTCTATGCCGTACCCTGGTCC
TGTGGGACGCTGGGTTTCCTGGTGGCCGCTGAGATCCGCATCATCCCTGCCAAGAAGTACGTCAAGCTGCGTTTC
GAGCCAGTGCGGGGCCTGGAGGCTATCTGTGCCAAGTTCACCCACGAGTCCCAGCGGCAGGAGAACCACTTCGTG
GAAGGGCTGCTCTACTCCCTGGATGAGGCTGTCATTATGACAGGGGTCATGACAGATGAGGCAGAGCCCAGCAAG
CTGAATAGCATTGGCAATTACTACAAGCCGTGGTTCTTTAAGCATGTGGAGAACTATCTGAAGACAAACCGAGAG
GGCCTGGAGTACATTCCCTTGAGACACTACTACCACCGCCACACGCGCAGCATCTTCTGGGAGCTCCAGGACATT
ATCCCCTTTGGCAACAACCCCATCTTCCGCTACCTCTTTGGCTGGATGGTGCCTCCCAAGATCTCCCTCCTGAAG
CTGACCCAGGGTGAGACCCTGCGCAAGCTGTACGAGCAGCACCACGTGGTGCAGGACATGCTGGTGCCCATGAAG
TGCCTGCAGCAGGCCCTGCACACCTTCCAAAACGACATCCACGTCTACCCCATCTGGCTGTGTCCGTTCATCCTG
CCCAGCCAGCCAGGCCTAGTGCACCCCAAAGGAAATGAGGCAGAGCTCTACATCGACATTGGAGCATATGGGGAG
CCGCGTGTGAAACACTTTGAAGCCAGGTCCTGCATGAGGCAGCTGGAGAAGTTTGTCCGCAGCGTGCATGGCTTC
CAGATGCTGTATGCCGACTGCTACATGAACCGGGAGGAGTTCTGGGAGATGTTTGATGGCTCCTTGTACCACAAG
CTGCGAGAGAAGCTGGGTTGCCAGGACGCCTTCCCCGAGGTGTACGACAAGATCTGCAAGGCCGCCAGGCACTGA
GCTGGAGCCCGCCTGGAGAGACAGACACGTGTGAGTGGTCAGGCATCTTCCCTTCACTCAAGCTTGGCTGCTTTC
CTAGATCCACACTTTCAAAGAGAAACCCCTCCAGAACTCCCACCCTGACAGCCCAACACCACCTTCCTCCTGGCT
TCCAGGGGGCAGCCCAGTGGAATGGAAAGAATGTGGGATTTGGAGTCAGACAAGCCTGAGTCCAGTTCCCCGTTT
AGAACTCATTAGCTGTGTGACTCTGGGTGAGTCCCTTAACCCCTCTGAGCCCGGGTCTCTTCATTAGTTGAAAGG
GATAGTAATACCTACTTGCAGGTTGTTGTCATCTGAGTTGAGCACTGGTCACATTGAAGGTGCTGGGTAAGTGGT
AGCTCTTGTTGCTTCCCGTTCAGCGTCACATCTGCAGTGGAGCCTGAAAAGGCTCCACATTAGGTCACCTGTGCA
CAGCCATGGCTGGAATGATGAAGGGGATACGCTGGAGTTGCCCTGCCATCGCCTCCATCAGCCAGACGAGGTCCT
CACAGGAGAAGGACAGCTCTTCCCCACCCTGGGATCTCAGGAGGGCAGCCACGGAGTGGGGAGGCCCCAGATGCG
CTGTGCCAAAGCCAGGTCCGAGGCCAAAGTTCTCCCTGCCATCCTTGGTGCCGTCCTGCCCCTTCCTCCTTCATG
CCTGGGCCTGCAGGCCCACCCCAGCCACCACTGAGTCCACTCGGAGTGCCCTGTGTTCCTGGAGAAGGCATTCCA
GGGTTGAATCTTGTCCCAGCCTCAGCCTGGGACACCTAGGTGGAGAGAGTGGTCTCCGCTCTGAATTGGATCCAG
GGGACCTGGGCTCATTCTTCTTGGCTCACCAACCCTGCAGGCCTCATCTTTCCCAAAACCCACTTTGTCTTGGTG
GGAGTGGGTCCGCGCTGCTCTGCAGCAGGGGCTGGGGAGTGGACAGCATCAGGTGGGAAAGTGGAGTCCACCCTC
ATGTTTCTGTAGGATTCTCACCGTGGGGCTGGAAGAAAAGAGCATCGACTTGATTTCTCCAACCACTCATCCCTC
TTTTTCTTTCTTCCACCACTCCCCACCCCAGCTGTAGTTAATTTCAGTGCCTTACAAATCCTAAGCTCAGAGAAA
GTTCCATTTCCGTTCCAGAGGGAAGGGAACCTCCCTAGGTCCTTCCCTGGCTTGTTATAACGCAAAGCTTGGTTG
TTTATGCAACTCTATCTTAAGAACTGCCCAGCCTCAGCTGAAAACCCGAATCTGAGAAGGAATTGCGTCATGTAA
GGGAAGCTGGAATTAAGGGAGCTGAGCCAGTCATGGTTGTGGCGTGTGAGTCAGGAGACCTAGGTTTCAGCCCCT
CTCTACTGTCAGCGAGCTGTGCAACGTGGGCAAGTCATTGTCCTCTGAGCTGCAGTTTCCTCATCTGTCACATCG
CTACAGACAAGACCTCCCTGGAACCCTTCTGATTGTCTTAGACACTGTGGTTGCAAAACCCACGGAAAGCCTCAT
TTGTGTGGAAAGTCAGAGGAAAAATGATCCAGTGGACACTTGGGGATTATCTGTCATTCAAGATCCTTCCTTCAA
CCCCAAGGTCAGCTCCCATCTCATTTCCAGAAAGGCTCATACCTGGCTTGCAGGGAAGCATCTGTCTTGTCATTC
CAGGTGCCAGAATCCTCTCAGAGTCATTGAAGGGTGTTCACCCATCCCACCCAAGGCTTGGCACACTGCCAGTGT
CTTAGCAGGGTCTTGTGAGGGCTGGGGGCATCCAGGCACTCAGAAGGCAAAGGAACCACCCTACCCATTTGGCCT
CTGGAGGGGGCAGAAGAAAGAAATAAACCTCATCCTATATTTTACAAAGCATGTGAATTCTGGCATTAGCTCTCA
TAGGAGACCCATGTGCTTCCTTGCTCAGTGCAAAACTGATGATTCTACTTGCTGTAGATGAATGGTTAACACGAG

FIGURE 249B

CTAGTTAAACAGTGCCATTGTTTTGCCAGTGAAGCCTCCAACCCTAAGCCACTGGGACGGTGGCCAGAGATGCCA
GCAGCCTCTGTCGCCCTTAGTCATATAACCAAAATCCAGACCTTATCCACAACCCGGGGCTTGGAAAGGAAGGTA
TTTTGGAATCACACCCTCCGGTTATGTTGCTCCAGTAAAATCTTGCCTGGAAAGAGGCAGTCTTCTTAGCATGGT
GAGCTGAGTTCATGGCTTTTTTTTGTAGCCAGTCCTGTCCCTGGCCATCCATGTGATGGTTTTGGATGGAGTTAA
ACTTGATGCCAGTGGGCAGTGCATGTGGAAAGTATCAGAGTAAGGCTCTCCCCTCCAGAGCCCTGAGTTTCTTGG
CTGCATGAAGGTTTTCTTTAGAATCAGAATTGTAGCCAGTTTCTTTGGCCAGAAGGATGAATACTTGGATATTAC
TGAAAGGGAGGGGTGGAGATGGGTGTGGCAGTGTATGGTGTGTGATTTTTATTTTCTTCTTTGGTCATGGGGGCC
AAGGAGAAAGGCATGAATCTTCCCTGTCAGGCTCTTACAGCCACAGGCACTGTGTCTACTGTCTGGAAGACATGT
CCCCATGGCTGTGGGGCCGCTGCTTCTGTTTAAATAAAAGTGGCCTGG

FIGURE 250

GACATCATGGGCTATTTTTAGGGGTTGACTGGTAGCAGATAAGTGTTGAGCTCGGGCTGGATAAGGGCTCAGAGT
TGCACTGAGTGTGGCTGAAGCAGCGAGGCGGGAGTGGAGGTGCGCGGAGTCAGGCAGACAGACAGACACAGCCAG
CCAGCCAGGTCGGCAGTATAGTCCGAACTGCAAATCTTATTTTCTTTTCACCTTCTCTCTAACTGCCCAGAGCTA
GCGCCTGTGGCTCCCGGGCTGGTGTTTCGGGAGTGTCCAGAGAGCCTGGTCTCCAGCCGCCCCCGGGAGGAGAGC
CCTGCTGCCCAGGCGCTGTTGACAGCGGCGGAAAGCAGCGGTACCCACGCGCCCGCCGGGGGGAAGTCGGCGAGCG
GCTGCAGCAGCAAAGAACTTTCCCGGCTGGGAGGACCGGAGACAAGTGGCAGAGTCCCGGAGCCAACTTTTGCAA
GCCTTTCCTGCGTCTTAGGCTTCTCCACGGCGGTAAAGACCAGAAGGCGGCGGAGAGCCACGCAAGAGAAGAAGG
ACGTGCGCTCAGCTTCGCTCGCACCGGTTGTTGAACTTGGGCGAGCGCGAGCCGCGGCTGCCGGGCGCCCCCTCC
CCCTAGCAGCGGAGGAGGGGACAAGTCGTCGGAGTCCGGGCGGCCAAGACCCGCCGCCGGCCGGCCACTGCAGGG
TCCGCACTGATCCGCTCCGCGGGGAGAGCCGCTGCTCTGGGAAGTGAGTTCGCCTGCGGACTCCGAGGAACCGCT
GCGCACGAAGAGCGCTCAGTGAGTGACCGCGACTTTTCAAAGCCGGGTAGCGCGCGCGAGTCGACAAGTAAGAGT
GCGGGAGGCATCTTAATTAACCCTGCGCTCCCTGGAGCGAGCTGGTGAGGAGGGCGCAGCGGGGACGACAGCCAG
CGGGTGCGTGCGCTCTTAGAGAAACTTTCCCTGTCAAAGGCTCCGGGGGGCGCGGGTGTCCCCCGCTTGCCACAG
CCCTGTTGCGGCCCCGAAACTTGTGCGCGCAGCCCAAACTAACCTCACGTGAAGTGACGGACTGTTCTATGACTG
CAAAGATGGAAACGACCTTCTATGACGATGCCCTCAACGCCTCGTTCCTCCCGTCCGAGAGCGGACCTTATGGCT
ACAGTAACCCCAAGATCCTGAAACAGAGCATGACCCTGAACCTGGCCGACCCAGTGGGGAGCCTGAAGCCGCACC
TCCGCGCCAAGAACTCGGACCTCCTCACCTCGCCCGACGTGGGGCTGCTCAAGCTGGCGTCGCCCGAGCTGGAGC
GCCTGATAATCCAGTCCAGCAACGGGCACATCACCACCACGCCGACCCCCACCCAGTTCCTGTGCCCCAAGAACG
TGACAGATGAGCAGGAGGGCTTCGCCGAGGGCTTCGTGCGCGCCCTGGCCGAACTGCACAGCCAGAACACGCTGC
CCAGCGTCACGTCGGCGGCGCAGCCGGTCAACGGGGCAGGCATGGTGGCTCCCGCGGTAGCCTCGGTGGCAGGGG
GCAGCGGCAGCGGCGGCTTCAGCGCCAGCCTGCACAGCGAGCCGCCGGTCTACGCAAACCTCAGCAACTTCAACC
CAGGCGCGCTGAGCAGCGGCGGCGGGGCGCCCTCCTACGGCGCGGCCGGCCTGGCCTTTCCCGCGCAACCCCAGC
AGCAGCAGCAGCCGCCGCACCACCTGCCCCAGCAGATGCCCGTGCAGCACCCGCGGCTGCAGGCCCTGAAGGAGG
AGCCTCAGACAGTGCCCGAGATGCCCGGCGAGACACCGCCCCTGTCCCCCATCGACATGGAGTCCCAGGAGCGGA
TCAAGGCGGAGAGGAAGCGCATGAGGAACCGCATCGCTGCCTCCAAGTGCCGAAAAAGGAAGCTGGAGAGAATCG
CCCGGCTGGAGGAAAAAGTGAAAACCTTGAAAGCTCAGAACTCGGAGCTGGCGTCCACGGCCAACATGCTCAGGG
AACAGGTGGCACAGCTTAAACAGAAAGTCATGAACCACGTTAACAGTGGGTGCCAACTCATGCTAACGCAGCAGT
TGCAAACATTTTGAAGAGAGACCGTCGGGGGCTGAGGGGCAACGAAGAAAAAAAAATAACACAGAGAGACAGACTT
GAGAACTTGACAAGTTGCGACGGAGAGAAAAAAGAAGTGTCCGAGAACTAAAGCCAAGGGTATCCAAGTTGGACT
GGGTTGCGTCCTGACGGCGCCCCCAGTGTGCACGAGTGGGAAGGACTTGGCGCGCCCTCCCTTGGCGTGGAGCCA
GGGAGCGGCCGCCTGCGGGCTGCCCCGCTTTGCGGACGGGCTGTCCCCGCGCGAACGGAACGTTGGACTTTTCGT
TAACATTGACCAAGAACTGCATGGACCTAACATTCGATCTCATTCAGTATTAAAGGGGGGAGGGGGAGGGGGTTA
CAAACTGCAATAGAGACTGTAGATTGCTTCTGTAGTACTCCTTAAGAACACAAAGCGGGGGGGAGGGTTGGGGAGG
GGCGGCAGGAGGGAGGTTTGTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTGGCCTGCCTTCGTTAACTG
TGTATGTACATATATATATTTTTTAATTTGATGAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAG
TTATTTCTTGTTTGTTTGTTTGGGTATCCTGCCCAGTGTTGTTTGTAAATAAGAGATTTGGAGCACTCTGAGTTT
ACCATTTGTAATAAAGTATATAATTTTTTTATGTTTTGTTTCTGAAAATTCCAGAAAGGATATTTAAGAAAATAC
AATAAACTATTGGAAAGTACTCCCCTAACCTCTTTTCTGCATCATCTGTAGATACTAGCTATCTAGGTGGAGTTG
AAAGAGTTAAGAATGTCGATTAAAATCACTCTCAGTGCTTCTTACTATTAAGCAGTAAAAACTGTTCTCTATTAG
ACTTTAGAAATAAATGTACCTGATGTACCTGATGCTATGGTCAGGTTATACTCCTCCTCCCCCAGCTATCTATAT
GGAATTGCTTACCAAAGGATAGTGCGATGTTTCAGGAGGCTGGAGGAAGGGGGGGTTGCAGTGGAGAGGGACAGCC
CACTGAGAAGTCAAACATTTCAAAGTTTGGATTGTATCAAGTGGCATGTGCTGTGACCATTTATAATGTTAGTAG
AAATTTTACAATAGGTGCTTATTCTCAAAGCAGGAATTGGTGGCAGATTTTACAAAAGATGTATCCTTCCAATTT
GGAATCTTCTCTTTGACAATTCCTAGATAAAAAGATGGCCTTTGCTTATGAATATTTATAACAGCATTCTTGTCA
CAATAAATGTATTCAAATACC

FIGURE 251A

GTTAACAAAAGGATTAATGGGTTGCTTAAATTAGTGAGCTTCATCAGTTTTATTTTTAATTCCTTGAGATAATGA
ATTTTAAAAGCAATAAATACAATGCTGTAGTTTTTGACTTCTTTTCTAAATATTTACATGGATTTACATGAAAGA
ACTAAAGAGATAGTATTTGTGGAACCAATTTAAACTCTTACATGCCTTTCAGGATTTGGGAATGTATTAACACCT
GCTGCTTTGTATCCAGTCTAAGGGAGCCTATTTGTTTGTTATCACATTGACTTCCTTTGATGTCTTTTAGTGTTA
CCCTCACTCAGACCCAAGGATTATGTCTTTTGGGGCTCCCATCATCCTGAGCTAGAGACACGTGACAGGGGTACA
CTCTCCTACAAAACCAGCCAGTTACTCAGTAAAGTGGACGATAGAAGAAAAAGAGCTGTTTGAACAAGGGCTGGC
TAAATTTGGCCGAAGATGGACCAAAATTTCAAAGCTAATTGGAAGCCGCACTGTTTTACAAGTGAAGAGTTATGC
AAGACAGTATTTTAAAAATAAGGTCAAATGCGGTCTGGATAAAGAAACACCAAATCAGAAGACCGGCCATAATCT
TCAAGTTAAAAATGAAGATAAAGGGACAAAGGCATGGACACCATCATGTTTAAGGGGACGTGCTGATCCCAACTT
GAATGCTGTAAAAATTGAAAAGTTATCTGATGATGAAGAAGTAGACATCACAGATGAGGTGGACGAGTTGTCTTC
TCAAACACCCCAGAAGAATTCTAGCAGTGATCTCTTGTTAGACTTTCCTAATAGTAAA**ATG**CATGAAACCAATCA
AGGAGAATTCATTACTTCTGACAGCCAGGAAGCTCTCTTTTCTAAGTCTTCCAGGGGCTGTCTTCAAAATGAAAA
GCAAGATGAAACACTTTCAAGCTCAGAAATTACACTGTGGACTGAGAAACAGAGCAATGGTGACAAAAAATCAAT
TGAATTAAATGACCAGAAATTTAATGAATTGATTAAAAACTGCAACAAGCATGATGGAAGGGGAATAATAGTTGA
TGCCAGGCAGTTGCCTTCTCCAGAGCCTTGTGAAATTCAGAAAAATTTGAATGATAATGAAATGCTTTTTCATTC
TTGCCAAATGGTAGAGGAAAGCCATGAGGAAGAAGAGCTTAAGCCACCAGAACAGGAAATAGAAATAGATAGAAA
TATCATTCAAGAAGAAGAAAAACAAGCAATTCCTGAGTTTTTTGAGGGGCGCCAAGCTAAAACACCAGAACGCTA
TTTGAAAATTAGAAATTATATTTTGGATCAATGGGAGATATGCAAACCAAAATACTTAAATAAGACCTCAGTACG
TCCTGGCCTGAAGAACTGTGGAGATGTTAATTGTATTGGACGGATTCATACATACCTCGAATTGATAGGAGCAAT
CAATTTTGGATGTGAACAGGCTGTGTATAATAGGCCACAAACAGTTGACAAAGTACGAATCAGAGACAGAAAAGA
TGCAGTAGAAGCATACCAACTTGCCCAGCGTCTGCAGTCTATGCGTACAAGGAGACGTAGGGTCCGAGACCCATG
GGGAAACTGGTGTGATGCAAAGGACTTAGAAGGACAAACGTTTGAGCATCTCTCTGCTGAGGAGTTGGCAAAAAG
AAGAGAAGAGGAAAAAGGCAGACCTGTTAAATCTTTAAAAGTGCCAAGACCAACAAAAAGCTCGTTTGATCCCTT
CCAACTGATACCTTGTAATTTTTTTAGTGAAGAAAAGCAGGAGCCATTTCAGGTGAAAGTGGCTTCAGAAGCACT
TTTAATAATGGATTTGCATGCTCATGTTTCTATGGCAGAAGTGATTGGTCTGTTAGGAGGAAGATACTCAGAAGT
TGATAAAGTAGTTGAAGTCTGTGCAGCAGAACCATGTAACAGTCTGAGTACAGGACTACAGTGTGAGATGGATCC
TGTATCACAAACACAGGCCTCAGAAACCTTGGCTGTTAGAGGCTTCAGTGTTATTGGATGGTATCATTCTCATCC
TGCTTTTGATCCTAATCCTTCCTTACGAGATATTGACACACAAGCTAAATACCAGAGTTACTTCTCCAGAGGAGG
TGCAAAGTTCATTGGGATGATTGTTAGTCCCTATAATCGAAATAATCCCTTACCATATTCTCAGATTACCTGCCT
GGTTATAAGTGAGGAAATTAGCCCAGATGGCTCTTATCGCTTACCTTACAAATTTGAAGTACAGCAGATGTTAGA
AGAACCTCAGTGGGGATTAGTATTTGAAAAGACAAGATGGATAATAGAAAAATACAGGCTCTCCCATAGCAGCGT
CCCCATGGATAAAATCTTTCGCCGGGATTCTGACCTGACTTGTTTGCAGAAACTTTTGGAGTGTATGAGGAAGAC
TCTGAGCAAAGTGACCAATTGCTTTATGGCTGAAGAATTCTTGACTGAAATAGAAAATTTGTTCCTTTCCAATTA
TAAAAGCAACCAAGAGAATGGAGTAACCGAAGAGAACTGTACAAAGGAATTGTTAATG**TGA**TTATTTTAAAGTTA
AGACATTTTAATCTTGACACAGTAGATCTTACTTTCAAAGTTATAAACTTGAAGTGATTGTAGTTAACATTGGCA
CAGCTTTGGTATTTTTTCTCTATTTCACAAAATCCAAACTTTGCCACATAAATCATGTGAAAAGGAAGAGATACA
AATTTGTTTTCATATAGTGATTATCAGAGTGTTCTGCAAACCAGGGTCCACCACGGTGTTCTAGTCCTTTACTGA
GCAATGCTGTAGGCTGTGAAACTAAGCAACCTGGTCGGCTTTACTGTTGTGTTCAGCTTGGGATTTGGACTATGT
CTCTAAGTCATTTCTTCCCTGAACTAGTCATTTATGTTCCATTGTGGTATCTCCTATTTCATTTAAAAGCACTTC
CATTCTTTCCATATATTCTGCTGAGATTTGTTTATGGCTATAAATGAGATATGGATGGGTGGTCACTGAGATAAT
TAATATGGTTTAGAACTACTGATTAATAAATCTAACAGGAGACCAGGAGAGGCATGACAAGAAAATCTTAAAAAC
AGGAAAAACCCAAAGGAGAGAACTAAATTACCAGTTTCTAATCATAGATACTATCTTCCATTTCATTGTATAGCA
GTAGTATCATAAGATATGCCATTTTCTCAGCTATCTGAAAATTTTTAACCAATTTTACACACATAAAATAATTAG
CTTCAATTGTGAGTCCACTTACATTAGTAGGTGTGATAAAACCTCATTTAACTGGAACATAGGTAATCATAACTC
AAACTTTTTTTCTACTGCCTACTACTAGGAGAAAGAGGCAAATGATAATAAAGCTGGAATAAATCAGAGATTTAA
TTTTTAAAACAAGCCTTTCAGGACATGTTACATATTCAGCCCAGTTTCATATGCTTTCTGAATCTATAATGGAGG
TCAGTGAACTTTTTTAATGTAAAGGGCCAGTTTGTAAATAATTTTGGCTTTTCAGGCCACATATGATGTCTATGA
GACATTCTTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTTACAGCCCTTTAAAATGATAAAAA

FIGURE 251B

CCATTGTTAACTCACAGGCCTCATAAAACATAGGCTGTTGGCTATTATTCTCCAACCCTTGATCTAGAGAATTTT
AAACATTAGAATTTTGTTTTACATTTGTTAAGCTTTACGTCATCTTCAAATGACACCAAAACTCAGAATTATGAT
CTGCATTTAAGCCAATTTTAAAATAAAATAAGCAGTCAATGCTGCCTCATTTATTGAAATTCAGTAGATTTTAGT
TTATTTCTTAGTAGTCAGAGAATTGATTTATAGCTATTCACCAAACATTCTTACTAACGTTTCCTTATATCTAAA
TCAGATTGATTCTATATTTTGCTTTGTTTGTAATCAATAGCCAATGAAGAATAAGGAGTATTGGAAGAAGCAGTG
AGTCAGCTTTAGGTGACCTGGTTCTTGTCTCAACTTTGTGATTTGGGGAGATACAGTTTACTTTCCCTGAGCCTT
AATTCTTGTGTAACTGAAGTCTAACTTAACTTCTTAATGTCCTTCCAGAACTAAAATTTTATTGTTCATTCTAAT
CGTTGGACTACTCTTGTGAAGTTTATATTTTGAGTTAATACAGTTTCCAAATTAACATACATTTAAAAAAAAAAG
GGTAGTATTTTTCCATTTCTCTGTGTGCACTTAGGATAAACAGTGAAGTATAGCTTATAAAACAATTAGTTTGAG
GGCTGAGAGTGTAAGAGGAACTATACCAAAAGTCAGGAAACCTGAGCTCTTACCCTAACTCTGTTACCAACTTTG
CTGTGTGACCTTAATCAAAACACATAACCTGGACCCCATGCTCCTCACCAGTAAATCAAGGGCCTGAATTTTATG
GCTTAGTATTCCCTTCCAAGCTCCGAAGTTGCGTGATTCTGTGAAAGGCAGTGATTGATTCCTTTGTACTCATCT
TCCTTTTGACCTGTTTCCTCATGATATATTGGGGAACAAATACTAAAAAGTGTTTTATACTAGCTTTCTTGATTG
ACATTTCCCTATAATACTGATGAATTTGGGTGATGGAAAGTAATGGAAATTGTTAAAAGTTCTGCTCTCAAATCT
GAGTCTCCTTGCCCTGTGTGCCAATGTTTAACCATATTTGCTAATCTAAGCCATATTGCGAGGATCTCAAGGATG
ATACTTGTCAAGAGTTTGGGGCCTTGAGAGCACAGTTTTCAAAATAATACTTAGTATTTTCTGACTATAGAGTAC
ATTTGTCTTGTAAAGTATATTTTAAAATACAGAGAAGTGTGAAGTACAAATATCTCAGTGCTACTATTTAAAAAA
ACACAATTAGTATATAAATCCTTCCCCATTTTTTTGACAGTATAATTTTAGTATGTTAAACTTGGTTACTTCTTT
CTCTCTTCCTCCATCATTTTCCCTGCTTCCTTTTTCTTTTGTCATATTCTTAAAACAATTTTGCAACCACAGGTA
CCCACATTGCTGGCACTACCAGCCTTGGGCTACTACCGAGGATAATGGAGCCAGGGCCTTGTAGAAGCACAGAGG
AAGTCTAGAACTGAGGGGGCCTATGATACAGGAAGTTCAGGAGGCAGAGTCTCAAAGGAACACCTGCCTTTAATA
ATGTTTACAGAAGTGGAGAAAGGACTAAAGGACTTAAAGACATGCAGGTGTCTTCATCCTGATTCTGTCTTTGTT
ATTGCACAATGACTATAAAATAATGACCTAATTTTTTTTTTTTCTGGCTTGGCTAATGGAAATCGACACTAGCG
CTTCCCCAGTATTAGACTTAATCTAATTCCAAAGTAACATTCAAGAAAAGAAAAACCAGTGGAACAGGATCAGTA
AGCTCAGACTCTCCATCTCCATTATTTTAGCCTTGACCATTCTTCTCTAATCCTTTTAAATTATCTTCAGTTTCC
AGTTCAAGTTACATTGCTTCAGTTACAGTTTGTTTGACCCTGTATTCAGAGCTGCATTATGATTCTTGTGGGCCC
TAGATAGTTTTGCCATCTTAGACCCCTTCTTCCATACAAAATTAAAAGTGATATTTTACAATTGTATCTGTATGA
AATGAATGTATTAATATTTTAGATTAAAACATTTTGTTTAGAAGTTCAGTTTTTTCTTATGAGGCTAAAAAAAAT
TAAAACATTTTTGTGGGCTTCTAAAAAACTGTGGGCCTTAGGTACTGTGCCTAATGGATAAGTTGGCATTGCCTG
TATTCTGAAGGGCATCATTGGAAAAATAGCAGTCATTATTCTGTCCCCTTCTCCCACCACCACAGTCCTTGGAGA
AGCCTTTGCCACTCCATCCAGGAGCACTGCAGTTTCCACGGTTATAGATCTATAGACTTGAACTTACTTCCTTCC
CAACCTAACGAAAACTCACAAGGATTACTTGGGACCATTCATCCTCAAAAAAGATAGGAGGCAGTGGTTTGTTTT
AGTCTTCAGATATTTTTGTTTTGGTCAGTCCCTAATCTGTAGTTTTGAAACTCGTGCCACACTTGAAAGGGAAAC
ATCCTACTACCTTTCTTTCCTCTCCATTTCCCACAAACCCTTTCCTTCATCATCACTCCCTGCATTCTTACTTCT
CAGCATATAAATACAAGACCCTTCTTTCTATTATTTGTTGAAAGCTAGGCCTGTAAAATAGAGATGGACAGACCA
TGCATGTTTCCATGAAGCTATTTAATGCTGCTCCCAGTCTTCTGTCCATACCATTCCTTCCCTGCCCCTAGGAGT
GGGGTTGAGGTCTGTGACATGCAGACTGTAAGCACAGTCAGAACCTCTGCAGCTCTCAACCCAACAGAGGAGACT
GTGGCTTCAACATGCCAACCTGAGCAGGTCTCCTCTGCATTACCTTCCTCCCATTTCTCTTCCTGGGTCCTGATG
AGGTGAGCTGGAGGAACCAATAGTCAGGATGCCCTGGAATTGATGTTGCTCTGTTTTGTGCTCACAAAACAGCCA
TGTAACACATGAGCACCTGAGTTGAAGCCATCCAGTCGCAAGTCAGCAGACAGCAGTTGATGGAATTCTCAGTAG
AAATTCAGTAAGGGTGCCCAAATTTTATTTTTTTTTTCACCTATACTCTACCAATATATGGTATTTAGGAAAACT
TCTTTTATCCAAGCACAAAGAAAAGCACACACATTTTTATAATCATCTGCTTCATCAGGGTAAATAAATAATTTA
ACAAATTTGATCAGCATCTCTAGTTTACCAGTACTTTAATATTAGTTTTCTTACAAATTAATGTATTTTGCAATA
TTTCCAGAAAATCACTGTGGGAGAATAATGTAATATACTTTAGGATATATTTCCTGACCTTTTCTTAAATGGCTT
CATGTGCTATTCCCCCAAATTCTGCTTTCTCTATTTTCTTTTTTATTTAACCTATAATTATACTTTCTAGTATAT
TCTGAGTCTATCTTCTAAGCCACCTTACATTTTTCCTGGAACAAGGGAGGGAATAAATAGTTGCCTCCACTAAAT
CAGGAAAAAATAAAAATATCCCAGGGGAGCTGTGATTATGCCAAGAGCTCTAAACAGAAGTTTGAGAAGGTAAAA
ATTAAGTTGTAGTATCTGAGTTGTTTTTATTTTCTTCCTTTGGTGTTTATGAAGGTATTCATAAGAACTTTAATT

FIGURE 251C

TCAGGGGAAAAAAATGCCTGATTTGCTATTTTTGACATTTCCTCGTCTCTTAAGAAGTCAGTTAAATATGTTTTC
ATAGTTTATATTCCTGTTTCATAGATTACTGTGAAACATGTATTTAAACCTATGAATTATAAAATAGTATTTAGA
TTCTAGCGTGAGTTAAATAGATTAGTCATATATCTTTTAGATTTGTGGATTTGACATGTAAATTATGTGTTGTGT
ATAAGTAAGTTAGTTACTAAACATATGGCATGGTTATTGATAAACTTGTTGCTATTTTTTTCCAAATGCTATCAG
TGTTTGTGGACTTTTAAAAATTAGTTTGAATTTTGGAATGTTCTGTGATAAAATGTAATTTCAACTATTTTGTAC
ATTTAAATATGCCATGTTGTATATGTCTGTATTTAAAAATGTTGTAAATACCTGCATTTTAAGAATTATGAAAGA
TTTTCCTCAAAAATGACAGAACTCTCCATACTTAATTGTGACACATTATAAGATATCTGATTTTAAGCTTTTGGA
TTTTGTTCTAAAAATTAAGTTTAAACATGCTGAAAATTCCATAAAAATAAAATTTTGAAAATAAA

FIGURE 252

MHETNQGEFITSDSQEALFSKSSRGCLQNEKQDETLSSSEITLWTEKQSNGDKKSIELNDQKFNELIKNCNKHDG
RGIIVDARQLPSPEPCEIQKNLNDNEMLFHSCQMVEESHEEEELKPPEQEIEIDRNIIQEEEKQAIPEFFEGRQA
KTPERYLKIRNYILDQWEICKPKYLNKTSVRPGLKNCGDVNCIGRIHTYLELIGAINFGCEQAVYNRPQTVDKVR
IRDRKDAVEAYQLAQRLQSMRTRRRRVRDPWGNWCDAKDLEGQTFEHLSAEELAKRREEEKGRPVKSLKVPRPTK
SSFDPFQLIPCNFFSEEKQEPFQVKVASEALLIMDLHAHVSMAEVIGLLGGRYSEVDKVVEVCAAEPCNSLSTGL
QCEMDPVSQTQASETLAVRGFSVIGWYHSHPAFDPNPSLRDIDTQAKYQSYFSRGGAKFIGMIVSPYNRNNPLPY
SQITCLVISEEISPDGSYRLPYKFEVQQMLEEPQWGLVFEKTRWIIEKYRLSHSSVPMDKIFRRDSDLTCLQKLL
ECMRKTLSKVTNCFMAEEFLTEIENLFLSNYKSNQENGVTEENCTKELLM

