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Compounds for immunotherapy of prostate cancer and methods for their use

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| (54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE                                                                                                                                                                                                                                                                                                                                                               |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |
| (57) Abstract<br><p>Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.</p> |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |

COMPOUNDS FOR IMMUNOTHERAPY  
OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

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Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### Example I

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of  $H_2O$ , heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l  $H_2O$  to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l  $H_2O$ . Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68  $^{\circ}C$  water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l  $H_2O$ , mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68  $^{\circ}C$  for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR  
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

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of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### Example 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

The reference to any prior art in this specification is not, and should not be taken as, an acknowledgment or any form of suggestion that that prior art forms part of the common general knowledge in Australia.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun  
Dillin, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER  
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SEED and BERRY LLP
  - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 23-FEB-1998
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Maki, David J.
  - (B) REGISTRATION NUMBER: 31,392
  - (C) REFERENCE/DOCKET NUMBER: 210121.427C3
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

|                                                                   |     |
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| ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACCTC CCCCCATAGT GAATCAGCTT | 120 |
| CCAGGGGGTC CAGTCCCTCT CTTACTTCA TCCCCATCCC ATGCCAAAGG AAGACCCCTCC | 180 |
| CTCCTTGGCT CACAGCCTTC TCTAGGCTTC CCAGTGCCTC CAGGACAGAG TGGGTTATGT | 240 |
| TTTCAGCTCC ATCCTTGCTG TGAGTGTCTG GTGCGTTGTG CCTCCAGCTT CTGCTCAGTG | 300 |
| CTTCATGGAC AGTGTCCAGC ACATGTCACT CTCCACTCTC TCAGTGTGGA TCCACTAGTT | 360 |
| CTAGAGCGGC CGCCACCGCG GTGGAGCTCC AGCTTTGTGT CCCTTTAGTG AGGGTTAATT | 420 |

GCGCGCTTGG CGTAATCATG GTCATAACTG TTTCTGTGT GAAATTGTTA TCCGCTCACA 480  
ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAG CCTGGGGTGC CTAATGAGTG 540  
ANCTAACTCA CATTAAATTGC GTTGGCGTCA CTGNCCGCTT TCCAGTCNGG AAAACTGTGC 600  
TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCGGGGAAAA GCGGTTTGGC TTTGGGGGC 660  
TCTTCCGCTT CTCGCTCACT NANTCCTGCG CTCGGTCNTT CCGCTGCGGG GAACGGTATC 720  
ACTCCTCAAA GGNNGTATTA CGGTTATCCN NAAATCNGGG GATACCCNGG AAAAAANTTT 780  
AACAAAAGGG CANCAAAGGG CNGAACGTA AAAA 814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

ACAGAAATGT TGGATGGTGG AGCACCTTTC TATACGACTT ACAGGACAGC AGATGGGGAA 60  
TTTCATGGCTG TTGSAGCAAT AGAACCCAG TTCTACGAGC TGCTGATCAA AGGACTTGGA 120  
CTAAAGTCTG ATGAACCTCC CAATCAGATG AGCATGGATG ATTGGCCAGA AATGAAGAAG 180  
AAGTTTGAGC ATGTATTTGC AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC 240  
ACAGATGCCT GTGTGACTCC GGTTCGACT TTTGAGGAGG TTGTTCACTA TGATCACAAC 300  
AAGGAACGGG GCTCGTTTAT CACCAGTGAG GAGCAGGACG TGAGCCCCCG CCTGCACTC 360  
CTGCTGTAA ACACCCAGC CATCCCTTCT TTCAAAAGG ATCCACTAGT TCTAGAAGCG 420  
GCGGCCACCG CGGTGGAGCT CCAGCTTTTG TTCCTTTAG TGAGGGTTAA TTGCGCGCTT 480  
GGCGTAATCA TGGTCATAGC TGTTCTCTGT GTGAAATTGT TATCCGCTCA CAATTCCCCC 540  
AACATACGAG CCGGAACATA AAGTGTTAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN 600  
CATTAAATGC GTTGGCGTCA CTGCCCCGCTT TCCAGTCGGG AAAACTGTGC TGCCACTGCN 660  
TTANTGAATC NGCCACCCCC CGGGAAAAGG CGGTTGCNTT TTGGGCTCT TCGCTTTCC 720  
TCGCTCATG ATCCTNGCNC CCGGTCTTCG GCTGCGNGA ACGGTTCACT CCTCAAAGGC 780  
GGTNTNCCGG TTATCCCCAA ACNGGGGATA CCCNGA 816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

CTTTTGAAG AAGGGATGCG TGGGTGTTT AACAGCAGAG GTGCAGGGCG GGGGCTCAG 60  
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TCCTCAAAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCAC 180  
TCTGCTTCG TCTTCTTTGC AAATACATCT GCAAACCTCT TCTTCATTTC TGGCCAATCA 240  
TCCATGCTCA TCTGATTGGG AAGTTCACTA GACTTTAGTC CANNCTCTT GATCAGCAGC 300  
TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAAT CCCCCTCTGC TGCTCTGTAA 360  
GTGCTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTCGAGGGGG GGGCCGGTAC 420  
CCAATTGCGC CTATANTGAG TCGTATTACG CGCGCTCACT GCGCGTCGTT TTACAACGTC 480  
GTGACTGGGA AAACCTGGG CGTTACCAAC TTAATCGCCT TGCAGCATAT CCCCCTTTCG 540  
CCAGCTGGGC GTAATANCGA AAAGGCCCGC ACCGATCGCC CTTCCAACAG TTGCGCACCT 600  
GAATGGGNAA ATGGGACCCC CCGTTACCG CGCATTNAAC CCCCNGGGG TTTNGTTGTT 660  
ACCCCAACNT NNACCGCTTA CACTTTGCCA GCGCCTTANC GCGCGCTCCC TTTNCCTTT 720  
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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

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CCTCCTGAGT CCTACTGACC TGTGCTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG      60
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TCGGAACACT GGCTGTCTCT GAAGACTTCT CGCTCAGTTT CAGTGAGGAC ACACACAAAG      180
ACGTGGGTGA CCAATGTTGTT TGTGGGTGC AGAGATGGGA GGGGTGGGCG CCACCTGGA      240
AGAGTGGACA GTGACACAAG GTGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC      300
ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGTGTCTCT      360
GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAAG AAGGGGAGGA TCCACTAGTT      420
CTANAGCGCG CGCCACGCGG GTGGANCTCC ANCTTTTGT CCCTTTAGTG AGGGTTAATT      480
GCGCGCTTGG CNTAATCATG GTCATANCTN TTTCTGTGT GAAATTGTTA TCCGCTCACA      540
ATTCCACACA ACATACGANC CGGAAACATA AANTGTAAAC CTGGGGTGCC TAATGANTGA      600
CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAATCNGGAA ACCTGTCTTG      660
CCNCTTGCAAT TNATGAATCN GCCAACCCCC GGGGAAAAGC GTTTGCGTTT TGGGCGCTCT      720
TCGCTTCCTT CNCTCANTTA NTCCCTNCNC TCGGTCATTC CGGTGTCNGC AAACCGGTTT      780
ACCNCTCCA AAGGGGTAT TCCGGTTTCC CCNAATCCGG GGANANCC      828

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## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

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TTTTTTTTT TTTTACTGA TAGATGGAAT TTATTAAGCT TTTACATGT GATAGCACAT      60
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ATTTTATAAC AATCAACACC TGTGGCTTTT AAAATTGTTT TTTATAAGA TAATTTATAC      180
TGAAGTAAAT CTAGCCATGC TTTTAAAAAA TGCTTTAGGT CACTCCAAGC TTGGCAGTTA      240
ACATTTGGCA TAAACAATAA TAAACAATC ACAATTTAAT AAATAACAAA TACAACATTG      300
TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG      360
AATAGAATAC CTTGGCCTCT ATGCAAAATAT GTCTAGACAC TTTGATTAC TCAGCCCTGA      420
CATTCAGTTT TCAAGTAGG AGACAGGTTT TACAGTATCA TTTTACAGTT TCCAACACAT      480
TGAAAACAAG TAGAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA      540
TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTGCTGTGTC      600
TTATTTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT      660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTTGA ACTGGAACAT      720
TGNATNACAG TGTTCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA      780
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## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

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TGTAAGTGA AATATTAGTT GCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT      180
GACGTGAAGT CCGTGGAAGC CTGTGGCTAC AAAAAATGTT GAGCCGTAGA TGCCGTCGGA      240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGTTAAAT AGAGACCCAG      300
TAAATTTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG      360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC      420
TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCCIA GTTGGGGGGT      480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCCAAGAAAA AAACCTTCTGA      540
GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC      600
TTGGTATGTG CTTTCTCGTG TTACATCCCG CCATCATTTG TATATGGTTA GTGTGTTGGG      660
TTANTANGGC CTANTATGAA GAACCTTTGG ANTGGAAATTA AATCAATNGC TTGGCCGGAA      720
GTCAATANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTTA CCNACCCAT      780
GGAATNCNC CCCCGACNA NTGNATCCCT ATTCTTAA      818
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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

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CGGGCCCTAT TTCAAAGATT TTAGGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT      120
GGTTTGCTCC ACAGATTTC AAGCATTGAC CGTAGTATAC CCCCGGTCGT GTAGCGGTGA      180
AAGTGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG      240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGGCT TCAATCGGGA      300
GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGCTCGCC TGGTTCTAGG AATAATGGGG      360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC      420
ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT TGAACCTCGT TGTATGTAA      480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT      540
TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTTNGTTATT      600
GAATNTTNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG      660
CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCACNCNN      720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCNC CTTTTGTTCC      780
CTTNANTGAN GGTATTTCNC CCCTNGCNTT ATCANCC      817
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```
CATTTCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG      60
CATAAGGAGA ACTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT      120
```

CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG 180  
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCTGGGG 240  
TGGGTGGCCG ANGCTGANC CGCTCTGCCT TGCTGCCCCC ANGTTGGGCG CCACCCCTG 300  
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCACANGG 360  
GGATTTTGCT CCTANANTAA GGCTCATCTG GGCTCGGCC CCCCCACCTG GTTGGCCTTG 420  
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCTG GACCACCTT NGGGAGTGT 480  
CTCCTTACAA CCACANNATG CCGGCTCCT CCGGAAACC ANTCCANCC TNGAAGGAT 540  
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGAACC CACCTTNTGT 600  
TCCTTTTNT TNAGGGTTAA TNNCGCCTTG GCCTNCCAN NGTCCTNCNC NTTTTCCNNT 660  
GTTNAAATG TTANGCNCCC NCCNNTCCN CNMNCNAN CCGACCCNN ANNTTNANN 720  
NCCTGGGGT NCCNCCNGAT TGACCCNCC NCCCTNTANT TGCNTTNGG NNCNNTGCC 780  
CTTTCCTCT NGGGANNC 799

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

ACGCCTTGAT CTTCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG 60  
TAANGATGAC ACTCCCAAAG GTGTCCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT 120  
CAAGGACAAG GCCACCAAGT GCGGGGGCCG AAGCCACAT GATCCTTACT CTATGAGCAA 180  
AATCCCCTGT GGGGGCTTCT CTTGAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG 240  
CAGGTCATGG GGTGTGNGC CAACTGGGG CCNCAACGCA AAANGGCNCA GGGCCTCNGN 300  
CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG 360  
TTCNTACCCG CGNATNTGTC CCANCTGTTT CNGTGCCNAC TCCANCTTCT NGGACGTGCG 420  
CTACATACGC CCGANTCNC NCTCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATTT 480  
CNCNTANTG CACCNATTC CACNTTTNNC AGNTTCCNC NNCNGGCTTC CTNTAAAAG 540  
GGTTGANCCC CGGAAAATNC CCCAAAGGG GGGGGCCNGG TACCCAACN CCCCCTNATA 600  
GCTGAANTCC CCATNACCNN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT 660  
GGGAANANCC CTCGNCNTN CCCCNTTAA TCCNCCTTG CNANGNNCNT CCCCNNNTCC 720  
NCCCNNTNG GCNTNTNANN CNAAAAGGC CCNNANCAA TCTCCTNNCN CCTCANTTCG 780  
CCANCCCTCG AAATCGGCCN C 801

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

CAGTCTATNT GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC 60  
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCTCACCAG GTTCACCTTC TCAGCCCTGC 120  
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCCTGCCCA 180  
AATACCGAGG GGACACTGGA GTGTCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCTGC 240  
CAGGCCCTAA GCCTGGAGCT CCCTTCCTA ATGGACACGT GGGTCTGGA GGCAGTGGCC 300  
TGCTCCACCC TCCACCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG 360  
TGGTGGGTGA GCCCACCAGN GCCAGGGTGG TTCCGGGCGG GGGCATCTGC CTGGACCTCG 420  
CCATCCTGGA TAGTGCTTCC TGCTGTCCCA NGTGGCCCCA TCCCTGTTA TGGGCTCCAT 480  
TGTCAGCTC AGCCAGTCTG TCACTGCCTA TATGTGTCT GCCGACGGC TGGGTCTGGT 540

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CCCATTACT  | TTGCTACACA | GGTANTATTT | GACAAGAACG | ANTTGGCCAA | ATACTCAGCG | 600 |
| TTAAAAAATT | CCAGCAACAT | TGGGGGTGGA | AGGCCTGCCT | CACTGGGTCC | AATCCCCGC  | 650 |
| TCCTGTAAAC | CCCATGGGGC | TGCCGGCTTG | GCCGCCAATT | TCTGTTGCTG | CCAAANTNAT | 720 |
| GTGGCTCTCT | GCTGCCACCT | GTGCTGGCT  | GAAGTGCNTA | CNGCNCANCT | NGGGGGGTNG | 780 |
| GGNGTTCCC  |            |            |            |            |            | 789 |

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| CCCACCTAC  | CCAAATATTA  | GACACCAACA | CAGAAAAGCT | AGCAATGGAT | TCCCTTCTAC  | 60  |
| TTTGTAAAT  | AAATAAGTTA  | AATATTTAAA | TGCCTGTGTC | TCTGTGATGG | CAACAGAAGG  | 120 |
| ACCAACAGGC | CACATCTGA   | TAAAAGGTAA | GAGGGGGGTG | GATCAGCAAA | AAGACAGTGC  | 180 |
| TGTGGGCTGA | GGGGACCTGG  | TTCTTGTGTG | TTGCCCTCA  | GGACTCTTCC | CCTACAAATA  | 240 |
| ACTTTCATAT | GTTCAAATCC  | CATGGAGGAG | TGTTTCATCC | TAGAAACTCC | CATGCAGAGAG | 300 |
| CTACATTAA  | CGAAGCTGCA  | GGTTAAGGGG | CTTANAGATG | GGAAACCAGG | TGACTGAGTT  | 360 |
| TATTCAGCTC | CCAAAAACCC  | TTCTCTAGGT | GTGTCTCAAC | TAGGAGGCTA | GCTGTTAAACC | 420 |
| CTGAGCCTGG | GTAATCCACC  | TGCAGAGTCC | CCGCATTCCA | GTGCATGGAA | CCCTTCTGGC  | 480 |
| CTCCCTGTAT | AAGTCCAGAC  | TGAAACCCCC | TTGGAAGGNC | TCCAGTCAGG | CAGCCCTANA  | 540 |
| AACTGGGGAA | AAAAGAAAAG  | GACGCCCCAN | CCCCCAGCTG | TGCANCTACG | CACCTCAACA  | 600 |
| GCACAGGGTG | GCAGCAAAAA  | AACCACCTTA | CTTTGGCACA | AACAAAAACT | NGGGGGGGCA  | 660 |
| ACCCCGGCAC | CCCNANGGGG  | GTAAACAGGA | ANCNGGGNAA | CNTGGAACCC | AATTNAGGCA  | 720 |
| GGCCCNCCAC | CCCNAAATNTT | GCTGGGAAAT | TTTCTCTCCC | CTAAATNTTT | TC          | 772 |

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GCCCCAATTC | CAGCTGCCAC  | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTACATACAA | 60  |
| AGCTGATTGA | AGCAACCTTC  | TACTTTTGG  | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT  | GTCAATTGCA | CAGAAATGGG | GAAAGGCACT | GTTCTCTTTG | 180 |
| AAGTANGGTG | AGTCCTCAAA  | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGGTGT | TCCACACTTG  | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG  | GGAAGTGCTC | AGCCATTGTG | GTGTACACCA | AGGCGACCAC | 360 |
| AGCAGCTGCN | ACCTCAGCAA  | TGAAGATGAN | GAGGANGATG | AAGAAGAAGC | TCNCGAGGCG | 420 |
| ACACTTGCTC | TCAGTCTTAN  | CACCATANCA | GCCCNTGAAA | ACCAANANCA | AAGACCACNA | 480 |
| CNCCGGCTGC | GATGAAGAAA  | TNACCCCNCG | TTGACAAACT | TGCATGGCAC | TGGGANCCAC | 540 |
| AGTGGCCCN  | AAAATCTTCA  | AAAAGGATGC | CCCATCNATT | GACCCCCCAA | ATGCCCACTG | 600 |
| CCAACAGGGG | CTGCCCCACN  | CNCNNAACGA | TGANCCNATT | GNACAAGATC | TNCNTGGTCT | 660 |
| TNATNAACNT | GAACCCCTGCN | TNGTGGCTCC | TGTTCAGGNC | CNNGGCCTGA | CTTCTNAANN | 720 |
| AANGAACTCN | GAAGNCCCA   | CNGGANANNC | G          |            |            | 751 |

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```
GAGCCAGGCG TCCCTCTGCC TGCCCACTCA GTGGCAACAC CCGGAGCTG TTTTGTCTT 60
TGTGGANCTT CAGCAGTNCC CTCTTTTCTA ACTCANTGCC AAGANCCCTG AACAGGAGCC 120
ACCATGCAGT GCTTCAGCTT CATTAAGACC ATGATGATCC TCTTCAATTT GCTCATCTTT 180
CTGTGTGGTG CAGCCCTGTT GGCAGTGGGC ATCTGGGTGT CAATCGATGG GGCATCCTTT 240
CTGAAGATCT TCGGGCCACT GTCGTCCAGT GCCATGCAGT TTGTCAACGT GGGCTACTTC 300
CTCATCGCAG CCGGCGTTGT GGTCTTAGCT CTAGGTTTCC TGGGCTGCTA TGGTGCTAAG 360
ACTGAGAGCA AGTGTGCCCT CGTGACGTTT TTCTTCATCC TCCTCCTCAT CTTCATTGCT 420
GAGGTTGCAA TGCTGTGGTC GCCTTGGTGT ACACCACAAT GCGTGAGCAC TTCCTGACGT 480
TGCTGGTAAT GCGTGCCATC AANAAAAGAT TATGGGTTCC CAGGAANACT TCACTCAAGT 540
GTTGGAACAC CACCATGAAA GGGCTCAAGT GCTGTGGCTT CNCCAACTA TACGGATTTT 600
GAAGANTCAC CTACTTCAA GAAAANAGTG CCTTCCCCC ATTTCTGTTG CAATTGACAA 660
ACGTCCCAA CACAGCCAAT TGAAAACCTG CACCAACCC AAANGGGTCC CCAACCANAA 720
ATTNAAGGG 729
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```
TGCTCTTCTT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG 60
TGTTGCTGTA AGGGGTTGTA GTACCAAGCG GGGATGCTCT CCTTGACAGT TCCTGTGTCT 120
GGCAGGTCCA CGCAGTGCCC TTTGTCACTG GGGAAATGGA TCCGCTGGAG CTCGTCAAAG 180
CCACTCGTGT ATTTTTCACA GGCAGCCTCG TCCGACGCGT CCGGGCAGTT GGGGTGTCT 240
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGGCTGA 300
CANGTGCCAG AGCACACTGG ATGGCGCCTT TCCATGMNAN GGGCCCTGNG GGAAAGTCCC 360
TGANCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACA CCGGACAGG CTAGAATGGA 420
ATCTTCTTCC CGAAAGGTAG TTNTTCTGT TGCCCAANCC ANCCCNATAA ACAAACTCTT 480
GCANATCTGC TCCGNGGGGG TCNTANTACC ANCGTGGGAA AAGAACCCCA GGCNGCGAAC 540
CAANCTTGTG TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGACA GCACCANTNA 600
CTGTNNANCT TTAGNCCNTG GTCCTCNTGG GTTGNNCTTG AACCTAATCN CNNTCAACT 660
GGGACAAGGT AANTNGCNT CCTTTNAATT CCCNANCNTN CCCCTGTTT TGGGGTTTTN 720
CNCNCTCCTA CCCCAGAAAN NCCGTGTTCC CCCCCAATA GGGGCCNAAA CNNTTNTTC 780
CACAAACCCTN CCCCACCAC GGGTTCNGNT GGTNG 816
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG      60
ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA      120
AAGACCCAAA CCAGGTGGAA CTGTGGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA      180
CAGTGACTAG CTCAGACCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA      240
CCAAGCAGAC AGAAGACTAC TGCTTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT      300
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTTCGTT TATGGAGGCT      360
GCTTGGGCAA CAAGAACAAC TACCTTCGGG AAGAAGAGTG CATTTCTANCC TGTGNGGGTG      420
TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCTT      480
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCGCTGCA      540
NCAATGGCTG CTGCATCNAC ANTTTCCTNG AATTGTGACA ACACCCCCCA NTGCCCCCAA      600
CCCTCCCAAC AAAGCTTCCC TGTNAAAAA TACNCCANTT GGCTTTTAC AAACNCCCGG      660
CNCCTCCNTT TTCCCCNNTN AACAAAGGCG NCTNGCNTTT GAACTGCCCN AACCCNGGAA      720
TCTNCCNNGG AAAAANTNCC CCCCTGGTCT CTTNNAANCC CCTCCNCAA ANCTNCCCCC      780
CCC

```

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```

CCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTCGGAT GTCATACAAA      60
AGCTGATTGA AGCAACCTTC TACTTTTGG TCGTGAGCCT TTTGCTTGGT GCAGGTTTCA      120
TTGGCTGTGT TGGTGACGTT GTCAATTGCAA CAGAATGGGG GAAAGGCACT GTTCTCTTTG      180
AAGTAGGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC      240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA      300
GGCACTACCA GCAACGTCAG GAAGTGCTCA GCCATTGTGG TGTACACCAA GGCAGACCACA      360
GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA      420
CACTTGCTCT CCGTCTTAGC ACCATAGCAG CCCANGAAAC CAAGAGCAAA GACCACAACG      480
CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGGCCACT GGACGACAGT      540
TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATCGATTG AACACCCANA TGCCCACTGC      600
CNACAGGGCT GCNCCNCCN GAAAGAATGA GCCATTGAAG AAGGATCNTC NTGCTCTTAA      660
TGAAGTAAA CCNTGCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGAA TTCTGANAAA      720
AAGGAACNGC NTNAGCCCCC CCAAANGANA AACACCCCC GGGTGTGTGCC CTGAATTGGC      780
GGCCAAGGAN CCCTGCCCN G

```

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 740 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```

GTGAGAGCCA GCGTCCCTC TGCTGCCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT      60
CCTTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG      120
AGCCACCATG CAGTGCTTCA GCTTCATTAA GACCATGATG ATCCTCTTCA ATTTGCTCAT      180
CTTTCTGTGT GGTGCAGCCC TGTGGCAGT GGCATCTGG GTGTCAATCG ATGGGGCATC      240
CTTCTGAAG ATCTTCGGGC CACTGTCGTC CAGTGCCATG CAGTTTGTCA ACGTGGGCTA      300
CTTCCTCATC GCAGCCGGCG TTGTGGTCTT TGCTCTTGGT TTCCTGGGCT GCTATGGTGC      360

```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TAAGACGGAG | AGCAAGTGTG | CCCTCGTGAC | GTTCTTCTTC | ATCCTCCTCC | TCATCTTCAT | 420 |
| TGCTGAAGIT | GCAGTGCTG  | TGGTCGCCTT | GGTGACACC  | ACAATGGCTG | AACCATTCCT | 480 |
| GACGTGCTG  | GTANTGCCTG | CCATCAANAA | AGATTATGGG | TCCCAGGAA  | AAATTCATC  | 540 |
| AANTNTGAA  | CACCNCCATG | AAAAGGGCTC | CAATTCTGN  | TGGCTTCCCC | AACATACCG  | 600 |
| GAATTTGAA  | AGANTCNCCC | TACTTCCAAA | AAAAANANT  | TGCCTTTNCC | CCNTTCTGT  | 660 |
| TGCAATGAAA | ACNTCCCAAN | ACNGCCAATN | AAACCTGCC  | CNNNCAAAA  | GGNTCNCAAA | 720 |
| CAAAAAAANT | NNAAGGTTN  |            |            |            |            | 740 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| CCGCTGGTTG | CGCTGGTCCA | GNGNAGCCAC | GAAGCACGTC  | AGCATAACAC | GCCTCAATCA | 60  |
| CAAGGTCTTC | CAGCTGCCGC | ACATTACGCA | GGGCAAGAGC  | CTCCAGCAAC | ACTGCATATG | 120 |
| GGATACACTT | TACTTTAGCA | GCCAGGGTGA | CAACTGAGAG  | GTGTCGAGC  | TTATTCTTCT | 180 |
| GAGCCTCTGT | TAGTGGAGGA | AGATTCCGGG | CTTCAGCTAA  | GTAGTCAGCG | TATGTCCCAT | 240 |
| AAGCAAAAC  | TGTGAGCAGC | CGGAAGGTAG | AGGCAAGATC  | ACTCTCAGCC | AGCTCTCTAA | 300 |
| CATTGGGCAT | GTCCAGCAGT | TCTCCAAACA | CGTAGACACC  | AGNGGCCTCC | AGCACCTGAT | 360 |
| GGATGAGTGT | GGCCAGCGCT | GCCCCCTTGG | CCGACTTGGC  | TAGGAGCAGA | AATTGCTCCT | 420 |
| GGTTCGCCCC | TGTCACCTTC | ACTTCCGCAC | TCATCACTGC  | ACTGAGTGTG | GGGGACTTGG | 480 |
| GCTCAGGATG | TCCAGAGACG | TGGTCCGCCC | CCCTCNCTTA  | ATGACACCGN | CCANNCAACC | 540 |
| GTGGGCTCCC | GCCGANTGNG | TTCGTGCTNC | CTGGGTGAGG  | GTCTGCTGGC | CNCTACTTGC | 600 |
| AANCTTCGTC | NGGCCCATGG | AATTACCCNC | ACCGGAACCTN | GTANGATCCA | CTNNTTCTAT | 660 |
| AAACCGNCGC | CACCGCNNTT | GGAATCCAC  | TCTTNTTNC   | TTACTTGAG  | GGTTAAGGTC | 720 |
| ACCTTNNCG  | TTACCTTGGT | CCAAACCTN  | CCNTGTGTCG  | ANATNGTNAA | TCNGNGCCNA | 780 |
| TNCCANCCNC | ATANGAAGCC | NG         |             |            |            | 802 |

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

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

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| CNAAGCTTCC  | AGGTNACGGG  | CCGCNAANCC | TGACCCNAGG | TANCANAANG | CAGNCNGCGG | 60  |
| GAGCCACCCG  | TCACNGGNG   | GNGTCTTTAT | NGGAGGGGGC | GGAGCCACAT | CNCTGGACNT | 120 |
| CNTGACCCCA  | ACTCCCNCC   | NCNCANTGCA | GTGATGAGTG | CAGAACTGAA | GGTNACGTGG | 180 |
| CAGGAACCAA  | GANCAAAANNC | TGCTCCNNTC | CAAGTCGGCN | NAGGGGGCGG | GGCTGGCCAC | 240 |
| GCNCATCCNT  | CNAGTGCTGN  | AAAGCCCCNN | CCTGTCTACT | TGTTTGGAGA | ACNGCNNGA  | 300 |
| CATGCCCCAGN | GTANATAAC   | NGGCNGAGAG | TNANTTTGCC | TCTCCCTTCC | GGCTGCGCAN | 360 |
| CGNGTNTGCT  | TAGNGGACAT  | AACCTGACTA | CTTAACTGAA | CCCNNGAATC | TNCCNCCCCT | 420 |
| CCACTAAGCT  | CAGAACAAAA  | AACCTCGACA | CCACTCANTT | GTCACTGNC  | TGCTCAAGTA | 480 |
| AAGTGATCCC  | CATNCCCAAT  | GTNTGCTNGA | NGCTCTGNCC | TGCNTTANGT | TCGGTCTGCG | 540 |
| GAAGACCTAT  | CAATTNAAGC  | TATGTTTCTG | ACTGCCTCTT | GCTCCCTGNA | ACAANCNACC | 600 |
| CNNCNTCCA   | AGGGGGGGNC  | GGCCCCCAAT | CCCCCAACC  | NTNAATTNAN | TTTANCCCCN | 660 |
| CCCCNCGCC   | CGGCCTTTTA  | CNANCNTCNC | NNACNGGGNA | AAACNNNGC  | TTTNCCTAAC | 720 |
| NNAATCCNCC  | T           |            |            |            |            | 731 |