FIGURE 253

CTCTCTCTGGTCCGTGCCTCCAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCAC
GTGCAGCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGACATTCGTCATTCGA
AACATAGTGAAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTG
TATGTGAAGCTACATTACTGTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
AAGGACCGAACACCCCCATCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGA
GCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTT

FIGURE 254A

ATGGCACAACCGGGCAAATGCTCTGAAAAACGGATAAATAAAATGCTGGTCACAGATGAGAACATCAGTCTAGCA
GAGCTTGCGAAGGCAGCAGGGAGGAGAAAACCTCTGAGCTGTGTTTTGCCCAGTGTCCACAGAGGGTTAGGAGGA
CCCAATGAAGGAATGACCCTGAAATGTGAACAGGGCGAAGAACTAGGCCCCAGCTCCCTGCAGAGAAGATACATC
AAAGCCCCACATGAGGATTTTTATAGCTCCACATTGGACAAGCTTCCTCTTCCTGAGATAGAGCCTACAGGGAAG
GGACAGATTTGGGGCAAGGAGAGGAGTCTGAAAGAGATGGGGTACGCCGTAGTGAAAGCTGGAGTGAGAGCCTTC
GTATTCGAAGGCGGGGACTCGGGCGCTGTTGGCAGCTGGCGACGCGGGGCGAAGCCGCGGCTGGCGGCGCCTGGC
CAGTCCCGCATCCGCCGCGTGCACCCGGAGGTTGCGTGCGCTCCGAAGCCGGGGTGTGCGCCTAGCTGCCCCGGC
CCCGTGCACCGCGGGCCGCCTCGCGCAGGACTTCCGCAGCTCGCCAAGCCTGGGGTCTGCGACAGAAAAGGAGCG
GGGCTGCTCGGGCTGCCCAAAGGGTCATGGTTATTAAGGAAGAAAACACAGAATGGGCCCTTGTATGGACTCTAT
TACCAAGTGCCATTGGACACGCAGGCAGTGTACTGGGAGACAGTCGTGGTGTGCTCAGAGGTATTGCCACGGCCT
GAAGTTCCTCTCTTGGCCGCAGCTGCCCCCACTCTGCTGCAATCTTCTGGGGAGGGCTTCACCTGCCACTGCCTC
CTGCATGCCAGCATCGCCTGCTGCAGACTGCAGAGCTGGGGTGCCAAAGACCAGTCCTCTCAGGGGGATGAAGAG
AAAGACCCTCCGAAGAGCCACCCTTATTCTGTGGAGACCCCATATGGCTTTCATTTAGACCTGGACTTCCTCAAG
TATGTGGATGACATCGAGAAGGGAAACACTATCAAAAGAATTCCTATCCACAGAAGGGCCAAGCAGGCCAAATTT
AGCACTCTGCCCCGAAACTTCAGCCTTCCTGACAGTGGGGCTCGCCCCCCTGCAGCCCCGCCCCTCCAAAACTGG
TCTCCCGTGGTGCCAAGGGAGGCATCACTTGGGACACAGGAGCAAAACCAGTCACCACCGCTTGGTAATGCCCCC
CAGGCCTCAACAAGCAGGAGTGAGGTGAGCTACCACAGGAAGGCTCTGTTGGCAGAGGCCACCAGACAGTTGGAA
GCTGCTGAGCCAGAGGATGCCGAGCTCACTTTTGGGAGTGGACGGCCCCAGCTCTTGAGAGCATCCAGCATGCCT
GCCACGCTGCTGCACAGCAGGGCTTCTGAGGAGCCAGGCCTGAGCCTGGGGCCCCCTGCCCCTCCTGCCCTCCCT
CCCCTTCAGGGTGAAGGCAGTGTCTGTGATGGCACCTTTGAACCTGCAGAAGGATTGGCAGGTTTCCACAGCTCC
AGCCCACGAGCATCAACTCGGATTCCAGAGCTGGTCCAGGAGGGAGCTGAGCCTCCAGAGGGTGTGGTGAAGGTT
CCAAATCACCTCCCTCTCCCAGGCCCTCCTTTCTCATTCCAGAATGTGCTTGTAGTTCTAGAGGACAAGGAAGAT
GAACACAATGCCAGAGAAGCAGAGGTGTTGTTCACCCCTGGCTCCCCTACGCCAAGCCCGCCACCTCTGCCATCA
CCCATCCCTGAGAATGAGCTCCTCCTGGAAGAAATCGAGCTCAACATCAGCGAGATTCCACCCCCGCCACCTGTA
GAGGTGGACATGAGAAGCATTGGCATCAGGGTAACTGAGGAAAGCCTGGGCCTTGCCAGGGTGGATCCAGGCAGC
ATCTCCAGCCTGAAACAGCAGGTCTCGGCCCTGGAGGGAGAGTTGTCTGGAAGAACCGAGGAACTGGCACAGGTC
AGAACTGCTCTCCAGCAGCAGGAAGAGGAAATCAAAGCTAGGGAGCAAAGAATTCGAGAGCTGGAGTTCACTGTA
GCCCAACTGGAAGGACAGTTTCACCAAGAGAACGCCAAAGACACTCAGGGCCAGACGGACGTGATGGTGAACACT
GACCCTGTCCATGGACTCTTGACCAGGGAGTCGTGTGATAAGGGCATTGAAGTCAACCTTCTAGGCAGCATGGAG
TCTGAAAGCTGGGGGCACCGAGGAGAGGAGAATGGCCTCCTATGGGGGCCAGATGGTCATAAACAAGGGAATCAG
AGCCCAGCAGAACGTGTGCTTCTGCCCCAGCTGTCACTGCCACAGGGACCCGAGCAGGTCCTTACCTCCTCTGTA
CATAGCTTCCTCTCCACTGAACTCAGGATTGAAGAAGCAGGCACTGAACAGGAAGGAGGCCCTCAGGGAGGAACC
AGGGGAGCAGGAGGCTTTCTGTGGGGCAGCGACAGAAAGACTCCCCCAGCAGGGAGGGAGGAGACCAGTTCCAAT
CTCCCAGGGAAGGAGCACCCGGGAAGGCCACCAAGCTCGCCAACGGATGCCACTATTGGGCAGTATGTGAAGAAG
ATCCAGGAGCTCCTGCAGGAGCAGTGGAACTGCCTGGAGCATGGGTACCCGGAGCTGGCCAGCGCCATCAAGCAG
CCAGCCTCCAAGCTCAGCAGCATCCAGAGCCAGCTGCTGAGCTCCCTCAACCTGCTGCTGTCGGCCTACTCGGCC
CAGGCTCACCCACCCAAGGAGCCACCGGCCTCCTCCTCCTCCCCGCCAGTGGAGATCTCCCCATCGACCAGCCTT
AAATCCATAATGAAAAAGAAAGACTATGGCTTCCGTGCAGGAGGTAATGGGACCAAAAAGAACCTTCAGTTTGTT
GGGGTTAACGGTGGGTATGAGACCACCTCAAGTGAGGAGACCAGCGGTGAGGACAGCACCCCAGAGGACTTGTCT
GACAGCGAGGCAGAGAAGAAGTGTGACGGCCCAGATCACAAGCATGTCAAAGATGCCCATCTCACCTGCGAGGCT
GGGCAGGGCATCCCTGAGGGCACCTGCCATGCTGCCCAGGAAAGTGGGCCTGGGGAAGAAGTCCCCCACTCCAAG
GCCGAGAGCCGGAAGTCGTCTAGCCCCGCCGTGGTGGCCTCCTACCTCCACGAGGTCCAGCCTCACTCCCCACAC
TTCCTGAAACTGCTTGTCAACTTGGCCGATCACAACGGGAACACGGCCCTTCACTACAGCGTGTCCCACTCCAAC
TTCTCCATCGTGAAGCTGCTGCTGGAGACAGGCGTCTGCAATGTGGACCATCAGAACAAAGCTGGCTACACTGCC
GTAATGATCACTCCCTTGGCTTCCGCAGAGACCAATGAAGACATGGCTGTTGTCTGGAAGCTCTTAAGAGAAGGA
AATGTGAACATTCAAGCTACTCAGGGAGGCCAGACTGCGCTGATGCTGGGAGTCAGCCACGACAGGGAGGACATG
GTTCAAGCGCTGCTTAGCTGCCAGGCAGATGTCAATCTGCAGGACCACGATGGATCCTCGGCCCTCATGGTGGCC
TGTCACCATGGCAACGTGGACCTGGTGCGGCTGCTCCTGGCACACCCAGCCTGCGACAGCAGCCTGACTGACAAG

FIGURE 254B

GCTGGCCGCACAGCTTTGTCCATCGCTCTGAAGTCACCCACCCATATGGAAATTGCTGGGCTTCTGAGAGCCCAC
GCGGAGCAGGGCAGGTCCCTGGGGCTGTAG

FIGURE 255

MASVQEVMGPKRTFSLLGLTVGMRPPQVRRPAVRTAPQRTCLTARQRRSVTAQITSMSKMPISPARLGRASLRAP
AMLPRKVGLGKKSPTPRPRDINPQKNFLMHAGH

FIGURE 256A

GCGGCGGCCGCGGAGTATCCTGGAGCTGCAGACAGTGCGGGCCTGCGCCCAGTCCCGGCTGTCCTCGCCGCGACC
CCTCCTCAGCCCTGGGCGCGCGCACGCTGGGGCCCCGCGGGGCTGGCCGCCTAGCGAGCCTGCCGGTCGACCCCA
GCCAGCGCAGCGACGGGGCGCTGCCTGGCCCAGGCGCACACGGAAGTGCGCTTCTCTGAAGTAGCTTTGGAAAGT
AGAGAAGAAAATCCAGTTTGCTTCTTGGAGAACACTGGACAGCTGAATAAATGCAGTATCTAAATATAAAAGAGG
ACTGCAATGCCATGGCTTTCTGTGCTAAAATGAGGAGCTCCAAGAAGACTGAGGTGAACCTGGAGGCCCCTGAGC
CAGGGGTGGAAGTGATCTTCTATCTGTCGGACAGGGAGCCCCTCCGGCTGGGCAGTGGAGAGTACACAGCAGAGG
AACTGTGCATCAGGGCTGCACAGGCATGCCGTATCTCTCCTCTTTGTCACAACCTCTTTGCCCTGTATGACGAGA
ACACCAAGCTCTGGTATGCTCCAAATCGCACCATCACCGTTGATGACAAGATGTCCCTCCGGCTCCACTACCGGA
TGAGGTTCTATTTCACCAATTGGCATGGAACCAACGACAATGAGCAGTCAGTGTGGCGTCATTCTCCAAAGAAGC
AGAAAAATGGCTACGAGAAAAAAAAGATTCCAGATGCAACCCCTCTCCTTGATGCCAGCTCACTGGAGTATCTGT
TTGCTCAGGGACAGTATGATTTGGTGAAATGCCTGGCTCCTATTCGAGACCCCAAGACCGAGCAGGATGGACATG
ATATTGAGAACGAGTGTCTAGGGATGGCTGTCCTGGCCATCTCACACTATGCCATGATGAAGAAGATGCAGTTGC
CAGAACTGCCCAAGGACATCAGCTACAAGCGATATATTCCAGAAACATTGAATAAGTCCATCAGACAGAGGAACC
TTCTCACCAGGATGCGGATAAATAATGTTTTCAAGGATTTCCTAAAGGAATTTAACAACAAGACCATTTGTGACA
GCAGCGTGTCCACGCATGACCTGAAGGTGAAATACTTGGCTACCTTGGAAACTTTGACAAAACATTACGGTGCTG
AAATATTTGAGACTTCCATGTTACTGATTTCATCAGAAAATGAGATGAATTGGTTTCATTCGAATGACGGTGGAA
ACGTTCTCTACTACGAAGTGATGGTGACTGGGAATCTTGGAATCCAGTGGAGGCATAAACCAAATGTTGTTTCTG
TTGAAAAGGAAAAAAATAAACTGAAGCGGAAAAAACTGGAAAATAAACACAAGAAGGATGAGGAGAAAAACAAGA
TCCGGGAAGAGTGGAACAATTTTTCTTACTTCCCTGAAATCACTCACATTGTAATAAAGGAGTCTGTGGTCAGCA
TTAACAAGCAGGACAACAAGAAAATGGAACTGAAGCTCTCTTCCCACGAGGAGGCCTTGTCCTTTGTGTCCCTGG
TAGATGGCTACTTCCGGCTCACAGCAGATGCCCATCATTACCTCTGCACCGACGTGGCCCCCCCGTTGATCGTCC
ACAACATACAGAATGGCTGTCATGGTCCAATCTGTACAGAATACGCCATCAATAAATTGCGGCAAGAAGGAAGCG
AGGAGGGGATGTACGTGCTGAGGTGGAGCTGCACCGACTTTGACAACATCCTCATGACCGTCACCTGCTTTGAGA
AGTCTGAGCAGGTGCAGGGTGCCCAGAAGCAGTTCAAGAACTTTCAGATCGAGGTGCAGAAGGGCCGCTACAGTC
TGCACGGTTCGGACCGCAGCTTCCCCAGCTTGGGAGACCTCATGAGCCACCTCAAGAAGCAGATCCTGCGCACGG
ATAACATCAGCTTCATGCTAAAACGCTGCTGCCAGCCCAAGCCCCGAGAAATCTCCAACCTGCTGGTGGCTACTA
AGAAAGCCCAGGAGTGGCAGCCCGTCTACCCCATGAGCCAGCTGAGTTTCGATCGGATCCTCAAGAAGGATCTGG
TGCAGGGCGAGCACCTTGGGAGAGGCACGAGAACACACATCTATTCTGGGACCCTGATGGATTACAAGGATGACG
AAGGAACTTCTGAAGAGAAGAAGATAAAAGTGATCCTCAAAGTCTTAGACCCCAGCCACAGGGATATTTCCCTGG
CCTTCTTCGAGGCAGCCAGCATGATGAGACAGGTCTCCCACAAACACATCGTGTACCTCTATGGCGTCTGTGTCC
GCGACGTGGAGAATATCATGGTGGAAGAGTTTGTGGAAGGGGGTCCTCTGGATCTCTTCATGCACCGGAAAAGCG
ATGTCCTTACCACACCATGGAAATTCAAAGTTGCCAAACAGCTGGCCAGTGCCCTGAGCTACTTGGAGGATAAAG
ACCTGGTCCATGGAAATGTGTGTACTAAAAACCTCCTCCTGGCCCGTGAGGGCATCGACAGTGAGTGTGGCCCAT
TCATCAAGCTCAGTGACCCCGGCATCCCCATTACGGTGCTGTCTAGGCAAGAATGCATTGAACGAATCCCATGGA
TTGCTCCTGAGTGTGTTGAGGACTCCAAGAACCTGAGTGTGGCTGCTGACAAGTGGAGCTTTGGAACCACGCTCT
GGGAAATCTGCTACAATGGCGAGATCCCCTTGAAAGACAAGACGCTGATTGAGAAAGAGAGATTCTATGAAAGCC
GGTGCAGGCCAGTGACACCATCATGTAAGGAGCTGGCTGACCTCATGACCCGCTGCATGAACTATGACCCCAATC
AGAGGCCTTTCTTCCGAGCCATCATGAGAGACATTAATAAGCTTGAAGAGCAGAATCCAGATATTGTTTCAGAAA
AAAAACCAGCAACTGAAGTGGACCCCACACATTTTGAAAAGCGCTTCCTAAAGAGGATCCGTGACTTGGGAGAGG
GCCACTTTGGGAAGGTTGAGCTCTGCAGGTATGACCCCGAAGGGGACAATACAGGGGAGCAGGTGGCTGTTAAAT
CTCTGAAGCCTGAGAGTGGAGGTAACCACATAGCTGATCTGAAAAAGGAAATCGAGATCTTAAGGAACCTCTATC
ATGAGAACATTGTGAAGTACAAAGGAATCTGCACAGAAGACGGAGGAAATGGTATTAAGCTCATCATGGAATTTC
TGCCTTCGGGAAGCCTTAAGGAATATCTTCCAAAGAATAAGAACAAAATAAACCTCAAACAGCAGCTAAAATATG
CCGTTCAGATTTGTAAGGGGATGGACTATTTGGGTTCTCGGCAATACGTTCACCGGGACTTGGCAGCAAGAAATG
TCCTTGTTGAGAGTGAACACCAAGTGAAAATTGGAGACTTCGGTTTAACCAAAGCAATTGAAACCGATAAGGAGT
ATTACACCGTCAAGGATGACCGGGACAGCCCTGTGTTTTGGTATGCTCCAGAATGTTTAATGCAATCTAAATTTT
ATATTGCCTCTGACGTCTGGTCTTTTGGAGTCACTCTGCATGAGCTGCTGACTTACTGTGATTCAGATTCTAGTC
CCATGGCTTTGTTCCTGAAAATGATAGGCCCAACCCATGGCCAGATGACAGTCACAAGACTTGTGAATACGTTAA

FIGURE 256B

AAGAAGGAAAACGCCTGCCGTGCCCACCTAACTGTCCAGATGAGGTTTATCAACTTATGAGGAAATGCTGGGAAT
TCCAACCATCCAATCGGACAAGCTTTCAGAACCTTATTGAAGGATTTGAAGCACTTTTAAAATAAGAAGCATGAA
TAACATTTAAATTCCACAGATTATCAAGTCCTTCTCCTGCAACAAATGCCCAAGTCATTTTTTAAAAATTTCTAA
TGAAAGAAGTTTGTGTTCTGTCCAAAAAGTCACTGAACTCATACTTCAGTACATATACATGTATAAGGCACACTG
TAGTGCTTAATATGTGTAAGGACTTCCTCTTTAAATTTGGTACCAGTAACTTAGTGACACATAATGACAACCAAA
ATATTTGAAAGCACTTAAGCACTCCTCCTTGTGGAAAGAATATACCACCATTTCATCTGGCTAGTTCACCATCAC
AACTGCATTACCAAAAGGGGATTTTTGAAAACGAGGAGTTGACCAAAATAATATCTGAAGATGATTGCTTTTCCC
TGCTGCCAGCTGATCTGAAATGTTTTGCTGGCACATTAATCATAGATAAAGAAAGATTGATGGACTTAGCCCTCA
AATTTCAGTATCTATACAGTACTAGACCATGCATTCTTAAAATATTAGATACCAGGTAGTATATATTGTTTCTGT
ACAAAAATGACTGTATTCTCTCACCAGTAGGACTTAAACTTTGTTTCTCCAGTGGCTTAGCTCCTGTTCCTTTGG
GTGATCACTAGCACCCATTTTTGAGAAAGCTGGTTCTACATGGGGGGATAGCTGTGGAATAGATAATTTGCTGCA
TGTTAATTCTCAAGAACTAAGCCTGTGCCAGTGCTTTCCTAAGCAGTATACCTTTAATCAGAACTCATTCCCAGA
ACCTGGATGCTATTACACATGCTTTTAAGAAACGTCAATGTATATCCTTTTATAACTCTACCACTTTGGGGCAAG
CTATTCCAGCACTGGTTTTGAATGCTGTATGCAACCAGTCTGAATACCACATACGCTGCACTGTTCTTAGAGGGT
TTCCATACTTACCACCGATCTACAAGGGTTGATCCCTGTTTTTACCATCAATCATCACCCTGTGGTGCAACACTT
GAAAGACCCGGCTAGAGGCACTATGGACTTCAGGATCCACTAGACAGTTTTCAGTTTGCTTGGAGGTAGCTGGGT
AATCAAAAATGTTTAGTCATTGATTCAATGTGAACGATTACGGTCTTTATGACCAAGAGTCTGAAAATCTTTTTG
TTATGCTGTTTAGTATTCGTTTGATATTGTTACTTTTCACCTGTTGAGCCCAAATTCAGGATTGGTTCAGTGGCA
GCAATGAAGTTGCCATTTAAATTTGTTCATAGCCTACATCACCAAGGTCTCTGTGTCAAACCTGTGGCCACTCTA
TATGCACTTTGTTTACTCTTTATACAAATAAATATACTAAAGACTTT

FIGURE 257

CTCTTCATAAGCCGGCGCTCGGCGAGTTCTCCCAGGAGAAGGCC**ATG**TTCAGTTCGAGCGCCAAGATCGTGAAAC
CCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGGCATCTCCCAGGCTCTTCTGGAGCTGGAGATGAACTCAGAAC
TCAAGGCTCAGCTCAGAGAGCTGAATATTACGGCAGCCAAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCA
TAATACTTGTTCCCGTTACTCAACTGAAATCTTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAA
AGTTCAGTGGGAAGCATGTCGTCTTTATCGCTCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAA
AAAATAAGCAAAAGCGTCCCAGGAGCAGCACTGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCC
CAAGTGAAATTGTGGGCAAGAAAATCCGCGTCAAACTAGATGGCAGCCGGCTCATAAAGGTTCATTTGGACAAAG
CACAACAGAACAATGTGGAACACAAGGTTGAAACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTA
ATTGTGAATTCCCAGAGTTTCAATAG**TAA**ACAAAAATGACTAAATAAAAATATATATATTCATAGT

FIGURE 258

MFSSSAKIVKPNGEKPEEFESGISQALLELEMNSELKAQLRELNITAAKEIEVGGGRKAIIILVPVTQLKSFQKI
QIRLVSELEKKFSGKHVVFIAQRRILPKPTRKSCTKNKQKRPRSSTVTAVHDAILEDLVFPSEIVGKKIRVKLDG
SRLIKVHLDKAQQNNVEHKVETFSGVYKKLMGKDVNCEFPEFQS

FIGURE 259

GGAGAAGGCCATGTTCAGTTCGAGCGCCAAGATCGTGAAACCCAACGGCGAGAAGCCGGAGGAGTTCGAGTCCGG
CATCTCCCAGGAAATTGAAGTTGGTGGTGGTCGGAAAGCTATCATAATACTTGTTCCCGTTACTCAACTGAAATC
TTTCCAGAAAATCCAAATCCGGCTAGTAAGTGAATTGGAGAAAAAGTTCAGTGGGAAGCATGTCGTCTTTATCGC
TCAGAGGAGAATTCTGCCTAAGCCAACTCGAAAAAGCTGTACAAAAAATAAGCAAAAGCGTCCCAGGAGCAGCAC
TGTGACAGCTGTGCACGATGCCATCCTTGAGGACTTGGTCTTCCCAAGTGAAATTGTGGGCAAGAAAATCCGCGT
CAAACTAGATGGCAGCCGGCTCATAAAGGTTCATTTGGACAAAGCACAACAGAACAATGTGGAACACAAGGTTGA
AACTTTTTCTGGTGTCTATAAGAAGCTCATGGGCAAGGATGTTAATTGTGAATTCCCAGAGTTTCAATAGTAAAC
AAAAATGACTAAATAAAAATATATATATTCATAGTAAAAAAAAAAAAAAAAATCTC

FIGURE 260

GGGGGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTGGAGGAACGCGCCGCCG
AGCCACCATC**ATG**CCTGGGCACTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATTCGACCAGTTATTTGA
CGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAAGAAGCCGGCGGGGGCGGCGTTGG
GGGCCCTGGGGCCAAGAGCGCAGCTCAGGCCGCGGCCCAGACCAACTCCAACGCGGCAGGCAAACAGCTGCGCAA
GGAGTCCCAGAAAGACCGCAAGAACCCGCTGCCCCCCAGCGTTGGCGTGGTTGACAAGAAAGAGGAGACGCAGCC
GCCCGTGGCGCTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACTTCAGGGTGAAGGGAA
AATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTCGAAAAGCCACTTGAAGAAAAGGGTGA
AGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTCGAGGTCGTGGTGGTCTTGGAAGAGGTCG
AGGGGGCCGTGGACGTGGAATGGGCCGAGGAGATGGATTTGATTCTCGTGGCAAACGTGAATTTGATAGGCATAG
TGGAAGTGATAGATCTGGCCTGAAGCACGAGGACAAACGTGGAGGTAGCGGATCTCACAACTGGGGAACTGTCAA
AGACGAATTAACTGACTTGGATCAATCAAATGTGACTGAGGAAACACCTGAAGGTGAAGAACATCATCCAGTGGC
AGACACTGAAAATAAGGAGAATGAAGTTGAAGAGGTAAAAGAGGAGGGTCCAAAAGAGATGACTTTGGATGAGTG
GAAGGCTATTCAAAATAAGGACCGGGCAAAAGTAGAATTTAATATCCGAAAACCAAATGAAGGTGCTGATGGGCA
GTGGAAGAAGGGATTTGTTCTTCATAAATCAAAGAGTGAAGAGGCTCATGCTGAAGATTCGGTTATGGACCATCA
TTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATCAATTTTGGAGACCTTGGCCGCCCAGGACGTGG
CGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCAAACCGTGGCAGCAGGACCGACAAGTCAAGTGC
TTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGCTCTGGCT**TAA**CTGGATGCCATAAGACAACCCTGGTT
CCTTTGTGAACCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGATTCCAAACGACTAAGAAATTAAAAAAAAAAAG
ACTGTCATTCATACCATTCACACCTAAAGACTGAATTTTATCTGTTTTAAAAATGAACTTCTCCCGCTACACAGA
AGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTGGTAGCAGGGATGTTTTCATAATTTTCAGAGAT
TATGCATTCTTCATGAATACTTTTGTATTGCTGCTTGCAAATATGCATTTCCAAACTTGAAATATAGGTGTGAAC
AGTGTGTACCAGTTTAAAGCTTTCACTTCATTTGTGTTTTTTAATTAAGGACTTAGAAGTTCCCCCAATTACAAA
CTGGTTTTAAATATTGGACATACTGGTTTTAATACCTGCTTTGCATATTCACACATGGTCAACTGGGACATGTTA
AACTTTGATTTGTCAAATTTTATGCTGTGTGGAATACTAACTATATGTATTTTAACTTAGTTTTAATATTTTCAT
TTTGGGGGAAAAATCTTTTTTCACTTCTCATGATAGCTGTTATATATATATGCTAAATCTTTATATACAGAAATA
TCAGTACTTGAACAAATTCAAAGCACATTTGGTTTATTAACCCTTGCTCCTTGCATGGCTCATTAGGTTCAAATT
ATAACTAATTTACATTTTCAGCTATATTTACTTTTTAAATGCTTGAGTTTCCCATTTTAAAATCTAAACTAGACA
TCTTAATTGGTGAAAGTTGTTTAAACTACTTATTGTTGGTAGGCACATCGTGTCAAGTGAAGTAGTTTTATAGGT
ATGGGTTTTTTCTCCCCCTTCACCAGGGTGGGTGGAATAAGTTGATTTGGCCAATGTGTAATATTTAAACTGTTC
TGTAAAATAAAAAAAAAAAAAAAAAA

FIGURE 261

MPGHLQEGFGCVVTNRFDQLFDDESDPFEVLKAAENKKKEAGGGGVGGPGAKSAAQAAAQTNSNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVALKKEGIRRVGRRPDQQLQGEGKIIDRRPERRPPRERRFEKPLEEKGEGGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFDSRGKREFDRHSGSDRSGLKHEDKRGGSGSHNWGTVKDEL
TDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKPNEGADGQWKK
GFVLHKSKSEEAHAEDSVMDHHFRKPANDITSQLEINFGDLGRPGRGGRGGRGGRGRGGRPNRGSRTDKSSASAP
DVDDPEAFPALA

FIGURE 262

ACCTTTAAGCGTCACGGGTGGGGCTGCAGCTTCTGGACCTAGGACTTTGAAC**ATG**TCGCGCCTGAAGCGGATAGC
GGGGCAGGATCTCCGCGCTGGTTTCAAAGCAGGTGGAAGAGACTGCGGTACCTCGGTACCCCAAGGGCTGTTGAA
GGCAGCGAGGAAGAGCGGCCAGTTAAACCTGTCGGGTAGAAACCTCAGTGAAGTGCCGCAGTGTGTCTGGAGAAT
AAATGTGGATATCCCTGAGGAAGCTAATCAGAATCTTTCGTTTGGTGCTACTGAAAGATGGTGGGAGCAGACAGA
TTTGACCAAACTAATAATATCAAACAATAAACTTCAGTCACTTACAGATGACCTGCGACTCTTGCCTGCACTGAC
TGTTCTTGATATACATGATAATCAGTTGACATCCCTTCCTTCTGCTATAAGAGAGCTAGAAAATCTTCAGAAACT
TAATGTCAGCCATAATAAACTGAAAATACTCCCTGAAGAAATTACAAACCTAAGAAACCTGAAGTGCCTGTATCT
CCAGCATAATGAATTAACCTGCATATCAGAGGGATTTGAACAACTTTCCAATTTAGAAGATTTAGATCTTTCAAA
CAATCATCTTACAACTGTTCCTGCTAGTTTTTCTTCTCTGTCCAGTCTGGTGCGACTCAATCTTTCTAGTAATGA
ACTGAAGAGTTTGCCAGCAGAAATAAATAGAATGAAAAGGTTGAAGCATTTGGATTGTAATTCAAATCTCTTGGA
AACTATACCTCCTGAATTGGCTGGCATGGAATCACTAGAATTGCTTTATTTGCGGAGGAATAAATTACGTTTTCT
ACCAGAATTTCCTTCTTGTAGTCTATTGAAGGAATTGCACGTAGGTGAAAACCAGATTGAAATGTTAGAGGCAGA
ACATCTTAAACATCTGAATTCAATTCTTGTGCTAGACCTGAGGGATAACAAGTTAAAATCTGTTCCAGATGAAAT
TATACTACTACGGTCCTTGGAAAGGCTTGACCTAAGCAACAATGATATTAGTAGTCTTCCCTATTCATTGGGGAA
CCTTCATTTGAAATTTTTGGCATTAGAAGGAAATCCTTTGAGAACAATTCGAAGAGAAATTATAAGTAAAGGAAC
ACAAGAAGTCCTAAAATATCTACGAAGCAAGATCAAAGATGATGGACCTAGCCAAAGTGAGTCTGCTACTGAGAC
TGCCATGACACTACCAAGTGAATCCAGAGTCAATATACATGCCATCATTACATTAAAAATATTAGACTATAGTGA
TAAACAAGCAACTTTGATTCCTGATGAGGTGTTTGATGCAGTAAAAAGCAACATCGTCACTTCTATTAACTTCAG
TAAGAATCAACTATGTGAAATTCCAAAAAGGATGGTAGAACTGAAGGAAATGGTTTCTGATGTCGATCTCAGTTT
TAATAAACTTTCCTTTATATCCTTGGAGTTATGTGTGCTTCAGAAATTGACTTTTTTAGATCTCAGGAACAATTT
TTTAAATTCTTTGCCAGAAGAAATGGAATCACTGGTAAGACTGCAAACGATCAATCTTTCCTTTAATAGGTTTAA
AATGCTACCTGAAGTTCTATATCGTATCTTCACACTTGAAACAATTCTGATTAGTAATAATCAGGTTGGATCTGT
GGACCCTCAGAAAATGAAGATGATGGAAAATCTGACCACGTTGGACCTTCAAAATAATGACCTCTTACAAATTCC
ACCAGAGCTCGGTAATTGTGTAAACTTAAGAACATTACTATTGGATGGAAATCCATTCCGAGTTCCTCGAGCAGC
CATATTAATGAAAGGAACAGCTGCTATACTTGAATATTTGAGAGACCGAATTCCTACT**TAA**CATGGAGTTGCTTT
ATAACCCTTGTCATGTATTATTAACCCTGGTTAATTCTAAGGAGGATGTAACATTTGTTTTAGTATCATCTTAAA
AGGTGATTATTGTAATTGATCTTGTAGTTTCCCAGTATCACCTACCCGTTGGTATAATTAGCCTGGGCCATATTC
ACTGCCAGTAAATATTTTTACATTTTTATTTAAGATTTTTGTAAGGTGTTGTGTACATTTGTAATGGTGATAACC
ACAATGTGTTCATACATTTGTTCTAAATGTTTTGCTTATGATTTATCCTGCTAACTTTCATTTTCTTATAGCAAG
CAGTTTTTTCAAAAATGAATTTTTATTTAATGTGGTTCAGTATTATAATAACAAAGCATTTTTGTAGAACTGGTT
TTTTTTCTCATTTATTTTTGTATTCCATACAATGTGACCAATTGACTTGAATATGACTAGCCAGTTTCTATGTTT
TTGTTAGATATAAAATTAAATCGAATTTTGTTGAATACTGTTCTTTGGCATTTAAAAAATAAGACCTTCTTATCT
TGGGCCACATGTCAAAAGAAAAAGGAAACAAAAATATATTAAAAATAAGACTTTTCATTACCCATGATAGGACTT
TTGTGATATGGCTAATCTCAGTACACATTTCAACTTAAAACCTTTTTATTTACAGCACCATAATTTTAAAATTTA
CTTGCAATCTTGGTAAGACTAAACTTGCAGTGTTTTTCTAAAAGGGAATTTGATAGGTAAACTTGATTTAATAAA
AATTAAATATCATTTTTGTTTACACCAAAATTATCAGAAGTAGGTTGATTAGTCATTATAACACTTACCATATGA
TTCTATTAAGAAGTCAATTCAGTAGCATGTATATCAATTTATATAGATAGGTAGATAGCTTTTGGATGATTGAGG
CATGCTTATATTATGAAAAAAATTGCTAATAAAGATAAATACTACATGTTCAGAATAAAAGTTACATTTTTC