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```
TTTTTTTTTT TTTTTTTTTT TAAAAACCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC      60
CAACCCCTC NTCCAAATNN CCNTTCCCG GNGGGGGTTC CAAACCCAAN TTANNTTGG      120
ANNTTAAATT AAATNTTNTT TGGNGGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA      180
TNANCTTNAA TNCCTGGAAA CCNGTNGNTT CCAAAAATNT TTAACCCCTTA ATCCCTCCG      240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTGTTT GAAGGNTNAA TNAAAAANCC      300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTCC NTTAAANAA      360
GGNNANCCCC GGTANTNAA TCCCCCNCC CCAATTATA CCGANTTTT TNGAATTGG      420
GANCCNCGG GAATTAACGG GGNNTTCCC TTTGGGGGG CNGGNNCCCC CCCNTCGGG      480
GGTTNGGNC AGNCNNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC      540
CCAGGTGAG NNTNGGGTT NCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTGG      600
GGGGCCTGG ATTTNTTTC CCTNTTNC TCCCCCCCC CCNGGGANAG AGGTTNGNT      660
TTGNTCNCC GGGCCNCCN AAGANCTTN CCGANTTNAN TAAATCCNT GCCTNGGCGA      720
AGTCNTTGN AGGNTAAAN GGCCCCCTNN CGGG      754
```

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 755 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

```
ATCANCCTAT GACCCNAAC NNGGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA      60
NNGTNAGNCC ACTCNNTTN NATCACNCCC CNCCNACTAC GCCCNANANC CNACGCNCTA      120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN      180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCCT CNAAGTATTN      240
NNCNANATAT GATTTTCCTN ANCCGATTAC CCNTNCCCCC TANCCTCC CCCCCAACNA      300
CGAAGGCNCT GGNCCNAAGG NNGCGNCCNC CCGCTAGNTC CCCNCAAGT CNCNCNCTA      360
AACTCANCCN NATTACNCGC TTCTGAGTA TCACTCCCGG AATCTCAGCC TACTCAATC      420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT      480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATTT CCNAANGGCT      540
CTTTCNGACA GCATNTTTTG GTTCCNNTT GGGTCTTAN NGAATTGCC TICTNNGAAC      600
GGGCTCTCT TTTCTTCGG TTANCCCTGGN TTCNNCCGGC CAGTTATTAT TTTCCNTTTT      660
AAATTCNTNC CNTTTANTTT TGGCNTTCA AACCCCGGGC CTTGAAAACG GCCCCTGGT      720
AAAAGGTTGT TTTGANAAAA TTTTGTGTT GTTCC      755
```

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 849 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

TTTTTTTTT TTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT      60
ACGCTNGGAN TAANGCGACC CGANTTCTAG GANNCNCCCT AAAATCANAC TGTGAAGATN      120
ATCCTGMNNA CGGAANGGTC ACCGGNNGAT NNTGCTAGGG TGNCNCTCC CANNNCNTTN      180
CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCNG NGNCCGGGCC CGGGTCATTN      240
GMNTTAACCN CACTNNGCNA NCGGTTTCCN NCCCNCCNG ACCCNGGCGA TCCGGGGTNC      300
TCTGTCTTCC CCTGNAGNCN ANAAANTGGG CCNCGNCCC CTTTACCCCT NNACAAGCCA      360
CNGCCNTCTA NCCNCGCCC CCCCTCCANT NNGGGGACT GCCNANNGCT CCGTTNCTNG      420
NNACCCCNMN GGGTNCCTCG GTTGTGANT CNACCGNANG CCANGGATTC CNAAGGAAGG      480
TGCGTTNTTG GCCCCTACCC TTCGCTNCGG NNCACCCCTC CCGACNANGA NCCGCTCCCG      540
CNCNCCGNGG CCTCNCTCG CAACACCCGC NCTCNTNGT NCGGNNMCCC CCCCACCCGC      600
NCCCTCNCNC NGNCGNANCN CTCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC      660
NTCANCCACN GGNNGACNNG NAGCNCNNTC GCNCCGCGCN GCGNCCCTC CGCCNCGAA      720
CTNCTCNGG CCANTNCGC TCAANCCNNA CNAACGCGC CTGCGCGGCC CGNAGCGNCC      780
NCCTCCNCGA GTCCTCCCGN CTTCCNACC ANGNNTTCCN CGAGGACACN NNACCCCGCC      840
NMCANGCGG

```

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GCGCAAACTA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTTCTC CGCAACCATG      60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAACT GANTAACACA      120
CACACNCNAN AGANAATCC NCTGCCTTCC ANAGTANACN ATTGAACNNG AGAACCCANGC      180
NGGCGAATCG TAATNAGGCG TGCGCGGCGA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC      240
CTNCCNACC TACNTCTTCN NAGCTGTCCN ACCCCTNGTN CGNACCCCCC NAGGTGGGGA      300
TCGGGTTTNN NNTGACCGNG CNNCCCTTCC CCCCTCCAT NACGANCCNC CCGCACCCACC      360
NANNGCNCGC NCCCCGNNCT CTTGCGCNCC CTGTCTNTN CCCCTGTNGC CTGGCNCNGN      420
ACCGCATTGA CCCTCGCCNN CTNCCNGAAA NCGNANACGT CCGGGTTGNN ANNANCGCTG      480
TGGGNNNGCG TCTGCNCCG GTTCCTTCCN NCNCTTCCA CCATCTTCNT TACNNGGTCT      540
CCNCGCNC TCNNNCACNC CCTGGGACGC TNCCTNTGC CCCCCTTAC TCCCCCCTT      600
CGNCGTGNC CGNCCCCACC NTCATTNCA NACGNTCTC ACAANNNCCT GGNNTNCTCC      660
CNANCNGNCN GTCANCCNAG GGAAGGGNGG GGNCCNNTG NTGACGTTG NGGNGANGTC      720
CGAANANTCC TCNCCNTCAN CNCTACCCCT CGGGCGNNCT CTCNGTTNCC AACTTANCAA      780
NTCTCCCCCG NGNCCNCTC TCAGCCTCNC CCNCCCNCT CTCGTGANTG TNCTCTGCTC      840
TNACCNNTAC GANTNTTCGN CNCCCTCTTT CC

```

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

GCATGCAAGC TTGAGTATTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA      60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNNGTA      120

```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TCNTNCATTA | GTAACAANTG | TNNTGTCCAT | CCTGTCNGAN | CANATTCCCA | TNNATTNCGN | 180 |
| CGCATTCNCN | GCNCANTATN | TAATNGGGAA | NTCNNNTNNN | NCACCNNCAT | CTATCNTNCC | 240 |
| GCNCCTGAC  | TGGNAGAGAT | GGATNANTTC | TNNTNTGACC | NACATGTICA | TCTTGGATTN | 300 |
| AANANCCCC  | CGCNGNCCAC | CGGTTNGNNG | CNAGCCNNTC | CCAAGACCTC | CTGTGGAGGT | 360 |
| AACCTGCGTC | AGANNATCA  | AACNTGGGAA | ACCCGCNNCC | ANGTNNAAGT | NGNNNCANAN | 420 |
| GATCCCGTCC | AGGNTTNACC | ATCCCTTCNC | AGCGCCCCCT | TNNGTGCCTT | ANAGNGNAGC | 480 |
| GTGTCCNANC | CNCTCAACAT | GANACGCGCC | AGNCCANCCG | CAATTNGGCA | CAATGTCGNC | 540 |
| GAACCCCTA  | GGGGGANTNA | TNCAAAANCC | CAGGATTGTC | CNCNCANGAA | ATCCCNANC  | 600 |
| CCNCCCTAC  | CCNCTTTGG  | GACNGTGACC | AANTCCCGGA | GTNCCAGTCC | GGCCNGNCTC | 660 |
| CCCCACCGGT | NNCCTGGGG  | GGGTGAANCT | CNGNNTCANC | CNGNCGAGGN | NTCGNAAGGA | 720 |
| ACCGGNCCTN | GGNCGAANNG | ANCNNTCNGA | AGNGCCNCNT | CGTATAACCC | CCCCTCNCCA | 780 |
| NCCNACNGNT | AGNTCCCCC  | CNGGGTNCGG | AANGG      |            |            | 815 |

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CCGAGATGTC | TCGCTCCGTG | GCCTTAGCTG | TGCTCGCGCT | ACTCTCTCTT | TCTGGCCTGG | 60  |
| AGGCTATCCA | GGCTACTCCA | AAGATTACAG | TTTACTCAGC | TCATCCAGCA | GAGAATGGAA | 120 |
| AGTCAAATTT | CCTGAATTGC | TATGTGTCTG | GGTTTCATCC | ATCCGACATT | GAANTTGACT | 180 |
| TACTGAAGAA | TGGANAGAGA | ATTGAAAAAG | TGGAGCATTG | AGACTTGCTT | TTAGCAAGG  | 240 |
| ACTGGTCTTT | CTATCTCNTG | TACTACACTG | AATTCACCCC | CACTGAAAAA | GATGAGTATG | 300 |
| CCTGCCGTGT | GAACCATGTG | ACTTTGTAC  | AGCCCAAGAT | AGTTAAGTGG | GATCGAGACA | 360 |
| TGTAAGCAGN | CNNCATGGAA | GTTTGAAGAT | GCCGCATTG  | GATTGGATGA | ATTCCAAATT | 420 |
| CTGCTTGCTT | GCNTTTTAAT | ANTGATATGC | NTATACACCC | TACCCCTTAT | GNCCCCAAAT | 480 |
| TGTAGGGGTT | ACATNANTGT | TCNCTNNGA  | CATGATCTTC | CTTTATAANT | CCNCCNTTCG | 540 |
| AATTGCCCGT | CNCCCNGTTN | NGAATGTTTC | CNNAACCACG | GTTGGCTCCC | CCAGGTCNCC | 600 |
| TCTTACGGAA | GGGCCTGGGC | CNCTTTNCAA | GGTTGGGGGA | ACCNAAAAAT | TCNCTTNTGC | 660 |
| CCNCCNCCA  | CNNTCTTGNG | NNCNCANNTT | GGAACCCCTC | CNATTCCCTT | TGGCTCNNA  | 720 |
| NCCTTNNCTA | ANAAAACTTN | AAANCGTNGC | NAAANNNTTN | ACTTCCCCC  | TTACC      | 775 |

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ANATTANTAC | AGTGAATCT  | TTTCCAGAG  | GTGTGTANAG | GGAACGGGGC | CTAGAGGCAT | 60  |
| CCCANAGATA | NCTTATANCA | ACAGTGCTTT | GACCAAGAGC | TGCTGGGCAC | ATTTCCTGCA | 120 |
| GAAAAGGTGG | CGGTCCCCAT | CACTCCTCCT | CTCCCATAGC | CATCCAGAG  | GGGTGAGTAG | 180 |
| CCATCANGCC | TTCCGTGGGA | GGGAGTCANG | GAAACAACAN | ACCACAGAGC | ANACAGACCA | 240 |
| NTGATGACCA | TGGCGGGGAG | CGAGCCTCTT | CCCTGNACCG | GGGTGGCANA | NGANAGCCTA | 300 |
| NCTGAGGGGT | CACACTATAA | ACGTTAACGA | CCNAGATNAN | CACCTGCTTC | AAGTGCACCC | 360 |
| TTCTACCTG  | ACNACCAGNG | ACCNNNAACT | GCNGCCTGGG | GACAGCCTG  | GGANCACTA  | 420 |
| ACNNAGCACT | CACCTGCCCC | CCCATGGCCG | TNCGCNTCCC | TGGTCCTGNC | AAGGGAAGCT | 480 |
| CCCTGTTGGA | ATTNCGGGGA | NACCAAGGGA | NCCCCCTCCT | CCANCTGTGA | AGGAAAAANN | 540 |
| GATGGAATTT | TNCCCTTCCG | GCCNNTCCCC | TCTTCCTTTA | CACGCCCCCT | NNTACTCNTC | 600 |

```

TCCCTCTNTT NTCCTGNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TCGGANNNCTN   660
GANATTCCAC TNNCGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGGAT   720
GGGNCCCTCG NTCATCCTCT CTTTTTCNCT ACCNCCNNTT CTTTGCCTCT CCTTNGATCA   780
TCCAACCNTC GNTGGCCNTN CCCCCCENN TCCTTTNCCC   820

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAACTCTCT   60
TGTTTCTTCT CCGAGCCCA GGCAGCGGTG ATTCAGCCCT GCCCAACCTG ATTCTGATGA   120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGCGC   180
CTGCTGAGCA CTTCCGCCCC TCACCTTGCC CAGCCCTGCG CATGAGCTCT GGGCTGGGTC   240
TCCGCCTCCA GGGTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC   300
TTCTTCTGCG CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCTGTGC ANGCNCCCTG   360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTCTTGANN TCTTCANTTA ACTNTGANTT   420
TATNACCNAN TGNCTGTNC TGTCTNACTT TAATGGGCGC GACCGGCTAA TCCCTCCCTC   480
NCTCCCTTCC ANTTCTNNNA ACCNGCTTNC CNTCNTCTCC CCNTANCCCG CCNGGGAANC   540
CTCCTTTGCC CTNACCANGG GCCNNNACCG CCCNTNNTN GGGGGGCGNG GTNNTCNCNC   600
CTGNTNNCCC CNCTCNCNNT TNCCTCGTCC CNNCNNCGCN NNGCANNTTC NCNGTCCCN   660
TNNCTCTCN NGTNTCGNAA NGNTCNCNTN TNNNNNGNCN NGNTNNTCN TCCCTCTCNC   720
CNNTGNANG TNNTTNNNNC NCNGNCCCC MNMNCNNNN NGGNNTNNN TCTNCNCNGC   780
CCCNCCCCC NGNATTAAGG CCTCCNNTCT CCGGCCNC   818