FIGURE 263

MSRLKRIAGQDLRAGFKAGGRDCGTSVPQGLLKAARKSGQLNLSGRNLSEVPQCVWRINVDIPEEANQNLSFGAT
ERWWEQTDLTKLIISNNKLQSLTDDLRLLPALTVLDIHDNQLTSLPSAIRELENLQKLNVSHNKLKILPEEITNL
RNLKCLYLQHNELTCISEGFEQLSNLEDLDLSNNHLTTVPASFSSLSSLVRLNLSSNELKSLPAEINRMKRLKHL
DCNSNLLETIPPELAGMESLELLYLRRNKLRFLPEFPSCSLLKELHVGENQIEMLEAEHLKHLNSILVLDLRDNK
LKSVPDEIILLRSLERLDLSNNDISSLPYSLGNLHLKFLALEGNPLRTIRREIISKGTQEVLKYLRSKIKDDGPS
QSESATETAMTLPSESRVNIHAIITLKILDYSDKQATLIPDEVFDAVKSNIVTSINFSKNQLCEIPKRMVELKEM
VSDVDLSFNKLSFISLELCVLQKLTFLDLRNNFLNSLPEEMESLVRLQTINLSFNRFKMLPEVLYRIFTLETILI
SNNQVGSVDPQKMKMMENLTTLDLQNNDLLQIPPELGNCVNLRTLLLDGNPFRVPRAAILMKGTAAILEYLRDRI
PT

FIGURE 264

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCCACGAAA
TCACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACTT
TACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCT
GGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTG
AACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCC
GGACCTACAGAGCTCATGGTCGGATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAA
AGGAACAGATTGTTCCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAAC
AAAAACTTATGGCACGGGAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGGAAAAATAAAAAATAAAAATAA
ATAAATAAATAAATAAAAAAAAAAAAAAAAAAAAG

FIGURE 265

GCTCTTTCCCTAAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTACTCACTTGACCCGGAGAACCCCACGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACAAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACCATTCCGACGTTAC
AATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCGGATTAACCCA
TACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAAACCAGAAGAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTAAATTCAGCAT
TAAAATAAATGTAATTAAAAGG

FIGURE 266

MVRYSLDPENPTKSCKSRGSNLRVHFKNTRETAQAIKGMYIQKGTKYLKDVTLQKQCIPFRHYNGGVGRCAQAKQ
WGWTQGRWPKKSAEFLLHVLKNTESNAELKGRFSGH

FIGURE 267

CGGGAAGGATTGAATACGAGACGCTGTCTGCTTGCTGCCTTAAGACAGCTAGCTGAATTGCTGATTAACTTTTAA
AATACCCAGCTTGGTTTATTTTTCTTAGAATCTGTTGCTAAGACTGGGGACGCTGTTTTCTTTTACAAAGGGAAA
TCTAAGTTAATTTCAAGGCATTCGAA**ATG**GGGAAAGACTATTATTGCATTTTGGGAATTGAGAAAGGAGCTTCAG
ATGAAGATATTAAAAAGGCTTACCGAAAACAAGCCCTCAAATTTCATCCGGACAAGAACAAATCTCCTCAGGCAG
AGGAAAAATTTAAAGAGGTCGCAGAAGCTTATGAAGTATTGAGTGATCCTAAAAAGAGAGAAATATATGATCAGT
TTGGGGAGGAAGGGTTGAAAGGAGGAGCAGGAGGTACTGATGGACAAGGAGGTACCTTCCGGTACACCTTTCATG
GCGATCCTCATGCTACATTTGCTGCATTTTTCGGAGGGTCCAACCCCTTTGAAATTTTCTTTGGAAGACGAATGG
GTGGTGGTAGAGATTCTGAAGAAATGGAAATAGATGGTGATCCTTTTAGTGCCTTTGGTTTCAGCATGAATGGAT
ATCCAAGAGACAGGAATTCTGTGGGGCCATCCCGCCTCAAACAAGATCCTCCAGTTATTCATGAACTTAGAGTAT
CACTTGAAGAGATATATAGTGGTTGTACCAAACGGATGAAGATTTCTCGAAAAAGGCTAAACGCTGATGGAAGGA
GTTACAGATCTGAGGACAAAATTCTTACCATTGAGATTAAAAAAGGGTGGAAAGAAGGCACCAAAATTACTTTTC
CAAGAGAAGGAGATGAAACACCAAATAGTATTCCAGCAGACATTGTTTTTATCATTAAAGACAAAGATCATCCAA
AATTTAAAAGGGATGGATCAAATATAATTTATACTGCTAAAATTAGTTTACGAGAGGCATTGTGTGGCTGCTCAA
TTAATGTACCAACACTGGATGGAAGAAACATACCTATGTCAGTAAATGATATTGTGAAACCCGGAATGAGGAGAA
GAATTATTGGATATGGGCTGCCATTTCCAAAAAATCCTGACCAACGTGGTGACCTTCTAATAGAATTTGAGGTGT
CCTTCCCAGATACTATATCTTCTTCATCCAAAGAAGTACTTAGGAAACATCTTCCTGCCTCA**TAG**AATGAAGAAC
TTTGTTACACATATTTTGATAAGGCACTGAAAATATAAAAGGACTGGTAGTTTACTGATGTAGATGTGAATTCTG
TATAAAGATGTGTAAATTGTTTTGAGGGTTCATTAAATTGCAT

FIGURE 268

MGKDYYCILGIEKGASDEDIKKAYRKQALKFHPDKNKSPQAEEKFKEVAEAYEVLSDPKKREIYDQFGEEGLKGG
AGGTDGQGGTFRYTFHGDPHATFAAFFGGSNPFEIFFGRRMGGGRDSEEMEIDGDPFSAFGFSMNGYPRDRNSVG
PSRLKQDPPVIHELRVSLEEIYSGCTKRMKISRKRLNADGRSYRSEDKILTIEIKKGWKEGTKITFPREGDETPN
SIPADIVFIIKDKDHPKFKRDGSNIIYTAKISLREALCGCSINVPTLDGRNIPMSVNDIVKPGMRRRIIGYGLPF
PKNPDQRGDLLIEFEVSFPDTISSSSKEVLRKHLPAS

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FIGURE 269

GCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGCCGCGCTCGCCCCGGGCTACTCCTGCGCG
CCACA**ATG**AGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCT
CCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACG
GCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCA
AGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGAC
CCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTA
TTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTC
GGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGG
ACCAGGACGGCCTCCTTGGTAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGA
TTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGATCCCTGTTTTTGGAATGGAGCCTCGCATCCGATACAACCCTT
TACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCA
CACGAGTTACCAATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGAC
AGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTA
CTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGCCGATGCTGCA
CGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGA
TGATCCAGTCCTGCAAATGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCA
ATGACATTCACAAATTTAGGGAC**TAA**ATGCTACCTGGGTTTCCAGGGCACACCTAGACAAACAAGGGAGAAGAGT
GTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGATGGGACTCATTGTAGAAAGGAAGCCTTG
CTCATTCTTGAGGAGCATTAAGGTATTTCGAAACTGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACG
ATTGGAGAATACTTTGCTTCATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACT
TTCTGTTTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTCTACAGTCG
TAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTGACAAAAGTAAATGGGAGGGCAT
TCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTGTGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAG
AAATCAGGTGTTTTAAGACTGAATGTTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACT
GGAATAATTTGTAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATAAAG
AAATATTTACCT

FIGURE 270

MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQLNEDCSKTQPCDHTKG
LECNFGASSTALKGICRAQSEGRPCEYNSRIYQNGESFQPNCKHQCTCIDGAVGCIPLCPQELSLPNLGCPNPRL
VKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKELGFDASEVELTRNNELIAVGKGSSLKRIPVFGMEPRIRYNPLQ
GQKCIVQTTSWSQCSKTCGTGISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
AGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFRCEDGETFSKNVMMIQSCKCNYNCPHANEAAFPFYRLFND
IHKFRD

FIGURE 271

GCTCTGTCAGTAACACATGTGTAAGAGCCGCGGAGGGAGCGAGCGAGCCGGCTAGAGGCCAGCGCCGCCGCCGCC
GCCGCCTCCGAGCCGGGCAGCAACAGCCCCGGCAGCGGCGCAGGCTCCAGCGCGCCGGGCCCGGCCGGCCGCAGC
CCCCGACGCCTGGGTGCGCCTGCCTGCCGGCCTCCGCACCGTCCGCCGCCGCTCCCGGGGCTGTTGTGTCTGCGA
CTGCTCCCGGCCGGAGGTGCAGGGAGCTCAGCCGAGCCGCCGCTGCCATCCCGGAGCGAGCAAGCGAGCGAGCGC
GCGGGAGGGAGGAAGGCGGCGGCGGAGGAGGAGGAGGAGCGGGAGGAGCGCGGGCGGGGGCGGGGGCCGCCGGGC
GGGGGAATATACAAAGTGAAGCCACATTGCCAAACTTGCAGCAGCGATTGCAGCAGTTGCTGCCGCTGCGCCGCG
CCTGAAGCCGCGCCGCGCGGGCCGAGGGCTCCTGCAGCTGCTCGCGCGCAGTCGGAGGCGGAGAAGGACGAAGAC
TGAGACTGACACTTCTGCTCCCGGCCGCCCGGCACTTACGCGGGGGCCCCCCAACCCGCCCCAGAGCAACGCGAT
TTAAAAAAAAAAAAAAAGCCGCCCTTAGCCCCCTCCTCTCCTTTCCTGCTTCTGCGAGAACTCCCTCCCTCCCTC
CAGCTCCGCCAGCCCAGGCGCCCCTTCCCTGGAAGCCGAGCGGCTTCGCTCGCATTTCACCGCCGCCGCCTCTCG
CAATATTGCAATATAGGGGAAAAGCAGACC**ATG**GTGAATCCGGGCAGCAGCTCGCAGCCGCCCCCGGTGACGGCC
GGCTCCCTCTCCTGGAAGCGGTGCGCAGGCTGCGGGGGCAAGATTGCGGACCGCTTTCTGCTCTATGCCATGGAC
AGCTATTGGCACAGCCGGTGCCTCAAGTGCTCCTGCTGCCAGGCGCAGCTGGGCGACATCGGCACGTCCTGTTAC
ACCAAAAGTGGCATGATCCTTTGCAGAAATGACTACATTAGGTTATTTGGAAATAGCGGTGCTTGCAGCGCTTGC
GGACAGTCGATTCCTGCGAGTGAACTCGTCATGAGGGCGCAAGGCAATGTGTATCATCTTAAGTGTTTTACATGC
TCTACCTGCCGGAATCGCCTGGTCCCGGGAGATCGGTTTCACTACATCAATGGCAGTTTATTTTGTGAACATGAT
AGACCTACAGCTCTCATCAATGGCCATTTGAATTCACTTCAGAGCAATCCACTACTGCCAGACCAGAAGGTCTGC
TAAAAGGTCAGAGTAATGCAGAATGCGTGCCTTCATCTCAGATTTGTTCATCACAGGTGGATCCCATGTGTCTTC
AGTAGACAAGTCACCTTTGTAGCTAGCACCAGTGCCAGCTCCATGCCATTGCACCTTCTTTAGTCTTGATTGCCC
TTCCCGCATTTATTGGTGTATTAAAATGACTGAATATGAACATTAAGGACTCCATGAACCTGGGCTAATGGGAGA
CTGTAGAGAAAATGAAAAAAGATCCACCAGAGGACATCTTGGGGAGGGGGAGGGAGCTGGGGGGGAGGGAAATGA
CTAATGAAGCTAATTAAAAGAAGCATTCAAATCTGCTTTCTACCCTCATTAACAATTAGCAGGGCACTGGCCAGA
GTTTGTACCCTGTGTTTTACCTTAACAACATTCTATTTGCTCTTTGTATATTTAAGTGTTGTAAGGAAACGTGTT
TCAATCAAAACTGACCATGAGATAAAGGAAAGAGATGTGGCTTTTGTGATATTCTATCACAAACACTTATTGTAT
CTCTGTAAAATACAATGTATGTATGCATGTAAGTGTTTTTGTCCTAATGTTGCTACTCCCATGGCAAAGAAAAAA
AAAAGAATGAAAAAAAGAAAAAAAATTTGGAAAAAAAAATCAGGCTCATAGCAGCTACTGTGTAGAAAATTCCCC
CTACTTCTAATTTGCTGAATGAAGAAAAAAAAAAATCTTTTATTTGTGATATTTTCAGAGACATTTGCTCTAGTA
TGGTGTATTTAAATAATAAAAACTTAAAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 272

MVNPGSSSQPPPVTAGSLSWKRCAGCGGKIADRFLLYAMDSYWHSRCLKCSCCQAQLGDIGTSCYTKSGMILCRN
DYIRLFGNSGACSACGQSIPASELVMRAQGNVYHLKCFTCSTCRNRLVPGDRFHYINGSLFCEHDRPTALINGHL
NSLQSNPLLPDQKVC

FIGURE 273

AGCG**ATG**GCGGCTGGGCCGAGTGGGTGTCTGGTGCCGGCGTTTGGGCTACGGTTGTTGTTGGCGACTGTGCTTCA
AGCGGTGTCTGCTTTTGGGGCAGAGTTTTCATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTG
CAGCTCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGA
AGCACAATTTGAAACCAAAAAGCTGTATGCAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCC
TCAAGTCCAAGCTTTTGTTAGGAGTGATAAACCCAAACTGTTCAGAGGACTGCAAATCAAGTATGTCCGTGGTTC
AGACCCTGTATTAAAGCTTTTGGACGACAATGGGAACATTGCTGAAGAACTGAGCATTCTCAAATGGAACACAGA
CAGTGTAGAAGAATTCCTGAGTGAAAAGTTGGAACGCATA**TAA**ATCTTGCTTAAATTTTGTCCTATCCTTTTGTT
ACCTTATCAAATGAAATATTACAGCACCTAGAAAATAATTTAGTTTTGCTTGCTTCCATTGATCAGTCTTTTACT
TGAGGCATTAAATATCTAATTAAATCGTGAAATGGCAGTATAGTCCATGATATCTAAGGAGTTGGCAAGCTTAAC
AAAACCCATTTTTTATAAATGTCCATCCTCCTGCATTTGTTGATACCACTAACAAAATGCTTTGTAACAGACTTG
CGGTTAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACGAACAACAGATTTCTAAATTAGAGAGGT
TAACAAGACAGATGATTACTATGCCTCATGTGCTGTGTGCTCTTTGAAAGGAATGACAGCAGACTACAAAGCAAA
TAAGATATACTGAGCCTCAACAGATTGCCTGCTCCTCAGAGTCTCTCCTATTTTTGTATTACCCAGCTTTCTTTT
TAATACAAATGTTATTTATAGTTTACAATGAATGCACTGCATAAAAACTTTGTAGCTTCATTATTGTAAAACATA
TTCAAGATCCTACAGTAAGAGTGAAACATTCACAAAGATTTGCGTTAATGAAGACTACACAGAAAACCTTTCTAG
GGATTTGTGTGGATCAGATACATACTTGGCAAATTTTTGAGTTTTACATTCTTACAGAAAAGTCCATTTAAAAGT
GATCATTTGTAAGACCAAAATATAAATAAAAAGTTTCAAAAATCTATCTGAATTTGGAATTCTTCTGGTTTGTTC
TTTCATGTTTAAAAATGATGTTTTTCAATGCATTTTTTTCATGTAAGCCCTTTTTTTAGCCAAAATGTAAAAATG
GCTGTAATATTTAAAACTTATAACATCTTATTGTTGGTAATAGTGCTTTATATTTGTCTGATTTTATTTTTCAAA
GTTTTTTCATTTATGAACACATTTTCATTGGTATATTATTTAAGGAATATCTCTTGATATAGAATTTTTATATTA
AAAATGATTTTTCTTTGGC

FIGURE 274

MAAGPSGCLVPAFGLRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEA
QFETKKLYAGAILEVCGENWEGSLKSKLLLGVINPNCSEDCKSSMSVVQTLYLKLLDDNGNIAEELSILKWNTDS
VEEFLSEKLERI

FIGURE 275

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCAC
TTTACAGAAACAGTGCATACCATTCCGACGTTACAATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGG
CTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATAC
TGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCG
CCGGACCTACAGAGCTCATGGTCGGATTAACTCATACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGA
AAAGGAACAGATTGTTCCTAAACCAGAAAAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAA
ACAAAAACTTATGGCCCGGAAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGGAAAAAAAAAAAAAAAAAAA
AAAAAAAAAG

FIGURE 276

GCTCTTTCCCTAAGCAGCCTGAAGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCATGAAA
TCATGCAAATCAAGAGGTTCCAATCTTCGTGTTCACTTTAAGGACACTCGTGAAACTGCTCAGGCCATCAAGGGT
ATGCATATACGAAAAGCCACGAAGTATCTTAAAGATGTCACTTTACAGAAACAGTGCATACCATTCCGACGTTAC
AATGGTGGAGTTGGCAAGTGTGCGCAGGCCAAGCAGTGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCT
GAATTTTTGCTGCACATGTTTAAAAACGCAGAGGGTAATACTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTC
ATTGAGTATATCCAAGTGAACAAAGCACCTAAGATGCTCCGCCGGACCTACAGAGCTCATGGTCGGATTAACTCA
TACATGAGCTCTCCCTGGCACATTGAGATGATCCTTACTGAAAAGGAACAGATTGTTCCTAAACCAGAAAAGGAG
GTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCCCGGAAGTAAATTCAGCAT
TAAAATAAATGTAATTAAAAGG

FIGURE 277

CTTTTTCACAACGGGTTTGCTGCCAGAACACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAAGAA
AAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTAC
AAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTC
AAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAA
TTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTCATCAAAAACATGATTACA
GGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTTGGTGAATTTGAAGCTGGTATCTCCAAG
AATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTAATTGTTGATGTTAACAAA
ATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAG
AAAATTGGCTACAACCCCAACACAGTAGCATTTGTGCCAATTTCTGGTTAGAATGGTGACAAC**ATG**CTGGAGCCA
AGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCATGCTGCTT
GAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTCCAGGATGTCTAC
AAAATTGGTGGTATTGGTACTGTTCTTGTTGGCCGAGTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACC
TTTGCTCCAGTCAGCGTTACAACAGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCT
GGGGACAATATGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCATCGTGGCAACGTTGCTGGTGACAGC
AAAAATGACCCACCAATGGAAGCAGCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGT
CGCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGA
GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAA**TGA**ATATTATCCCTAATACCTGCCACCCCA
CTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGAC
TGGTTAATGATAATAATGCAACATAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTT
TTTCGCATGCAGCAGTTTTAAGTTATTAGTTTTTAAAATCAGTACTTTTTAAATGGAAACAACTTGACCAAAAAT
TTGTCACAGAATTTTGAGACCCATTAAAAAAGTTTAATGAG

FIGURE 278

MLEPSANMPWFKGWKVTHKDGNASGTMLLEALDCILPPTRPTDKPLRLPLQDVYKIGGIGTVLVGRVETGILKPG
MVVTFAPVSVTTEVKSVEMHHEALNEALPGDNMGFNVKNVSVKDVHRGNVAGDSKNDPPMEAAGKPMCVESFSDY
PPLGRFTVHDMRQTLAVGVIKAVDKKAAGAGKVTKSAQKAQKAK

FIGURE 279

CACAGGTGTCGTGAAAACTACCCCTAAAAGCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTG
GACACGTAGATTCGGGCAAGTCCACCACTTCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAA
TTGAAAAATTGCAGAAAGAGGCTGCTGAGATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGA
AAGCTGAGCGTGAACGTGGTATCACCATTGATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTA
TCATTGATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTAATTGTTGATGTTAACAAAATGGATTCCACTG
AGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAAATCAGCACTTACATTAAGGGTGACAACATGC
TGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGGAAAGTCACCCATAAGGATGGCAATGCCAGTGGAACCA
TGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCGGCCAAATAAGCTCTGGCTA
TGCACCTGTATTGGATTGCCACACAGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCG
TTCTGGTAAAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGG
CAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTACTGTTCATGATATGAGACAGAC
ACTTGCGGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAA
AGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGG

FIGURE 280

GCCAAAATGGGAAAAGAAAAGACTCATATCAACATTGTCGTCATTGGACACGTAGATTCGGGCAAGTCCACCACT
TCTGGCCATCTGATCTACAAATGCGGTGGCATCGACAAAAGAACAATTGAAAAATTGCAGAAAGAGGCTGCTGAG
ATGGGAAAGGGCTCCTTCAAGTATGCCTGAGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATT
GATATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACTTC
ATCAAAAACATGATTACAGGGACATCTCAGGCTGGTTGTGCTGTCCTAATTGTTGCTGCTGGTGTTGGTGAATTT
GAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCATATACACTGGGTGTGAAACAACTA
ATTGTTGATGTTAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATGAGGAAATTGTTAAGGAA
ATCAGCACTTACATTAAGAAAATTGGCTACAACCCCAACACAGTAGCATTTGTGCCAAATTCTTGAAGTCTGGTG
ATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTC
GCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTG

FIGURE 281

GTGGAGACTGGTATTCTCAAACCTGGTATGGTGGTCACCTTTGCTCCAGTCAGCGTTACAACAGAAGTAAAATCT
GTCGAAATGCACCATGAAGCTTTGAATGAAGCTCTTCCTGGGGACAATATGGGCTTCAATGTCAAGAATGTGTCT
GTCAAGGATGTTCATCGTGGCAACGTTGCTGGTGACAGCAAAAATGACCCACCAATGGAAGCAGCTGGCTTCACT
GCTCAGGTGATTATCCTGAACCATCCGGGCCAAATAAGCTCTGGCTATGCACCTGTATTGGATTGCCACACAGCT
CACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCT
AAATTCTTGAAGTCTGGTGATGCTGCCATTGCTGATATGGTTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCA
GACTATCCACCTTTGGGTCGCTTTACTGTTCATGATATGAGACAGACACTTGCGGTGGGTGTCATCAAAGCAGTG
GACAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCC
CTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTA
AGTTTAGTAGTAAATTTTGTGGACCACTTTGGTT

FIGURE 282

GTTACTCAAAGACTACCTACTGCGTGGTGCTCCAAGTGAAATTCGTGAAGAATTAGAAAAGCAGCTTTATTCTTG
TATTGCTCTCAAAGTCACAGCAAATCAAATGGAAATGGAACATTCTTTGATACTAAATAACCTAAAAACATTATT
GTGGAAGAAAATTTCCTACACTAATGACTCTTAGTTCATTTGGACATAATTACCATTTTAAGAAACCTGCCACTT
TTAAAGAACAATTTTGAGCATTAAAAAAAAATGGCTTCAAATTCCGGCCAGTTACACAAAACTCCTTCCCCCCAG
GCCTGAGAAGCCATCAGTATGTGATCACTGAAGTAATGGCAGGTGTAGGATCAACAGGTCCCCAAGATGTCATTC
CTGCCCTTTTAGAAGCCCTGTTACATCTCCGAAGTACATTCATTGTGTAACTATTTTGACTGACTTTAAAAACCA
ATGCTGTGAAAAGCTTCATTCCATAAACATCAACAGTGAGTGATTTGTAGATTTACCTTAGCCAAAATACCAATG
CTGGAAGCATTGTGTTTGCATTGAAGCTGCTGTTCAACAAGAAAATTTATAAATTTACTAATGTCTTAGCATGGT
AAAGTTTGCACATTAACAGAAATTAAGACTGCAAAGCAGGTTAAACTTGCTTCTTTATAAAACAGATGTTGGGTT
AATAGCATGGTTTACTGTATTAAAGACTTATACACCCATTTTTAACCTCATTCAGACATCAAGTTATGTGTAGCT
TCACAATGGTTCAAGTGGCTTACTTCAAGAAATCTTATACTTGACAGTACACCAATTTTATTGACTAAAAATGGA
TGAACTTTCCTAAAGATTCAAAGGGCCCATCTTAGTATCACGCAGCTGACTGAGCCCTTCAAAACTGACATCTTA
AGGCCCAATCAAGATCCACATATCCTGATTTTGAACTATGTGAAAGTGGGACTGTAAGTGCAAGACTAAAATAAA
TTATAGCAGACTTTTTAGTAATAACTTTCCATTTTCAAACAGTATATCCTGTGGGCCAAAGGGCTATTTCTTAAA
GAGGCATGTAAATGTATTTATTTATCTA**ATG**TTTTTTTCCCCATGTAAACTTGATATACAAGGTTTAGTATTTGC
TCCTCTTTCATATTATTTTCACACGTATACTCAGATTTGGCATGTACCTTTCAACATCTCCATAAAATTAAACAC
CTTTTGGAGAAAAGAACCACTATTTTCTGCTCAAAGGTTTCGCCTACCTAAAGTGGAACATGTTAAAAATCTATG
TGACCATCACTGGACAGCTTTCTCTCAAAACTTTCCTTCAACGCCATGGATTAGCACCAGTTTTGTTTACTTTAA
GGTACTTTTCCCATTCATCATCTGGTTA**TAA**TAAATGGATGGAAGAAATATTTCCCACTGATGGTTGGTCTGTTG
CTTGCCAAATTTTTAGGGAGAGCTGTTCATCATACAACATAAGGGATAATGACTCCTGTCAGGTAAAACAGAAGC
CCAAGAAATAACAACTTTTTTTCTTAAAAAGTTAGTTACACTTGTTTTCTTGGAGAAAAAAACCTGTCAACTCCT
TTGCTTTTCCAAAATATTTCAGGGTATTTCCTATAAGGTTCATAAGAATAAGAGCTTAACACAGAAATAGTTGCT
GTTCATAAGTTTATTATCTATATCTGAAAAAATCATAGAAAATTGCTGGGTTTAGCTCTCAGCAGCCCGCTCCTG
AGCTCTGAGGAAGCTTGCCTTCTTTTGAGCTACCCGATCCTTCTTCTGAGCAAGGGACATTTTGGGACGGTTCCA
CCTACAAAAGATAGGAATATATATTTTTTAAACTATAACTGAAGAGAATAGAATATTTAATTTAAAATTTTAATA
AAATTTAATTTTGATAGAGAATATTTAAGACTTTGCAATCAGAAGGTTAAATAATCCAAGTTCAAATACATTTAC
TTATGTATGATCTTAAGCTAACTTTCCCAAACCCCAACTTCTGTGATGTCCTACTACCATAGGGCCAAAAGTCAA
ATAGAAGACATGTTAGATTCAGTAATACCACTTCTAGGTATTTGCCCAAATGTTTTGAAATCAGTTTGTCCAAGA
GAGTGGCACTCCCATGTTCATTGCAGCACTATATATTAATAGCAACAGATAAATGGATAAAGGAAATGTGGTATA
CATATACATAATGGATTATTACCCAGTCTTTAAAAATGATGGAAATTCTGTCATTTGCAACATGAATGAAGTGGA
GAATATTGTGCTCAGTGAAATAAGCCAGGCACAAAAAGACAAATACTTCATATTCATATAGAATCTAAAACAATG
GAACTCACAGAAGCAGAGAGCAGAATGGTGGTTACAGAGGCTGGTGGGTGCAAAGAATGGGCAGATGATAGTCAA
GTATAAAATCTCCAACAGGAGGAGTATGATTTTGTTTTTAGTTCTATTGCACAGCATGATGAATATAGAATATCG
TACATTTCACAATTAAGAGAATAAATTTCAAATGTTGTTGCCACAAAGTGTTAAGTATTTGAGGTGAATATGTTA
AATACATTGATTTAATTACTATACATTGTATTTGTGGGCCATCACATCACTTTATGCTTACATGTTCATTAAGTA
TTACTTTCTATTCCATTTAAAGATCAAAACATGAAAGATCAACAAAAAGCAACTTGTCAGCCAATAAAAAAATGC
AGTAACCAGTACTTAGACTGTACTAGGATAGAAAGAACCACCTCAGTAGTGTCTGAGGCTAACACATTTCCATCA
CCACAGTTACTTTTGCAAACCTGGTTCCCTTCGCTTCTGCCACATCACGCAGAGCTAGTGATCGAGTTTGCACAA
TTACACCAACAGTCTGCCCCACGTGGGAACCATTCCCAACCTGTTTTCTTGAAAAGACAAAAAAAAAAGACGACAT
ACCTCTTCTTTTTAACTTCTTTCTTGGGCTTCTTTTCATAGACTGGATTCTCTCGTATAGCAGCATGAGCTTTCT
TATACATCTCCTCCATCTGAAACAAAGGAAAGCAAACAGTACTTGGTTTCATTTCATGTGCCCTACTATATTAAT
GCAACCATAACTTATCTTGTCCTTCTAAGCCAGATTCTCAAAAGGAACTAAACTAAATCAATGTTGGTAAACACT
TTAACTTCTAAATGTAACTCACCTTTTCCTAACAAATTCCCAATTTTCACCTTATGCAATGTGAATTATCACTAC
AGAACTCCATCTTACTCAAGAAAAAAATCAGGCCAGGTGTGGTGGTTCATGCCTGTAATCTCAAGCACTTTGGGA
GTCTGAAGTGGGAGGATCACTTCAGCCCAGGAGTTTGAGACCAGCTAAGGCAACACAGTGAGACCTGTCTCCATA
AAAAAACTAATTAGCCAGGTGGCAATTATTAATGGTGGCATGCACCTGTAGTCCCAGCTACAGGACTACACGTGA
GTCCAGGAGGTCAAGGCTGCAGTGGCACAATCACAGCTCACTGGACCCCAGCCTAGATGACAGAATGAGACCTCA
TCTCTACCAAAAATTAAAAAAAAAAAAAAAAAATTAGCAGGG

FIGURE 283

MFFSPCKLDIQGLVFAPLSYYFHTYTQIWHVPFNISIKLNTFWRKEPLFSAQRFRLPKVEHVKNLCDHHWTAFSQ
NFPSTPWISTSFVYFKVLFPFIIWL

FIGURE 284

CCTAGCGCCGCTGGGCCTGCAGGTCTCTGTCGAGCAGCGGACGCCGGTCTCTGTTCCGCAGG**ATG**GGGTTTGTTA
AAGTTGTTAAGAATAAGGCCTACTTTAAGAGATACCAAGTGAAATTTAGAAGACGACGAGAGGGTAAAACTGATT
ATTATGCTCGGAAACGCTTGGTGATACAAGATAAAAATAAATACAACACACCCAAATACAGGATGATAGTTCGTG
TGACAAACAGAGATATCATTTGTCAGATTGCTTATGCCCGTATAGAGGGGGATATGATAGTCTGCGCAGCGTATG
CACACGAACTGCCAAAATATGGTGTGAAGGTTGGCCTGACAAATTATGCTGCAGCATATTGTACTGGCCTGCTGC
TGGCCCGCAGGCTTCTCAATAGGTTTGGCATGGACAAGATCTATGAAGGCCAAGTGGAGGTGACTGGTGATGAAT
ACAATGTGGAAAGCATTGATGGTCAGCCAGGTGCCTTCACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCA
CTGGCAATAAAGTTTTTGGTGCCCTGAAGGGAGCTGTGGATGGAGGCTTGTCTATCCCTCACAGTACCAAACGAT
TCCCTGGTTATGATTCTGAAAGCAAGGAATTTAATGCAGAAGTACATCGGAAGCACATCATGGGCCAGAATGTTG
CAGATTACATGCGCTACTTAATGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACA
GCGTAACTCCAGACATGATGGAGGAGATGTATAAGAAAGCTCATGCTGCTATACGAGAGAATCCAGTCTATGAAA
AGAAGCCCAAGAAAGAAGTTAAAAAGAAGAGGTGGAACCGTCCCAAAATGTCCCTTGCTCAGAAGAAGGATCGGG
TAGCTCAAAAGAAGGCAAGCTTCCTCAGAGCTCAGGAGCGGGCTGCTGAGAGC**TAA**ACCCAGCAATTTTCTATGA
TTTTTTCAGATATAGATAATAAACTTATGAACAGCAACTAAAAAAAAAAAAAAAAAAA

FIGURE 285

MGFVKVVKNKAYFKRYQVKFRRRREGKTDYYARKRLVIQDKNKYNTPKYRMIVRVTNRDIICQIAYARIEGDMIV
CAAYAHELPKYGVKVGLTNYAAAYCTGLLLARRLLNRFGMDKIYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGL
ARTTTGNKVFGALKGAVDGGLSIPHSTKRFPGYDSESKEFNAEVHRKHIMGQNVADYMRYLMEEDEDAYKKQFSQ
YIKNSVTPDMMEEMYKKAHAAIRENPVYEKKPKKEVKKKRWNRPKMSLAQKKDRVAQKKASFLRAQERAAES

FIGURE 286

ATGGTAAATGTTAAGACAAATCTTGGGAGAAACATTTATCAATTCCAATACCTCTCTCCACCCCAATACTGTATG
CTCTTGGAAGAAGATGAAGATGCTTACAAGAAACAGTTCTCTCAATACATAAAGAACAGTGTAACTCCAGACATG
ATGGAGGAGATGTATAAGAAAGCTCATGCTGCTGTACCAGAGAATCCGGTCTATGAAAAGAAGCCCAAGAAAGAA
GTTAAAAAGAAGAGGTGGAACCGTTCCAAAATGTCCCTTGCTCAGAAGAAGGATTGGGTAGCTCAAAAGAAGGCA
AGCTTCCTCAGAGCT**TAG**

FIGURE 287

MVNVKTNLGRNIYQFQYLSPPQYCMLLEEDEDAYKKQFSQYIKNSVTPDMMEEMYKKAHAAVPENPVYEKKPKKE
VKKKRWNRSKMSLAQKKDWVAQKKASFLRA

FIGURE 288

GCTGACTCCAGTGTCCCGAGAGGCGCCGCTTCTTCCGCTTTCTCGTCAGGCTCCTGCAACCCCAGGCATGAACCA
AGGTTTCTGAACTACTGGGCGGGAGCCAACGTCTCTTCTTTCTCCCGCTCTGGCGGAGGCTTTGTCGCTGCGGGC
TGGGCCCCAGGGTGTCCCCC**ATG**GCGGGGCCGCGGGTGGAGGTCGATGGCAGCATCATGGAAGGGGGCGGCCAGA
TCCTGAGAGTCTCTACGGCCTTGAGCTGTCTCCTAGGCCTCCCCTTGCGGGTGCAGAAGATCCGAGCCGGCCGGA
GCACGCCAGGCCTGAGGCCTCAACATTTATCTGGACTGGAAATGATTCGAGATTTGTGTGATGGGCAACTGGAGG
GGGCAGAAATTGGCTCAACAGAAATAACCTTTACACCAGAGAAGATCAAAGGTGGAATCCACACAGCAGATACCA
AGACAGCAGGGAGTGTGTGCCTCTTGATGCAGGTCTCAATGCCGTGTGTTCTCTTTGCTGCTTCTCCATCAGAAC
TTCATTTGAAAGGTGGAACTAATGCTGAAATGGCACCACAGATCGATTATACAGTGATGGTCTTCAAGCCAATTG
TTGAAAAATTTGGTTTCATATTTAATTGTGACATTAAAACAAGGGGATATTACCCAAAAGGGGGTGGTGAAGTGA
TTGTTCGAATGTCACCAGTTAAACAATTGAACCCTATAAATTTAACTGAGCGTGGCTGTGTGACTAAGATATATG
GAAGAGCTTTCGTTGCTGGTGTTTTGCCATTTAAAGTAGCAAAAGATATGGCAGCGGCAGCAGTTAGATGCATCA
GAAAGGAGATCCGGGATTTGTATGTTAACATCCAGCCTGTTCAAGAACCTAAAGACCAAGCATTTGGCAATGGAA
ATGGAATAATAATTATTGCTGAGACCTCCACTGGCTGTTTGTTTGCTGGATCATCGCTTGGTAAACGAGGTGTAA
ATGCAGACAAAGTTGGAATTGAAGCTGCCGAAATGCTATTAGCAAATCTTAGACATGGTGGTACTGTGGATGAGT
ATCTGCAAGACCAGCTGATTGTTTTCATGGCATTAGCCAATGGAGTTTCCAGAATAAAAACAGGACCAGTTACAC
TCCATACGCAAACCGCGATACATTTTGCTGAACAAATAGCAAAGGCTAAATTTATTGTGAAGAAATCAGAAGATG
AAGAAGACGCCGCTAAAGATACTTATATTATTGAATGCCAAGGAATTGGGATGACAAATCCAAATCTA**TAG**AGTA
TTTGCCTCTTAAATGATACCTCATTGATATATTGCACTATTTCATAAATACTATAAAATAATGACTAGGAAGTAA
CTTATTAAAGGCTATGACTTAAATTTGAAGATGAAGTACAGTGTTCTAGGTTTGCTGAGAAGGCTTCATTAAATT
AATCTCACTTTGAATATCTCCTGAGAGATGGACAATGAAATATCAGTTGGTGGATATGTGTGATAGCTGATTTCA
ATATTGAAGTATTGAAATAAAATATTCTTTACACCTGAG

FIGURE 289

MAGPRVEVDGSIMEGGGQILRVSTALSCLLGLPLRVQKIRAGRSTPGLRPQHLSGLEMIRDLCDGQLEGAEIGST
EITFTPEKIKGGIHTADTKTAGSVCLLMQVSMPCVLFAASPSELHLKGGTNAEMAPQIDYTVMVFKPIVEKFGFI
FNCDIKTRGYYPKGGGEVIVRMSPVKQLNPINLTERGCVTKIYGRAFVAGVLPFKVAKDMAAAAVRCIRKEIRDL
YVNIQPVQEPKDQAFGNGNGIIIIAETSTGCLFAGSSLGKRGVNADKVGIEAAEMLLANLRHGGTVDEYLQDQLI
VFMALANGVSRIKTGPVTLHTQTAIHFAEQIAKAKFIVKKSEDEEDAAKDTYIIECQGIGMTNPNL

FIGURE 290

GCTTTTCCTTGCTACCTGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAAACTTT
CACA**ATG**TCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTT
AGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATCATAAA
TCTGAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGGTCGTGCTATTGTTGCCATTGAAAACCCTGCTGATGTCAG
TGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAATTTGCTGCTGCCACTGGAGCCACTCCAATTGC
TGGCCGCTTCACTCCTGGAACCTTCACTAACCGGATCCAGGCAGCCTTCCGGGAGCCACGGCTTGTTGTGGTTAC
TGACCCCAGGGCTGACCACCAGCCTCTCACAGAGGCATCTTATGTTAACCTACCTACCATTGCGCTGTGTAACAC
AGATTCTCCTCTGTGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAACTCACTCAGTGGGTTTGATGTG
GTGGATGCTGGCTCGGGAAGTTCTGCGCATGTGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGA
TCTGTACTTCGACAGAGATCCTGAAGAGATTGAAAAAGAAGAGCAGGCTGCTGCTGAGAAGGCAGTGACCAAGGA
GGAATTTCAGGGTGAATGGACTGCTCCAGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAGACTGGTCTGA
AGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGAAGACTGGAGCGCTCAGCCTGCCACGGAAGA
CTGGTCTGCAGCTCCCACTGCTCAGGCCACTGAATGGGTAGGAGCAACCACTGACTGGTCT**TAA**GCTGTTCTTGC
ATAGGCTCTTAAGCAGCATGGAAAAATGGTTGATGGAAAATAAACATCAGTTTCT

FIGURE 291

MSGALDVLQMKEDVLKFLAAGTHLGGTNLDFQMEQYIYKRKSDGIYIINLKRTWEKLLLAGRAIVAIENPADVSV
ISSRNTGQRAVLKFAAATGATPIAGRFTPGTFTNRIQAAFREPRLVVVTDPRADHQPLTEASYVNLPTIALCNTD
SPLCYVDIAIPCNNKGTHSVGLMWWMLAREVLRMCGTISREHPWEVMPDLYFDRDPEEIEKEEQAAAEKAVTKEE
FQGEWTAPAPEFTATQPEVADWSEGVQVPSVPIQQFPTEDWSAQPATEDWSAAPTAQATEWVGATTDWS

FIGURE 292

GGCACGAGGAAGAATCAGGAGCTTAGGATGTATTAACACCAACTCATTAATATACTAACCGGACAATGTTCTACA
AACAATTCTACATTGTAAAGGACTGGATTGGCACAAAATAAAATAATTTTATTTTATTCAGCTTATAATATGACT
CGATGGAGGAAAATTTGATAAGC**ATG**AGAGAAGACCATTCTTTTCATGTTCGTTACAGAATGGAAGCTTCTTGCC
TAGAGCTGGCCTTGGAAGGGGAACGTCTATGTAAATCAGGAGACTGCCGCGCTGGCGTGTCATTCTTTGAAGCTG
CAGTTCAAGTTGGAACTGAAGACCTAAAAACACTTAGCGCTATTTACAGCCAGTTGGGCAATGCTTATTTCTATT
TGCATGATTATGCCAAAGCATTAGAATATCACCATCATGATTTAACCCTTGCAAGGACTATTGGAGACCAGCTGG
GGGAAGCGAAAGCTAGTGGTAATCTGGGAAACACCTTAAAAGTTCTTGGGAATTTTGACGAAGCCATAGTTTGTT
GTCAGCGACACCTAGATATTTCCAGAGAGCTTAATGACAAGGTGGGAGAAGCAAGAGCACTTTACAATCTTGGGA
ATGTGTATCATGCCAAAGGGAAAAGTTTTGGTTGCCCTGGTCCCCAGGATGTAGGAGAATTTCCAGAAGAAGTGA
GAGATGCTCTGCAGGCAGCCGTGGATTTTTATGAGGAAAACCTATCATTAGTGACTGCTTTGGGTGACCGAGCGG
CACAAGGACGTGCCTTTGGAAATCTTGGAAACACACATTACCTCCTTGGCAACTTCAGGGATGCAGTTATAGCTC
ATGAGCAGCGTCTCCTTATTGCAAAAGAATTTGGAGATAAAGCAGCTGAAAGAAGAGCATATAGCAACCTTGGAA
ATGCATATATATTTCTTGGTGAATTTGAAACTGCCTCGGAATACTACAAGAAGACACTACTGTTGGCCCGACAGC
TTAAAGACCGAGCTGTAGAAGCACAGTCTTGTTACAGTCTTGGAAATACATATACTTTACTTCAAGACTATGAAA
AGGCCATTGATTATCATCTGAAGCACTTAGCAATTGCTCAAGAGCTGAATGATAGAATTGGTGAAGGAAGAGCAT
GTTGGAGCTTAGGAAATGCATACACAGCACTAGGAAATCATGATCAAGCAATGCATTTTGCTGAAAAGCACTTGG
AAATTTCAAGAGAGGTTGGGGATAAAAGTGGTGAACTAACAGCACGACTTAATCTCTCAGACCTTCAAATGGTTC
TTGGTCTGAGCTACAGCACAAATAACTCCATAATGTCTGAAAATACTGAAATTGATAGCAGTTTGAATGGTGTAC
TCCCCAAGTTGGGACGCCGGCATAGTATGGAAAATATGGAACTTATGAAGTTAACACCAGAAAAGGTACAGAACT
GGAACAGTGAAATTCTTGCTAAGCAAAAACCTCTTATTGCCAAACCTTCTGCAAAGCTACTCTTTGTCAACAGAC
TGAAGGGGAAAAAATACAAAACGAATTCCTCCACTAAAGTTCTCCAAGATGCCAGTAATTCTATTGACCACCGAA
TTCCAAATTCTCAGAGGAAAATCAGTGCAGATACTATTGGAGATGAAGGGTTCTTTGACTTATTAAGCCGATTTC
AAAGCAATAGGATGGATGATCAGAGATGTTGCTTACAAGAAAAGAACTGCCATACAGCTTCAACAACAACTTCTT
CCACTCCCCCTAAAATGATGCTAAAAACATCATCTGTTCCTGTGGTATCCCCCAACACGGATGAGTTTTTAGATC
TTCTTGCCAGCTCACAGAGTCGCCGTCTGGATGACCAGAGGGCTAGTTTCAGTAATTTGCCAGGGCTTCGTCTAA
CACAAAACAGCCAGTCGGTACTTAGCCACCTGATGACTAATGACAACAAAGAGGCTGATGAAGATTTCTTTGACA
TCCTTGTAAAATGTCAAGGATCCAGATTAGATGATCAAAGATGTGCTCCACCACCTGCTACCACAAAGGGTCCGA
CAGTACCAGATGAAGACTTTTTCAGCCTTATTTTACGGTCCCAGGGAAAGAGAATGGATGAACAGAGAGTTCTTT
TACAAAGAGATCAAAACAGAGACACTGACTTTGGGCTAAAGGACTTTTTGCAAAATAATGCTTTGTTGGAGTTTA
AAAATTCAGGGAAAAAATCGGCAGACCAT**TAG**TTACTATGGATTTATTTTTTTTCCTTTCAAACACGGTAAGGAA
ACAATCTATTACTTTTTTCCTTAAAAGGAGAATTTATAGCACTGTAATACAGCTTAAAATATTTTTAGAATGATG
TAAATAGTTAA

FIGURE 293

MREDHSFHVRYRMEASCLELALEGERLCKSGDCRAGVSFFEAAVQVGTEDLKTLSAIYSQLGNAYFYLHDYAKAL
EYHHHDLTLARTIGDQLGEAKASGNLGNTLKVLGNFDEAIVCCQRHLDISRELNDKVGEARALYNLGNVYHAKGK
SFGCPGPQDVGEFPEEVRDALQAAVDFYEENLSLVTALGDRAAQGRAFGNLGNTHYLLGNFRDAVIAHEQRLLIA
KEFGDKAAERRAYSNLGNAYIFLGEFETASEYYKKTLLLARQLKDRAVEAQSCYSLGNTYTLLQDYEKAIDYHLK
HLAIAQELNDRIGEGRACWSLGNAYTALGNHDQAMHFAEKHLEISREVGDKSGELTARLNLSDLQMVLGLSYSTN
NSIMSENTEIDSSLNGVLPKLGRRHSMENMELMKLTPEKVQNWNSEILAKQKPLIAKPSAKLLFVNRLKGKKYKT
NSSTKVLQDASNSIDHRIPNSQRKISADTIGDEGFFDLLSRFQSNRMDDQRCCLQEKNCHTASTTTSSTPPKMML
KTSSVPVVSPNTDEFLDLLASSQSRRLDDQRASFSNLPGLRLTQNSQSVLSHLMTNDNKEADEDFFDILVKCQGS
RLDDQRCAPPPATTKGPTVPDEDFFSLILRSQGKRMDEQRVLLQRDQNRDTDFGLKDFLQNNALLEFKNSGKKSA
DH

FIGURE 294

AAGCAGCCTGAGGTAATCTGTGAAAATGGTTCGCTATTCACTTGACCCGGAGAACCCCACGAAATCATGCAAATC
AAGAGGTTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTATGCATATACG
AAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACCATTCCGACGTTACAATGGTGGAGT
TGGCAGGTGTGCGCAGGCCCTGCACATGCTTAAAAACACAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGA
TTCTCTGGTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCG
GATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAAACC
AGAAGAGGAGGTTGCCCAGAAGAAAAGGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTA
AATTCAGCAT

FIGURE 295

GCAGGCTCTGCCTGTGGCCACTAGCAGAGAAGCTGCTGTCCTTCCACCACCAGCACCGGACCACCTGCTCCAAGA
CCAGCCTCCTGGGGGGACCAGGCACCCGGCCTTCACTGGCACCCAGGGAGCCGTCCTCAGCAGCGTCAACATGTC
AAGGCCCAGCAGCAGAGCCATTTACTTGCACCGGAAGGAGTACTCCCAGAACCTCACCTCAGAGCCCACCCTCCT
GCAGCACAGGGTGGAGCACTTGATGACATGCAAGCAGGGGAGTCAGAGAGTCCAGGGGCCCGAGGATGCCTTGCA
GAAGCTGTTCGAGATGGATGCACAGGGCCGGGTGTGGAGCCAAGACTTGATCCTGCAGGTCAGGGACGGCTGGCT
GCAGCTGCTGGACATTGAGACCAAGGAGGAGCTGGACTCTTACCGCCTAGACAGCATCCAGGCCATGAATGTGGC
GCTCAACACATGTTCCTACAACTCCATCCTGTCCATCACCGTGCAGGAGCCGGGCCTGCCAGGCACTAGCACTCT
GCTCTTCCAGTGCCAGGAAGTGGGGGCAGAGCGACTGAAGACCAGCCTGCAGAAGGCTCTGGAGGAAGAGCTGGA
GCAAAGACCTCGACTTGGAGGCCTTCAGCCAGGCCAGGACAGATGGAGGGGGCCTGCTATGGAAAGGCCGCTCCC
TATGGAGCAGGCACGCTATCTGGAGCCGGGGATCCCTCCAGAACAGCCCCACCAGAGGACCCTAGAGCACAGCCT
CCCACCATCCCCAAGGCCCCTGCCACGCCACACCAGTGCCCGAGAACCAAGTGCCTTTACTCTGCCTCCTCCAAG
GCGGTCCTCTTCCCCCGAGGACCCAGAGAGGGACGAGGAAGTGCTGAACCATGTCCTAAGGGACATTGAGCTGTT
CATGGGAAAGCTGGAGAAGGCCCAGGCAAAGACCAGCAGGAAGAAGAAATTTGGGAAAAAAAACAAGGACCAGGG
AGGTCTCACCCAGGCACAGTACATTGACTGCTTCCAGAAGATCAAGCACAGCTTCAACCTCCTGGGAAGGCTGGC
CACCTGGCTGAAGGAGACAAGTGCCCCTGAGCTCGTACACATCCTCTTCAAGTCCCTGAACTTCATCCTGGCCAG
GTGCCCTGAGGCTGGCCTAGCAGCCCAAGTGATCTCACCCCTCCTCACCCCTAAAGCTATCAACCTGCTACAGTC
CTGTCTAAGCCCACCTGAGAGTAACCTTTGGATGGGGTTGGGCCCAGCCTGGACCACTAGCCGGGCCGACTGGAC
AGGCGATGAGCCCCTGCCCTACCAACCCACATTCTCAGATGACTGGCAACTTCCAGAGCCCTCCAGCCAAGCACC
CTTAGGATACCAGGACCCTGTTTCCCTTCGGCGGGGAAGTCATAGGTTAGGGAGCACCTCACACTTTCCTCAGGA
GAAGACACACAACCATGACCCTCAGCCTGGGGACCCCAACTCCAGGCCCTCCAGCCCCAAACCTGCCCAGCCAGC
CCTGAAAATGCAAGTCTTGTACGAGTTTGAAGCTAGGAACCCACGGGAACTGACTGTGGTCCAGGGAGAGAAGCT
GGAGGTTCTGGACCACAGCAAGCGGTGGTGGCTGGTGAAGAATGAGGCGGGACGGAGCGGCTACATTCCAAGCAA
CATCCTGGAGCCCCTACAGCCGGGGACCCCTGGGACCCAGGGCCAGTCACCCTCTCGGGTTCCAATGCTTCGACT
TAGCTCGAGGCCTGAAGAGGTCACAGACTGGCTGCAGGCAGAGAACTTCTCCACTGCCACGGTGAGGACACTTGG
GTCCCTGACGGGGAGCCAGCTACTTCGCATAAGACCTGGGGAGCTACAGATGCTATGTCCACAGGAGGCCCCACG
AATCCTGTCCCGGCTGGAGGCTGTCAGAAGGATGCTGGGGATAAGCCCTTAGGCACCAGCTTAGACACCTCCAAG
AACCAGGCCCCGCTGATGCAAGATGGCAGATCTGATACCCATTAGAGCCCCGAGAATTCCTCTTCTGGATCCCAG
TTTGCAGCAAACCCCACACCCCAGCTCACACAGCAAAAACAATGGACAGGCCCAGAGGCTGAAGCAAACAGTGTC
CCTTCTGGCTGTGTTGGAGCCTCCCCAGTAACCACCTATTTATTTTACCTCTTTCCCAAACCTGGAGCATTTATG
CCTAGGCTTGTCAAGAATCTGTTCAGTCCCTCTCCTTCTCAATAAAAGCATCTTCAAGCTTGT

FIGURE 296

GGGAGAAAGCCTGTTGCGTGGAAGATAAGGCGGCGCGGGAAGTGGACACAGGGTGGGCTGGAGCTCAGATCTAAC
TGGACTCTCGCTCCTGCTGGCTGGAC**ATG**GAGGATTTGGAGGAAGATGTAAGGTTTATTGTGGATGAGACCTTGG
ACTTTGGGGGGCTGTCACCATCTGACAGCCGTGAGGAGGAAGACATAACAGTGTTGGTGACTCCAGAGAAACCAC
TTCGACGGGGCCTCTCCCACCGAAGTGACCCAAATGCAGTGGCACCTGCCCCCCAGGGTGTGAGGCTCAGCCTAG
GCCCCCTCAGTCCAGAGAAGCTGGAGGAGATCCTCGATGAGGCCAACCGGCTGGCCGCTCAGCTGGAGCAGTGTG
CCCTGCAGGATCGGGAGAGCGCAGGCGAGGGCCTGGGGCCTCGCCGAGTGAAGCCCAGTCCTCGGCGGGAGACCT
TTGTGCTGAAGGATAGTCCTGTCCGAGACCTGCTGCCCACTGTGAACTCTTTGACGCGGAGCACCCCCTCCCCAA
GCAGCCTGACGCCTCGACTCCGGAGTAATGATAGGAAGGGGTCAGTCAGGGCTCTCCGGGCTACATCTGGAAAGA
GGCCCTCCAACATGAAGAGGGAGTCACCCACTTGCAATCTGTTCCCTGCATCCAAAAGCCCAGCATCTTCTCCTC
TTACCCGATCGACTCCCCCAGTCCGGGGGAGAGCCGGGCCCAGTGGGAGAGCAGCAGCCAGCCCACCCACCCCCA
TCAGATCCGTCCTGGCCCCACAGCCTTCTACCAGCAACTCTCAACGCCTGCCCCGGCCGCAGGGAGCAGCTGCTA
AATCTTCCAGTCAACTGCCCATTCCCTCGGCCATCCCCAGGCCTGCCAGCCGAATGCCACTCACCAGCCGGAGTG
TGCCACCTGGCAGAGGTGCCCTACCTCCGGATTCTCTGTCAACTCGAAAAGGGCTTCCAAGACCAAGCACTGCAG
GACACAGAGTGCGGGAAAGTGGACACAAGGTTCCTGTTTCCCAGCGACTAAATCTTCCTGTCATGGGTGCCACTC
GCAGCAATCTGCAGCCCCCCAGGAAAGTGGCAGTCCCAGGACCTACCAGG**TAA**AGAGATCAGGACAGCAAGCAAG
ACTTCAGTAGCAAACCACTACAGTCAGTACCTGGACTCGCCTCTACCCAGCAGACCCTGACTCCAGCAGATTCTG
GCCCAGGGACAGGAGGAAGAGATGCCACCAGGGCTGGTCTCCCAGGAGTAGAGACCATGGGAAATGGGGTGGATT
AGGATTGAGCTGGAGAAGACTTAAACTCTCTGGGTTGAAAGAAGATTAGGGGAAAAGAGGTCACCTTCCAGCAGT
GAAATGAACAAATAGAAGATGAGAAGTACAGGCAAGTGGTTTGTCTTTATCCACCCCCACTGTTGTGGTCAGCCC
CAGAGAATTTTATCTTCTTCCTTGGCATTGGTTCACTGGACATTTCCACGTGAGCGGCCTCCGTAGCTAACCTCC
CTGCCCTCTGAGGAGCCATCTTCCTGAATCGCATTCTCTACTGGACTCTGGCCTGCTTGGAGAGGTGGCAGCAGG
CACCTGGTCTTCAGAAATTGTTTCCTGTGAATTCTGTGACTCCTAATAGGCCAGTTTGTGATAAGCTTACTCTAT
GAGTCTTCATTTTTCTAAAATAAAGTGAATGTATTTTTAAAAAAAAAAAAAAAAAAA

FIGURE 297

MEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVLVTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLE
EILDEANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSPVRDLLPTVNSLTRSTPSPSSLTPRLRS
NDRKGSVRALRATSGKRPSNMKRESPTCNLFPASKSPASSPLTRSTPPVRGRAGPSGRAAASPPTPIRSVLAPQP
STSNSQRLPRPQGAAAKSSSQLPIPSAIPRPASRMPLTSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGH
KVPVSQRLNLPVMGATRSNLQPPRKVAVPGPTR

FIGURE 298

GCAGTGCGGCGGTCACAGGCTGAGTGCTGCGGCGCGATCCTTGCTTCCCTGAGCGTTGGCCCGGGAGGAAAGAAG
ATGGTGCTGGATCTGGATTTGTTTCGGGTGGATAAAGGAGGGGACCCAGCCCTCATCCGAGAGACGCAGGAGAAG
CGCTTCAAGGACCCGGGACTAGTGGACCAGCTGGTGAAGGCAGACAGCGAGTGGCGACGATGTAGATTTCGGGCA
GACAACTTGAACAAGCTGAAGAACCTATGCAGCAAGACAATCGGAGAGAAAATGAAGAAAAAAGAGCCAGTGGGA
GATGATGAGTCTGTCCCAGAGAATGTGCTGAGTTTCGATGACCTTACTGCAGACGCTTTAGCTAACCTGAAAGTC
TCACAAATCAAAAAAGTCCGACTCCTCATTGATGAAGCCATCCTGAAGTGTGACGCGGAGCGGATAAAGTTGGAA
GCAGAGCGGTTTGAGAACCTCCGAGAGATTGGGAACCTTCTGCACCCTTCTGTACCCATCAGTAACGATGAGGAT
GTGGACAACAAAGTAGAGAGGATTTGGGGTGATTGTACAGTCAGGAAGAAGTACTCTCATGTGGACCTGGTGGTG
ATGGTAGATGGCTTTGAAGGCGAAAAGGGGGCCGTGGTGGCTGGGAGTCGAGGGTACTTCTTGAAGGGGGTCCTG
GTGTTCCTGGAACAGGCTCTCATCCAGTATGCCCTTCGCACCTTGGGAAGTCGGGGCTACATTCCCATTTATACC
CCCTTTTTCATGAGGAAGGAGGTCATGCAGGAGGTGGCACAGCTCAGCCAGTTTGATGAAGAACTTTATAAGGTG
ATTGGCAAAGGCAGTGAAAAGTCTGATGACAACTCCTATGATGAGAAGTACCTGATTGCCACCTCAGAGCAGCCC
ATTGCTGCCCTGCACCGGGATGAGTGGCTCCGGCCGGAGGACCTGCCCATCAAGTATGCTGGCCTGTCTACCTGC
TTCCGTCAGGAGGTGGGCTCCCATGGCCGTGACACCCGTGGCATCTTCCGAGTCCATCAGTTTGAGAAGATTGAA
CAGTTTGTGTACTCATCACCCCATGACAACAAGTCATGGGAGATGTTTGAAGAGATGATTACCACCGCAGAGGAG
TTCTACCAGTCCCTGGGGATTCCTTACCACATTGTGAATATTGTCTCAGGTTCTTTGAATCATGCTGCCAGTAAG
AAGCTTGACCTGGAGGCCTGGTTTCCGGGCTCAGGAGCCTTCCGTGAGTTGGTCTCCTGTTCTAATTGCACGGAT
TACCAGGCTCGCCGGCTTCGAATCCGATATGGGCAAACCAAGAAGATGATGGACAAGGTGGAGTTTGTCCATATG
CTCAATGCTACCATGTGCGCCACTACCCGTACCATCTGCGCCATCCTGGAGAACTACCAGACAGAGAAGGGCATC
ACTGTGCCTGAGAAATTGAAGGAGTTCATGCCGCCAGGACTGCAAGAACTGATCCCCTTTGTGAAGCCTGCGCCC
ATTGAGCAGGAGCCATCAAAGAAGCAGAAGAAGCAACATGAGGGCAGCAAAAAGAAAGCAGCAGCAAGAGACGTC
ACCCTAGAAAACAGGCTGCAGAACATGGAGGTCACCGATGCT**TGA**ACATTCCTGCCTCCCTATTTGCCAGGCTTT
CATTTCTGTCTGCTGAGATCTCAGAGCCTGCCCAACAGCAGGGAAGCCAAGCACCCATTCATCCCCCTGCCCCCA
TCTGACTGCGTAGCTGAGAGGGGAACAGTGCCATGTACCACACAGATGTTCCTGTCTCCTCGCATGGGCATAGGG
ACCCATCATTGATGACTGATGAAACCATGTAATAAAGCATCTCTGGGGAGGGCTTAGGACTCTTCCTCAGTCTTC
TTCCCCGGGCTTGAACCCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 299

MVLDLDLFRVDKGGDPALIRETQEKRFKDPGLVDQLVKADSEWRRCRFRADNLNKLKNLCSKTIGEKMKKKEPVG
DDESVPENVLSFDDLTADALANLKVSQIKKVRLLIDEAILKCDAERIKLEAERFENLREIGNLLHPSVPISNDED
VDNKVERIWGDCTVRKKYSHVDLVVMVDGFEGEKGAVVAGSRGYFLKGVLVFLEQALIQYALRTLGSRGYIPIYT
PFFMRKEVMQEVAQLSQFDEELYKVIGKGSEKSDDNSYDEKYLIATSEQPIAALHRDEWLRPEDLPIKYAGLSTC
FRQEVGSHGRDTRGIFRVHQFEKIEQFVYSSPHDNKSWEMFEEMITTAEEFYQSLGIPYHIVNIVSGSLNHAASK
KLDLEAWFPGSGAFRELVSCSNCTDYQARRLRIRYGQTKKMMDKVEFVHMLNATMCATTRTICAILENYQTEKGI
TVPEKLKEFMPPGLQELIPFVKPAPIEQEPSKKQKKQHEGSKKKAAARDVTLENRLQNMEVTDA

FIGURE 300

CAGAGTGCCCTTTCTCCCCGCCTCTTCCCCCTCCCGGGAGCTGCCAGTACTTGACGTGGCGTCACCGCCCTCTAC
CCTCGCTTTGCGTGCGTGTTTGCGTACAGCGGAGGTGGCGGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCT
GGTTCTCTTGTGGCCACCGTCGCTGTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTC
AGAAGCCGACGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGCGGGCAG
GCGGGCGGGCGCCAGAGGGGGAAAGAGGCGGGGGCGGCGGGTCAGCCGCTGGCCGGGCCGGCGGGGGA**ATG**TCGA
TGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGT
ACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCA
AATTCCCCACCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAG
CTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAAGGGCAGCA
GCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGT
CTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACAC
ACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTA
ACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCG
AGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGG
ATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGG
AAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACG
TCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGA
GGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTG
CTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGG
ATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGA
ATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAG
AAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCT
GGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCT
TTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACA
AGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCC
ACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATT
ACAGATAC**TAA**TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTAAGAT
AACTTTTATTTTCTTCTTACTCCTTTCCTCTTGATTTTTTTCCTATAATTTCATTCTTGTTTTTTCATCTCATTA
TCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTCCCTCACTC
TAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAG
TCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGC
CTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCTAC
CCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAG
GTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGT
ATAGCCCTTCCTCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTA
ATTTTGTCCTCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAAAAA

FIGURE 301

MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDSY
SSAASYTDSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALISLRKRAQGEKPLAGAKIVG
CTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANM
ILDDGGDLTHWVYKKYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDG
LKRTTDVMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVIRQVDVVITCTG
NKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVVLLAEGRLLNLSCSTV
PTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKP
NYYRY