```

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

AGGAAGGCGG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG   60
TCCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTTANN CCNGGTGGGT   120
GATTNAACCC CATGTATGG AGNNAAAGN TTTNAGGGAT TTTTCGGCTC TTATCAGTAT   180
NTANATTCTT GTNAATCGGA AATNATNTT TCNNCGGAA AATNTTGCTC CCATCCGNAA   240
ATTNCTCCCG GGTAGTGCA TTTNGGGGNN CNGCCANGTT TCCAGGCTG CTANAATCGT   300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG   360
TNNNTTNCCT TCGCCCTNTG ACTCTGCNNG AGCCCAATAC CCNNGNGNAT GTCNCCNNG   420
NNNGCGNCNC TGAANNNNC TCGNGGCTNN GANCATCANG CGGTTTCGCA TCAAAGCANN   480
CGTTTCNCAT NAAGGCACTT TNGCCTCATC CAACCNCTNG CCCTCNCCA TTNGCCGCTC   540
NGGTTNCCT ACGCTNNTNG CNCCTNNNTN GANATTTTC CCGCCTNGGG NAANCCTCCT   600
GNAATGGGTA GGGNCTTNTC TTTTACCNN GNGGTNTACT AATCNCNTNC ACGCNTNCTT   660
TCTNACCCC CCCCCTTTT CAATCCANC GGCNAATGGG GTCTCCCN CGANGGGGG   720
NNNCCANN C   731

```

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT    60
CGCTCANACC TCACANCCCT CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNNT    120
ATNTNTACNC TCATANNCCT CNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN    180
TNNCTANTCT NTGCCGCGCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC    240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN    300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTTCNC ATNANCTCCT AATTTGAATC    360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC    420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCTCCG ATCCCCNNAC AACCCCCCTC    480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCATTTAN    540
CCACTGGAAT CACNATNGGA NAAAAAAAC CCNAACTCTC TANCNCNNAT CTCCTAANA    600
AATNCTCCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTTTT    660
TANATCCCTT CTTTCGAAAA CCNACCCCTT ANNNCCCAAC CTTTNGGGCC CCCCNCCTNC    720
CCNAATGAAG GNCNCCCAAT CNANGAAACG NCCNTGAAAA ANCNAGGCNA ANANNNTCCG    780
CANATCCTAT CCCTTANTTN GGGGNCCTT NCCNNGGGCC CC                        822
```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 787 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
CGGCCGCTG CTCTGGCACA TGCCTCCTGA ATGGCATCAA AAGTGATGGA CTGCCCATG    60
CTAGAGAAGA CCTTCTCTCC TACTGTCAAT ATGGAGCCCT GCAGACTGAG GGCTCCCCCT    120
GTCTGCAGGA TTTGATGTCT GAAGTCGTGG AGTGTGGCTT GGAGCTCCTC ATCTACATNA    180
GCTGGAAGCC CTGGAGGGCC TCTCTCGCCA GCCTCCCCCT TCTCTCCACG CTCTCCANGG    240
ACACCAGGGG CTCCAGGCAG CCCATTATTC CCAGNANGAC ATGGTGTTTC TCCACGCGGA    300
CCCATGGGGC CTGNAAGGCC AGGGTCTCCT TTGACACCAT CTCTCCCGTC CTGCCTGGCA    360
GGCCGTGGGA TCCACTANTT CTANAACGGN CGCCACCNCG GTGGGAGCTC CAGCTTTTGT    420
TCCCNTTAAT GAAGGTTAAT TGCNCGCTTG GCGTAATCAT NGGTCANAAC TTTTCTCTGT    480
GTGAAATTGT TTNTCCCTC NCNATTCCNC NCNACATACN AACCCGGAAN CATAAAGTGT    540
TAAAGCCTGG GGGTNGCCTN NNGAATNAAC TNAACTCAAT TAAATGCGTT GGCTCATGGC    600
CCGCTTTCN TTNCGAAAA CTGTCNTCCC CTGCNTTNTT GAATCGGCCA CCCCNCNGG    660
AAAAGCGGTT TGCNTTTTNG GGGGNTCCTT CCNCTTCCC CCTCNCTAAN CCCTNCGCCT    720
CGGTCTGTTN NGGTNGCGGG GAANGGGNAT NNNCTCCNC NAAGGGGGNG AGNNNGNTAT    780
CCCCAAA                                         787
```

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 799 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
TTTTTTTTTT TTTTTTTTGGC GATGCTACTG TTTAATTGCA GGAGGTGGGG GTGTGTGTAC      60
CATGTACCAG GGCTATTAGA AGCAAGAAGG AAGGAGGGAG GGCAGAGCGC CCTGCTGAGC      120
AACAAAGGAC TCCTGCAGCC TTCTCTGTCT GTCTCTTGGC GCAGGCACAT GGGGAGGCGT      180
CCCGCAGGGT GGGGGCCACC AGTCCAGGGG TGGGAGCACT ACANGGGGTG GGAGTGGGTG      240
GTGGCTGGTN CNAATGGCCT GNCACANATC CCTACGATTC TTGACACCTG GATTTCACCA      300
GGGGACCTTC TGTTCCTCCA NGGNAACCTC NTNNATCTCN AAAGAACACA ACTGTTTCTT      360
CNGCANTTCT GGCTGTTTCA GGAAGGCACA GGTGTCCNAT TTNGGCTGGG ACTTGGTACA      420
TATGGTTCCG GCCCACCTCT CCCNTCNAAN AAGTAATTCA CCCCCCCCN CCNTCTNTTG      480
CCTGGGCCCT TAANTACCCA CACCGGAAC TANTTANTTA TTCATCTTNG GNTGGGCTTG      540
NTNATCNCCN CCTGAANGCG CCAAGTTGAA AGGCCACGCC GTNCCCNCTC CCCATAGNAN      600
NTTTNNCNT CANCTAATGC CCCCCNNGC AACNATCCAA TCCCCCCCN TGGGGGGCCC      660
AGCCCCANGC CCCCNGCTCG GGNNNCCNGN CNGNANTCC CCAGGNTCTC CCANTCNGN      720
CCNNNGCNCC CCGCACGCA GAACANAAGG NTNGAGCCNC CGCANNNNNN NGGTNNCNAC      780
CTCGCCCCC CCNNCGNNG                                     799
```

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
TTTNNCCNAG GGCAGGTTTA TTGACAACCT CCGGGACAC AANAGGCTG GGGACAGGAC      120
GGCAACAGGC TCCGGCGGCG GCGGCGGCGG CCTACCTGC GGTACCAAT NTGCAGCCTC      180
CGCTCCCGCT TGATNTTCTT CTGCAGCTGC AGGATGCCNT AAAACAGGGC CTCGGCCNTN      240
GGTGGGCACC CTGGGATTTN AATTTCCACG GGCACAATGC GGTGCGANCC CCTCACCACC      300
NATTAGGAAT AGTGGTNTTA CCNCCNCCG TTGGCNCAC CCCCNTGGAA ACCACTTNTC      360
GCGGCTCCGG CATCTGGTCT TAAACCTTGC AAACNCTGGG GCCCTCTTTT TGGTTANTNT      420
NCCNGCCACA ATCATNACTC AGACTGGCNC GGGCTGGCCC CAAAAAANCN CCCCCAAACC      480
GGNCCATGTC TTNNCGGGGT TGCTGCNATN TNCATCACCT CCGGGGCNCA NCAGGNCAAC      540
CCAAAGTTC TTNGNGCCCN CAAAAAANC CCGGGGGGNC CCAGTTTCAA CAAAGTCATC      600
CCCCTTGGCC CCAAATCCT CCCCCGNTT NCTGGGTTTG GGAACCCACG CCTCTNNCTT      660
TGGNNGGCAA GNTGGNTCCC CTTTCGGGCC CCGGTGGGC CCNNCTCTAA NGAAACNCC      720
NTCCTNNNCA CCATCCCCC NNGNNACGNC TANCAANGNA TCCCTTTTTT TANAAACGGG      780
CCCCCNCG                                     789
```

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
GACAGAACAT GTTGATGGT GGAGCACCTT TCTATACGAC TTACAGGACA GCAGATGGGG      60
AATTCATGGC TGTGGAGCA ATANAACCCC AGTTCTACGA GCTGCTGATC AAAGGACTTG      120
GACTAAAGTC TGATGAATTT CCAATCAGA TGAGCATGGA TGATTGGCCA GAAATGAANA      180
AGAAAGTTGC AGATGTATTT GCAAAGAAGA CGAAGGCAGA GTGGTGTCAT ATCTTTGACG      240
GCACAGATGC CTGTGTGACT CCGTTTCTGA CTTTGGAGGA GGTGTTCAT CATGATCACA      300
```

```

ACAANGAACG GGGCTCGTTT ATCACCANTG AGGAGCAGGA CGTGAGCCCC CGCCCTGCAC 360
CTCTGCTGTT AACACCCCCA GCCATCCCTT CTTCAAAAAG GGATCCACTA CTTCTAGAGC 420
GGNCGCCACC GCGGTGGAGC TCCAGCTTTT GTTCCCTTTA GTGAGGGTTA ATTGCGCGCT 480
TGGCGTAATC ATGGTCATAN CTGTTTCCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC 540
ACAACATACG ANCCGGAAGC ATNAAATTTT AAAGCCTGGN GGTNGCCTAA TGANTGAAC 600
NACTCACATT AATTGGCTTT GCGCTCACTG CCCGCTTTCC AGTCCGAAA ACCTGTCCTT 660
GCCAGCTGCC NTTAATGAAT CNGGCCACCC CCCGGGGAAA AGGCNGTTTG CTTNTGGGG 720
CGCNCCTCCC GCTTCTCGC TTCCTGAANT CCTTCCCCC GGTCTTTCGG CTTGCGGCNA 780
ACGGTATCNA CCT 793

```

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GGCGCGACCG GCATGTACGA GCAACTCAAG GGCGAGTGGA ACCGTAAAAG CCCCAATCTT 60
ANCAAGTGCG GGGAAAGCT GGGTCGACTC AAGCTAGTTC TTCTGGAGCT CAACTTCTTG 120
CCAACCACAG GGACCAAGCT GACCAAAACAG CAGCTAATTC TGGCCCGTGA CATACTGGAG 180
ATCGGGGGCC AATGGAGCAT CCTACGCAAN GACATCCCTT CCTTCGAGCG CTACATGGCC 240
CAGCTCAAAT GCTACTACTT TGATTACAA GAGCAGCTCC CCGAGTCAGC CTATATGCAC 300
CAGCTCTTGG GCCTCAACCT CCTCTTCCTG CTGTCCCAGA ACCGGGTGGC TGANTNCCAC 360
ACGGANTTGG ANCGGCTGCC TGCCCAANGA CATAACANACC AATGTCTACA TCNACCACCA 420
GTGTCTTGGG GCAATACTGA TGGANGGCAG CTACCNCAA GINTTCTCTG CCNAGGGTAA 480
CATCCCCCGC CGAGAGCTAC ACCTTCTTCA TTGACATCCT GCTCGACACT ATCAGGGATG 540
AAAATCGCNG GGTGCTCCA GAAAGGCTNC AANAANATCC TTTTCNCTGA AGGCCCCCGG 600
ATNCNCTAGT NCTAGAATCG GCCCCCATC GCGGTGGANC CTCCAACCTT TCGTNTCCCT 660
TTACTGAGGG TINATTGCCG CCCTTGGCGT TATCATGGTC ACNCCNGTIN CCTGTGTGA 720
AATTNTTAAC CCCCCACAT TCCACGCCNA CATNG 756

```

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GGGGATCTCT ANATNACCT GNATGCATGG TTGTCGGTGT GGTGCGTGTC GATGAANATG 60
AACAGGATCT TGCCCTTGAA GCTCTCGGCT GCTGINTTTA AGTTGCTCAG TCTGCCGTCA 120
TAGTCAGACA CNCTCTTGGG CAAAAAACAN CAGGATNTGA GTCTTGATTT CACCTCCAAT 180
AATCTTCNGG GCTGTCTGCT CGGTGAACCT GATGACNANG GGCAGCTGGT TGTGTNTGAT 240
AAANTCCANC ANGTTCTCCT TGGTGACCTC CCCTTCAAAG TTGTTCCGGC CTTTCATCAA 300
CTTCTNNAAN ANGANNANCC CANCTTTGTC GAGCTGGNAT TTGGANAACA CGTCACTGTT 360
GGAAACTGAT CCAAAATGGT ATGTCATCCA TCGCCTCTGC TGCCTGCAAA AAACCTTGCTT 420
GGCNCAAATC CGACTCCCCN TCCTTGAAAG AAGCCNATCA CACCCCTCTC CTGGACTCC 480
NNCAANGACT CTNCCGCTNC CCCNTCCNNG CAGGGTTGGT GGCANNCCGG GCCNTGCCG 540
TTCTTCAGCC AGTTCAACNAT NTTATCAGC CCCTCTGCCA GCTGTTNTAT TCCTTGGGG 600
GGAANCCGTC TCTCCCTTCC TGAANNACT TTGACCGTNG GAATAGCCGC GCNTCNCNTT 660
ACNTNCTGGG CCGGGTTCAA ANTCCCTCCN TTGNCNNTCN CCTCGGGCCA TTCTGGATTT 720
NCCNAACCTT TTCCTTCCCC CNCCCNCCG NGTTTGGNTT TTTCATNGGG CCCCACCTCT 780

```

GCTNTTGGCC ANTCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCTNG GGCC

834

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
CGNCGCTTT CCGCCGCGC CCGTTTCCA TGACNAAGGC TCCCTTCANG TTAAATACNN      60
CCTAGNAAAC ATTAATGGGT TGCTCTACTA ATACATCATA CNAACCAGTA AGCCTGCCCA      120
NAACGCCAAC TCAGGCCATT CCTACCAAAG GAAGAAAGGC TGGTCTCTCC ACCCCCTGTA      180
GGAAAGGCCT GCCTTGTAAG ACACCACAAT NCGGCTGAAT CTNAAGTCTT GTGTTTACT      240
AATGGAAAAA AAAAAATAAC AANAGGTTTT GTTCTCATGG CTGCCCACCG CAGCCTGGCA      300
CTAAACANCC CCAGCGCTCA CTCTGCTTGG GANAAATATT CTTTGCTCTT TTGGACATCA      360
GGCTTGATGG TATCACTGCC ACNTTTCAC CCAGCTGGGC NCCCTTCCCC CATNTTGTG      420
ANTGANCTGG AAGGCCTGAA NCTTAGTCTC CAAAAGTCTC NGCCCAAG ACCGGCCACC      480
AGGGGANGTC NTTTNCAGTG GATCTGCCAA ANANTACCCN TATCATCNNT GAATAAAAG      540
GCCCCGTAAC GANATGCTTC CANCANCTT TAAGACCCAT AATCCTNGAA CCATGGTGCC      600
CTCCCGTCT GATCCNAAAG GAATGTTCTT GGTCCCANNT CCCTCCTTTG TTNCTTACGT      660
TGTNTTGGAC CCNTGCTNGN ATNACCCAAN TGANATCCCC NGAAGCACCC TNCCTTGGC      720
ATTGANTTT CNTAAATTCT CTGCCCTACN NCTGAAAGCA CNATTCCTTN GGCNCCNAAN      780
GGNGAACTCA AGAAGGTCTN NGAAAAACCA CNCN                                814
```

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
GCATGCTGCT CTTCCTCAAA GTTGTCTTTG TTGCCATAAC AACCACCATA GGTAAAGCGG      60
GCGCAGTGTT CGCTGAAGGG GTTGTAGTAC CAGCGCGGGA TGCTCTCCTT GCAGAGTCCT      120
GTGTCTGGCA GGTCCACGCA ATGCCCTTTG TCACTGGGGA AATGGATGCG CTGGAGCTCG      180
TCNAANCCAC TCGTGATTTT TTCACANGCA GCCTCCTCCG AAGCNTCCGG GCAGTTGGGG      240
GTGTCGTAC ACTCCACTAA ACTGTCGATN CACAGCCCA TTGCTGCAGC GGAAGTGGT      300
GGGCTGACAG GTGCCAGAAC AACTGGATN GGCCTTTCCA TGGAAGGGCC TGGGGGAAAT      360
CNCCTNANCC CAAACTGCCT CTCAAAGGCC ACCTTGACA CCCCACAGS CTAGAAATGC      420
ACTCTTCTC CCAAGGTAG TTGTCTTGT TGCCAAGCA NCCTCCANCA AACCAAAANC      480
TTGCAAAATC TGCTCCGTGG GGTTCATNN TACCANGGTT GGGGAANAA ACCCGGCNGN      540
GANCCNCCTT GTTTGAATGC NAAGGNAATA ATCCTCCTGT CTTGCTTGGG TGGAAAGCA      600
CAATTGAACT GTTAACNTTG GGCCGNGTTC CNCTNGGGTG GTCTGAAACT AATCACCGTC      660
ACTGGAAAAA GGTANGTGCC TTCCTTGAAT TCCCAAANT CCCCTNGNTI TGGGTNNTTT      720
CTCCTCTNCC CTAAAAATCG TTTTCCCCC CCNTANGGCG                                760
```