FIGURE 302A

GCTTATGGCGGCGCTGGAGAGGGGGCGCTGAGCTGTTGGGTATGAAGTGTAACAGAACAGACTTTACCACCTGAA
ACTGCTGCTTCAAGTTCAGATCAGGCAAGGAACAAACCTCGTAACAACTAACAAGACCAAAGAAGAGTACACTTA
AGTTGAAGACACAACACTTGATCTGAAACAAGAAGTTTGTGCCTACTCAACAGCTTTGAAAGAGCACTTCCCAAC
GCTGCTAGTAGTCTTTGTTTTCTTCAGTGCTGTACTGTGAGATTGCCCGGTACAGCAGCAGTTGTATTCTTTATT
AGCTTGGTAGATCATTTTCTCTCGCTCTTTTTTTTAATACTAGCAACTTTCATCCTTTGAAACGTGTGCTGAAAA
AGAAGAATCAGCAAATACTACTGAAAGTGCAATATTTGAGTATCACTGCGAG**ATG**AGCTTTGATCCAAACCTTCT
CCACAACAATGGACATAATGGGTACCCTAATGGTACTTCAGCAGCACTGCGTGAAACTGGGGTTATTGAAAAACT
GTTAACCTCTTACGGATTTATTCAGTGTTCAGAACGTCAAGCTAGACTTTTCTTCCACTGTTCACAGTATAATGG
CAACCTGCAAGACTTAAAAGTAGGAGATGATGTTGAATTTGAAGTATCATCGGACCGACGGACTGGGAAACCCAT
TGCTGTTAAACTGGTGAAGATAAAACAAGAAATCCTCCCTGAAGAACGAATGAATGGACAAGTTGTGTGCGCTGT
TCCTCACAACTTAGAGAGTAAATCTCCAGCTGCCCCGGGTCAGAGTCCAACAGGGAGTGTATGCTACGAACGTAA
TGGGGAAGTGTTTTATCTGACTTACACCCCTGAAGATGTCGAAGGGAACGTTCAGCTGGAAACTGGAGATAAAAT
AAACTTTGTAATTGATAACAATAAACATACTGGTGCTGTAAGTGCTCGCAACATTATGCTGTTGAAAAAGAAACA
AGCCCGCTGTCAGGGAGTAGTTTGTGCCATGAAGGAGGCATTTGGCTTTATTGAAAGAGGTGATGTTGTAAAAGA
GATATTCTTTCACTATAGTGAATTTAAGGGTGACTTAGAAACCTTACAGCCTGGCGATGATGTGGAATTCACAAT
CAAGGACAGAAATGGTAAAGAAGTTGCAACAGATGTCAGACTATTGCCTCAAGGAACAGTCATTTTTGAAGATAT
CAGCATTGAACATTTTGAAGGAACTGTAACCAAAGTTATCCCAAAAGTACCCAGTAAAAACCAGAATGACCCATT
GCCAGGACGCATCAAAGTTGACTTTGTGATCCCTAAAGAACTTCCCTTTGGAGACAAAGATACGAAATCCAAGGT
GACCCTGCTGGAAGGTGACCATGTTAGGTTTAATATTTCAACAGACCGACGTGACAAATTAGAGCGAGCAACCAA
TATAGAAGTTCTGTCAAATACATTTCAGTTCACTAATGAAGCCCGAGAAATGGGTGTGATTGCTGCCATGAGAGA
TGGTTTTGGTTTCATCAAGTGTGTGGATCGTGATGTTCGTATGTTCTTCCACTTCAGTGAAATTCTGGATGGGAA
CCAGCTCCATATTGCAGATGAAGTAGAGTTTACTGTGGTTCCTGATATGCTCTCTGCTCAAAGAAATCATGCTAT
TAGGATTAAAAAACTTCCCAAGGGCACGGTTTCATTTCATTCCCATTCAGATCACCGTTTTCTGGGCACGGTAGA
AAAAGAAGCCACTTTTTCCAATCCTAAAACCACTAGCCCAAATAAAGGCAAAGAGAAGGAGGCTGAGGATGGCAT
TATTGCTTATGATGACTGTGGGGTGAAACTGACTATTGCTTTTCAAGCCAAGGATGTGGAAGGATCTACTTCTCC
TCAAATAGGAGATAAGGTTGAATTTAGTATTAGTGACAAACAGAGGCCTGGACAGCAGGTTGCAACTTGTGTGCG
ACTTTTAGGTCGTAATTCTAACTCCAAGAGGCTCTTGGGTTATGTGGCAACTCTGAAGGATAATTTTGGATTTAT
TGAAACAGCCAATCATGATAAGGAAATCTTTTTCCATTACAGTGAGTTCTCTGGTGATGTTGATAGCCTGGAACT
GGGGGACATGGTCGAGTATAGCTTGTCCAAAGGCAAAGGCAACAAAGTCAGTGCAGAAAAAGTGAACAAAACACA
CTCAGTGAATGGCATTACTGAGGAAGCTGATCCCACCATTTACTCTGGCAAAGTAATTCGCCCCCTGAGGAGTGT
TGATCCAACACAGACTGAGTACCAAGGAATGATTGAGATTGTGGAGGAGGGCGATATGAAAGGTGAGGTCTATCC
ATTTGGCATCGTTGGGATGGCCAACAAAGGGGATTGCCTGCAGAAAGGGGAGAGCGTCAAGTTCCAATTGTGTGT
CCTGGGCCAAAATGCACAAACTATGGCTTACAACATCACACCCCTGCGCAGGGCCACAGTGGAATGTGTGAAAGA
TCAGTTTGGCTTCATTAACTATGAAGTAGGAGATAGCAAGAAGCTCTTTTTCCATGTGAAAGAAGTTCAGGATGG
CATTGAGCTACAGGCAGGAGATGAGGTGGAGTTCTCAGTGATTCTTAATCAGCGCACTGGCAAGTGCAGCGCCTG
TAATGTTTGGCGAGTCTGTGAGGGCCCCAAGGCTGTTGCAGCTCCTCGACCTGATCGGTTGGTCAATCGCTTGAA
GAATATCACTCTGGATGATGCCAGTGCTCCTCGCCTAATGGTTCTTCGTCAGCCAAGGGGACCAGATAACTCAAT
GGGGTTTGGTGCAGAAAGAAAGATCCGTCAAGCTGGTGTCATTGAC**TAA**CCACATCCACAAAGCACACCATTAAT
CCACTATGATCAAGTTGGGGGGGAATCTGGTGAAGGGTTCTGAATATCTCCCTCTTCATCCCTCCCGAAATCTGGA
ATACTTATTCTATTGAGCTATTACACCAGTTTTAACACCTTCCTCGTGTTATGTTTAAAAAAATAAATAAATTTA
AGAAAACCATTTTAAATAATGCACAGTTGCAGCCTGGAAAAACTTAAGGTGGCGCCTTATAGTATCAATTTTAGG
AGCTTTATTTGGTGCATTTAACGCAACTGGTAATTGCAGAATCCACTTTGCCTGTGTAAGTGAAAAATATAGACT
GTTATCTTGTTGGCCCTATGAAATTCTGCACTTTTCATTATATACTCTACCTTCATTAATTACTTCTGGCAAGAT
GTTCTGCCTTAGCACTCAGTTGCATTCTTTTCCTTTTTCTTCCTGTTCATTATGCTTTAATTCTGAGGACCATAT
GAGGGTAGAATATATTATCTTTTAAAAATTACAAAAATTTGTATAGGCAAACCATTTCTTAAAGTTGATGGCCAA
ATTTTAAAATGTTATTTTTCATATCATTTATAATCTTGTCACAATCCACTTAAAGAAGTTTGGTTATATTTCAGT
GAAAATTTTCTTCCAGAGTAGGTTTTTTTTCGTGGGTTGGGGGGTAACTTTACTACAATTAGTAAGTATGGTGCA
GAATTTCATGCAAATGAGGAGTGCCAGCAGTGTGATAATTTAAACATATTTAAACAAAAACAAAAAAAATGAATG

FIGURE 302B

CACAAACTTGCTGCTGCTTAGATCACTGCAGCTTCTAGGACCCGGTTTCTTTTACTGATTTAAAAACAAAACAAA
AAAAAATAAAAAAGTTGTGCCTGAAATGAATCTTGTTTTTTTTTATAAGTAGCCGCCTGGTTACTGTGTCCTGTA
AAATACAGACACTTGACCCTTGGTGTAGCTTCTGTTCAACTTTATATCACGGGAATGGATGGGTCTGATTTCTTG
GCCCTCTTCTTGAATTGGCCATATACAGGGTCCCTGGCCAGTGGACTGAAGGCTTTGTCTAAGATGACAAGGGTC
AGCTCAGGGGATGTGGGGGAGGGCGGTTTTATCTTCCCCCTTGTCGTTTGAGGTTTTGATCTCTGGGTAAAGAGG
CCGTTTATCTTTGTAAACACGAAACATTTTTGCTTTCTCCAGTTTTCTGTTAATGGCGAAAGAATGGAAGCGAAT
AAAGTTTTACTGATTTTTGAGACACT

FIGURE 303

MSFDPNLLHNNGHNGYPNGTSAALRETGVIEKLLTSYGFIQCSERQARLFFHCSQYNGNLQDLKVGDDVEFEVSS
DRRTGKPIAVKLVKIKQEILPEERMNGQVVCAVPHNLESKSPAAPGQSPTGSVCYERNGEVFYLTYTPEDVEGNV
QLETGDKINFVIDNNKHIGAVSARNIMLLKKKQARCQGVVCAMKEAFGFIERGDVVKEIFFHYSEFKGDLETLQP
GDDVEFTIKDRNGKEVATDVRLLPQGTVIFEDISIEHFEGTVTKVIPKVPSKNQNDPLPGRIKVDFVIPKELPFG
DKDTKSKVTLLEGDHVRFNISTDRRDKLERATNIEVLSNTFQFTNEAREMGVIAAMRDGFGFIKCVDRDVRMFFH
FSEILDGNQLHIADEVEFTVVPDMLSAQRNHAIRIKKLPKGTVSFHSHSDHRFLGTVEKEATFSNPKTTSPNKGK
EKEAEDGIIAYDDCGVKLTIAFQAKDVEGSTSPQIGDKVEFSISDKQRPGQQVATCVRLLGRNSNSKRLLGYVAT
LKDNFGFIETANHDKEIFFHYSEFSGDVDSLELGDMVEYSLSKGKGNKVSAEKVNKTHSVNGITEEADPTIYSGK
VIRPLRSVDPTQTEYQGMIEIVEEGDMKGEVYPFGIVGMANKGDCLQKGESVKFQLCVLGQNAQTMAYNITPLRR
ATVECVKDQFGFINYEVGDSKKLFFHVKEVQDGIELQAGDEVEFSVILNQRTGKCSACNVWRVCEGPKAVAAPRP
DRLVNRLKNITLDDASAPRLMVLRQPRGPDNSMGFGAERKIRQAGVID

FIGURE 304

GCTGAAG**ATG**GGAGCCACTCTCAAAATCATGCTGGATAACACCTACATGAAAAAGTGTGACGAGAACATCCTGTG
GCTGGACTACAAGAACATCTGCAAGGTGATGGAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCT
CCAGGTAAAGCAGAAAGGTGCTGACTTCCTGGTGACGGAGGTGGAAACTGGTGGTTCCTCGGGCAGCAAGAAGGG
TGTGAACCTTCCTGGGGCTGCTGTGGACTTGCCTGCTGTGTCAGAGGACATCCAGGACCTGAATTTTGGGGTCGA
GCAGGATGTCGATATGGTGTTTGCGTCGTTCATCCGCAAGGCATCTGATGTCCATGAAGTTAGGGAGGCCCTGGG
AGAGAAGGGAAAGAAAACACTCCACCCTCCACCTTCCATTTTCCCCCACTACTGCAGCACCTCCGGGCCTGTTGC
TATAGAGCCTACCTGTATATCAATAAACAACAGC**TGA**AG

FIGURE 305

MGATLKIMLDNTYMKKCDENILWLDYKNICKVMEVGSKIYVDDGLISLQVKQKGADFLVTEVETGGSSGSKKGVN
LPGAAVDLPAVSEDIQDLNFGVEQDVDMVFASFIRKASDVHEVREALGEKGKKTLHPPPSIFPHYCSTSGPVAIE
PTCISINNS

FIGURE 306

AGAAGAAGCTGGCCAAGGATATGGGAGCAACCACC**ATG**GACCAGAAGTCTCTCTGGGCAGGTGTAGTGGTCTTGC
TGCTTCTCCAGGGAGGATCTGCCTACAAACTGGTTTGCTACTTTACCAACTGGTCCCAGGACCGGCAGGAACCAG
GAAAATTCACCCCTGAGAATATTGACCCCTTCCTATGCTCTCATCTCATCTATTCATTCGCCAGCATCGAAAACA
ACAAGGTTATCATCAAGGACAAGAGTGAAGTGATGCTCTACCAGACCATCAACAGTCTCAAAACCAAGAATCCCA
AACTGAAAATTCTCTTGTCCATTGGAGGGTACCTGTTTGGTTCCAAAGGGTTCCACCCTATGGTGGATTCTTCTA
CATCACGCTTGGAATTCATTAACTCCATAATCCTGTTTCTGAGGAACCATAACTTTGATGGACTGGATGTAAGCT
GGATCTACCCAGATCAGAAAGAAAACACTCATTTCACTGTGCTGATTCATGAGTTAGCAGAAGCCTTTCAGAAGG
ACTTCACAAAATCCACCAAGGAAAGGCTTCTCTTGACTGCGGGCGTATCTGCAGGGAGGCAAATGATTGATAACA
GCTATCAAGTTGAGAAACTGGCAAAAGATCTGGATTTCATCAACCTCCTGTCCTTTGACTTCCATGGGTCTTGGG
AAAAGCCCCTTATCACTGGCCACAACAGCCCTCTGAGCAAGGGGTGGCAGGACAGAGGGCCAAGCTCCTACTACA
ATGTGGAATATGCTGTGGGGTACTGGATACATAAGGGAATGCCATCAGAGAAGGTGGTCATGGGCATCCCCACAT
ATGGGCACTCCTTCACACTGGCCTCTGCAGAAACCACCGTGGGGGCCCCTGCCTCTGGCCCTGGAGCTGCTGGAC
CCATCACAGAGTCTTCAGGCTTCCTGGCCTATTATGAGATCTGCCAGTTCCTGAAAGGAGCCAAGATCACGCGCC
TCCAGGATCAGCAGGTTCCCTACGCAGTCAAGGGGAACCAGTGGGTGGGCTATGATGATGTGAAGAGTATGGAGA
CCAAGGTTCAGTTCTTAAAGAATTTAAACCTGGGAGGAGCCATGATCTGGTCTATTGACATGGATGACTTCACTG
GCAAATCCTGCAACCAGGGCCCTTACCCTCTTGTCCAAGCAGTCAAGAGAAGCCTTGGCTCCTTG**TGA**AGGATTA
ACTTACAGAGAAGCAGGCAAGATGACCTTGCTGCCTGGGGCCTGCTCTCTCCCAGGAATTCTCATGTGGGATTCC
CCTTGCCAGGCTGGCCTTTGGATCTCTCTTCCAAGCCTTTCCTGACTTCCTCTTAGATCATAGATTGGACCTGGT
TTTGTTTTCCTGCAGCTGTTGACTTGTTGCCCTGAAGTACAATAAAAAAAATTCATTTTGCTCCAGTA

FIGURE 307

MDQKSLWAGVVVLLLLQGGSAYKLVCYFTNWSQDRQEPGKFTPENIDPFLCSHLIYSFASIENNKVIIKDKSEVM
LYQTINSLKTKNPKLKILLSIGGYLFGSKGFHPMVDSSTSRLEFINSIILFLRNHNFDGLDVSWIYPDQKENTHF
TVLIHELAEAFQKDFTKSTKERLLLTAGVSAGRQMIDNSYQVEKLAKDLDFINLLSFDFHGSWEKPLITGHNSPL
SKGWQDRGPSSYYNVEYAVGYWIHKGMPSEKVVMGIPTYGHSFTLASAETTVGAPASGPGAAGPITESSGFLAYY
EICQFLKGAKITRLQDQQVPYAVKGNQWVGYDDVKSMETKVQFLKNLNLGGAMIWSIDMDDFTGKSCNQGPYPLV
QAVKRSLGSL

FIGURE 308

GGGGAGACTTGTGAGCGGCCATCTTGGTCCTGCCCTGACAGATTCTCCTATCGGGGTCACAGGGACGCTAAGATT
GCTACCTGGACTTTCGTTGACC**ATG**CTGTCCCGGGTGGTACTTTCCGCCGCCGCCACAGCGGCCCCCTCTCTGAA
GAATGCAGCCTTCCTAGGTCCAGGGGTATTGCAGGCAACAAGGACCTTTCATACAGGGCAGCCACACCTTGTCCC
TGTACCACCTCTTCCTGAATACGGAGGAAAAGTTCGTTATGGACTGATCCCTGAGGAATTCTTCCAGTTTCTTTA
TCCTAAAACTGGTGTAACAGGACCCTATGTACTCGGAACTGGGCTTATCTTGTACGCTTTATCCAAAGAAATATA
TGTGATTAGCGCAGAGACCTTCACTGCCCTATCAGTACTAGGTGTAATGGTCTATGGAATTAAAAAATATGGTCC
CTTTGTTGCAGACTTTGCTGATAAACTCAATGAGCAAAAACTTGCCCAACTAGAAGAGGCGAAGCAGGCTTCCAT
CCAACACATCCAGAATGCAATTGATACGGAGAAGTCACAACAGGCACTGGTTCAGAAGCGCCATTACCTTTTTGA
TGTGCAAAGGAATAACATTGCTATGGCTTTGGAAGTTACTTACCGGGAACGACTGTATAGAGTATATAAGGAAGT
AAAGAATCGCCTGGACTATCATATATCTGTGCAGAACATGATGCGTCGAAAGGAACAAGAACACATGATAAATTG
GGTGGAGAAGCACGTGGTGCAAAGCATCTCCACACAGCAGGAAAAGGAGACAATTGCCAAGTGCATTGCGGACCT
AAAGCTGCTGGCAAAGAAGGCTCAAGCACAGCCAGTTATG**TAA**ATGTATCTATCCCAATTGAGACAGCTAGAAAC
AGTTGACTGACTAAATGGAAACTAGTCTATTTGACAAAGTCTTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTA
CCCTTCCTAAAAATGAAAAGTTTGTTTCATATAGTGAGAGAACGAAATCTCTATCGGCCAGTCAGATGTTTCTCA
TCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCACTTCTGAATAAGCAGTTTGCCTTTATAAAAACTTGCTGC
CTGACTAAAGATTAACAGGTTATAGTTTAAATTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAAT
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 309

MLSRVVLSAAATAAPSLKNAAFLGPGVLQATRTFHTGQPHLVPVPPLPEYGGKVRYGLIPEEFFQFLYPKTGVTG
PYVLGTGLILYALSKEIYVISAETFTALSVLGVMVYGIKKYGPFVADFADKLNEQKLAQLEEAKQASIQHIQNAI
DTEKSQQALVQKRHYLFDVQRNNIAMALEVTYRERLYRVYKEVKNRLDYHISVQNMMRRKEQEHMINWVEKHVVQ
SISTQQEKETIAKCIADLKLLAKKAQAQPVM

FIGURE 310

GCGGGGAGCCGGCCCGGAGCGCAGTTTCCAGTGGGGCCGGGGTTTCACCCGGGCCCTCTCTGTTTGAACCGAACC
CGACAAATGGGCGC**ATG**ACGATGGAGAGCAGGGAAATGGACTGCTATCTCCGTCGCCTCAAACAGGAGCTGATGT
CCATGAAGGAGGTGGGTGATGGCTTACAGGATCAGATGAACTGCATGATGGGTGCACTGCAAGAACTGAAGCTCC
TCCAGGTGCAGACAGCACTGGAACAGCTGGAGATCTCTGGAGGGGGTCCTGTGCCAGGCAGCCCTGAAGGTCCCA
GGACCCAGTGCGAGCACCCTTGTTGGGAGGGTGGCAGAGGTCCTGCCAGGCCCACAGTCTGTTCCCCCTCCAGTC
AACCTTCTCTTGGCAGCAGCACCAAGTTTCCATCCCATAGGAGTGTCTGTGGAAGGGATTTAGCCCCCTTGCCCA
GGACACAGCCACATCAAAGCTGTGCTCAGCAGGGGCCAGAGCGAGTGGAACCGGATGACTGGACCTCCACGTTGA
TGTCCCGGGGCCGGAATCGACAGCCTCTGGTGTTAGGGGACAACGTTTTTGCAGACCTGGTGGGCAATTGGCTAG
ACTTGCCAGAACTGGAGAAGGGTGGGGAGAAGGGTGAGACTGGGGGGGCACGTGAACCCAAAGGAGAGAAAGGCC
AGCCCCAGGAGCTGGGCCGCAGGTTCGCCCTGACAGCAAACATCTTTAAGAAGTTCTTGCGTAGTGTGCGGCCTG
ACCGTGACCGGCTGCTGAAGGAGAAGCCAGGCTGGGTGACACCCATGGTCCCTGAGTCCCGAACCGGCCGCTCAC
AGAAGGTCAAGAAGCGGAGCCTTTCCAAGGGCTCTGGACATTTCCCCTTCCCAGGCACCGGGGAGCACAGGCGAG
GGGAGAATCCCCCCACAAGCTGCCCCAAGGCCCTGGAGCACTCACCCTCAGGATTTGATATTAACACAGCTGTTT
GGGTC**TGA**ATCCTAGAGACAGAAAGTTGACTGAGCCTGAAAGGGCCAGGTCCCAGTGCTGGGCCCCTGGGGAGGA
GGGAGGGTGGGCGGTATGGCTCTCGAAAGCCCAACTCCAAGTTCCTTTCCCCCAGAAAGCGGGGAGAAGCCAGAG
TTCTTGGCTCAGGACTGAAGGGAAGGTGGTTGGGAGAGGCTGTCTTGGGGGCTAGCTGGTGGAGGAGGTAAGAGT
AGCTGGAGAGTGAGCTGTGCGTGTGTGTGTGTGTGTGTGCATGTGTGTGTCTGTCTGGCATGCATGCACTCACTT
TGGGGCTGGAGGTGACAGTAGGTGAGGGCAGAGGAGGAGATCAGAAAATCCCTCTGACATCTCCACTGCCCCCAA
AGACCTCCGTTGAACATTCTGTATGGAAAAGAGCCCTGGAGCATCAGGTTCCCCAGATAGGCCCCCAAATAAAGA
CCTGTCTATGGCTCTCCCAA

FIGURE 311

MTMESREMDCYLRRLKQELMSMKEVGDGLQDQMNCMMGALQELKLLQVQTALEQLEISGGGPVPGSPEGPRTQCE
HPCWEGGRGPARPTVCSPSSQPSLGSSTKFPSHRSVCGRDLAPLPRTQPHQSCAQQGPERVEPDDWTSTLMSRGR
NRQPLVLGDNVFADLVGNWLDLPELEKGGEKGETGGAREPKGEKGQPQELGRRFALTANIFKKFLRSVRPDRDRL
LKEKPGWVTPMVPESRTGRSQKVKKRSLSKGSGHFPFPGTGEHRRGENPPTSCPKALEHSPSGFDINTAVWV

FIGURE 312A

GGCACGAGGCTGGGGCGCAGAGCAGCGGCGGGAGGAGGCGGACACGTGGCAACAGCGGTAGCAGCCCGGGCGGCG
GCAGCAACAGCGGCGGCGGCATCGGCCCGAGCCGCCGGCCGCCCTCCCACCCTCCCGCCCCGCGGCAGCCCTAGC
TCCCTCCACTTGGCTCCCCTGGTCCCGCTCGCTCGGCCGGGAGCTGCTCTGTGCTTTTCTCTCTGATTCTCCAGC
GACAGGACCCGGCGCCGGGCACTGAGCACCGCCACC**ATG**GGGAAGGGGGTTGGACGTGATAAGTATGAGCCTGCA
GCTGTTTCAGAACAAGGTGATAAAAAGGGCAAAAAGGGCAAAAAAGACAGGGACATGGATGAACTGAAGAAAGAA
GTTTCTATGGATGATCATAAACTTAGCCTTGATGAACTTCATCGTAAATATGGAACAGACTTGAGCCGGGGATTA
ACATCTGCTCGTGCAGCTGAGATCCTGGCGCGAGATGGTCCCAACGCCCTCACTCCCCCTCCCACTACTCCTGAA
TGGATCAAGTTTTGTCGGCAGCTCTTTGGGGGGTTCTCAATGTTACTGTGGATTGGAGCGATTCTTTGTTTCTTG
GCTTATAGCATCCAAGCTGCTACAGAAGAGGAACCTCAAAACGATAATCTGTACCTGGGTGTGGTGCTATCAGCC
GTTGTAATCATAACTGGTTGCTTCTCCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAC
ATGGTCCCTCAGCAAGCCCTTGTGATTCGAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGTGGTTGGG
GATCTGGTGGAAGTAAAAGGAGGAGACCGAATTCCTGCTGACCTCAGAATCATATCTGCAAATGGCTGCAAGGTG
GATAACTCCTCGCTCACTGGTGAATCAGAACCCCAGACTAGGTCTCCAGATTTCACAAATGAAAACCCCCTGGAG
ACGAGGAACATTGCCTTCTTTTCAACCAATTGTGTTGAAGGCACCGCACGTGGTATTGTTGTCTACACTGGGGAT
CGCACTGTGATGGGAAGAATTGCCACACTTGCTTCTGGGCTGGAAGGAGGCCAGACCCCCATTGCTGCAGAAATT
GAACATTTTATCCACATCATCACGGGTGTGGCTGTGTTCCTGGGTGTGTCTTTCTTCATCCTTTCTCTCATCCTT
GAGTACACCTGGCTTGAGGCTGTCATCTTCCTCATCGGTATCATCGTAGCCAATGTGCCGGAAGGTTTGCTGGCC
ACTGTCACGGTCTGTCTGACACTTACTGCCAAACGCATGGCAAGGAAAAACTGCTTAGTGAAGAACTTAGAAGCT
GTGGAGACCTTGGGGTCCACATCCACCATCTGCTCTGATAAAACTGGAACTCTGACTCAGAACCGGATGACAGTG
GCCCACATGTGGTTTGACAATCAAATCCATGAAGCTGATACGACAGAGAATCAGAGTGGTGTCTCTTTTGACAAG
ACTTCAGCTACCTGGCTTGCTCTGTCCAGAATTGCAGGTCTTTGTAACAGGGCAGTGTTTCAGGCTAACCAGGAA
AACCTACCTATTCTTAAGCGGGCAGTTGCAGGAGATGCCTCTGAGTCAGCACTCTTAAAGTGCATAGAGCTGTGC
TGTGGTTCCGTGAAGGAGATGAGAGAAAGATACGCCAAAATCGTCGAGATACCCTTCAACTCCACCAACAAGTAC
CAGTTGTCTATTCATAAGAACCCCAACACATCAGAGCCCCAACACCTGTTGGTGATGAAGGGCGCCCCAGAAAGG
ATCCTAGACCGTTGCAGCTCTATCCTCCTCCACGGCAAGGAGCAGCCCCTGGATGAGGAGCTGAAAGACGCCTTT
CAGAACGCCTATTTGGAGCTGGGGGGCCTCGGAGAACGAGTCCTAGGTTTCTGCCACCTCTTTCTGCCAGATGAA
CAGTTTCCTGAAGGGTTCCAGTTTGACACTGACGATGTGAATTTCCCTATCGATAATCTGTGCTTTGTTGGGCTC
ATCTCCATGATTGACCCTCCACGGGCGGCCGTTCCTGATGCCGTGGGCAAATGTCGAAGTGCTGGAATTAAGGTC
ATCATGGTCACAGGAGACCATCCAATCACAGCTAAAGCTATTGCCAAAGGTGTGGGCATCATCTCAGAAGGCAAT
GAGACCGTGGAAGACATTGCTGCCCGCCTCAACATCCCAGTCAGCCAGGTGAACCCCAGGGATGCCAAGGCCTGC
GTAGTACACGGCAGTGATCTAAAGGACATGACCTCCGAGCAGCTGGATGACATTTTGAAGTACCACACTGAGATA
GTGTTTGCCAGGACCTCCCCTCAGCAGAAGCTCATCATTGTGGAAGGCTGCCAAAGACAGGGTGCTATCGTGGCT
GTGACTGGTGACGGTGTGAATGACTCTCCAGCTTTGAAGAAAGCAGACATTGGGGTTGCTATGGGGATTGCTGGC
TCAGATGTGTCCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCAATTGTGACTGGAGTAGAG
GAAGGTCGTCTGATCTTTGATAACTTGAAGAAATCCATTGCTTATACCTTAACCAGTAACATTCCCGAGATCACC
CCGTTCCTGATATTTATTATTGCAAACATTCCACTACCACTGGGGACTGTCACCATCCTCTGCATTGACTTGGGC
ACTGACATGGTTCCTGCCATCTCCCTGGCTTATGAGCAGGCTGAGAGTGACATCATGAAGAGACAGCCCAGAAAT
CCCAAAACAGACAAACTTGTGAATGAGCGGCTGATCAGCATGGCCTATGGGCAGATTGGAATGATCCAGGCCCTG
GGAGGCTTCTTTACTTACTTTGTGATTCTGGCTGAGAACGGCTTCCTCCCAATTCACCTGTTGGGCCTCCGAGTG
GACTGGGATGACCGCTGGATCAACGATGTGGAAGACAGCTACGGGCAGCAGTGGACCTATGAGCAGAGGAAAATC
GTGGAGTTCACCTGCCACACAGCCTTCTTCGTCAGTATCGTGGTGGTGCAGTGGGCCGACTTGGTCATCTGTAAG
ACCAGGAGGAATTCGGTCTTCCAGCAGGGGATGAAGAACAAGATCTTGATATTTGGCCTCTTTGAAGAGACAGCC
CTGGCTGCTTTCCTTTCCTACTGCCCTGGAATGGGTGTTGCTCTTAGGATGTATCCCCTCAAACCTACCTGGTGG
TTCTGTGCCTTCCCCTACTCTCTTCTCATCTTCGTATATGACGAAGTCAGAAAACTCATCATCAGGCGACGCCCT
GGCGGCTGGGTGGAGAAGGAAACCTACTAT**TAG**CCCCCCGTCCTGCACGCCGTGGAGCATCAGGCCACACACTCT
GCATCCGACACCCACCCCCTCTTTGTGTACTTCAGTCTTGGAGTTTGGAACTCTACCCTGGTAGGAAAGCACCGC
AGCATGTGGGGAAGCAAGACGTCCTGGAATGAAGCATGTAGCTCTATGGGGGGAGGGGGGAGGGCTGCCTGAAAA
CCATCCATCTGTGGAAATGACAGCGGGGAAGGTTTTTATGTGCCTTTTTTGTTTTTGTAAAAAAGGAACACCCGGA

FIGURE 312B

AAGACTGAAAGAATACATTTTATATCTGGATTTTTACAAATAAAGATGGCTATTATAATGGAAAAAAAAAAAAAA
AAAAA

FIGURE 313

MGKGVGRDKYEPAAVSEQGDKKGKKGKKDRDMDELKKEVSMDDHKLSLDELHRKYGTDLSRGLTSARAAEILARD
GPNALTPPPTTPEWIKFCRQLFGGFSMLLWIGAILCFLAYSIQAATEEEPQNDNLYLGVVLSAVVIITGCFSYYQ
EAKSSKIMESFKNMVPQQALVIRNGEKMSINAEEVVVGDLVEVKGGDRIPADLRIISANGCKVDNSSLTGESEPQ
TRSPDFTNENPLETRNIAFFSTNCVEGTARGIVVYTGDRTVMGRIATLASGLEGGQTPIAAEIEHFIHIITGVAV
FLGVSFFILSLILEYTWLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICS
DKTGTLTQNRMTVAHMWFDNQIHEADTTENQSGVSFDKTSATWLALSRIAGLCNRAVFQANQENLPILKRAVAGD
ASESALLKCIELCCGSVKEMRERYAKIVEIPFNSTNKYQLSIHKNPNTSEPQHLLVMKGAPERILDRCSSILLHG
KEQPLDEELKDAFQNAYLELGGLGERVLGFCHLFLPDEQFPEGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVP
DAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPRDAKACVVHGSDLKDMTS
EQLDDILKYHTEIVFARTSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGIAGSDVSKQAADMIL
LDDNFASIVTGVEEGRLIFDNLKKSIAYTLTSNIPEITPFLIFIIANIPLPLGTVTILCIDLGTDMVPAISLAYE
QAESDIMKRQPRNPKTDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDVED
SYGQQWTYEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILIFGLFEETALAAFLSYCPGMG
VALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIRRRPGGWVEKETYY