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTAAAAA CCCCTCCAT TGAATGAAAA    60
CTTCCNAAAT TGTCCAACCC CCTCNCCAA ATNNCCATTT CCGGGGGGGG GTTCCAAACC    120
CAATTAATTT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA    180
AATTTAACCC ATTATNAACT TAAATNCCCN GAAACCCNTG GNTTCCAAAA ATTTTAAACC    240
CTTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT    300
NGATTTAAAC CCCCTTNANT TTTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGTTC    360
TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNCCCT AANCCAATTA AACCGAATTT    420
TTTTTGAATT GGAATATCCN NGGGAATINA CCGGGGTTT TCCNTTTGG GGGCCATNCC    480
CCNCTTTTCG GGGTTTGGGN NTAGGTTGAA TTTTNNANG NCCCAAAAAA NCCCCAANA    540
AAAAAATCC CAAGNNTTAA TTNGAATNTC CCCCTTCCA GGCCTTTTG GAAAGNGGG    600
TTTNTGGGG CCNGGGANTT CNTTCCCCN TTNCNCCCC CCCCCNGGT AAANGGTTAT    660
NGNNTTTGGT TTTTGGGCC CTTNANGGAC CTTCGGATN GAAATTAAT CCCCAGGNGC    720
GCCG                                         724
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
TTTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGAATTTTTT TAATGCTGCA    60
CAACACAATA TTTATTTTCT TGTCTTCTT TATTTTCTT TATTTGTTG CTGCTGCTGT    120
TTTATTTAT TTTACTGAAA GTGAGAGGGA ACTTTGTGG CCTTTTTC TTTTCTGTA    180
GGCCGCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT    240
CGCAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTTGTAA TCATGCCCTA TGGTGGGTGA    300
TTAACTGCTT GTACAATTAC NTTTCACTT TAATTAATTG TGCTNAANGC TTTAATTANA    360
CTTGGGGGTT CCCCTCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAAATNATG    420
TCCCGGCNNT CNTTGAACA CACNGCNGAA NGTCTCATT NTCCCNCCNC CAGGTNAAAA    480
TGAAGGGTTA CCAATNTTAA CNCCACCTCC ACNTGGCNCN GCCTGAATCC TCNAAAANCN    540
CCCTCAANCN AATTNCTNNG CCCCAGTCNC GCNTNNGTCC CCCCCGGGT CCGGGAANTN    600
CACCCCNCA ANNCNNTNNC NAACNAAAT CCGAAATAT TCCNNTCNC TCAATTCACC    660
CNNAGACTNT CCTCNCCNAN CNCAATTTTC TTTTNTTAC GAACNCGNNC CNNAAAATGN    720
NNNCCNCTC CNCTNGTCCN NAATCNCCAN C                                         751
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
GTGGTATTTT CTGTAAGATC AGGTGTTCTT CCTCGTAGG TTAGAGGAA ACACCCTCAT    60
AGATGAAAAC CCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG    120
CGCCCTATGC ACAGCTGGGC CTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA    180
```

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TGGTCTGGAA | GCGGCGGCTG | TACCTGCGTA | GGGGCACACC | GTGAGGGCCC | ACCAGGAACT | 240 |
| TCTCAAAGTT | CCAGGCAACN | TCGTTGCGAC | ACACCGGAGA | CCAGGTGATN | AGCTTGGGGT | 300 |
| CGGTCATAAN | CGCGGTGGCG | TCGTGCGCTG | GAGCTGGCAG | GGCCTCCCGC | AGGAAGGCNA | 360 |
| ATAAAAGGTG | CGCCCCCGCA | CCGTTCAACT | CGCACTTCTC | NAANACCATG | ANGTTGGGCT | 420 |
| CNAACCCACC | ACCANNCCGG | ACTTCCTTGA | NGGAATTCCC | AAATCTCTTC | GNTCTTGGGC | 480 |
| TTCTNCTGAT | GCCCTANCTG | GTGCCCCNGN | ATGCCAANCA | NCCCCAANCC | CCGGGGTCCT | 540 |
| AAANCACCCN | CCTCCTCNTT | TCATCTGGGT | TNTTNTCCCC | GGACCNCTGT | TCCTCTCAAG | 600 |
| GGANCCCAT  | TCTCNACCAN | TACTCACCN  | NCCCCCCNT  | GNNACCCANC | CTTCTANNNG | 660 |
| TTCCCNCCG  | NCCTCTGGCC | CNTCAAANAN | GCTTNCACNA | CCTGGGCTG  | CCTTCCCCCC | 720 |
| TNCCCTATCT | GNACCCNCN  | TTTGTCTCAN | TNT        |            |            | 753 |

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACTATATCCA | TCACAACAGA | CATGCTTCAT | CCCATAGACT | TCTTGACATA | GCTTCAAATG | 60  |
| AGTGAACCCA | TCCTTGATTT | ATATACATAT | ATGTTCTCAG | TATTTTGGGA | GCCTTTCCAC | 120 |
| TTCTTTAAAC | CTTGTTCAAT | ATGAACACTG | AAAATAGGAA | TTGTGAAGA  | GTAAAAAGT  | 180 |
| TATAGCTTGT | TTACGTAGTA | AGTTTTTGAA | GTCTACATTC | AATCCAGACA | CTTAGTTGAG | 240 |
| GTTTAAACTG | TGATTTTAA  | AAAATATCAT | TTGAGAATAT | TCTTTCAGAG | GTATTTTCAT | 300 |
| TTTACTTTT  | TGATTAAATG | TGTTTATAT  | ATTAGGTAG  | T          |            | 341 |

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTACTGAA | TTTAGTTCTG | TGCTCTTCCT | TATTTAGTGT | TGTATCATAA | ATACTTTGAT | 60  |
| GTTCAAACA  | TTCTAAATAA | ATAATTTTCA | GTGGCTTCAT | A          |            | 101 |

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCTCACCCT    60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT    120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA    180
CCTCTTGAGA GGTCACTAAA GAGGACTTAA TATTTTCATAT CTACAAAATG ACCACAGGAT    240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC    300
TCGAA                                         305
```

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTTCT    60
GATTATTTGG TGTGTGTTTT GGTGTTGTGC CAAAGTATTG GCAGCTTCAG TTTTCATTTT    120
CTCTCCATCC TCGGGCATTG TCCCAAAT TATATACCAG TCTTCGTCCA TCCACACGCT    180
CCAGAATTTT TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC    240
TGCTGTTGTT CTTCTTTTAA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCCTGA    300
AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA    360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC    420
ACTTGGCAGG GGGGTCTTGC TCCTTTTTC TATCAGGTGA CTCTGCAACA GGAAGGTGAC    480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG    540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTC ATGATGGAAG    600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC    660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG    720
CCGCCCGGGT GAACTCTGTC AACTCATGTC TGCAAAGGTG CTCGCCGTGT ATGTCGAACT    780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGTTGTGC CAGGAGGTGA TGGAGCCACT    840
CCCACACCTG GT                                         852
```

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
ACAACAGACC CTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG    60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGAACCTCTT    120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCACTGCG    180
```

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 590 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA   | 60  |
| ATTGTAGAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA | 120 |
| AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATGACACA TTATCCTTTA | 240 |
| AAAGCTTTCA AAANAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT  | 300 |
| CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT | 360 |
| TTACAATGGC TTAATGTCAN GGAAGGAGCA GTGGAAGTAG GGAAGTANTC AAGGTCCTTC | 420 |
| TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT | 540 |
| GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT            | 590 |

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 774 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCC  | 60  |
| TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGGA GGTTCAGAC  | 120 |
| GCTTCACTGC TTGAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG  | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA | 240 |
| AACATCAAAG AAAGGAAGGT GGCCTCATACT CCCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCTGTGTG | 360 |
| CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC | 420 |
| CCACACTCCT TGAACACACA TCCCAGGTT ATATTCCTGG ACATGGCTGA ACCTCCTATT  | 480 |
| CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCCTCAC CCTCCAAACC  | 540 |
| ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGAA CAATCCCTGA | 600 |
| TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT | 720 |
| TCACTTCTAT GGGNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT        | 774 |

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 124 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CANAAATTGA AATTTTATAA AAAGGCATT TTCTCTTATA TCCATAAAAT GATATAATTT   | 60  |
| TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTTCCTT AATTACAGCT CAACGCAACT | 120 |
| TGGT                                                               | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT | 60  |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTTT TACGGGTGAT TGCAAAAATT | 120 |
| TTAGGCACC CATATCCCAA GCANTGT                                      | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC | 60  |
| ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTTGGGA GAGGGGT               | 107 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

(2) INFORMATION FOR SEQ ID NO:52:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

(2) INFORMATION FOR SEQ ID NO:53:

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| ACATAATTTA | GCAGGGCTAA | TTACCATAAG | ATGCTATTTA | TTAANAGGTN  | TATGATCTGA | 60  |
| GTATTAAACG | TTGCTGAAGT | TGGTATTTT  | TATGCAGCAT | TTTCTTTTGT  | CTTGATATAC | 120 |
| ACTACAGAAC | CCTTAAGGAA | ACTGAAATTT | AGTAAGTAA  | GTTCTAGAAAT | ATTAGTCTGT | 180 |
| CAATCAAATC | TCTACATAAC | ACTATAGTAA | TTAAAAAGTT | AAAAAAAAGT  | GTGAAATCT  | 240 |
| GCACATAGAT | ANACCGCTCC | TGTCAGAGTA | ANACTGTTT  | GGAAACAGAA  | GGGAAAAAAC | 300 |
| AGCTTTTGAT | TTCTTTGTGC | TGATANAGG  | AAAGGCTGAA | TTACCTTGGT  | CCCTCTCCCT | 360 |
| AATGATTGGC | AGGTCNGGTA | AATNCCAAAA | CATATTCCAA | CTCAACACTT  | CTTTTCCNCG | 420 |
| TANCTTGANT | CTGTGTATTC | CAGGANCAGG | CGGATGGAA  | GGGCCAGCCC  | NCGGATGTTT | 480 |
| CANT       |            |            |            |             |            | 484 |

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG      60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAACAC AAATCCTTGG CACTGGCTAG      120
TCTATGTCCT CTCAAGTGCC TTTTGTGTG T                               151
```

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
ACCTGGCTTG TCTCCGGGTG GTTCCCGCG CCCCCACGG TCCCCAGAAC GGACACTTTC      60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T                               91
```

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT      60
TGGATTTTGT GTATCTGTGG GTTGGGGGGA CGTCCAGGA ACCAATACCC CATGGATACC      120
AAGGGACAAC TGT                               133
```

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC | 60  |
| GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGCT                                     | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAATAAC ATTGAATTTT CTGTATACTC | 60  |
| TGATTACATA CATTATCCT TAAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA    | 120 |
| ATTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAGTAGTT | 180 |
| TTGACTTCTA AGTTTGCT                                              | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT   | 60  |
| CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAAGTTA TCRAAACTC ACTCAATTTT  | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG | 240 |
| CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCRAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTGAAGAGT                                   | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60  |
| GTCTGGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC | 120 |
| TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGGC ATTCCCGTGC CTGGT      | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT | 60  |
| GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC | 120 |
| TGGACTGCAC AGCCCCGGGG CTCACATTG CTGT                              | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

|                                  |    |
|----------------------------------|----|
| CGCTCGAGCC CTATAGTGAG TCGTATTAGA | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| ACAAGTCATT TCAGCACCTT TTGCTCTTCA AAAGTGACCA TCTTTTATAT TTAATGCTTC | 60 |
| CTGTATGAAT AAAAATGGTT ATGTCAAGT                                   | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCGCG | 60 |
| AATCAGTGCA TCCAGGATTG GTCCTGGAT CTGGGGT                         | 97 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACAACAANA NTCCCTTCTT TAGGCCACTG ATGGAACCT GGAACCCCT TTTGATGGCA    | 60  |
| GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCA ACCGCACACC  | 120 |
| CCAACCCG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT   | 180 |
| TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA | 240 |
| GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CTTGGCATTC GCCGCTGAAC TATGAACCCG | 300 |
| TGGGGGTGAA CTACCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG  | 360 |
| GGCGGGGAGG AGCATGT                                                | 377 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
ACGCCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG      60
AGAACCCGTC TGCCCTTCC CACCATATCC ACCCTCGCTC CATCTTTGAA CTCAAACAGC      120
AGGAACCTAAC TGCACCCCTG TCCTCTCCCC AGTCCCAGT TCACCTCCA TCCCTCACCT      180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGTTT      240
TTATATATTT TTTAATAAGA TGCACCTTAT GTCATTTTTT AATAAAGTCT GAAGAATTAC      300
TGTTT                                     305
```

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 385 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTGA GGAATGCTGA      60
GGTCGGACCA CCCACATCTC ATGTGCAAGA TTGCCAGCA GACATCAGGT CTGAGAGTTC      120
CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC      180
TGTCGTGTGC TGGAGATTCA CTTTGTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG      240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG      300
CCTCTCCAG GGGCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC      360
CATAGTTTCT GTGCTAGTGG ACCGT                                     385
```

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA      60
GTTTTTTTAA TGG                                     73
```

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTAGTCCAG TGTGGTGGAA TICCATTGTG TTGGGGGCTC TCACCTCCTC CTCTGCAGC  | 60  |
| TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCCAG CATCTGAGTA CCCTGCTGCT | 120 |
| CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT | 180 |
| CCCCGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACTT | 240 |
| CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT | 300 |
| ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG | 360 |
| CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC | 420 |
| AGAACTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCTT GGGGAGAACA | 480 |
| GAANGTCCCT GGGTGAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC      | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATGACCCCTA ACAGGGGGCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT | 60  |
| TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA | 120 |
| CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT | 180 |
| CCAAAAGGC CTTGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC   | 240 |
| AGGGATTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC  | 300 |
| ACTGGCCCC AACAGGCATC ACCCCGCTAA ATCCCCTAGA AGTCCCACCT CTAAACACAT  | 360 |
| CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA | 420 |
| ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT    | 477 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAACACA TTTTCTACAT AGATAGTACT  | 60  |
| AGGTATTAAT AGATATGTAA AGAAAGAAAT CACACCATTA ATAATGGTAA GATTGGTTTA | 120 |
| TGTGATTTTA GTGGTATTTT TGGCACCTT ATATATGTTT TCCAACTTT CAGCAGTGAT   | 180 |
| ATTATTTCCA TAACTTAAAA AGTGAGTTG AAAAAGAAAA TCTCCAGCAA GCATCTCATT  | 240 |
| TAAATAAAGG TTTGTCTCTT TAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC   | 300 |
| AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA | 360 |
| AGTCAGTTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG | 420 |
| CTTCGTAATT TTGGAGTANG AGGTTCCTC CTCAATTTG TATTTTAAA AAGTACATGG    | 480 |

TAAAAAAAAA AATTCACAAC AGTATATAAG GCTGTAAAT GAAGAATTCT GCC

533

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 511 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA  | 60  |
| AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAGAGGG ACAAGGCTAA   | 120 |
| AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTGGG TTGGCTGGAG GAGCTGTGGA   | 180 |
| AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATTGTT ATTACANAGT  | 240 |
| GAGGTTCTCT GTGTGCCCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA | 300 |
| CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAAANAC | 360 |
| GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCCC GTCTGTTATG  | 420 |
| ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTCTAAGCA AACNCAGGTG ATGATGGCNA   | 480 |
| AAATACACCC CCTCTGAAG NACCNGGAGG A                                  | 511 |

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 499 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC  | 60  |
| CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC   | 120 |
| TGGCCTTGGT GGAGCTGGTG CCAGCACCCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA  | 180 |
| CAAGTGAGAT TTTAGATATT GTTAATCCTG CCAGTCTTTC TCTCAAGCC AGGGTGCAATC  | 240 |
| CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA  | 300 |
| CTCTGCATTA AATCTATTTG CCATTCTGA AAAAAAAAAA AAAAAAGGG CGGCCGCTCG    | 360 |
| ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTTGCCAGC  | 420 |
| CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT | 480 |
| GTCTTTCTCT AANTAAAT                                                | 499 |

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 537 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTGAGCC GCGAAGAGAT    60
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT    120
TCCAGGCCCA CGGCTCAAGT GAATTTGAAT ACTGCATTTA CAGTGTAGAG TAACACATAA    180
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA    240
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG    300
GGCTTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC    360
CAGTTTGCTT GATATATTG TGTATATTAA GATTCTTGAC TTATATTTTG AATGGGTTCT    420
ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA CACTCTTGAT    480
TCTACAATGT AGAAAATGAA GGAATGCCC CAAATTGTAT GGTGATAAAA GTCCCGT      537
```

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
CAANACAAT TGTTCAAAG ATGCAAATGA TACTACTCTG CTGCAGCTCA CAAACACCTC    60
TGCAATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA    120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG    180
TGGCACAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAAGCGT CTCTGAGGA    240
TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA    300
TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAG TCTGTAATAA    360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC    420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN      467
```

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
AAGCTGACAG CATTGGGGCC GAGATGTCTC GCTCCGTGGC CTAGCTGTG CTCGCGCTAC    60
TCTCTCTTTC TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTCAGGTT TACTCAGTTC    120
ATCCAGCAGA GAATGGAAAG TCAAATTTCC TGAATTGCTA TGTGCTGGG TTTCATCCAT    180
CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTCAG    240
ACTTGCTTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA    300
CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG    360
```

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCCGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT    | 60  |
| CCAGCTGCCC CGGCGGGGGA TGCGAGGCTC GGAGCACCTT TCCCCGGCTG TGATTGCTGC  | 120 |
| CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA  | 180 |
| GTTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA | 240 |
| AAAAAAA                                                            | 248 |

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGCCCCAA CACAATGGCT ACCTTTAACA | 60  |
| TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT | 180 |
| GATTTAAAAA AAAAAAAAAA A                                           | 201 |

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 552 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TCCTTTTGT AGGTTTITGA GACAACCCTA GACCTAAACT GTGTCACAGA CTCTGAATG    | 60  |
| TTTAGGCAGT GCTAGTAAT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT   | 120 |
| CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAAGGTAG | 180 |

TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT 240  
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT 300  
CTGTTCCCTG GCTAGAAAAA ATTATAAACA GGACTTTGTT AGTTTGGGAA GCCAAATTGA 360  
TAATATTCTA TGTTCATAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGAATTTTA 420  
TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC 480  
CNGTTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA 540  
AAAAAAAAAA AA 552

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 476 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCCTCT TATTTTCAGA 60  
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT 120  
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT 180  
GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA 240  
AGGTTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC 300  
TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGTTGAT AGGAANTNTC 360  
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGTTGAC GCNTAAAAAT 420  
GCTGAAAAAA TTAATATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAA AAAAAA 476

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGA GGAGCCCAGT 60  
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCTCCCA TTCCCAGCCT 120  
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG 180  
ACTCAGTCAG CGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT 232

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC 60
AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG 120
GTGCCAGCCT GACCGCCACT CTCACATTG GGTCTTTCGC TGGCCTTGGT GGAGCTGGTG 180
CCAGCACCCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA CAAGTGAGAT TTTAGATATT 240
GTTAATCCTG CCAGTCTTTC TCTCAAGCC AGGCTGCATC CTCAGAAACC TACTCAACAC 300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG 360
CCATTTCAAA AAAAAAAAAA AAA 383
```

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA 60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC 120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA 180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTFAAACTG 240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TCGGACTGTG 300
AGCCCTGATG CCTTTTGGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GCGGATTGAT 360
TATGCTTGTC TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAAACACAT TTGANTTTTT 420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA 480
AAAAAAAAA AAAA 494
```

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA 60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCAG 120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG 180
GCACACCCCTC CTGGGGCCCA GCGGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG 240
GTGCTGCTCC TCGTCATCTT CCGTCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG 300
CCATGTTTCA TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC 360
AGCGTTNCCG CCTCATCCG 380
```

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTCTGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAAGC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCNT TGGTGGNNGC GCNTNCTTT      480
T                                          481
```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGGAAAA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCAACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCAATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTAC ACCTGTTAAA AGGGCGCTAA GCATTTTGA TTCAACATCT TTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTTGA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG          472
```

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
AGAAACCACT ATCTCTNAAA ACAACCTCTC ATACCTTGTC GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTINGT      240
TTTATTCGAC ATGAAGGAAA TTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG      300
GGGACAAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA      360
ACAGAAATTG GGTNGTATAT TGAANANNG CATCATNAA ACGTTTTTTT TTT              413
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCCTCCC CGCGTCCCGC      60
GTCCTAGCCN ACCATGGCCG GGCCCTTGGC CGCCCGCTG CTCCTGCTGG CCATCTTGGC      120
CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCTTGGT      180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGCCTG GACTTTGCCG      240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC      300
CCCAANCAAA TTGTACTNG GGTAAANTAA TTCTTGAAG TTGAACCTGG GCCAAACNNG      360
TTTACCAGAA CCNAGCCAAT TNGAACAATT NCCCCTCCAT AACAGCCCT TTTAAAAGG      420
GAANCANTCC TGNTCTTTTC CAAATTTT              448
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA      60
GTAGTGATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAATGTCA AAAAATTAGC      120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT      180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CTTTGCATC      240
TTTATGTTN AGACTTGCTT CTNTNAAATT GCTTTGTNT TCTGCAGTA CTATCTGTGG      300
TTTAACAAAA TAGAANNACT TCTTGCTTN GAANATTGA ATATCTTACA TCTNAAAATN      360
AATTCCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN      420
AATTCNNANA ANTTCAAGTN TCATACAACA NAACNGGANC CCC              463
```

(2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTCANCCA CCAACTCTAC AAGTTGCTGT      60
CTTCCACTCA CTGTCTGTAA GCNTNTTAA CAGACTGTA TCTTCATAAA TAGAACAAAT      120
TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTCAG TTAGTATAAG CTCTTCCACT      180
TCCTTTGTTA AGACTTCATC TGGTAAAGTC TTAAGTTTGT TAGAAAGGAA TTTAATTGCT      240
CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCTT      300
TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCAA      360
GAGTCATCTG TCTGAAAAG TTGCGTTAGT ATATCTGCCA      400
```

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT      60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC      120
ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT      180
TGTGGAAAAA CTGGCACTTG NCTGGAACTA GCAAGACATC ACTTACAAAT TCACCCACGA      240
GACACTTGAA AGGTGTAACA AAGCGACTCT TGCATTGCTT TTTGTCCCTC CGGCACCAGT      300
TGTCAATACT AACCCGCTGG TTTGCCTCCA TCACATTGTG GATCTGTAGC TCTGGATACA      360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT      420
NGATCAGGTT CCCATTTCCT AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA      480
```

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
ATACAGCCCA NATCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TCGGGTCACT    60
GGTCCCCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGTTTGATGC TGCACCTCCTT    120
CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTGG GGTGACGGT    180
TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCGACT GTGCGGGACC    240
TGCAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCAGG GCCTTGCCCA    300
GAACCTTCCG CCTGTTCTCT GGCCTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG    360
ACCAGCGGAC AAACGGCGTT GAACAGCCGC ACCTCACGGA TGCCCANCTGT GTCGCGCTCC    420
AGGAACGGCN CCAGCGTGTC CAGGTCAATG TCGGTGAANC CTCGCGGGT AATGGCG    477
```

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
GAACGGCTGG ACCTTGCCCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC    60
AGTCCGAGCA GCCCCAGACC GCTGCCGCCC GAAGCTAAGC CTGCCTCTGG CCTTCCCCTC    120
CGCCTCAATG CAGAACCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN    180
TGATTTTACT TGGGAATTTC CTCTGTATA TAGCTTTTCC CAATGCTAAT TTCAAACAA    240
CAACAACAAA ATAACATGTT TGCCTGTINA GTTGATATAA AGTANGTAT TCTGTATNTA    300
AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTATTGG TNCTCTGGAA    360
ATAAATATAT TATTAAA    377
```

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 495 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
CCCTTGAGG GGTAGGGTC CAGTCCCAG TGAAGAAAC AGGCCAGGAG AANTGCGTGC    60
CGAGCTGANG CAGATTTCCT ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT    120
CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGCG AGGACCTAGA GGCACCAAGG    180
GAAGGCCCCA TTCCGGGGCT GTTCCCGAG GAGGAAGGGA AGGGGCTCTG TGTGCCCCC    240
ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAAA    300
TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGGCC    360
ACACCCACCC AGANCANCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG    420
TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAACC CTGCTNANA    480
AAAAAANA AAAAA    495
```

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
GGTIACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCAATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
TAGCTGTTTT GAGTTGATTC GCACCACTGC ACCACAACCTC AATATGAAAA CTATTNACT      180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTTGT TCATACTGTA TTTATCAAGT      240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTIN AATTATGATT GCCATTATTA      300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GAACTTCAC      360
TTGGTTATTT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA      420
TTTANTTCAN TAATTCTTTT CCTTGTTTAC GTTAATTTTG AAAAGAATGC AT              472
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCAATTGAT ACCTGTAGTA AGTTGACAAT      60
GTGCTGAAAT TTCAAAATTA TATGTAACTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT      120
TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT      180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAAGTGTCTT GNGCANAATG TTCTAGNTAT      240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCAAAAT      300
TGTGTTAGTC TCAATTCCTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT      360
GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAGAAAGT ACATCTGCGT      420
TACAAAGTCT ATCTTCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT      476
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCAT AGAATGGATA      60
```

```

AAATAATGCT GCAAACCTAA TGTTCCTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA 120
CAATCGCAAA TCAAAACCTCA CAAGTGCTCA TCTGTGTAG ATTTAGTGTA ATAAGACTTA 180
GATTGTGCTC CTCGGATAT GATTGTTTCT CANATCTGG GCAATNTTCC TTAGTCAAAT 240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT 300
GTGATTATNA AATTAATCAC AAATTTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT 360
NTNNTTTTAA NATCAAAGTA TTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG 420
TTCNATCTTA TTTTTCCTN GACNACTANT TNCTTTTAA GGGNCTATTC TGANCCATC 479

```

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCAGTGACA ATCAGACCTA 60
TGCTAGTTCC TGTCTATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA 120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA 180
AGTGATTGAG TTTCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA 240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACA GAGAAATAAA CTCAGAAAAA 300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT 360
TTAAGAAAAA CTACCACATG TTGTGTAICC TGGTGCCGGC CGTTTATGAA CTGACCACCC 420
TTTGAATAAA TCTTGACGCT CCTGAACCTG CTCCTCTGCG A 461