FIGURE 314A

TTCCAAAACTGTTCTCTGGAGCTATAAGTGGATTGCCAGAAATGAGAGATTAGGAGCTGGGAGAAGAGGAAGCGC
CTTGTGTTGTGTCTCCTGGAGGCTGCCGACATGAAGTGCTTTTTCCCGGTGCTGAGCTGTCTGGCTGTGCTGGGT
GTGGTGTCAGCACAGCGGCAGGTCACCGTTCAGGAAGGACCCTTGTACCGCACGGAGGGCTCCCACATCACTATC
TGGTGCAATGTGAGTGGCTACCAGGGACCTTCTGAGCAGAATTTCCAGTGGTCCATTTACCTGCCTTCGTCGCCA
GAGCGAGAGGTGCAGATCGTCAGCACCATGGACTCTTCCTTCCCCTATGCCATCTACACCCAGCGCGTCCGCGGA
GGGAAGATCTTCATAGAAAGAGTCCAGGGGAACTCAACCCTATTGCACATCACAGATCTTCAGGCCCGGGATGCC
GGGGAGTATGAATGCCACACACCCAGCACTGATAAGCAATACTTTGGGAGTTACAGTGCAAAGATGAACCTAGTG
GTGATCCCAGACTCCCTGCAGACCACTGCCATGCCCCAGACTCTGCACAGAGTGGAGCAGGACCCGCTGGAGCTC
ACTTGTGAGGTGGCCTCAGAGACCATTCAGCACAGCCACCTGTCTGTGGCCTGGCTCCGGCAGAAAGTTGGCGAG
AAGCCCGTGGAGGTCATCTCCCTGAGCCGAGATTTCATGCTTCACTCCAGCAGCGAATATGCCCAGAGGCAGAGC
CTGGGGGAGGTGCGGCTGGACAAGCTGGGGAGGACCACCTTCCGCCTCACCATCTTCCACCTGCAGCCTTCTGAC
CAGGGCGAATTCTACTGCGAGGCCGCCGAGTGGATCCAGGATCCGGATGGGTCGTGGTATGCTATGACCCGAAAG
CGTTCCGAGGGAGCCGTGGTCAACGTCCAGCCAACTGACAAAGAATTCACTGTTCGGCTGGAGACAGAGAAGCGG
CTGCACACGGTGGGCGAGCCGGTGGAGTTCAGATGCATCCTGGAGGCTCAGAATGTTCCCGACCGTTACTTTGCT
GTCTCCTGGGCCTTCAACAGCTCGCTCATCGCCACCATGGGTCCTAACGCTGTGCCTGTCCTCAACAGCGAATTT
GCTCACCGGGAAGCCAGGGGACAGCTTAAGGTGGCCAAAGAGAGCGACAGTGTCTTTGTGCTGAAGATCTACCAC
CTCCGCCAGGAAGATAGCGGGAAATACAACTGCCGGGTGACTGAGCGAGAGAAAACCGTGACCGGGGAATTCATT
GATAAGGAGAGCAAGCGTCCCAAGAACATCCCCATCATAGTCCTCCCCCTCAAGAGCAGCATCTCCGTGGAGGTG
GCCAGCAATGCCAGCGTCATCCTTGAGGGCGAGGACCTGCGCTTCTCCTGCAGTGTCCGCACGGCAGGCAGGCCG
CAGGGTCGCTTCTCTGTCATCTGGCAGCTTGTGGACAGGCAGAACCGCCGCAGCAATATCATGTGGCTAGACCGG
GATGGCACCGTGCAGCCAGGCTCGTCCTACTGGGAGCGCAGCAGCTTTGGGGGCGTCCAGATGGAGCAGGTGCAG
CCCAACTCGTTCAGCCTGGGCATCTTCAACAGCAGGAAGGAGGACGAGGGCCAGTATGAATGCCATGTGACTGAA
TGGGTGCGGGCAGTGGATGGCGAGTGGCAGATTGTTGGGGAGCGCCGGGCCAGCACTCCCATCTCCATCACAGCT
CTTGAAATGGGCTTCGCAGTCACAGCCATCTCCCGGACACCGGGGGTGACCTACAGCGACTCCTTTGACTTGCAG
TGTATCATCAAACCCCACTACCCTGCCTGGGTCCCCGTGTCGGTGACATGGCGGTTCCAGCCGGTGGGCACGGTG
GAGTTCCATGACTTGGTGACCTTCACCCGGGACGGAGGGGTCCAGTGGGGGGGACAGGTCCTCCAGCTTCCGAACC
CGAACTGCCATCGAGAAGGCTGAGTCCAGCAACAACGTCCGCCTAAGCATCAGCCGAGCCAGTGACACGGAAGCA
GGCAAGTACCAGTGTGTGGCAGAGCTGTGGCGGAAGAACTACAACAACACCTGGACGCGACTGGCGGAGAGGACC
TCCAACCTGCTGGAGATCAGGGTGCTGCAGCCAGTGACAAAGCTGCAGGTGAGCAAATCGAAGAGGACCCTCACC
CTGGTGGAAAACAAGCCCATTCAGTTGAACTGCTCAGTCAAGTCTCAGACTAGCCAGAACTCCCACTTTGCGGTG
CTCTGGTATGTCCACAAGCCCTCGGATGCCGATGGCAAGCTTATCCTGAAGACCACCCACAACTCCGCCTTTGAA
TACGGTACTTACGCCGAGGAGGAGGGCCTGAGAGCCAGGCTCCAGTTTGAGAGGCATGTGTCGGGGGGCCTGTTC
AGCCTCACCGTCCAGAGAGCCGAGGTCAGCGACAGCGGCAGCTACTACTGCCACGTGGAGGAGTGGCTGCTGAGC
CCCAACTACGCCTGGTACAAGCTGGCAGAGGAGGTTTCTGGGCGCACAGAAGTCACTGTGAAACAGCCAGACAGC
CGCCTGAGGCTCAGCCAAGCCCAGGGGAACCTGTCGGTTCTGGAGACCCGGCAGGTACAGCTGGAGTGTGTGGTT
CTCAACCGCACCAGCATAACCTCCCAGCTCATGGTGGAATGGTTTGTATGGAAGCCCAACCACCCTGAGCGGGAG
ACTGTGGCCCGCTTGAGCCGTGACGCCACCTTCCACTATGGAGAGCAGGCAGCCAAGAACAATCTGAAGGGGCGG
CTGCATTTGGAGAGTCCTTCCCCCGGCGTGTACCGTCTCTTCATCCAGAACGTGGCTGTGCAGGACAGCGGGACC
TACAGCTGCCATGTGGAGGAGTGGCTGCCCAGCCCCAGTGGCATGTGGTATAAGCGGGCAGAGGACACCGCTGGG
CAGACAGCTCTGACAGTCATGCGACCAGATGCTTCCCTGCAGGTGGACACAGTGGTCCCCAATGCCACGGTCTCT
GAGAAGGCAGCTTTCCAGCTGGACTGTAGCATCGTGTCCCGCTCCAGCCAGGACTCCCGCTTCGCTGTGGCCTGG
TATTCCCTGAGGACTAAAGCTGGGGGGAAAAGGAGCAGCCCTGGCCTGGAAGAACAGGAAGAGGAAAGGGAGGAG
GAGGAGGAGGAGGACGACGACGACGACGACGACCCAACAGAGCGGACGGCCCTGCTGAGCGTGGGCCCAGATGCT
GTCTTTGGCCCAGAGGGCAGTCCTTGGGAGGGCAGGCTTCGCTTCCAGAGGCTCTCCCCGGTGCTCTACCGGCTC
ACAGTGCTGCAGGCAAGCCCCCAAGATACAGGCAATTACTCCTGCCATGTGGAGGAGTGGCTGCCCAGCCCTCAG
AAGGAATGGTACCGGCTGACGGAGGAGGAGTCAGCCCCCATCGGCATCCGTGTTCTAGATACAAGTCCCACCCTC
CAGTCCATCATCTGCTCCAACGACGCACTCTTCTACTTCGTCTTCTTCTACCCTTTCCCCATCTTTGGCATTCTT
ATCATCACCATCCTTCTGGTGCGTTTCAAGAGCCGGAACTCCAGCAAGAACTCTGATGGGAAGAATGGGGTGCCT

FIGURE 314B

CTGCTGTGGATCAAAGAGCCACACCTCAACTACTCCCCTACTTGCCTGGAGCCCCCTGTTCTCAGTATCCATCCA
GGGGCCATAGACTAAGCGGGTGATGCCCCAGCGGATGTTGGCCACGGAGGAGCTGAGGCTCTCCCTTTCTCTGTG
ATTGGACAGTTGACAGCACCCAAACTCTGGGGTGCATGTGTGTGGAAAGTTGTCAGACTTGAAAAGTGTTCCAAG
TTCCCAGTCAGTCACAGAGACAGACTGCCTCTCGGTGGCAGTCTTGGTTGGTTAGCTATTTGCGCGCAAATGTTG
TGATCCTGCCATTATAGATTTCTTGTTTCTGTTTTTAGTAATGTAGTGAGTAGCTCCAGGTGCCACATCTACTCA
CAGATTTATCTAGTATTCTCAGATAGATGTTACAGGGCTTCTTATTCTTTGTAATGTACTCTTTTTAAATCCCTT
TAGTTTACCCTTTTTGGATTCCTTAATGTGGACGAATTTCTCTTACGTACAACTGACAGCAAAAGGAAGGGCGAA
CTTTCTAGTGACAAGGAATCTCTTCCAAGACTTTGTTTTTGCACATTTGAAAATGCCACCCATGGATCAAAATAT
ACCCAAACGTTTTTTACTTTCTTAACAAGACTTAAGAATTGTGTGTAGTGTGGGCAAAATTTGTATGTTGTCTTT
TCCCTCAGCTGGAGTTATTGGAACCACTTTGTAGTCAAGACGAAAGCACTGAATTTTGCTTCAAAGAACTGTGTA
TGTACAAGAGAAATCCTGCATAACCCCATTAGGAGTAGATGGTGCCCGGCCTATCTGTCAGGGAGGCAAAAAAGG
CTTCATCCCATCCTTGCCAAAAAATAAGAAAACTGTCTTGGAGAATGGGTCAGAAGCCCCAAACGGCACACACTT
TCCAAATTAAAGTGGGCAGGGGCTGCTTTTAGCAGCTGCTGACCTGCAGATTTGTCAAAGCCAGTGACTAGAGAA
GGAAGGGAGAAAGGCTGGCTGTTGGCTTGCTCTGAGCTGCAAGGATGGTCTCTAACTGATTAACTGTGAGCAGGT
GGGCCTGTGTCTTCAGGTGCTTTGCCAAACTCTTAAAAGAAAGTGTCCAGTGAACTTGGAAGTGGGCCCCTGAGC
TGAGCACAGGGCCAAAGCAGCCATGGCAGACACCTGACGGAGGGCACGGGGCTGGCTGACACTAAGTTTGGTGGG
ACAGTGAGGGGTGGGAGGGGGGTTTCCAGGGCCTGGTGTTGGAGAGTGCAGAGAAATATCTACCTCCCTGGAGGT
GTGAAGACTAGGTTTTTCTTCTTCCTTCCAATTAGATTTTCCTTAATTATAGTGATGTCTTCCTTATTCATTTTT
CTCTCCCTGCCTCTCACTGCCATAAGAATATCAGCCTGGGGGCAGTCCAGACGCAGCCCTTTGTCATCCTTTCTG
TTTGCCTAGTCTCAGCAGACTGTGATCACAAGGCATTGTCTGTGGGATTTTTCCTTTCCCTTTCTTGATCTCTCT
TGTGGTTCTAGGTTGTTTGGTTGTTCATTGTTATGGTGGCTTTTTATTTTAACGCCCCTTGAGCCCCATGATGGC
TGGTGTCACCCTGTTCTTTTACACTGTTGGGCCAGGTGCTGCTTGTCCTTCTTAGGGCATCATCAATTGCAAATA
TTTCCTTTTGCTCCCTTTATGAAGATGTTCTTATACCCTTGCTTTCCCATATTTTTCTGGCCAAGCATGCCATCT
CCTTTACTCTGGGAACTTACATCCTGAATCCCAAGAGGGGGTCACAGTTTGGAAAAAGTCATCAGGGATTCTGGA
ACTAAGTCTGATAAAAGATTCCAGTGAAGCCCTGTTCTGAGAACGAGCAGACTGCAGGGGAGGCCATGGGATTCC
CCAGGCCAGTGTCTGTGCTGATCCTTCAAGGGTCTGCAGGTATGCAGGTGGCCTGGGCTGCTCGGCAGATACTTT
GCTGATTCCCAGCTGAGGGGAGCATGGTGGCGATTGCTCAGCCATTTTCTGACAGACACACAGACCTGCCTTTTC
TCCCCCAAGTATACCGTACCCTCCTGTGAGACAGTGTGTGCAGGCACCACCACCTTAATCCTGCTGTTGCCTGAC
ATGCTGATTCTCATTTATTATGCTGCATCAACACATTAGAGGTACAGGAGCGGCTCAGTCATGAAAAAAGAAGGT
CTTTTGCCCCATTTCTTTATTTCAGAGATGTGGGCTTTCAGTGGGAATTTGCTGACTCCTACTTTATAGGCTGAG
TCAATGAGGGAAGATGACTGGCGTTTCCTCTGTCTAAATGGGAGGTTGCCAGAGCGCTGGCTGGGACTAGGATGT
GTAACTAAGATTTCAGTTTGAAATCTTAGATTTCAGTTCACGGCGATAAAGAAGTAGGTGCTGCACACAAATATG
TAAAGCAATTGTAGGAAATTTGAAAGGAAAAAAAGAAACCGAAGCCAGTATTTTAATAATTGCTTTTTTCTGTGTA
TTTTGTATTGGGCTGGGGGATAGCATCAAAGGTTGAACTTTTTGAGCTTTCTATGAAAAACCCCAGGACCTTCTT
TCTTTGGCCATTTCTATGGAAATGCGATGTCAGATGGATGGTAATGGTGCCCTCCAGTGGCTGTGAGACCTCATT
GCGCATTGTCTACTGGAGCTTTAGTCTTCTGAGACGGAGGAAAACTGCTGAATACTCTGGATTCATCTATGTCTA
CAATGTTGCATTTATGAAAAACTACACTGTGCTAGGCGCATTCTAGGACATGAATATGACCACACCCTCTTTCAC
CGGGTGTTTCTGTAGCAAGTTTTCATATTCTTTTCAAACAATGGTTTCTCTGCGTTAATTATTGAGGAAAAAAAA
AGATGGGGTAAGAAAACTACCCATGCATGATGTAGAGAGCTGTTGATTTGTTTCTGTTTTTTTAAAGGAAAACTA
TTTGTAAGATGTTGCACTAAAACATTTTATATACACTTCAGAGACCTGTAGTAAATTATGTTGAAAAT

FIGURE 315A

GCTCTTTGCCGAGGGCGTGTGGTGAGAGTCCCCACAGCGACCCTGGTTCGAGTGGTGGGCACTGAGCTGGTCATC
CCCTGCAACGTCAGTGACTATGATGGCCCCAGCGAGCAAAACTTTGACTGGAGCTTCTCATCTTTGGGGAGCAGC
TTTGTGGAGCTTGCAAGCACCTGGGAGGTGGGGTTCCCAGCCCAGCTGTACCAGGAGCGGCTGCAGAGGGGCGAG
ATCCTGTTAAGGCGGACTGCCAACGACGCCGTGGAGCTCCACATAAAGAACGTCCAGCCTTCAGACCAAGGCCAC
TACAAATGTTCAACCCCCAGCACAGATGCCACTGTCCAGGGAAACTATGAGGACACAGTGCAGGTTAAAGTGCTG
GCCGACTCCCTGCACGTGGGCCCCAGCGCGCGGCCCCCGCCGAGCCTGAGCCTGCGGGAGGGGGAGCCCTTCGAG
CTGCGCTGCACCGCCGCCTCCGCCTCGCCGCTGCACACGCACCTGGCGCTGCTGTGGGAGGTGCACCGCGGCCCG
GCCAGGCGGAGCGTCCTCGCCCTGACCCACGAGGGCAGGTTCCACCCGGGCCTGGGGTACGAGCAGCGCTACCAC
AGTGGGGACGTGCGCCTCGACACCGTGGGCAGCGACGCCTACCGCCTCTCAGTGTCCCGGGCTCTGTCTGCCGAC
CAGGGCTCCTACAGGTGTATCGTCAGCGAGTGGATCGCCGAGCAGGGCAACTGGCAGGAAATCCAAGAAAAGGCC
GTGGAAGTTGCCACCGTGGTGATCCAGCCATCAGTTCTGCGAGCAGCTGTGCCCAAGAATGTGTCTGTGGCTGAA
GGAAAGGAACTGGACCTGACCTGTAACATCACAACAGACCGAGCCGATGACGTCCGGCCCGAGGTGACGTGGTCC
TTCAGCAGG**ATG**CCTGACAGCACCCTACCTGGCTCCCGCGTGTTGGCGCGGCTTGACCGTGATTCCCTGGTGCAC
AGCTCGCCTCATGTTGCTTTGAGTCATGTGGATGCACGCTCCTACCATTTACTGGTTCGGGATGTTAGCAAAGAA
AACTCTGGCTACTATTACTGCCACGTGTCCCTGTGGGCACCCGGACACAACAGGAGCTGGCACAAAGTGGCAGAG
GCCGTGTCTTCCCCAGCTGGTGTGGGTGTGACCTGGCTAGAACCAGACTACCAGGTGTACCTGAATGCTTCCAAG
GTCCCCGGGTTTGCGGATGACCCCACAGAGCTGGCATGCCGGGTGGTGGACACGAAGAGTGGGGAGGCGAATGTC
CGATTCACGGTTTCGTGGTACTACAGGATGAACCGGCGCAGCGACAATGTGGTGACCAGCGAGCTGCTTGCAGTC
ATGGACGGGGACTGGACGCTAAAATATGGAGAGAGGAGCAAGCAGCGGGCCCAGGATGGAGACTTTATTTTTTCT
AAGGAACATACAGACACGTTCAATTTCCGGATCCAAAGGACTACAGAGGAAGACAGAGGCAATTATTACTGTGTT
GTGTCTGCCTGGACCAAACAGCGGAACAACAGCTGGGTGAAAAGCAAGGATGTCTTCTCCAAGCCTGTTAACATA
TTTTGGGCATTAGAAGATTCCGTGCTTGTGGTGAAGGCGAGGCAGCCAAAGCCTTTCTTTGCTGCCGGAAATACA
TTTGAGATGACTTGCAAAGTATCTTCCAAGAATATTAAGTCGCCACGCTACTCTGTTCTCATCATGGCTGAGAAG
CCTGTCGGCGACCTCTCCAGTCCCAATGAAACGAAGTACATCATCTCTCTGGACCAGGATTCTGTGGTGAAGCTG
GAGAATTGGACAGATGCATCACGGGTGGATGGCGTTGTTTTAGAAAAAGTGCAGGAGGATGAGTTCCGCTATCGA
ATGTACCAGACTCAGGTCTCAGACGCAGGGCTGTACCGCTGCATGGTGACAGCCTGGTCTCCTGTCAGGGGCAGC
CTTTGGCGAGAAGCAGCAACCAGTCTCTCCAATCCTATTGAGATAGACTTCCAAACCTCAGGTCCTATATTTAAT
GCTTCTGTGCATTCAGACACACCATCAGTAATTCGGGGAGATCTGATCAAATTGTTCTGTATCATCACTGTCGAG
GGAGCAGCACTGGATCCAGATGACATGGCCTTTGATGTGTCCTGGTTTGCGGTGCACTCTTTTGGCCTGGACAAG
GCTCCTGTGCTCCTGTCTTCCCTGGATCGGAAGGGCATCGTGACCACCTCCCGGAGGGACTGGAAGAGCGACCTC
AGCCTGGAGCGCGTGAGTGTGCTGGAATTCTTGCTGCAAGTGCATGGCTCCGAGGACCAGGACTTTGGCAACTAC
TACTGTTCCGTGACTCCATGGGTGAAGTCACCAACAGGTTCCTGGCAGAAGGAGGCAGAGATCCACTCCAAGCCC
GTTTTTATAACTGTGAAGATGGATGTGCTGAACGCCTTCAAGTATCCCTTGCTGATCGGCGTCGGTCTGTCCACG
GTCATCGGGCTCCTGTCCTGTCTCATCGGGTACTGCAGCTCCCACTGGTGTTGTAAGAAGGAGGTTCAGGAGACA
CGGCGCGAGCGCCGCAGGCTCATGTCGATGGAGATGGAC**TAG**GCTGGCCCGGGAGGGGAGTGACAGAGGGACGTT
CTAGGAGCAATTGGGGCAAGAAGAGGACAGTGATATTTTAAAACAAAGTGTGTTACACTAAAAACCAGTCCTCTC
TAATCTCAGGTGGGACTTGGCGCTCTCTCTTTTCTGCATGTCAAGTTCTGAGCGCGGACATGTTTACCAGCACAC
GGCTCTTCTTCCCACGGCACTTTCTGATGTAACAATCGAGTGTGTGTTTTCCCAACTGCAGCTTTTTAATGGTTA
ACCTTCATCTAATTTTTTTTCTCCCACTGGTTTATAGATCCTCTGACTTGTGTGTGTTTATAGCTTTTGTTTCGC
GGGGTTGTGGTGAGGAAGGGGTGATGGCATGCGGAGTTCTTTATCTTCAGTGAGAATGTGCCTGCCCGCCTGAGA
GCCAGCTTCCGCGTTGGAGGCACGTGTTCAGAGAGCTGCTGAGCGCCACCCTCTACCCGGCTGACAGACAACACA
GACCTGTGCCGAAGGCTAATTTGTGGCTTTTACGACCCTACCCCACCCCCTGTTTTCAGGGGTTTAGACTACATT
TGAAATCCAAACTTGGAGTATATAACTTCTTATTGAGCCCAACTGCTTTTTTTTTTTTTTTTTTTGCTTCTCTGC
CCCTTTTCCATTTCTTTTGTATTTGTTTTCTGTGAGAGCACTGAAATGGCAGCCCTGGAATCTACAATTTGGCTC
TCCACTGAGCACCTTATCTTGCCACCTTAGCCTTAAGAATGAATATGAAGAAAAATACACAGCCACCTCTGTCCA
GGGCAGTAAGAAGGGCTGCAAGGAAGGGGAGGATGGGGACAAGGAAAGGATCAGATACCTGCTCCAGTAGTTGTG
AGGCCACTGTGTCTCAGGGGACTCCAGGAGGAGCAGAAGAGGGATCCCACGAAGTTATTCTTACGCAGCTGGGGC
CAGGAGGGTCAGAGTGGTGCCAGGTGCAAGTTAGGCTAAAGAAGCCACCACTATTCCTCTCTCTTGCCCATTGTG

FIGURE 315B

GGGGGCAAAGGCATTGGTCACCAAGAGTCTTGCAGGGGGACCCACAGATATGCCATGTCCTTCACACGTGCTTGG
GCTCCTTAACCTGAAGGCAAATTGCTACTTGCAAGACTGACTGACTTCAAGGAATCAGAAATTACCTAGAAGCAC
CATGTTTTTTCTATGACCTTTTCAGTCCTTCAGGTCATTTTAAGGTCCACTGCAGGGGGTTAGTGAGAAAGGGTA
TACTTTGTGGTATGTTTTGCTTTCCTAATAGGGACATGAAGGAAACCCAGCAATTTGCTGTTATGTGAATGGCCT
GTAGAGCAGAGTCAAGAGCGGTGTGCTTTGCCCGACTGCTCCCATCAGGAATAGGAGAGTAGACAGAGATCTTCC
ACATCCCAGGCTTCTGCTGCTGCTTTAAAAGCTCTGTCCTTGGAGCCTCCCGCTCCCTGAAGTGTCTCGCCCCCT
GCACAGCACTGGCCTTTCGGAAGCATCCCAGTAGGGTTTTCTGAGGCTCGCTGGTGACTCATGCCCTAATTGCAA
TCCTCTGCTTTTATCTTGACTTTGAAGGATCTAACACTGCTCTCTCTTCCAAAGGGGAAAAAAAGATTCATTTGT
TTTGAGCAATAAACTAATACAAAATGATGGCCATTCATGTGCAGCTCTTTGTCACCATGGGCCGGATGAGTTGTG
CTCCTCCTGGCTCACCATTTCCCCCTGCTCCCCCACAGCCGGTTCTGCACTTATCACCGAGTCGCCCCTGGAAGC
AGATTCCCATTGAGTTTTCCCCACCAAGGGGACCATGCACATGGTAGAAACATTAGATTCTGCATTGACAGTAGC
CTTTCCTTGGCCCGGGCCTGTGGTGGGAAGACGGGCAACAAGTATACCCCACCAGGGCCTGAGTGACTAGAGGAA
GAGGACGAGGCCTTGTTGGCACTAGATTTGGGTATTTTCTGCATGTCATAACATATCCTAACTGCTATTTCAGAA
GAGGCAGCTTGTAGGTGATTGTACAAGTGAGAATTAAAGAGAGAACAGATATTTAAACAGGTGCTGTATTAGTAA
CAGCCAGTGCCCTTTCAGCCCTTGCATCTATTAAAAGGAGATTCAGGATTTTATTGGCACAGGCCCTTCTTAGTA
GGAAGAAAGGGTGCTTAGCTTTGGACCTGACCGGGTGTGTGTAAAACCATGGACTGAGTCACAGCAGACACTCGA
TGGTGGTAAATGTGATGGGTGCTTACACACTGTACCTTTTCCTTTCATACTGATGCTGCAGTTCAGGGCTGGAGT
TGTTAAGGCATTGACCTCCACCCACCTGCCCCATGTCCACTGGGCTGCCCAAGCTGCATGTCACCTGAGGGCTGG
CAGGAAGGGGCGAGAAATCCCAGGGCATTGTACCAAGGACCTAGTTCCTTCTAGGGATATAAATTTCCAGGAATG
TGTATTTTTAATGTGGTGAGATGCACTCTTTTGTTGTACCAAATAGGGCTCCCCACCCCACCCCTGCGACAAGTG
CTCTTCTAGAACAGGTTCCTACCAGCAGCACTGGTGTGAATGAAAGAGAGACCCAGCCGCGTCTCACACAGGTGG
AATTGCACTTCTTAACAAAAAGGAACTTTATAAAAGTTTGGGATTTTTTTTCCTAATCATAAAAATAGCCCCAGA
AAGAGCCTAAGCTATGTTCAGATAGAAGCCTCGAAATTCCTGTAAATTGTTTACTTTATGATGTTTACATACACG
TTTCACTTTGAAAAAAAATGCAAATCGACTTTTTAACAACTGTTGAGATGTTTCATGGGACAGTAGAACTCTGAC
TCACCAACTGGGCTAAATTTTAATTTAAAAATGTATTTATTTGAGTGTCTTTCCCCCCCTCACCCTCACCATCTG
AGGGGCTCCCTGAGATCTTGGTAGAGGAGGCCCCTCCTGCCCAGACCTTCGTTTGTTTCCCCGGTGGCCCTTGCT
TCTTGCTTTGCAGACTGCCTGCAGCCATGATTTTGTCACTGACATCTGTGAGCCAAAGACTGAGCCTTTTTGGCA
GGAATAATAAGCAATACTACACAACTTGCTACTTTCAGAAAACTTTTTTTTTAGCTTCACCGATGACAACAGAGGA
AGAAGGGAACTGGGATTTGGGTAAGTTCTCCTCCACTGTTTGACCAAATTCTCAGTGATAAATATGTGTGCAGAT
CCCTAGAAGAGAAAACGCTGACTTTCTTTTTAAGTGTGGCACATAAGGATCTGCAGAATTTTCCGTAGACAAAGA
AAGGATCTTGTGTATTTTTGTCCATATCCAATGTTATATGAACTAATTGTATTGTTTTATACTGTGACCACAAAT
ATTATGCAATGCACCATTTGTTTTTTATTTCATTAAAGGAAGTTTAATTT

FIGURE 316

MPDSTLPGSRVLARLDRDSLVHSSPHVALSHVDARSYHLLVRDVSKENSGYYYCHVSLWAPGHNRSWHKVAEAVS
SPAGVGVTWLEPDYQVYLNASKVPGFADDPTELACRVVDTKSGEANVRFTVSWYYRMNRRSDNVVTSELLAVMDG
DWTLKYGERSKQRAQDGDFIFSKEHTDTFNFRIQRTTEEDRGNYYCVVSAWTKQRNNSWVKSKDVFSKPVNIFWA
LEDSVLVVKARQPKPFFAAGNTFEMTCKVSSKNIKSPRYSVLIMAEKPVGDLSSPNETKYIISLDQDSVVKLENW
TDASRVDGVVLEKVQEDEFRYRMYQTQVSDAGLYRCMVTAWSPVRGSLWREAATSLSNPIEIDFQTSGPIFNASV
HSDTPSVIRGDLIKLFCIITVEGAALDPDDMAFDVSWFAVHSFGLDKAPVLLSSLDRKGIVTTSRRDWKSDLSLE
RVSVLEFLLQVHGSEDQDFGNYYCSVTPWVKSPTGSWQKEAEIHSKPVFITVKMDVLNAFKYPLLIGVGLSTVIG
LLSCLIGYCSSHWCCKKEVQETRRERRRLMSMEMD

FIGURE 317

GTCCATTTTGTCGGTAGAGGCAGAAGGAGAAGGTCGGATTGTAGAAGCTGGGGTGGCCGGCAGCTCGCTCATCGG
TGTTCGTGGGCTTTGTCGGTCCGTGCCTCGTCTCTCCCTGGAAAGGGAGGGAGGCTTCAACGTCGAGAGGGAGCC
GCTGCCGCGTTAGTTCCGAGCTTGAAGTCACTAGGACTTCTCTCAAACTTGAGTGCTGAGGAGACTCAGATGTTG
GCCTCAGCTCCTAGGCTGAACTCAGCAGATCGGCCCATGAAAACTTCTGTATTGAGACAAAGGAAGGGATCTGTC
AGAAAGCAACACTTGTTATCTTGGGCTTGGCAGCAAGGAAGAGGACAGGTAGTGGAGATCCTGCAATCTGAAAAG
CAGACTGAAAGGTGACAAAGAAGCTGAAGATGGGTGGTAGAGAGAGGTATAACATTCCAGCCCCTCAATCTAGAA
ATGTTAGTAAGAACCAACAACAGCTTAACAGACAGAAGACCAAGGAACAGAATTCCCAGATGAAGATTGTTCATA
AGAAAAAAGAAAGAGGACATGGTTATAACTCATCAGCAGGTGCCTGGCAGGCCATGAAAAATGGGGGGAAGAACA
AAAATTTTCCAAATAATCAAAGTTGGAATTCTAGCTTATCAGGTCCCAGCTTACTTTTTAAATCTCAAGCTAAAC
AGAACTATGCTGGTGCCAAATTTAGTGAGCCGCCATCACCAAGTGTTCTTCCCAAACCACCAAGCCACTGGGTCC
CTGTTTCCTTTAATCCTTCAGATAAGGAAATAATGACATTTCAACTTAAAACCTTACTTAAAGTACAGGTATAAA
ATAAGACAAATGTTTAAGTTTAGTTATGTTCACAGATAGTTGTCAATTGGTCTGAAACAAATTTGCTAGGGAATC
TATTTGTGTAGAACTAATTAATGTAAAAAAAATAGACTTCATCTCGTGTTGTGTGCACTGTGATATAATGGTAGT
ATCAGTGCAACTTAAACTAATGATTGTAATTGATATTAAGTGTTCTCAACTGAGTAACTTTTAAGTGGAAACCAA
GTTTAGATTTGGGGAGTGGTAAAGGAATCAGCTTTTTCTATTGTTAGGGGAAGATAGTAATTTATCATTCATGGA
CCAGTAGATTGTTGAAAGTTGGTGAATCGGATTATAAGCTTCTGGCTAACACAAGGATTCAGAATTAGGTAAACA
TCTGAAGGTTTAGTATATTAGAAACACCCAAACCAGTAATATGCTAACCTGATGCACTGCTGAAAGAAAATGTGA
ATTTTTCGTAATAATTGCATTTTAGTGAATTGTACAGTGGGTGGAAAGGGCATTTGGAGCTCATTAGAATGAGAC
ATAGTACACCCCAATGGCCCTGTTTATTAAATGTAGTGGATTAAGTGTCTGTCAACAAATACACCAAAACCATTT
TTTATAGAAACAGTATTTAATGGTCACTCAATAGCTTTCAAAATACATTTTTGTATTACAGCACTGCACAAGCTA
TTCTAATAGTGATCTGGCCTCCTCATTCCTGCCAAGCTTGCTTTGGGGAGTTGGATAATGTGAAAATTTTAAGTA
CCTAGGGGAGAAAGAGCCATGTAAATATCTGTAATAAACTTGTAGCATATGTAAAGTTTTCTTGGCCTTTATCTT
ACAAAAATGGAATATTTTAGTATGAATTTGCTGAATGTAAGACCGTGGACTGTTTTTTATAATATGGCCTAATTT
TAAAGGTCCAAAATAACTTGTTTTTAAAGTTTGCCCTTGTGCTAAAGTGCCAGTGTATGTATGTTATACTTGATT
TGGTTGTAAACTATATTTCAAAGTAAACCCTAGTGTAATAAGTTTTATAACTAAAAAGGTTTAAGCTGCTAAAAC
TATTTTTAAGAGATGTGAAATGCAGTATGGGACTATCTTTTTTTCCTCCTCTAAGCCCAAAGATTAACTAGAGTC
CCTCCAACCTTATAGATTTTTGGCTTTCACAATCTTATAACCTAGGATACAGGTAGTTTCGAGTATGGTGCCAGT
GATGTTTTGTTTTTGTTTGGTCAAGGGGTAGGTGCAACCCAATGGACCACTTATGCAAAAGATGTAAACTCTTGC
ATAATACATCGATAACATGTTTTGCCAACTTTAAATGCTTAAACATAAGCGAAACCAGTAGCAAGTATGTGGGTC
AGTTTAAAAATTTTGATTGTTAATGCCCTATTTTCTAATTTGGCACCTCTTTTGATGCCTAAGCAGGTAAGCAGA
TGCCTAAGCTGTATTTCTCCAAATAAATCAAGAGGAAGTACTGCCCAAGTTAAATATTGATAGCCTAAAGACAAA
TTCATGTAGTACTTAATGTACATGATATGAATTTGAAGCATAAAATTAAATTTTTCCCCATTG