```

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT 60
CGGCGCCTCT GCGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCCT 120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGGTAC C 171

```

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGGACGAA GATTCTGCCA GCAGTTGGTC | 60  |
| CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC | 120 |
| AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCAC GACCTTGACG CCGTCGGGGA  | 180 |
| CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCTCGGG AAGGGCGGCC  | 240 |
| CGAGAGATAC GCAGGTGCAG GTGGCCGCC                                   | 269 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA   | 60  |
| GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTTC GTCAACTTCC TTGTCGTGG  | 120 |
| TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG | 180 |
| AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG | 240 |
| TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTT AGAGAGTCCA  | 300 |
| CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG | 360 |
| GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA                 | 405 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 470 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT       | 60  |
| GGCACTTAAT CCATTTTAT TTCAAAATGT CTACAAATTT AATCCCATTA TACGGTATTT  | 120 |
| TCAAAATCTA AATTATTCAA ATTAGCCAAA TCCTTACCAA ATAATACCCA AAAATCAAAA | 180 |
| ATATACTTCT TTCAGCAAAC TTGTACATA AATTAAAAAA ATATATACGG CTGGTGTTTT  | 240 |
| CAAAGTACAA TTATCTTAAC ACTGCAAACA TTTTAAGGAA CTAAATATAA AAAAAACACT | 300 |
| CCGCAAAGGT TAAAGGGAAC AACAAATTCT TTTACAACAC CATTATAAAA ATCATATCTC | 360 |
| AAATCTTAGG GGAATATATA CTTACACGG GATCTTAACT TTTACTCACT TTGTTTATTT  | 420 |
| TTTTAAACCA TTGTTTGGGC CCAACACAAT GGAATCCCC CTGGACTAGT             | 470 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
TTTTTTTTT TTTTTTTGA CCCCCCTCTT ATAAAAACA AGTTACCATT TTATTTTACT      60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC      120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAATC TGCCTAAAGT      180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTCTACT CTTGTAAAAC ATCCAAATTC      240
ATTTTCTTG TCTTTAAAAA TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATTT      300
GCTTCTCTAG CCTCATTTC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA      360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTCAT ATTTCTACCT      420
ACGTTAATAA AATAGCATT TGTGAAGCCA GCTCAAAGA AGGCTTAGAT CCTTTTATGT      480
CCATTTTAGT CACTAAACGA TATCAAAGTG CCAGAAATGA AAAGGTTTGT GAACATTTAT      540
TCAAAGCTA ATATAAGATA TTTCACATAC TCATCTTTCT G                          581
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 578 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
TTTTTTTTT TTTTTTTTTT TTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT      60
CACTCTCTAG ATAGGGCATG AAGAAAACTC ATCTTTCCAG CTTTAAATA ACAATCAAAT      120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTTCTCCTGA      180
AGGAAATCTG TTCATTCTTC TCATTCATAT AGTTATATCA AGTACTACCT TGCATATTGA      240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT      300
TTCATGCAAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATT      360
CAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC      420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT      480
AAAGGAACAT TTTAGCCTG GGTATAATTA GCTAATTCAC TTTACAAGCA TTTATTAGAA      540
TGAATTCACA TGTTATTATT CCTAGCCCAA CACAATGG                          578
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
TTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATT AAAATTCATA      60
GAAAAGTGCC TTACATTAA TAAAAGTTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT      120
GTCTTGAACA CCAATATTAA TTTGAGGAAA ATACACCAAA ATACATTAAG TAAATTATTT      180
AAGATCATAG AGCTTGTAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTA      240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTTTG TGATGAATAT      300
GGGGTGTCAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA      360
TGACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTTCT CTTTCTTCAA TCTTTTAAGG      420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTTCTA TGGAAGGATT      480
AGATATGTTT CCTTTGCCAA TATTAATAAA ATAATAATGT TTACTACTAG TGAAACCC      538
```

## (2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
TTTTTTTTT TTTTITAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTT      60
ATTTATTAGC TCTGCAACTT ACATATTTAA ATTAAGAGAA CGTTTTAGAC AACTGTACAA      120
TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCCT CCAAGAGTGG ATGTGTCCT      180
TCTCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT      240
GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG      300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAT      360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA      420
CCGCTTCCTC AAAGGCGCTG CCACATTGTG GGTCTTTGTC ACTTGTTCCT AAA          473
```

## (2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1621 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
CGCCATGGCA CTGCAGGGCA TCTCGGTTCAT GGAGCTGTCC GGCTTGGCCC CGGGCCCGTT      60
CTGTGCTATG GTCTGGCTG ACTTCGGGGC GCGTGTGTA CGCGTGGACC GGCCCGGCTC      120
CCGCTACGAC GTGAGCCGCT TGGCCCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA      180
GCCCGGGGGA GCCGCGGTGC TGCAGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC      240
CTTCCGCGGC GGTGTCATGG AGAAACTCCA GCTGGGCCCA GAGATTCTGC AGCGGGAAAA      300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGGTT      360
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAGGTGTT CTCTCAAAAA TTGCCAGAAG      420
TGGTGAGAAAT CCGTATGCCC CGCTGAATCT CCTGGGTGAC TTTGCTGGTG GTGGCCTTAT      480
GTGTGCACTG GGCATTATAA TGGCTCTTTT TGACCGCACA CGCACTGACA AGGGTCAGGT      540
```

```

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTAAAGT TCTTTTCTGT GGAAACTCA 600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT 660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGAGGCAA TAGAACCCCA 720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAATTTC CCAATCAGAT 780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTG CAAAGAAGAC 840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC 900
TTTGGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA 960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCAG CCATCCCTTC 1020
TTTCAAAAGG GATCCTTTCA TAGGAGAAAC CACTGAGGAG ATACTTGAAG AATTGSGATT 1080
CAGCCGCGAA GAGATTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA 1140
AGCTAGTCTC TAACTTCCAG GCCCAGCGCT CAAGTGAATT TGAATACTGC ATTTACAGTG 1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTTA 1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTTCTAAA 1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAAGTTTGGG TACTTATACT AAATTATGGT 1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA 1440
TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT 1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT 1560
AAAAGTCACG TGAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620
A 1621

```

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205

```

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210 215 220  
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
 225 230 235 240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245 250 255  
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
 260 265 270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275 280 285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
 290 295 300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305 310 315 320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
 325 330 335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
 340 345 350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
 355 360 365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCAGCAGGC TGGCCAGGG CCTGAGCGGA GGGGGGGGCA GCCTCGCCAG CGGGGGCCCC 60  
 GGGCCTGGCC ATGCCTCACT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC 120  
 CAGTGCAGCC TAGTGGCTCT CACCTGCTTC CTCTGGGCG TGGGCTGCCG GCTGACCCCG 180  
 GGTTTGTACC ACCTGGGGCG CACTGTCCTC TGCATCGACT TCATGGTTT CACGCTGCGG 240  
 CTGCTTCACA TCTTCACGGT CAACAAACAG CTGGGGCCCA AGATCGTCAT CGTAGCAAG 300  
 ATGATGAAGG ACGTGTCTTT TTCTCTCTTC TTCCTCGGCG TGTGGCTGGT AGCCTATGGC 360  
 GTGGCCACGG AGGGGCTCCT GAGGCCACGG GACAGTGAAT TCCCAAGTAT CCTGCGCCGC 420  
 GTCTTCTACC GTCCCTACCT GCAGATCTTC GGGCAGATTC CCCAGGAGGA CATGGACGTG 480  
 GCGCTCATGG AGCACAGCAA CTGCTCGTCG GAGCCCGGCT TCTGGGCACA CCCTCCTGGG 540  
 GCGCAGGCGG GCACCTGCGT CTCCAGTAT GCCAACTGGC TGGTGGTGCT GCTCCTCGTC 600  
 ATCTTCCTGC TCGTGGCCAA CATCTGCTG GTCAACTGCT TCATTGCCAT GTTCAGTTAC 660  
 ACATTCCGCA AAGTACAGGG CAACAGCGAT CTCTACTGGA AGGCGCAGCG TTACCGCCTC 720  
 ATCCGGGAAT TCCACTCTCG GCGCGGCTG GCGCCGCCCT TTATCGTCAT CTCCCACTTG 780  
 CGCCTCCTGC TCAGGCAATT GTGCAGGCGA CCGCGGAGCC CCCAGCGGTC CTCCCCGGCC 840  
 CTCGAGCATT TCCGGGTTTA CCTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGGAA 900  
 TCGGTGCATA AGGAGAACTT TCTGCTGGCA CGCGTAGGG ACAAGCGGGA GAGCGACTCC 960  
 GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAACAGCT GGGACACATC 1020  
 CGCGAGTACG AACAGCGCCT GAAAGTCTG GAGCGGAGG TCCAGCAGTG TAGCCGCGTC 1080  
 CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC TCTGCCCTGC TGCCCCAGG TGGCCGCCA 1140  
 CCCCCTGACC TGCCTGGGTC CAAAGACTGA GCCCTGCTGG CGGACTTCAA GGAGAAGCCC 1200  
 CCACAGGGGA TTTTGTCTCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG 1260  
 GCCTTGTCTT TGAGGTGAGC CCGATGTCCA TCTGGGCCAC TGTGAGGACC ACCTTTGGGA 1320  
 GTGTATCTCT TACAAACCAC AGCATGCCCG GCTCTCCCA GAACCACTCC CAGCCTGGGA 1380

GGATCAAGGC CTGGATCCCG GGCCGTTATC CATCTGGAGG CTGCAGGGTC CTGGGGTAA 1440  
 CAGGGACCAC AGACCCCTCA CCACTCAGAG ATTCCTCACA CTGGGGAAAT AAAGCCATTT 1500  
 CAGAGGAAAA AAAAAAAAAA AAAA 1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC CTGCACGCGC TGGCTCCGGG TGACAGCCGC GCGCCTCGGC CAGGATCTGA 60  
 GTGATGAGAC GTGTCCCAAC TGAGGTGCCC CACAGCAGCA GGTGTTGAGC ATGGGCTGAG 120  
 AAGCTGGACC GGCACCAAGG GGCTGGCAGA AATGGGCGCC TGGCTGATTC CTAGGCAGTT 180  
 GGCGGCAGCA AGGAGGAGAG GCCGCAGCTT CTGGAGCAGA GCCGAGACGA AGCAGTTCTG 240  
 GAGTGCCTGA ACGGCCCCCT GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG 300  
 GGTGAGCCGC CTGCTCGGCG ACCGGAAAGC CCAGCTCTTG CTGGTCAACC TGCTAACCTT 360  
 TGGCCTGGAG GTGTGTTTGG CCGCAGGCAT CACCTATGTG CCGCCTCTGC TGCTGGAAGT 420  
 GGGGGTAGAG GAGAAGTTCA TGACCATGGT GCTGGGCATT GGTCCAGTGC TGGGCTGGT 480  
 CTGTGTCCCG CTCCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCCGCCGCCG 540  
 GCCCTTCATC TGGCACTGT CCTTGGGCAT CCTGCTGAGC CTCTTTCTCA TCCCAAGGGC 600  
 CGGCTGGCTA GCAGGGCTGC TGTGCCCGGA TCCCAGGCCC CTGGAGCTGG CACTGCTCAT 660  
 CCTGGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTGC TTCACTCCAC TGGAGGCCCT 720  
 GCTCTCTGAC CTCTTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCTT 780  
 CATGATCAGT CTTGGGGGCT GCCTGGGCTA CCTCCTGCCT GCCATTGACT GGGACACCAG 840  
 TGCCCTGGCC CCTACCTGG GCACCCAGGA GGAGTGCCCT TTTGGCCTGC TCACCTCAT 900  
 CTTCTCTACC TGCCTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAGCGC TGGGCCCCAC 960  
 CGAGCCAGCA GAAGGGCTGT CGGCCCCCTC CTTGTGCGCC CACTGCTGTC CATGCCGGGC 1020  
 CCGCTTGCTT TTCCGGAACC TGGCGGCCCT GCTTCCCGCG CTGCACCAGC TGTGCTGCCG 1080  
 CATGCCCGGC ACCCTGCGCC GGCTCTTCGT GGCTGAGCTG TGCAGCTGGA TGGCACTCAT 1140  
 GACCTTCACG CTGTTTTACA CGGATTTTGT GGGCGAGGGG CTGTACCAGG GCGTGCCGAG 1200  
 AGCTGAGCCG GGCACCGAGG CCCGAGACCA CTATGATGAA GCGCTTCGGA TGGGCAGCCT 1260  
 GGGGCTGTTT CTGCACTGCG CCATCTCCCT GGTCTTCTCT CTGGTCATGG ACCGGCTGGT 1320  
 GCAGCGATTG GGCACCTCGAG CAGTCTATTG GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC 1380  
 CGGTGCCACA TGCTGTCCC ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCTCACCAGG 1440  
 GTTCACCTTC TCAGCCCTGC AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA 1500  
 GAAGCAGGTG TTCTGCCCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG 1560  
 CCTGATGACC AGCTTCTGCG CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT 1620  
 GGGTGTGGA GGCAGTGGCC TGCTCCCAAC TCCACCCGCG CTCTGCGGGG CCTCTGCTGT 1680  
 TGATGTCTCC GTACGTGTGG TGGTGGGTGA GCCCACCAGG GCCAGGGTGG TTCCGGGCCG 1740  
 GGGCATCTGC CTGGACCTCG CCATCCTGGA TAGTGCTTTC CTGCTGTCCC AGGTGGCCCC 1800  
 ATCCCTGTTT ATGGGCTCCA TTGTCCAGCT CAGCCAGTCT GTCACTGCCT ATATGGTGTG 1860  
 TGCCGCAGGC CTGGGTCTGG TCGCCATTTA CTTTGCTACA CAGGTAGTAT TTGACAAGAG 1920  
 CGACTTGGCC AAATACTCAG CGTAGAAAAC TTCCAGCACA TTGGGGTGA GGGCCTGCCT 1980  
 CACTGGGTCC CAGTCCCGG CTCCTGTTAG CCCCATGGGG CTGCCGGGCT GGGCGCCAGT 2040  
 TTCTGTTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGTGCTGCT GAGGTGCGTA 2100  
 GCTGCACAGC TGGGGGCTGG GCGCTCCCTC TCCTCTCTCC CCAGTCTCTA GGGCTGCCTG 2160  
 ACTGAGGGCC TTCCAAGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCCA GAAGGGCTCC 2220  
 ATGCACTGGA ATGCGGGGAC TCTGCAGGTG GATTACCCAG GCTCAGGGT AACAGCTAGC 2280  
 CTCCTAGTTG AGACACACCT AGAGAAGGGT TTTTGGGAGC TGAATAAACT CAGTCACCTG 2340  
 GTTTCCTATC TCTAAGCCCC TTAACCTGCA GCTTCGTTTA ATGTAGCTCT TGCATGGGAG 2400  
 TTTCTAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTTG TAGGGGAAGA 2460  
 GTCTTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC CACAGCACTG TCTTTTGTCT 2520

GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTTGCCATCA 2580  
CAGAGACACA GGCATTTAAA TATTTAACTT ATTTATTTAA CAAAGTAGAA GGAATCCAT 2640  
TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA 2700  
GGTCCCCCTGA GATAGCTGGT CATTTGGGCTG ATCATTGCCA GAATCTTCTT CTCTGGGGT 2760  
CTGGCCCCCCC AAAATGCCTA ACCCAGGACC TTGGAATTC TACTCATCCC AAATGATAAT 2820  
TCCAAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT 2880  
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTGGGCCAG CCTGGTTCCC CCCACTTCCA 2940  
CTCCCCCTTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAAT TTCCCCTACC 3000  
CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCCTGT TGGAGCTACT 3060  
GCAGGACCAG AAGCACAAAG TGGGGTTTCC CAAGCCTTGG TCCATCTCAG CCCCCAGAGT 3120  
ATATCTCTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG 3180  
GAGGTCTTAT CTCTCAGGGG GGGTTAAGT GCCGTTGCA ATAATGTCGT CTTATTATT 3240  
TAGCGGGGTG AATATTTTAT ACTGTAAGT AGCAATCAGA GTATAATGTT TATGGTGACA 3300  
AAATTAAAGG CTTTCTTATA TGTTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360  
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAATAA AAAAAAAAAA 3410

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCACTCAG TGGCAACACC CGGAGCTGT TTTGTCTTT 60  
GTGGAGCCTC AGCAGTCCCC TCTTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA 120  
CCATGCAGTG CTTAGCTTTC ATTAAGACCA TGATGATCCT CTTCAATTGG CTCATCTTTT 180  
TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTTC 240  
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTTC 300  
TCATCGCAGC CGGCGTTGTG GTCTTTGCTC TTGGTTTCTT GGGCTGCTAT GGTGCTAAGA 360  
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG 420  
AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT 480  
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT 540  
GGAACACCAC CATGAAAGGG CTCAGTGCT GTGGCTTCA CAACTATACG GATTTTGAGG 600  
ACTCACCCCTA CTTCAAAGAG AACAGTGCCT TTCCCCCATT CTGTTGCAAT GACAACGTCA 660  
CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT 720  
GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG 780  
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC 840  
TACAATAAGT CCACTTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAATC GTGAAGAGGC 900  
ACCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA 960  
GAATGGACCT GCCCTTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTAGCG 1020  
ATGCTGACT TTCCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140  
TAGTGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
TGTTACAATG TTAATAAAAA AAAAAAAAAA 1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1           5           10           15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20           25           30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35           40           45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50           55           60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65           70           75           80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85           90           95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100          105          110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
115          120          125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130          135          140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145          150          155          160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165          170          175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180          185          190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195          200          205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
210          215          220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225          230          235          240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
245          250          255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
260          265          270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
275          280          285