FIGURE 318A

TTTCAGCCAAACTTCGGGCGGCGGCTGAGGCGGCGGCCGAGGAGCGGCGGACTCGGGGCGCGGGGAGTCGAGGCA
TTTGCGCCTGGGCTTCGGAGCGTAGCGCCAGGGCCTGAGCCTTTGAAGCAGGAGGAGGGGAGGAGAGAGTGGGGC
TCCTCTATCGGGACCCCCTCCCCATGTGGATCTGCCCAGGCGGCGGCGGCGGCGGCGGAGGAGGAGGCGACCGAG
AAGATGCCCGCCCTGCGCCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGGCCCCCGCGCAT
GCATTGCAGTGTCGAGATGGCTATGAACCCTGTGTAAATGAAGGAATGTGTGTTACCTACCACAATGGCACAGGA
TACTGCAAATGTCCAGAAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCGCTGCCAG
AATGGTGGGACTTGTGTGGCCCAGGCCATGCTGGGGAAAGCCACGTGCCGATGTGCCTCAGGGTTTACAGGAGAG
GACTGCCAGTACTCAACATCTCATCCATGCTTTGTGTCTCGACCCTGCCTGAATGGCGGCACATGCCATATGCTC
AGCCGGGATACCTATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAATGGACGGATGCCTGCCTG
TCTCATCCCTGTGCAAATGGAAGTACCTGTACCACTGTGGCCAACCAGTTCTCCTGCAAATGCCTCACAGGCTTC
ACAGGGCAGAAATGTGAGACTGATGTCAATGAGTGTGACATTCCAGGACACTGCCAGCATGGTGGCACCTGCCTC
AACCTGCCTGGTTCCTACCAGTGCCAGTGCCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCCC
TGTGCACCCTCACCTTGTGTCAATGGAGGCACCTGTCGGCAGACTGGTGACTTCACTTTTGAGTGCAACTGCCTT
CCAGGTTTTGAAGGGAGCACCTGTGAGAGGAATATTGATGACTGCCCTAACCACAGGTGTCAGAATGGAGGGGTT
TGTGTGGATGGGGTCAACACTTACAACTGCCGCTGTCCCCCACAATGGACAGGACAGTTCTGCACAGAGGATGTG
GATGAATGCCTGCTGCAGCCCAATGCCTGTCAAAATGGGGGCACCTGTGCCAACCGCAATGGAGGCTATGGCTGT
GTATGTGTCAACGGCTGGAGTGGAGATGACTGCAGTGAGAACATTGATGATTGTGCCTTCGCCTCCTGTACTCCA
GGCTCCACCTGCATCGACCGTGTGGCCTCCTTCTCTTGCATGTGCCCAGAGGGGAAGGCAGGTCTCCTGTGTCAT
CTGGATGATGCATGCATCAGCAATCCTTGCCACAAGGGGGCACTGTGTGACACCAACCCCCTAAATGGGCAATAT
ATTTGCACCTGCCCACAAGGCTACAAAGGGGCTGACTGCACAGAAGATGTGGATGAATGTGCCATGGCCAATAGC
AATCCTTGTGAGCATGCAGGAAAATGTGTGAACACGGATGGCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCA
GGACCTCGTTGTGAGATGGACATCAATGAGTGCCATTCAGACCCCTGCCAGAATGATGCTACCTGTCTGGATAAG
ATTGGAGGCTTCACATGTCTGTGCATGCCAGGTTTCAAAGGTGTGCATTGTGAATTAGAAATAAATGAATGTCAG
AGCAACCCTTGTGTGAACAATGGGCAGTGTGTGGATAAAGTCAATCGTTTCCAGTGCCTGTGTCCTCCTGGTTTC
ACTGGGCCAGTTTGCCAGATTGATATTGATGACTGTTCCAGTACTCCGTGTCTGAATGGGGCAAAGTGTATCGAT
CACCCGAATGGCTATGAATGCCAGTGTGCCACAGGTTTCACTGGTGTGTTGTGTGAGGAGAACATTGACAACTGT
GACCCCGATCCTTGCCACCATGGTCAGTGTCAGGATGGTATTGATTCCTACACCTGCATCTGCAATCCCGGGTAC
ATGGGCGCCATCTGCAGTGACCAGATTGATGAATGTTACAGCAGCCCTTGCCTGAACGATGGTCGCTGCATTGAC
CTGGTCAATGGCTACCAGTGCAACTGCCAGCCAGGCACGTCAGGGGTTAATTGTGAAATTAATTTTGATGACTGT
GCAAGTAACCCTTGTATCCATGGAATCTGTATGGATGGCATTAATCGCTACAGTTGTGTCTGCTCACCAGGATTC
ACAGGGCAGAGATGTAACATTGACATTGATGAGTGTGCCTCCAATCCCTGTCGCAAGGGTGCAACATGTATCAAC
GGTGTGAATGGTTTCCGCTGTATATGCCCCGAGGGACCCCATCACCCCAGCTGCTACTCACAGGTGAACGAATGC
CTGAGCAATCCCTGCATCCATGGAAACTGTACTGGAGGTCTCAGTGGATATAAGTGTCTCTGTGATGCAGGCTGG
GTTGGCATCAACTGTGAAGTGGACAAAAATGAATGCCTTTCGAATCCATGCCAGAATGGAGGAACTTGTGACAAT
CTGGTGAATGGATACAGGTGTACTTGCAAGAAGGGCTTTAAAGGCTATAACTGCCAGGTGAATATTGATGAATGT
GCCTCAAATCCATGCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACACTTGCCACTGTGTGCTGCCA
TACACAGGCAAGAATTGTCAGACAGTATTGGCTCCCTGTTCCCCAAACCCTTGTGAGAATGCTGCTGTTTGCAAA
GAGTCACCAAATTTTGAGAGTTATACTTGCTTGTGTGCTCCTGGCTGGCAAGGTCAGCGGTGTACCATTGACATT
GACGAGTGTATCTCCAAGCCCTGCATGAACCATGGTCTCTGCCATAACACCCAGGGCAGCTACATGTGTGAATGT
CCACCAGGCTTCAGTGGTATGGACTGTGAGGAGGACATTGATGACTGCCTTGCCAATCCTTGCCAGAATGGAGGT
TCCTGTATGGATGGAGTGAATACTTTCTCCTGCCTCTGCCTTCCGGGTTTCACTGGGGATAAGTGCCAGACAGAC
ATGAATGAGTGTCTGAGTGAACCCTGTAAGAATGGAGGGACCTGCTCTGACTACGTCAACAGTTACACTTGCAAG
TGCCAGGCAGGATTTGATGGAGTCCATTGTGAGAACAACATCAATGAGTGCACTGAGAGCTCCTGTTTCAATGGT
GGCACATGTGTTGATGGGATTAACTCCTTCTCTTGCTTGTGCCCTGTGGGTTTCACTGGATCCTTCTGCCTCCAT
GAGATCAATGAATGCAGCTCTCATCCATGCCTGAATGAGGGAACGTGTGTTGATGGCCTGGGTACCTACCGCTGC
AGCTGCCCCCTGGGCTACACTGGGAAAAACTGTCAGACCCTGGTGAATCTCTGCAGTCGGTCTCCATGTAAAAAC
AAAGGTACTTGCGTTCAGAAAAAAGCAGAGTCCCAGTGCCTATGTCCATCTGGATGGGCTGGTGCCTATTGTGAC
GTGCCCAATGTCTCTTGTGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTTGAACACTTGTGCCAGCACTCAGGT

FIGURE 318B

GTCTGCATCAATGCTGGCAACACGCATTACTGTCAGTGCCCCCTGGGCTATACTGGGAGCTACTGTGAGGAGCAA
CTCGATGAGTGTGCGTCCAACCCCTGCCAGCACGGGGCAACATGCAGTGACTTCATTGGTGGATACAGATGCGAG
TGTGTCCCAGGCTATCAGGGTGTCAACTGTGAGTATGAAGTGGATGAGTGCCAGAATCAGCCCTGCCAGAATGGA
GGCACCTGTATTGACCTTGTGAACCATTTCAAGTGCTCTTGCCCACCAGGCACTCGGGGCCTACTCTGTGAAGAG
AACATTGATGACTGTGCCCGGGGTCCCCATTGCCTTAATGGTGGTCAGTGCATGGATAGGATTGGAGGCTACAGT
TGTCGCTGCTTGCCTGGCTTTGCTGGGGAGCGTTGTGAGGGAGACATCAACGAGTGCCTCTCCAACCCCTGCAGC
TCTGAGGGCAGCCTGGACTGTATACAGCTCACCAATGACTACCTGTGTGTTTGCCGTAGTGCCTTTACTGGCCGG
CACTGTGAAACCTTCGTCGATGTGTGTCCCCAGATGCCCTGCCTGAATGGAGGGACTTGTGCTGTGGCCAGTAAC
ATGCCTGATGGTTTCATTTGCCGTTGTCCCCCGGGATTTTCCGGGGCAAGGTGCCAGAGCAGCTGTGGACAAGTG
AAATGTAGGAAGGGGGAGCAGTGTGTGCACACCGCCTCTGGACCCCGCTGCTTCTGCCCCAGTCCCCGGGACTGC
GAGTCAGGCTGTGCCAGTAGCCCCTGCCAGCACGGGGGCAGCTGCCACCCTCAGCGCCAGCCTCCTTATTACTCC
TGCCAGTGTGCCCCACCATTCTCGGGTAGCCGCTGTGAACTCTACACGGCACCCCCCAGCACCCCTCCTGCCACC
TGTCTGAGCCAGTATTGTGCCGACAAAGCTCGGGATGGCGTCTGTGATGAGGCCTGCAACAGCCATGCCTGCCAG
TGGGATGGGGGTGACTGTTCTCTCACCATGGAGAACCCCTGGGCCAACTGCTCCTCCCCACTTCCCTGCTGGGAT
TATATCAACAACCAGTGTGATGAGCTGTGCAACACGGTCGAGTGCCTGTTTGACAACTTTGAATGCCAGGGGAAC
AGCAAGACATGCAAGTATGACAAATACTGTGCAGACCACTTCAAAGACAACCACTGTGACCAGGGGTGCAACAGT
GAGGAGTGTGGTTGGGATGGGCTGGACTGTGCTGCTGACCAACCTGAGAACCTGGCAGAAGGTACCCTGGTTATT
GTGGTATTGATGCCACCTGAACAACTGCTCCAGGATGCTCGCAGCTTCTTGCGGGCACTGGGTACCCTGCTCCAC
ACCAACCTGCGCATTAAGCGGGACTCCCAGGGGGAACTCATGGTGTACCCCTATTATGGTGAGAAGTCAGCTGCT
ATGAAGAAACAGAGGATGACACGCAGATCCCTTCCTGGTGAACAAGAACAGGAGGTGGCTGGCTCTAAAGTCTTT
CTGGAAATTGACAACCGCCAGTGTGTTCAAGACTCAGACCACTGCTTCAAGAACACGGATGCAGCAGCAGCTCTC
CTGGCCTCTCACGCCATACAGGGGACCCTGTCATACCCTCTTGTGTCTGTCGTCAGTGAATCCCTGACTCCAGAA
CGCACTCAGCTCCTCTATCTCCTTGCTGTTGCTGTTGTCATCATTCTGTTTATTATTCTGCTGGGGGTAATCATG
GCAAAACGAAAGCGTAAGCATGGCTCTCTCTGGCTGCCTGAAGGTTTCACTCTTCGCCGAGATGCAAGCAATCAC
AAGCGTCGTGAGCCAGTGGGACAGGATGCTGTGGGGCTGAAAAATCTCTCAGTGCAAGTCTCAGAAGCTAACCTA
ATTGGTACTGGAACAAGTGAACACTGGGTCGATGATGAAGGGCCCCAGCCAAAGAAAGTAAAGGCTGAAGATGAG
GCCTTACTCTCAGAAGAAGATGACCCCATTGATCGACGGCCATGGACACAGCAGCACCTTGAAGCTGCAGACATC
CGTAGGACACCATCGCTGGCTCTCACCCCTCCTCAGGCAGAGCAGGAGGTGGATGTGTTAGATGTGAATGTCCGT
GGCCCAGATGGCTGCACCCCATTGATGTTGGCTTCTCTCCGAGGAGGCAGCTCAGATTTGAGTGATGAAGATGAA
GATGCAGAGGACTCTTCTGCTAACATCATCACAGACTTGGTCTACCAGGGTGCCAGCCTCCAGGCCCAGACAGAC
CGGACTGGTGAGATGGCCCTGCACCTTGCAGCCCGCTACTCACGGGCTGATGCTGCCAAGCGTCTCCTGGATGCA
GGTGCAGATGCCAATGCCCAGGACAACATGGGCCGCTGTCCACTCCATGCTGCAGTGGCAGCTGATGCCCAAGGT
GTCTTCCAGATTCTGATTCGCAACCGAGTAACTGATCTAGATGCCAGGATGAATGATGGTACTACACCCCTGATC
CTGGCTGCCCGCCTGGCTGTGGAGGGAATGGTGGCAGAACTGATCAACTGCCAAGCGGATGTGAATGCAGTGGAT
GACCATGGAAAATCTGCTCTTCACTGGGCAGCTGCTGTCAATAATGTGGAGGCAACTCTTTTGTTGTTGAAAAAT
GGGGCCAACCGAGACATGCAGGACAACAAGGAAGAGACACCTCTGTTTCTTGCTGCCCGGGAGGGGAGCTATGAA
GCAGCCAAGATCCTGTTAGACCATTTTGCCAATCGAGACATCACAGACCATATGGATCGTCTTCCCCGGGATGTG
GCTCGGGATCGCATGCACCATGACATTGTGCGCCTTCTGGATGAATACAATGTGACCCCAAGCCCTCCAGGCACC
GTGTTGACTTCTGCTCTCTCACCTGTCATCTGTGGGCCCAACAGATCTTTCCTCAGCCTGAAGCACACCCCAATG
GGCAAGAAGTCTAGACGGCCCAGTGCCAAGAGTACCATGCCTACTAGCCTCCCTAACCTTGCCAAGGAGGCAAAG
GATGCCAAGGGTAGTAGGAGGAAGAAGTCTCTGAGTGAGAAGGTCCAACTGTCTGAGAGTTCAGTAACTTTATCC
CCTGTTGATTCCCTAGAATCTCCTCACACGTATGTTTCCGACACCACATCCTCTCCAATGATTACATCCCCTGGG
ATCTTACAGGCCTCACCCAACCCTATGTTGGCCACTGCCGCCCCTCCTGCCCCAGTCCATGCCCAGCATGCACTA
TCTTTTTCTAACCTTCATGAAATGCAGCCTTTGGCACATGGGGCCAGCACTGTGCTTCCCTCAGTGAGCCAGTTG
CTATCCCACCACCACATTGTGTCTCCAGGCAGTGGCAGTGCTGGAAGCTTGAGTAGGCTCCATCCAGTCCCAGTC
CCAGCAGATTGGATGAACCGCATGGAGGTGAATGAGACCCAGTACAATGAGATGTTTGGTATGGTCCTGGCTCCA
GCTGAGGGCACCCATCCTGGCATAGCTCCCCAGAGCAGGCCACCTGAAGGGAAGCACATAACCACCCCTCGGGAG
CCCTTGCCCCCCCATTGTGACTTTCCAGCTCATCCCTAAAGGCAGTATTGCCCAACCAGCGGGGGCTCCCCAGCCT

FIGURE 318C

CAGTCCACCTGCCCTCCAGCTGTTGCGGGCCCCCTGCCCACCATGTACCAGATTCCAGAAATGGCCCGTTTGCCC
AGTGTGGCTTTCCCCACTGCCATGATGCCCCAGCAGGACGGGCAGGTAGCTCAGACCATTCTCCCAGCCTATCAT
CCTTTCCCAGCCTCTGTGGGCAAGTACCCCACACCCCCTTCACAGCACAGTTATGCTTCCTCAAATGCTGCTGAG
CGAACACCCAGTCACAGTGGTCACCTCCAGGGTGAGCATCCCTACCTGACACCATCCCCAGAGTCTCCTGACCAG
TGGTCAAGTTCATCACCCCACTCTGCTTCTGACTGGTCAGATGTGACCACCAGCCCTACCCCTGGGGGTGCTGGA
GGAGGTCAGCGGGGACCTGGGACACACATGTCTGAGCCACCACACAACAACATGCAGGTTTATGCGTGAGAGAGT
CCACCTCCAGTGTAGAGACATAACTGACTTTTGTAAATGCTGCTGAGGAACAAATGAAGGTCATCCGGGAGAGAA
ATGAAGAAATCTCTGGAGCCAGCTTCTAGAGGTAGGAAAGAGAAGATGTTCTTATTCAGATAATGCAAGAGAAGC
AATTCGTCAGTTTCACTGGGTATCTGCAAGGCTTATTGATTATTCTAATCTAATAAGACAAGTTTGTGGAAATGC
AAGATGAATACAAGCCTTGGGTCCATGTTTACTCTCTTCTATTTGGAGAATAAGATGGATGCTTATTGAAGCCCA
GACATTCTTGCAGCTTGGACTGCATTTTAAGCCCTGCAGGCTTCTGCCATATCCATGAGAAGATTCTACACTAGC
GTCCTGTTGGGAATTATGCCCTGGAATTCTGCCTGAATTGACCTACGCATCTCCTCCTCCTTGGACATTCTTTTG
TCTTCATTTGGTGCTTTTGGTTTTGCACCTCTCCGTGATTGTAGCCCTACCAGCATGTTATAGGGCAAGACCTTT
GTGCTTTTGATCATTCTGGCCCATGAAAGCAACTTTGGTCTCCTTTCCCCTCCTGTCTTCCCGGTATCCCTTGGA
GTCTCACAAGGTTTACTTTGGTATGGTTCTCAGCACAAACCTTTCAAGTATGTTGTTTCTTTGGAAAATGGACAT
ACTGTATTGTGTTCTCCTGCATATATCATTCCTGGAGAGAGAAGGGGAGAAGAATACTTTTCTTCAACAAATTTT
GGGGGCAGGAGATCCCTTCAAGAGGCTGCACCTTAATTTTTCTTGTCTGTGTGCAGGTCTTCATATAAACTTTAC
CAGGAAGAAGGGTGTGAGTTTGTTGTTTTTCTGTGTATGGGCCTGGTCAGTGTAAAGTTTTATCCTTGATAGTCT
AGTTACTATGACCCTCCCCACTTTTTTAAAACCAGAAAAAGGTTTGGAATGTTGGAATGACCAAGAGACAAGTTA
ACTCGTGCAAGAGCCAGTTACCCACCCACAGGTCCCCCTACTTCCTGCCAAGCATTCCATTGACTGCCTGTATGG
AACACATTTGTCCCAGATCTGAGCATTCTAGGCCTGTTTCACTCACTCACCCAGCATATGAAACTAGTCTTAACT
GTTGAGCCTTTCCTTTCATATCCACAGAAGACACTGTCTCAAATGTTGTACCCTTGCCATTTAGGACTGAACTTT
CCTTAGCCCAAGGGACCCAGTGACAGTTGTCTTCCGTTTGTCAGATGATCAGTCTCTACTGATTATCTTGCTGCT
TAAAGGCCTGCTCACCAATCTTTCTTTCACACCGTGTGGTCCGTGTTACTGGTATACCCAGTATGTTCTCACTGA
AGACATGGACTTTATATGTTCAAGTGCAGGAATTGGAAAGTTGGACTTGTTTTCTATGATCCAAAACAGCCCTAT
AAGAAGGTTGGAAAAGGAGGAACTATATAGCAGCCTTTGCTATTTTCTGCTACCATTTCTTTTCCTCTGAAGCGG
CCATGACATTCCCTTTGGCAACTAACGTAGAAACTCAACAGAACATTTTCCTTTCCTAGAGTCACCTTTTAGATG
ATAATGGACAACTATAGACTTGCTCATTGTTCAGACTGATTGCCCCTCACCTGAATCCACTCTCTGTATTCATGC
TCTTGGCAATTTCTTTGACTTTCTTTTAAGGGCAGAAGCATTTTAGTTAATTGTAGATAAAGAATAGTTTTCTTC
CTCTTCTCCTTGGGCCAGTTAATAATTGGTCCATGGCTACACTGCAACTTCCGTCCAGTGCTGTGATGCCCATGA
CACCTGCAAAATAAGTTCTGCCTGGGCATTTTGTAGATATTAACAGGTGAATTCCCGACTCTTTTGGTTTGAATG
ACAGTTCTCATTCCTTCTATGGCTGCAAGTATGCATCAGTGCTTCCCACTTACCTGATTTGTCTGTCGGTGGCCC
CATATGGAAACCCTGCGTGTCTGTTGGCATAATAGTTTACAAATGGTTTTTTCAGTCCTATCCAAATTTATTGAA
CCAACAAAAATAATTACTTCTGCCCTGAGATAAGCAGATTAAGTTTGTTCATTCTCTGCTTTATTCTCTCCATGT
GGCAACATTCTGTCAGCCTCTTTCATAGTGTGCAAACATTTTATCATTCTAAATGGTGACTCTCTGCCCTTGGAC
CCATTTATTATTCACAGATGGGGAGAACCTATCTGCATGGACCTCTGTGGACCACAGCGTACCTGCCCCTTTCTG
CCCTCCTGCTCCAGCCCCACTTCTGAAAGTATCAGCTACTGATCCAGCCACTGGATATTTTATATCCTCCCTTTT
CCTTAAGCACAATGTCAGACCAAATTGCTTGTTTCTTTTTCTTGGACTACTTTAATTTGGATCCTTTGGGTTTGG
AGAAAGGGAATGTGAAAGCTGTCATTACAGACAACAGGTTTCAGTGATGAGGAGGACAACACTGCCTTTCAAACT
TTTTACTGATCTCTTAGATTTTAAGAACTCTTGAATTGTGTGGTATCTAATAAAAGGGAAGGTAAGATGGATAAT
CACTTTCTCATTTGGGTTCTGAATTGGAGACTCAGTTTTTATGAGACACATCTTTTATGCCATGTATAGATCCTC
CCCTGCTATTTTTGGTTTATTTTTATTGTTATAAATGCTTTCTTTCTTTGACTCCTCTTCTGCCTGCCTTTGGGG
ATAGGTTTTTTTTGTTTGTTTATTTGCTTCCTCTGTTTTGTTTTAAGCATCATTTTCTTATGTGAGGTGGGGAAGG
GAAAGGTATGAGGGAAAGAGAGTCTGAGAATTAAAATATTTTAGTATAAGCAATTGGCTGTGATGCTCAAATCCA
TTGCATCCTCTTATTGAATTTGCCAATTTGTAATTTTTGCATAATAAAGAACCAAAGGTGTAATGTTTTGTTGAG
AGGTGGTTTAGGGATTTTGGCCCTAACCAATACATTGAATGTATGATGACTATTTGGGAGGACACATTTATGTAC
CCAGAGGCCCCCACTAATAAGTGGTACTATGGTTACTTCCTTGTGTACATTTCTCTTAAAAGTGATATTATATCT
GTTTGTATGAGAAACCCAGTAACCAATAAAATGACCGCATATTCCTGACTAAACGTAGTAAGGAAAATGCACACT

FIGURE 318D

TTGTTTTTACTTTTCCGTTTCATTCTAAAGGTAGTTAAGATGAAATTTATATGAAAGCATTTTTATCACAAAATA
AAAAAGGTTTGCCAAGCTCAGTGGTGTTGTATTTTTTATTTTCCAATACTGCATCCATGGCCTGGCAGTGTTACC
TCATGATGTCATAATTTGCTGAGAGAGCAAATTTTCTTTTCTTTCTGAATCCCACAAAGCCTAGCACCAAACTTC
TTTTTTTCTTCCTTTAATTAGATCATAAATAAATGATCCTGGGGAAAAAGCATCTGTCAAATAGGAAACATCACA
AAACTGAGCACTCTTCTGTGCACTAGCCATAGCTGGTGACAAACAGATGGTTGCTCAGGGACAAGGTGCCTTCCA
ATGGAAATGCGAAGTAGTTGCTATAGCAAGAATTGGGAACTGGGATATAAGTCATAATATTAATTATGCTGTTAT
GTAAATGATTGGTTTGTAACATTCCTTAAGTGAAATTTGTGTAGAACTTAATATACAGGATTATAAAATAATATT
TTGTGTATAAATTTGTTATAAGTTCACATTCATACATTTATTTATAAAGTCAGTGAGATATTTGAACATG

FIGURE 319

GAGGAGGAGGAGGAGATGACTGGGGAGCGGGAGCTGGAGAATACTGCCCAGTTACTCTAGCGCGCCAGGCCGAAC
CGCAGCTTCTTGGCTTAGGTACTTCTACTCACAGCGGCCGATTCCGAGGCCAACTCCAGCAATGGCTTTTGCAAA
TCTGCGGAAAGTGCTCATCAGTGACAGCCTGGACCCTTGCTGCCGGAAGATCTTGCAAGATGGAGGGCTGCAGGT
GGTGGAAAAGCAGAACCTTAGCAAAGAGGAGCTGATAGCGGAGCTGCAGGACTGTGAAGGCCTTATTGTTCGCTC
TGCCACCAAGGTGACCGCTGATGTCATCAACGCAGCTGAGAAACTCCAGGTGGTGGGCAGGGCTGGCACAGGTGT
GGACAATGTGGATCTGGAGGCCGCAACAAGGAAGGGCATCTTGGTTATGAACACCCCCAATGGGAACAGCCTCAG
TGCCGCAGAACTCACTTGTGGAATGATCATGTGCCTGGCCAGGCAGATTCCCCAGGCGACGGCTTCGATGAAGGA
CGGCAAATGGGAGCGGAAGAAGTTCATGGGAACAGAGCTGAATGGAAAGACCCTGGGAATTCTTGGCCTGGGCAG
GATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTATGACCCCATCATTTCCCC
AGAGGTCTCGGCCTCCTTTGGTGTTCAGCAGCTGCCCCTGGAGGAGATCTGGCCTCTCTGTGATTTCATCACTGT
GCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCTTTGCCCAGTGCAAGAAGGGGGTGCG
TGTGGTGAACTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCCTGCTCCGGGCCCTGCAGTCTGGCCAGTGTGC
CGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCACGGGACCGGGCCTTGGTGGACCATGAGAATGTCATCAG
CTGTCCCCACCTGGGTGCCAGCACCAAGGAGGCTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTCAGTTCGTGGA
CATGGTGAAGGGGAAATCTCTCACGGGGGTTGTGAATGCCCAGGCCCTTACCAGTGCCTTCTCTCCACACACCAA
GCCTTGGATTGGTCTGGCAGAAGCTCTGGGGACACTGATGCGAGCCTGGGCTGGGTCCCCCAAAGGGACCATCCA
GGTGATAACACAGGGAACATCCCTGAAGAATGCTGGGAACTGCCTAAGCCCCGCAGTCATTGTCGGCCTCCTGAA
AGAGGCTTCCAAGCAGGCGGATGTGAACTTGGTGAACGCTAAGCTGCTGGTGAAAGAGGCTGGCCTCAATGTCAC
CACCTCCCACAGCCCTGCTGCACCAGGGGAGCAAGGCTTCGGGGAATGCCTCCTGGCCGTGGCCCTGGCAGGCGC
CCCTTACCAGGCTGTGGGCTTGGTCCAAGGCACTACGCCTGTACTGCAGGGGCTCAATGGAGCTGTCTTCAGGCC
AGAAGTGCCTCTCCGCAGGGACCTGCCCCTGCTCCTATTCCGGACTCAGACCTCTGACCCTGCAATGCTGCCTAC
CATGATTGGCCTCCTGGCAGAGGCAGGCGTGCGGCTGCTGTCCTACCAGACTTCACTGGTGTCAGATGGGGAGAC
CTGGCACGTCATGGGCATCTCCTCCTTGCTGCCCAGCCTGGAAGCGTGGAAGCAGCATGTGACTGAAGCCTTCCA
GTTCCACTTCTAACCTTGGAGCTCACTGGTCCCTGCCTCTGGGGCTTTTCTGAAGAAACCCACCCACTGTGATCA
ATAGGGAGAGAAAATCCACATTCTTGGGCTGAACGCGGGCCTCTGACACTGCTTACACTGCACTCTGACCCTGTA
GTACAGCAATAACCGTCTAATAAAGAGCCTACCCCC

FIGURE 320

MAFANLRKVLISDSLDPCCRKILQDGGLQVVEKQNLSKEELIAELQDCEGLIVRSATKVTADVINAAEKLQVVGR
AGTGVDNVDLEAATRKGILVMNTPNGNSLSAAELTCGMIMCLARQIPQATASMKDGKWERKKFMGTELNGKTLGI
LGLGRIGREVATRMQSFGMKTIGYDPIISPEVSASFGVQQLPLEEIWPLCDFITVHTPLLPSTTGLLNDNTFAQC
KKGVRVVNCARGGIVDEGALLRALQSGQCAGAALDVFTEEPPRDRALVDHENVISCPHLGASTKEAQSRCGEEIA
VQFVDMVKGKSLTGVVNAQALTSAFSPHTKPWIGLAEALGTLMRAWAGSPKGTIQVITQGTSLKNAGNCLSPAVI
VGLLKEASKQADVNLVNAKLLVKEAGLNVTTSHSPAAPGEQGFGECLLAVALAGAPYQAVGLVQGTTPVLQGLNG
AVFRPEVPLRRDLPLLLFRTQTSDPAMLPTMIGLLAEAGVRLLSYQTSLVSDGETWHVMGISSLLPSLEAWKQHV
TEAFQFHF

FIGURE 321

GGGCAGGGGTGCGGAGGGACCGACGGACGCACGGGCGGGCGGCCGGGAGCCATGGAGCGCGGCCCTGGGGCCCGG
GGGCGCGGGCCGGGGTGGGCTTCCCACGGCACGACATGGAGACCTGTGGTTGCGAGGCTCCCTGGGGCTCGGCTT
GGACCGCGATGGGGCTGGGCCCTGGCCTCCTAACGGGGCTGCTGTCTGGGGCGGTAGCTGGGGGGGCGCTCTCCC
CCCTGCCCGCGACTCGGAGCACCCCACCCCTCCCCTGCCGGGCCAGGCCGGGCGGCGTTGTTGGCGGGGGCCCCG
GTGGAGGCCCGGCCCGGGCGGCGCCCGCC**ATG**AACGGGCTGTCGCTGAGTGAGCTCTGCTGCCTCTTCTGCTGCC
CTCCCTGCCCCGGCCGCATCGCTGCCAAGCTCGCCTTCCTGCCGCCGGAGGCCACCTACTCCCTGGTGCCTGAGC
CCGAGCTGGGGCCTGGTGGGGCCGGGGCCGCCCCCTTGGGGACCCTGAGAGCCTCCTCGGGCGCACCCGGGCGCT
GGAAGCTGCACCTGACGGAGCGTGCCGACTTCCAGTACAGCCAGCGCGAGCTGGACACCATCGAGGTCTTCCCCA
CCAAGAGCGCCCGCGGCAACCGTGTCTCCTGCATGTATGTTCGCTGCGTGCCTGGTGCCAGGTACACGGTCCTCT
TCTCGCACGGCAATGCCGTGGACCTGGGCCAGATGAGCAGCTTCTACATTGGCCTGGGCTCCCGCCTCCACTGCA
ACATCTTCACCTACGACTCCTCCGGCTACGGTGCCAGCTCGGGCAGGCCTTCCGAGAGGAACCTCTATGCCGACA
TCGACGCCACCTGGCAGGCCCTGCGCACCAGGTACGGCATCAGCCCGGACAGCATCATCCTGTACGGGCAGAGCA
TCGGCACGGTGCCCACCATGGACCTGGCCTCGCGCTACGAGTGTGCCGCGGTGGTGCTGCACTCGCCGCTCACCT
CGGGCATGCGCGTCGCCTTCCGCGACACCAAGAAGACCTACTGCTTCGACGCCTTCCCTAACATCGAGAAGGTGT
CCAAGATCACGTCTCCCGTGCTCATCATCCACGGCAGGGAGGACGAGGTGATCGACTTCTCGCACGGGCTGGCGC
TCTACGAGCGCTGCCCCAAGGCGGTGGAGCCGCTGTGGGTGGAGGGCGCCGGGCACAACGACATCGAGCTCTACA
GCCAGTACCTGGAGCGCCTGCGTCGCTTCATCTCCCAGGAGCTGCCCAGCCAGCGCGCC**TAG**CGGCGGCCCCAAC
CAGCCGGACCTCAGCAATAAGGCGGCCCCCGGACCTCACCCCGCGCCGGCCCCCACCCAGGGGCTGCATGTGGAC
CCCCCCGGGCGGCCCAGGGGACCCCGCCCCGACCCAGGGGCTGTGGACGATGTACAGGCAACAGAGCTACGCACT
CCTTTCCTTTTGGAAGCAAGAAGAAAATACGTGAAAACGGAAATTAAAGATTTAAAATT

FIGURE 322

MNGLSLSELCCLFCCPPCPGRIAAKLAFLPPEATYSLVPEPELGPGGAGAAPLGTLRASSGAPGRWKLHLTERAD
FQYSQRELDTIEVFPTKSARGNRVSCMYVRCVPGARYTVLFSHGNAVDLGQMSSFYIGLGSRLHCNIFTYDSSGY
GASSGRPSERNLYADIDATWQALRTRYGISPDSIILYGQSIGTVPTMDLASRYECAAVVLHSPLTSGMRVAFRDT
KKTYCFDAFPNIEKVSKITSPVLIIHGREDEVIDFSHGLALYERCPKAVEPLWVEGAGHNDIELYSQYLERLRRF
ISQELPSQRA

FIGURE 323A

AGCGTGAACCTGGGAGGCAGAGCTTGCAGTGAGCCTAGATCGCGTCACTGCACTCCAGCCTGGGAGACAGAGTGA
GACTCTGTCTCAAAAAAAAAAAAAGTCAAAACAAGAGAACATACTAAATGATTCCATTTTTTTATTTATGACTT
CATGACTACCATTAAGAAAATATAACCTGTTGGGAAACTGTTTCTGCCTTGATGATGTTGTACAGACAAGAGATA
AACAGTGAGGAATGTGCTTAGATGTATTGGGAAAGACACGGGTCTGTGGCATTGTCACAAGGGTACACGAATACT
GAGAGTGAATGCTGAAGGAATGATCCCCATTGGTGGTGACCCTCAGGTGAGACTAGGGTGCCTGTGTTTCAGCAA
AGCCTGGGCAATTGGAATGCAGGGCTCCTAAGATTCCATGACACCCCCACCTTCTAATTCTGTTATTGCAACTGC
AGACCGTTACCTGGCACGCTGGCCACAATCTACCTCACTCTTATCAGAGTCTGAGCTACTGGCAGTGCTTTCAGC
TCTGAGTTGAGGCACCTCGAACCTTGTTTTTGTGGTGAAGGATCCTAAAGTGCTGTGGGAGTGATCACATTTTTC
ACAACAGTAAGTCCCTGACTCCACCTCTTCTGCCACAAACGTCAGCATGGTGGTATCAGCCGGCCCTTGGTCCAG
CGAGAAGGCAGAGATGAACATTCTAGAAATCAACGAGAAATTGCGCCCCCAGTTGGCAGAGAACAAACAGCAGTT
CGTAAACCTCAAAGAGATGTTTTCTAACTCAACTGGCCGGCTTCCTGGCCAACCGACAGAAGAAATACAGCAATA
TAAAGTCCTGGTTCACTCTCAGGAACGAGAGCTGACGCAGTTAAAGGAGAAGTTACAGGAAGGGAGAGATGCCTC
CCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCTGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCA
AGAACAGCTGGCTGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACGAAGATGA
GGATGAAGATGTTCAAGTTGAGGAGGATGAGAAAGTGCAGAAATCATCTGCCCCCAGGGAGGTGCAGAAGGCTGA
AGTGAGCAAAGTCCCTGAGGACTCACTGGAGGAATGTGCCATCACTTGTTCAAATAGCCACGGCCCTTGTGACTC
CAACCAGCCTCACAAGAACATCAAAATCACATTTGAGGAAGACGAAGTCAACTCAACTCTGGTTGTAGACAGAGA
ATCCTCTCATGATGAATGTCAGGATGCTCTAAACATTCTCCCAGTCCCTGGCCCCACCTCTTCTGCCACAAACGT
CAGCATGGTGGTATCAGCCGGCCCTTTGTCCAGCGAGAAGGCAGAGATGAACATTCTAGAAATCAATGAGAAATT
GCACCCCCAGCTGGCAGAGAAGAAACAGCAGTTCAGAAACCTCAAAGAGAAATGTTTTCTAACTCAACTGGCCGG
CTTCCTGGCCAACCAGCAGAACAAATACAAGTATGAAGAGTGTAAAGACCTCATAAAATTTATGCTGAGGAATGA
GCGACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGCTCAGGCAATATAAAGTCCTGGT
TCACGCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTGCGGGAAGGGAGAGATGCCTCCCGCTCATTGAA
TGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCAGGGGCAGGACCTCCAAGAACAGCTGGC
TGAGGGGTGTAGACTGGCACAGCACCTTGTCCAAAAGCTCAGCCCAGAAAATGACAACGATGACAATGAAGATGT
TCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTCTGCCCCCAGGGAGATGCAGAAGGCTGAAGAAAAGGAAGT
CCCTGAGGACTCACTGGAGGAATGTGCCATCACTTATTCAAATAGCCATGGCCCTTATGACTCCAACCAGCCACA
TAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCTCATTGGCTCATCCTCTCATGTTGAACG
GGAAGATGCTGTACACATTATTCCAGAAAATGAAAGTGATGATGAGGAAGAGGAAGAAAAAGGGCCAGTGTCTCC
CAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCCTGGGATGAAGGTTATTCGACTCCCTCAAT
TCCTCCTGAAATGTTGGCCTCGTACAAGTCTTACAGCAGCACATTTCACTCATTAGAGGAACAGCAAGTCTGCAT
GGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGACCAAGAGGCAACAGGTCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGGGCCTGAAGTCTTGCAGGACTCACTGTATAGATGTTATTCAACTCCTTCAGG
TTGTCTTGAACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTACGTATTGGAGCAACAGCGTGTTGGCTT
GGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGACCAAGACCCATCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGATGAGAAAGAGCCTGAAGTCTTGCAGGACTCACTGGGTAGATGGTATTCGACTCCTTCAGG
TTATCTTGAACTGCCTGACTTAGGCCAGCCCTACAGCAGTGCTGTTTACTCATTGGAGGAACAGTACCTTGGCTT
GGCTCTTGACTTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGACCAAGGCCCACCATGCCCCAGGCTCAG
CAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTCAACTCCTTCCAG
TTGTCTTGAACAGCCTGACTCCTGCCAGCCCTATGGAAGTTCCTTTTATGCATTGGAGGAAAAACATGTTGGCTT
TTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAGAAGGAAAG
AAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCCCAGGCTCAACGGCGTGCTGATGGAAGT
GGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATGGATGTTATTCTACTCCGTCAATGTACTTTGAACTACCTGA
CTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAACAGCACATCAGCTTCGCCCTTTACGTGGACAA
TAGGTTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTGTTCCAGATGGAAGTCATATTCCCACAATAAGCAGC
CCTTACTAAGCCGAGAGATGTCATTCCTGCAGGCAGGACCTATAGGCACGTGAAGATTTGAATGAAACTACAGTT
CCATTTGGAAGCCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATTCCTATTCTCAAACCATGCCAGTGGCAA
CCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTTCACATAACTGTGCAGCACATGCCGGGA

FIGURE 323B

GTGATCAGTCAGACATTTTAATTTGAACCACGTATCTCTGGGTAGCTACAAAATTCCTCAGGGATTTCATTTTGC
AGACATGTCTCTGAGCTTCTATACCTGCTCAAGGTCATTGTCATCTTTGTGTTTAGCTCATCCAAAGGTGTTACC
CTGGTTTCAATGAACCTAACCTCATTCTTCGTGTCTTCAGTGTTGGCTTGTTTTAGCTGATCCATCTGTAACACA
GGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCTTGACAATTGTTAACCCGCTAGGCTCCT
TTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACTTAGGAAGACCACAGCTAGATGGACAAA
CAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGAGAACAGGAGTCAGGAGCCGCTGGCAGG
AGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAACAATGCCATGTTCTTGCAGAAAACGCTTAGCCT
GAGTTTCATAGGAGGTAATCACCAGACAACTGCAGAATGTAGAACACTGAGCAGGACAACTGACCTGTCTCCTTC
ACATAGTCCTTATCACCACAAATCACACAACAAAAAGGAGAAGAGATATTTTGGGTTCAAAAAAAGTAAAAAGAT
AATGTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCCTCATCTTTTTGTTGTTGTCATGGATGGTGG
TGACATGGACTTGTTTATAGAGGACAGGTCAGCTGTCTGGCTCAATGATCTACATTCTGAAGTTGTCTGAAAATG
TCTTCATGATTAAATTCAGCCTAAACGTTTTGCCGGGAACACTGCAGAGACAATGCTGTGAGTTTCCAACCTCAG
CCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATATCAGGACTGGTTACTTGGTTAAGGAGG
GGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTACTTGGGAAAGCGGTTTTCAAGAGTAT
AAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTTATTAATCCTCCCTGCCTGTGTCTATTATT
ATATTCATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTTACTGTGCCTTTGTTTTTACTAGTGTCTGCTGTT
GCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTTGTCCAAAGTTAATTTTAATCTATACAATTAAAAC
CTTTTGCCTATCACTCTGGACTTTTGGATTGTTTTTTACATTCAGTGTTATAATATTTGATTATGCTGATTGGTT
TTGGTGGGTACTGATGCGAATTAATAAAAACATTTCATTTCC

FIGURE 324A

GTTTTGTAACTCAACTGGCCGGCTTCCTGGCCAAGCAGCAGAACAAATACAAATATGAAGAGTGCAAAGACCTCA
TAAAATCTATGCTGAGGAATGAGCTACAGTTCAAGGAGGAGAAGCTTGCAGAGCAGCTGAAGCAAGCTGAGGAGC
TCAGGTGAGGGGACCCCATGGGGGCAGGCAGGGGGGCAGGTGTGTAAATCTCTGAAGTACAACAGCTCGGTGGGG
AGACTTAAGAGCTAAGCTGGGCCAGGGGAAGGGCAGGAATTGCCATGGCAGGCTCGCTACACACAAATATTTATC
AAACAGAGAAGAAGGATAATAAAAATTTATGGGTTGCAGTGTTTCTCAGAGCCTGTTTTCTTTTTTCAAACAAGT
AATGTTGATGTGAAATTTACATAACACAAAATTAACCAAAGGAGTGTGAACCACACAGCAGCATTCAGTATACTC
AAAATGGTGTGCCATCACCACCCCACTTACCCTAGTGAGAATCACCTCCTGACTGACTGCGGCTTCTCATTCTTT
CACTCAATCAATGTTGCCTTCTCGACCCTGTCATTCTTTTCTTCTTTCGTCTTTTCAATTCGCCCTATCTGCATC
TGGCCTCATTTCTGTACATGGCTTTGTATCTAATGGCCGCAAGATGCACTATGTGTATTTTCACATGGAAATGTC
CATGGCCAGAGTGAGGAACTGAAAGGATGTCTTTTTGAAACGGAATTAGGAAGACACCTACTTTTGTTTACAGAG
GGGAAAGATGAATGGAACATCATCGAGGATCTTGCAGGAGCCCTCTCTGATACAGAGGAAGCCTGTAAACCATTT
TCTATTCTTTCTCTTGGCCACAGACATTCCTTTCAACATGTGCTGACCTTCTGCTTGGAGGTCTCCTTGAGGACA
TTGTCTCAGAAATCTCTGTTGCAATATTTGAACGGATCACTCAACCCTTTCCACTCTTAAATTTTCTCTACCGTC
TCACCTTAGGCAATATAAAGTCCTGGTTCACTCTCAGGAACGAGAGCTGACCCAGTTAAGGGAGAAGTTACGGGA
AGGGAGAGATGCCTCCCGCTCATTGAATGAGCATCTCCAGGCCCTCCTCACTCCGGATGAGCCGGACAAGTCCCA
GGGGCAGGACCTCCAAGAACAGCTGGCTGAGGGGTGTAGACTGGCACAACACCTTGTCCAAAAGCTCAGCCCAGA
AAATGATAACGATGACGATGAAGATGTTCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTCTTCCCCCAGGGA
GATGCAGAAGGCTGAAGAAAAGGAAGTCCCTGAGGACTCACTGGAGGAGTGTGCCATCACTTGTTCAAATAGCCA
TGGCCCTTATGACTCCAACCAGCCACATAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACTCAACTCT
CATTGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCCAGAAAATGAAAGTGATGATGAGGA
AGAGGAAGAAAAAGGGCCAGTGTCTCCCAGGAATCTGCAGGAGTCTGAAGAGGAGGAAGTCCCCCAGGAGTCCTG
GGATGAAGGTTATTCGACTCTCTCAATTCCTCCTGAAAGGTTGGCCTCATACCAGTCTTACAGCAGCACATTTCA
CTCATTAGAGGAACAGCAAGTCTGCATGGCTGTTGACATAGGCAGACATCGGTGGGATCAAGTGAAAAAGGAGGA
CCAAGAGGCAACAGGTCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCAGTTTATCTTGGACTGACTGACTCATGCCAGCCCTACAGAAGTGCCTTTTA
CGTATTGGAGCAACAGCGTGTTGGCTTGGCTGTTGACATGGATGAAATTGAAAAGTACCAAGAAGTGGAAGAAGA
CCAAGACCCATCATGCCCCAGGCTCAGCAGGGAGCTGCTGGCTGAGAAAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCGACTCCTTCAGGTTATCTTGAACTGCCTGACTTAGGCCAGCCCTACAGAAGTGCTGTTTA
CTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAATTAAAAAGGACCAAGAAGAGGAAGAAGA
CCAAGGCCCACCATGCCCCAGGCTCAGCAGGGAGCTGCTGGAGGTAGTAGAGCCTGAAGTCTTGCAGGACTCACT
GGATAGATGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCTGCCAGCCCTACAGAAGTTCCTTTTA
TGCATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGAAATTGAAAAGAAGGGGAAGGGGAAGAAAAG
AAGGGGAAGAAGATCAAAGAAGAAAAGAAGAAGGGGAAGAAAAGAAGGGGAAGAAGATCAAAACCCACCATGCCC
CAGGCTCAACAGCGTGCTGATGGAAGTGGAAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGATGTTATTCGAC
TCCATCAATGTACTTTGAACTACCTGACTCATTCCAGCACTACAGAAGTGTGTTTTACTCATTTGAGGAACAGCA
CATCACCTTTGCCCTTGACATGGACAATAGCTTTTTTACTTTGACGGTGACAAGTCTCCACCTGGTCTTCCAGAT
GGGAGTCATATTCCCACAATAAGCAGCCCTTACTAAGCCGAGAGGTGTCATTCCTGCAGGCAGGACCTATAGGCA
CCTGAAGATTTGAATGAAACTATAGTTCCATTTGGAAGCCCAGACATAGGATGGGTCAGTGGGCATGGCTCTATT
CCTATTCTCAGAGCATGCCAGTGGCAACCTGTGCTCAGTCTGAAGACAATGGACCCACGTTAGGTGTGACACGTT
CACATAACTGTGCAGCACATGCCGGGAGTGATCAGCCGGACATTTTAATTTGAACCATGTATCTCTGGGTAGCTA
CAAAATTCCTCAGGGATTTCATTTTGCAGGCATGTCTCTGAGCTTCTATACCTACTCAAGGTCAGTGTCATCTTT
GTGTTTAGTTCATCCAAAGGTGTTACCCTGGTTTCAATGAACCTAACCTCATTATTTGTGTCTTCAGTGTTGGCT
TGTTTTAGCTGATCCATCTGTAACACAGGAGGGATCCTTGGCTGAGGATTGTATTTCAGAACCACCAACTGCTCT
TGACAATTGTTAACCCGCTAGGCTCCTTTGGTTAGAGAAGCCACAGTCCTTCAGCCTCCAATTGGTGTCAGTACT
TAGGAAGACCACAGCTAGATGGACAAACAGCATTGGGAGGCCTTAGCCCTGCTCCTCTCAATTCCATCCTGTAGA
GAACAGGAGTCAGGAGCCGCTGGCAGGAGACAGCATGTCACCCAGGACTCTGCCGGTGCAGAATATGAGCAATGC
CATGTTCTTGCAGAAAACGCTTAGCCTGAGTTTCATAGGAGGTAATCACCAGACAACTGCAGAATGTAGAACACT
GAGCAGGACAACTGACCTGTCTCCTTCACATAGTCCATATCACCACAAATCACACAACAAAAAGGAGAAGAGATA

FIGURE 324B

TTTTGGGTTGAAAAAAAGTAAAAAGATAATTAGCTGCATTTCTTTAGTTATTTTGAACCCCAAATATTTCCTCAT
CTTTTTGTTGTTGTCATTGATGGTGGTGACATGGACTTGTTTATAGAGGACAGGTCAGCTCTCTGGCTCAATGAT
CTACATTCTGAAGTTGTCTGAAAATGTCTTCATGATTAAATTCAGCCTAAACTTTTTGCTGGGAACACTGCAGAG
ACAATGCTGTGAGTTTCCAACCTCAGCCCATCTGCGGGCAGAGAAGGTCTAGTTTGTCCATCACCATTATGATAT
CAGGACTGGTTACTTGGTTAAGGAGGGGTCTAGGAGATCTGTCCCTTTTAGAGACACCTTACTTATAATGAAGTA
CTTGGGAAAGCGGTTTTCAAGAGTATAAATATCCTGTATTCTAATGATCATCCTCTAAACATTTTATCATTTATT
AATCCTCCCTGCCTGTGTCTATTATTATATACATATCTCTACGCTGCAAATTTTGGGTCTCAATTTTTACTGTGC
CTTTGTTTTTACTAGTGTCTGCTGTTGCAAAAAGAAGAAAACATTCTCTGCCTGAGTTTTAATTTTTGTCCAAAG
TTAATTTTAATCTATACAATTAAAACCTTTTGCCTATC

FIGURE 325

MLRNELQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLNEHLQALLTPDEPDKSQGQDL
QEQLAEGCRLAQHLVQKLSPENDNDDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCSNSHGPYD
SNQPHRKTKITFEEDKVDSTLIGSSSHVEWEDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEGY
STLSIPPERTSVGSSEKGGPRGNRSQAQQGAAG

FIGURE 326

CTCCGCGGTCTTCTGAGCGGTCACGTGAACGGCTTCCTGCAGGCTGGCCATGGCGCTTCAAGTTCCCAAGGCTCC
GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAGAAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAATTCTGGG
CTGTGGTATCACTTCCTCTTCAGTATTGCATGGCATGGTTTTTAAGAAGGAAACAGAAGGTGATGTACATCTGTC
AAAGATGCAAAAATAGCAGTGTACTCTTGTCCTTTTGATGGCATGATAACAGAAACTAAGGGAACAGTGTTGATA
AAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGTCAAAGCTATTGCT
GATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAACAAATATAAT
ATGATGTTAGTGAAGCTAAACTCAAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGCTACAGCTCTTCCT
AGATTGACACCTCCTGTCCTTGAAGAAATGGGACACTGAGACAGTGTTTACCTCTCAGAAGTTGGAGATACTCAG
GTGGTGGTTTTTAAGCATGAAAAGGAAGATGGCATCATTTCTACCATAGTACTTCAGGGCTCTACAGACAATCTG
ATGGATGACATAGAAAGGGCAGTAGATGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTA
CCCGGAGGTGGAGCAACAGAAATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCCTGGACTTGAA
CAGTACGCTATTAAGAAGTTTGCTGAGGCGTTTGAAGCTATTCCCCGTGCACTGGCAGAAATACTCTGGAGAAAA
CTCTGGAGTTAAGGCCAATGAAGTAATCTCTAAACTTTATGCAGTACCTCAAGAAGGAAATAAAAATGTTGGATT
AGATACTGAGGCTGTAGTCCCTGCTGTAACGGACATGTTGGAAGCTGGTGTTCTAGATACTTACCTGGGAAAACA
CTGGTCTATCAAACTCGCTGCTAATGCTGCAGTCACTGTACTTAGAGTGGGTCAGGTAATCATGGCAAAACCAGA
TGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGACTGGGATGATGACCAAAATGATTGAAATTGGCTTAATTTTTA
CTGTAGGTGAAGGCTGTATTTGTAGTAGTATTCTAAGAATCGCGTGATGTTTTCTTATTCTCCTTACATTAAGAG
GTATTTTGTGTTTGTATTCTTGGCTGGATGTTATAATAAACATATTGTTACTGTC

FIGURE 327

GGGCTTCGCCCAGATGCTCAAGGAGGGAGCGAAACACTTTTCAGAATTAGAAGAGGCTGTGTATAGAAACATACA
AGCTTGCAAGGAGCTTGCCCAAACCACTCGTACAGCATATGGACGAAATGGAATGAAAAAAATGGTTATCAACTA
CTTGGAGAAGTTGTTTGTGACAAATGATGCAGCGACTATTTTAAGAGAACTAGAAGTACAGCATCCTGCTGCAAA
AATGACTGTAATGGCTTCTCATATGCAAGAGCAAGAAGTTGGAGATGGCACAAACATTGTTCTGGTATTTGCTGG
AGCTCTCCTGGAATTAGCTGAAGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAAT
AGCTTGCAGAAAAGCTCATGAGATTCTTCCTAATTTGGTACGTTGTTCTGCAAAAAACCTTCGAGATGTTGATGA
AGTCTCATCTCTACTTCGTACCTCTGTAATGTGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGT
TCAGGCATGCGTATCTATTTTTCCTGATTCTGGCCATTTCAAAGTTGATAACATCAGAGTTTGTAAAATTCTGGG
AACAGTGTTGATAAAGACTGATGAAGAATTGATGAATTTAAGTAAGGGAGAAGAAAATCTCATGGATGCATAAGT
CAAAGCTATTGCTGATACTGGTGCAAATGTTGTAGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGC
AAACAAATATAATATGATGTTAGTGAAGCTAAACTCAAAATGGGATGTCTGAAGACTCTGTAAAACAGTTGGTGC
TACAGCTCTTCCTAGATTGACACCTCCTGTCCTTG

FIGURE 328

GTGGGTAGGAGCTTGCTTATAGAAAAGTGGAATCGAGTAGTCCTTGCTGGTGGAGCCGCTGCCGCCAGGGAACTC
AGGGCCGGCTCCTGTTCCTTCAAGAGTGCTGGAGGCCAAACTTGAAATACAAGTTTAATGTTCCTCGTCGGGCAA
AAGATAAGGATCCGATCTCCCCCGGCCCGGTGTGCAGCAGGAGCGACCAACCCCGACCCGGGTTAAAACTCCCAG
GGACTCTTCGCTGCTGCCACCTCTTGTTCTCTCCCCCGTTCCCACTCGGGGTCTCCCTCAGGGCCGGGAGGCACA
GCGGTCCCTGCTTGCTGAGGGGCTGGATGTACGCATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCC
CGGCGCCCGCAGAAGACTTGTGTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACC**ATG**ATC
ACTGGTGTGTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACCAGCGG
CGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGCCTGCTGAAGTTGAAAATG
GTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCCGCTCCCGCTGGAGGAGCAGGTAGAGTGGAAC
CCCCAGCTATTAGAGGTCCCACCCCAAACTCAGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCA
TATTCTCCTTACGACTCTCAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTG
GGCATGCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTCTTTCACCA
ACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTGGAGTCCACCCGTTGTTTGCTG
GCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCATCCACACTGATGAAGCAGATTCAGAAGTCTTGTAT
CCCAACTACCAAAGCTGCTGGAGCCTGAGGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGA
ATCTCAGAGGATTTGAAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTC
CTGGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTGCACGGATGATC
GAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGCAGTAGGC
CCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAG
CTGTATCTCTATGCGGCTCATGATGTGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGG
CCACCGTTTGCTGTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTAT
TACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGTTCTTGAATGCCATG
TCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAAACTCAGGTGATGGAAGTTGGAAATGAA
GAG**TAA**CTGATTTATAAAAGCAGGATGTGTTGATTTTAAAATAAAGTGCCTTTATACAATGCCAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 329

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQVE
WNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQ
PGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEWFVQ
LYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

FIGURE 330

CTTAAAGTGAAATAATTTTTTGCAAAGGGGTTTCCTCGATTTGGAGCTTTTTTTTTCTTCCACCGTCATTTCTAA
CTCTTAAAACCAACTCAGTTCCATCATGGTGATGTTCAAGAAGATCAAGTCTTTTGAGGTGGTCTTTAACGACCC
TGAAAAGGTGTACGGCAGTGGCGAGAAGGTGGCTGGCCGGGTGATAGTGGAGGTGTGTGAAGTTACTCGTGTCAA
AGCCGTTAGGATCCTGGCTTGCGGAGTGGCTAAAGTGCATCCTCAACAACAATGTGCAGTGAGCATGTGGAAGAA
AAGAAGCAGCTTTACCTACTTGTTTCTTTTTGTCTCTCTTCCTGGACACTCACTTTTTCAGAGACTCAACAGTCT
CTGCAATGGAGTGTGGGTCCACCTTAGCCTCTGACTTCCTAATGTAGGAGGTGGTCAGCAGGCAATCTCCTGGGC
CTTAAAGGATGCGGACTCATCCTCAGCCAGCGCCCATGTTGTGATACAGGGGTGTTTGTTGGATGGGTTTAAAAA
TAACTAGAAAAACTCAGGCCCATCCATTTTCTCAGATCTCCTTGAAAATTGAGGCCTTTTCGATAGTTTCGGGTC
AGGTAAAAATGGCCTCCTGGCGTAAGCTTTTCAAGGTTTTTTGGAGGCTTTTTGTAAATTGTGATAGGAACTTTG
GACCTTGAACTTATGTATCATGTGGAGAAGAGCCAATTTAACAAACTAGGAAGATGAAAAGGGAAATTGTGGCCA
AAACTTTGGGAAAA

FIGURE 331

TGACTTGCTCACTATCATGAACTCAAAAGAAACTAGCAATTTTTTAGACTTCTTTTGGGATCCTTGTACCGCATC
CTATACTGCTTTTATGTTCATGTGTGCATTTGTGTACATGTATACACATATTACTCCATAACGAAGCACAGTCTT
CTTTTATACCTTTCCTGGTTGGGGTAGTAGAGGAATTTTACAGCCTACAATCAGACACATCCAGAAGAAGAGTGG
AATATGTATGATACCTTAAAAATCAGCACATTTAACAAAGTATAACTTACTCATGGTTACAACTAAGTTAATGTT
TTTTCCCTTTATTTTTCAAAAGGCTCATTTTTCTCCATTTCTCTACTATCAAAGTCAAGAACTGCCCAATGGCTC
TGTCAAGGAGGCTCCAGCTCCTACTCCCACTTCTCTGGAAGTCTCAAGTCCACCAGATACTACAGAGGAAGAAGA
TCATAAGCCTAAACTCTGCAGGCTGGCTAAAGGTGAAAATGGCTATGGCTTTCACTTAAATGCGATTCGGGGTCT
GCCAGGCTCATTCATCAAAGAGGTACAGAAGGGCGGTCCTGCTGACTTGGCTGGGCTAGAGGATGAGGATGTCAT
CATTGAAGTGAATGGGGTGAATGTGCTAGATGAACCCTATGAGAAGGTGGTGGATAGAATCCAGAGCAGTGGGAA
GAATGTCACACTTCTAGTCTGTGGAAAGAAGGCCTATGATTATTTCCAAGCTAAGAAAATCCCTATTGTTTCCTC
CCTGGCTGATCCACTTGACACCCCTCCAGATTCTAAAGAAGGAATAGTGGTGGAGTCAAAGCATGACTCGCACAT
GGCAAAAGAACGGGCCCACAGTACAGCCTCACATTCTTCTTCCAATTCTGAAGATACAGAGATGTGATGAAAACA
AGCGGCTATTGCAGACGGCTAATTTATGCTTAACTTAGGAAGAGATAAGGTTCCTTGAGCACCAAAGATGATTCA
TAACTCTGTATAGGTGACAGCTGCTTATAAAAGCATCTTAGCAGATAAGCCTATTAAAATTGTGCTTTTGTAACA
ATGTTGTGGTTGCTAGAATAAATACCATTAACAAA

FIGURE 332

GTCCCAACTCTTGGACTCCATTTGCTATTCTCTTCTTTCTCCCCCACACCTATCTGGTGGTGGTAGTGGGCGTTT
ATATTTGCGTTCCTTTTCATTCATTTCTAAATCTCTTAAAAATTTTGGGTTGGGGGTATTGGGGAAGGCAGGAAA
GGGAAAAGGAGAGTAGTAGCTGAAGAGCAAGAGGAGGAC**ATG**GAGATGAAGAAGAAGATTAACCTGGAGTTAAGG
AACAGATCCCCGGAGGAGGTGACAGAGTTAGTCCTTGATAATTGCCTGTGTGTCAATGGGGAAATTGAAGGCCTG
AATGATACTTTCAAAGAACTAGAATTTCTGAGTATGGCTAATGTGGAACTAAGTTCGCTGGCCCGGCTTCCCAGC
TTAAATAAACTTCGAAAATTGGAGCTTAGTGATAATATAATTTCTGGAGGCTTGGAAGTCCTGGCAGAGAAATGT
CCAAATCTTACCTACCTCAATCTGAGTGGAAACAAAATAAAAGATCTCAGTACAGTAGAAGCTCTGCAAAATCTT
AAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAGATCACAAACCTGGAAGATTATAGAGAAAGTATTTTTGAA
CTACTGCAGCAAATCACATACTTAGATGGATTTGATCAGGAGGATAATGAAGCGCCGGACTCTGAAGAGGAGGAT
GATGAGGATGGAGATGAAGATGATGAAGAGGAAGAGGAAAATGAAGCTGGTCCACCGGAAGGATATGAGGAAGAG
GAGGAGGAAGAGGAAGAGGAGGATGAGGATGAGGATGAAGATGAAGATGAAGCAGGTTCAGAGTTGGGAGAGGGA
GAAGAGGAAGTGGGCCTCTCATACTTAATGAAAGAAGAAATTCAGGATGAAGAAGATGATGATGACTATGTTGAA
GAAGGGGAAGAAGAGGAAGAAGAGGAAGAAGGAGGTCTTCGAGGGGAGAAGAGGAAACGAGATGCTGAAGACGAT
GGAGAGGAAGAAGATGAC**TAG**ATCATTCTAAGACCAGATTCTCTAATGTTTCTGGGTGTGCAATAGAGTGATCAC
ATCTTTGTTTCTTCATGTACGATAGCTATCCCTACAGAAGATAATGTGTAACTTTTTATAGGAAAAGTGTGGTTT
TACTATTTTTGCCTTATCATTCCAAATAAGAACTAGTCTGTTAATGATCATATTGTATGTAGAGAAAAATTTTCA
TTGACTCCCATTGTGGAATTCCCTAGCAATTTATTTAGACTTAATTTTTTAAATTCAAGCTTACTGTATTAGTCA
TTTTTAGCCCATAATTAAAACATGATCACTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 333

MEMKKKINLELRNRSPEEVTELVLDNCLCVNGEIEGLNDTFKELEFLSMANVELSSLARLPSLNKLRKLELSDNI
ISGGLEVLAEKCPNLTYLNLSGNKIKDLSTVEALQNLKNLKSLDLFNCEITNLEDYRESIFELLQQITYLDGFDQ
EDNEAPDSEEEDDEDGDEDDEEEEENEAGPPEGYEEEEEEEEEDEDEDEDEDEAGSELGEGEEEVGLSYLMKEE
IQDEEDDDDYVEEGEEEEEEEEGGLRGEKRKRDAEDDGEEEDD

FIGURE 334

GTGGGGTCGCGTTGCCACCCCACGCGGACTCCCCAGCTGGCGCGCCCCTCCCATTTGCCTGTCCTGGTCAGGCCC
CCACCCCCCTTCCCACCTGACCAGCC**ATG**GGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGG
CCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCATTTTTCT
GGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGACCGACCGGTCAGATGCCCGGC
TCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACA
AGCTGCTTAAGAAGGCAGATGAGGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGA
TGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCAC
TTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCTATTACTTCCTGACTTCAGCCTTTCTGACAGCAGCCA
TTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGAGGAGACGGTACTGGGCTTTGGGCC
TGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCA
TCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCA
GCTCTTGTGTAAGGACTGACTACCTGGAC**TGA**TCGCCTGACAGATCCCACCTGCCTGTCCACTGCCCATGACTGA
GCCCAGCCCCAGCCCGGGGTCCATTGCCCACATTCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGG
TTTTGCTTTGTCCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAGCAGCCTGGGTTCAGCCAGTCAGTGACT
GGTGGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCCTTGTTGTGTCCAGGACTCCCCCTGTGTCAGT
GCTCTGCTCTCACCCTGCCCAAGACTCACCTCCCTTCCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGCCTGGGGTGCCCTC
CTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAGGTTGCCAAGAAAAGGGACCTAGTTTA
GCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGA
CTGGACATCTTGGTCTTTTTCTCAGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCTAAACTGCCTTTT
TTTCTTTTTTGAGGTGGGGGGAGGGAGGAGGTATATTGGAACTCTTCTAACCTCCTTGGGCTATATTTTCTCTCC
TCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAA
GTGCATGTTTGGGAACTGGCATTACTGGAACTAATGGTTTTAACCTCCTTAACCACCAGCATCCCTCCTCTCCCC
AAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCAT
GACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTAT
AAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACTAATAAA
AAAGAATTTGTAAAAAA

FIGURE 335

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIH
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSSCVRTDYLD

FIGURE 336

TTCCGGTGGGCTAGGTACTGAGCGCGCGAGGCTCTACAGAGTGAAGGTTTAAATCCAAGGTC**ATG**GCAAAACATC
TGAAGTTCATCGCCAGGACTGTGATGGTACAGGAAGGGAACGTGGAAAGCGCATACAGGACCCTAAACAGAATCC
TCACTATGGATGGGCTCATTGAGGACATTAAGCATCGGCGGTATTATGAGAAGCCATGCCGCCGGCGACAGAGGG
AAAGCTATGAAAGGTGCCGGCGGATCTACAACATGGAAATGGCTCGCAAGATCAACTTCTTGATGCGAAAGAATC
GGGCAGATCCGTGGCAGGGCTGC**TGA**GGCCTGTGGGTGGGACACCCAGTGCGAAACCCTCATCCAGTTTTCTCTC
CATCTCTTTTCTTTGTACAATCCCATTTCCTATTACCATTCTCTGCAATAAACTCAAATCACATGTCTGCAAAAA

FIGURE 337

MAKHLKFIARTVMVQEGNVESAYRTLNRILTMDGLIEDIKHRRYYEKPCRRRQRESYERCRRIYNMEMARKINFL
MRKNRADPWQGC

DEMANDE OU BREVET VOLUMINEUX

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