```

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 553 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80

Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530

535

540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1           5           10           15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20           25           30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35           40           45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
50           55           60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65           70           75           80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
85           90           95

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
100          105          110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
115          120          125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
130          135          140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145          150          155          160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
165          170          175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
180          185          190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
195          200          205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
210          215          220

```

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GCTCTTTC   | TCCCTCCTC  | TGAATTTAAT | TCTTTCAACT | TGCAATTGTC | AAGGATTACA | 60  |
| CATTTCACTG | TGATGTATAT | TGTGTTGCAA | AAAAAAAAAA | GTGTCTTTGT | TTAAAATTAC | 120 |
| TTGGTTTG   | AATCCATCTT | GCTTTTCCC  | CATTGGAACT | AGTCATTAAC | CCATCTCTGA | 180 |
| ACTGGTAGAA | AAACATCTGA | AGAGCTAGTC | TATCAGCATC | TGACAGGTGA | ATTGGATGGT | 240 |
| TCTCAGAAC  | ATTTCACCCA | GACAGCCTGT | TTCTATCCTG | TTAATAAAAT | TAGTTGGGT  | 300 |
| TCTCTACATG | CATAACAAAC | CCTGCTCCAA | TCTGTCACAT | AAAAGTCTGT | GACTTGAAGT | 360 |
| TTAGTC     |            |            |            |            |            | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACAAAGATGA | ACCATTTCTC | ATATTATAGC | AAAATTAAAA | TCTACCCGTA | TTCTAATATT | 60  |
| GAGAAATGAG | ATNAAACACA | ATNTTATAAA | GTCTACTTAG | AGAAGATCAA | GTGACCTCAA | 120 |
| AGACTTTACT | ATTTTCATAT | TTTAAGACAC | ATGATTTATC | CTATTTTAGT | AACCTGGTTC | 180 |
| ATACGTTAAA | CAAAGGATAA | TGTGAACAGC | AGAGAGGATT | TGTTGGCAGA | AAATCTATGT | 240 |
| TCAATCTNGA | ACTATCTANA | TCACAGACAT | TTCTATTCTT | TT         |            | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA      60
TATTTATCCT CCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA      120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA      180
TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGGAA ACAGATGAGG TCACCTCTGT      240
GACTGCCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGAGAGAAAT      300
TGGGT                                         305
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAAATC TGAGTGAAAA      60
AANTCCTGGG T                                         71
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA      60
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC      120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACAAANC GGAATTAANT      180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT                                         212
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90
```

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA 60
GAATAAGATT TGCTAAAAGA TTGGGGGCTA AAACATGGTT ATTGGGAGAC ATTCTTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTGTGTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA 60  
TTATCAANTA TTGTGT 76

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT 60  
CAATGTGCTG GGTCAATATG AGGGGAGGAG ACTCTAAAT AGCCAATTTT ATTCTCTTGG 120  
TTAAGATTG T 131

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAAATGC GTTACCAACT ATACCACTGG 60  
CTTGAAAAAG AGGTGATAGC TCTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA 120  
CTACAGTCTG CATTGGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT 180  
TTGCCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG 240  
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC 300  
CATGGTGGGG GTCTTGATC TGTAGAATG GAATTGATT TGCTTTTGCA AGAATCTCAG 360  
CAGGAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC 420  
CTCTTGCTT GT 432

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAACTGA GCTGAAATTT CTAATTCAC TTTCTAACCAT 60  
AGTAAGAATG ATATTTCCTC CCAGGCATCA CCAATATTT ATAAAAATTT GT 112

## (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG 54

## (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCT CTACCAGCTC 60  
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA 120  
TTCTCTCTGA AGTCTAGGT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC 180  
CCAAAGCATT TGGACAGTT CTGTTGTGT TTAGAATGG TTTTCCTTT TCTTAGCCTT 240  
TTCTGCAAA AGGCTCACT AGTCCCTTG TTGCTCAGTG GACTGGGCTC CCCAGGGCCT 300  
AGGCTGCCTT CTTTCCATG TCC 323

## (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC 60  
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCATC 120

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG 180  
GATAAACAAA GT 192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTGA TGGAAAGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCCTTGACA 60  
TATAATGACG CAACAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA 120  
GTTTCCATG TGTTCGCGG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA 180  
TTCTGATTC CATTTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA 240  
CTTATTAAA AGCTCTTATT TTGTGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT 300  
TGACGAGGA AGCAOGTGTG GGTGTTGT AAAGCTCTTT GCTAATCTTA AAAAGTAATG 360  
GG 362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAG GATCGTGTC ACTCCTGTGG ACATCTTGGT TTAATGGAGT TTCCCATGCA 60  
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAATGAGA 120  
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC 180  
TTCTGAAC TAATTAGGCA GCTGTGTAAT CTGATGTGAT TTGGTTTATT ATCCAATAA 240  
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC 300  
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT 332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC      60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT      120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT      180
TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG      240
GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT      300
GTAACAATCT ACAATTGGTC CA                                           322

```

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

ACAAGCCTTC ACAAGTTTAA CTAAATGGG ATTAATCTTT CTGTANTTAT CTGCATAATT      60
CTTGTTTTTC TTTCCATCTG GCTCCTGGGT TGACAATTG TGAAACAAC TCTATTGCTA      120
CTATTAAAAA AAAATCACA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCTG      180
CTATTCTGT TTTGTCAAG AAATTATATT TTCAAATA TGTNTATTG TTTGATGGGT      240
CCCACGAAC ACTAATAAAA ACCACAGAGA CCAGCCTG                               278

```

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GTTTAAAAA CTGTTTAGC TCCATAGAGG AAAGAATGTT AAAGTTTGT TTTTAAAAA      60
TGATTCTCTG AGGTAAACT TGGTTTCAA ATGTTATTT TACTTGTATT TTGCTTTTGG      120
T                                           121

```

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTTANAACC ATGCCTAGCA CATCAGAATC CCTCAAAGAA CATCAGTATA ATCCTATACC | 60  |
| ATANCAAGTG GTGACTGGTT AAGCGTGCGA CAAAGGTCAG CTGGCACATT ACTTGTGTGC | 120 |
| AAACTTGATA CTTTGTCTT AAGTAGGAAC TAGTATACAG TNCCTAGGAN TGGTACTCCA  | 180 |
| GGGTGCCCCC CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTTCGCT | 240 |
| CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG | 300 |
| TTCCCAAGGA TGCAAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT            | 350 |

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT  | 60  |
| GCTGTGATTG TATCCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT  | 120 |
| GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA  | 180 |
| CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG  | 240 |
| AAAAGTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC   | 300 |
| TCCCAGGAAC CCGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCCCAC TGGCGTGATG | 360 |
| GGTGCAGANG GATGAAGCAG CCAGNTGTTT TGCTGTGGT                         | 399 |

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT | 60  |
| GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGGGCC GTGCTAAATG AGCTTCGGGA | 120 |
| TTGGCTGGTC CCACTGGTGG TCACTGTCTAT TGGTGGGGTT CCTGT                | 165 |

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC      60
TTAACTTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCCAA      120
TGCTGGGCAG TCTCCCATGC CTCCACAGT GAAAGGCTT GAGAAAAATC ACATCCAATG      180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGGG CATANANGGT      240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTTGCCAC TGTACATTCC CCATNTTTAA      300
AAAAACTGAT GCCTTTTTTT TTTTTTTT TAAATTC      338
```

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GGGAATCTTG GTTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA      60
GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA      120
ATTCAACACG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCT GCTCACGCC TATCATCTGC      180
ATTTGCCCTTA CTCAGGTGCT ACCGGACTCT GGGCCCTGAT GTCTGTAGTT TCACAGGATG      240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCTACTTCT TCGGATGTGT TTTTAATAAT      300
GTCAGCTATG TGCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG      360
GCCTGGAAC TGTTTAAAGT GT      382
```

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
ACCAAANCCT CTTTCTGTTG TGTNGATTT TACTATAGGG GTTNGCTTN TTCTAAANAT      60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTGCTCCAT ANAATTATTG      120
TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTT      180
ATATTGACGA TAAAGGAGAA      200
```

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
ACTTTATTTT CAAAACACTC ATATGTTGCA AAAACACAT AGAAAAATAA AGTTTGGTGG      60
GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTG      120
ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA      180
AATGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG      240
TTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG      300
ATTCAAAAC CAAGTAATTT TAAACAAAGA CACTT                                     335
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGATTTTA      60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT      120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA      180
CACATGGTCC AACAACTCTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC      240
TTCAAACATC ATAGCCAATG ATGCCCGCTG TGCCTATAAT CTCTCCGACA TAAACCACA      300
TCAACACCTC AGTGGCCACC AAACCATTCG GCACAGCTTC CTAACTGTG AGCTGTTTGA      360
AGCTACCAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT      420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGCGGTANT                                     459
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
ACATTTCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG      60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG      120
ACCATCCGAC TTCCTGTGT                                     140
```

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
ACTTCAGTAA CAACATACAA TAACAACATT AAGTGATAT TGCCATCTTT GTCATTTTCT    60
ATCTATACCA CTCTCCCTTC TGAACAACAA AATCACTANC CAATCACTTA TACAAATTTG    120
AGGCAATTAA TCCATATTTG TTTCAATAA GGAAAAAAG ATGT                          164
```

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
ACGTAGACCA TCCAACCTTG TATTGTAAAT GGCAACATC CAGNAGCAAT TCCTAAACAA    60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT    120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGTG ATAACTTCA    180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG    240
TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT    300
CAA                                     303
```

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC    60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTGAGAGA GCTCCTTTGC CAACAGGCCT    120
CCAAGTCAGG GCTGGGATTG GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT    180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGAACAAGC TGCCACTTTC TAAAGTAGCC    240
AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG    300
TAGGGGTGAG CTGTGTGACT CTATGGT                                     327
```

## (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG      60
ACTGGAACAC ATACCCACAT CTTTGTCTTG AGGGATAATT TTCTGATAAA GTCTTGCTGT      120
ATATTCAGGC ACATATGTTA TATATTATTC AGTTCATGT  TTATAGCCTA GTT          173
```

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACACAC TCACTGTGCC TTTCTATCCT      60
ATGGGATATA TTATTTGATG CTCCATTTC AATCACAATAT ATGAATAATA CACTCATACT      120
GCCCTACTAC CTGCTGCAAT AATCACAATC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG      180
GTGGTCTTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC      240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA      300
TAGATTATNT CCAAAATCAG TCAATTAAGT TACTATTAAC ACTCTACCGG ACATGTCCAG      360
CACCCTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT      420
CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTTAA TTACCATGCT ATGGTGG      477
```

## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC      60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT      120
```

GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA 180  
TTTCAGGCAG AGGGAACAGC AGTGAAA 207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTCCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60  
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC 60  
AGCAAGATGG CTTTGAATC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120  
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG 180  
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60  
CTTCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120  
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 285 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTGAG    60
CTTCTGCTCT TATGTCTCTA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA    120
GCACATCAAT AAAGTCCAAA GTCTTGGAAT TGGCCTTGGC TTGGAGGAAG TCATCAACAC    180
CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA    240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT                      285
```

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC    60
ACCCCAAATT TTTCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC    120
CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG    180
ATTGGCACAG GAGTCGAAGG TGTTCAGCTC CCTCTCTCCG TGAACGAGA CTCTGATTG    240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG    300
GTGAGGCTG TCTCATCCAT ATGGATCTTC CGG                                333
```

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```
ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG    60
GAAAGTGCTT TGGGAACGTG AAAGTGCCCTA ACACATGATC GATGATTTT GTTATAATAT    120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCAGCCCC    180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT    240
```

GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG 300  
GCCCTGGT 308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 295 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA 60  
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAAGTGA 120  
GAATAGGAGA TTATGTTTGG CCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT 180  
CTAATATATT CTCAATCAA TAAGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT 240  
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT 295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT 60  
GAAGAGCAAA ACAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC 120  
CTTAGT 126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 442 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTG TGAGAAAATG 60  
AANCCAGCAG GCTGCCCCCTA GTCAGTCCTT CCTTCCAGAG AAAAGAGAT TTGAGAAAGT 120  
GCCTGGGTAA TTCACCATTA ATTTCTCCC CCAACTCTC TGAGTCTTCC CTTAATATTT 180

CTGTTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTGGGATCC CAGTGAAGTA 240  
NATGTTTGTA GCCTTGCGATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG 300  
CCAACCCTGT TTTCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA 360  
NACAGACGGG CTCTTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG 420  
TGTTCAATTCT CTGATGTCCT GT 442

## (2) INFORMATION FOR SEQ ID NO:159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAGT ATGGGTGACG TTGTAGGTTC 60  
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG 120  
GCTGCTGTGG ACTGTTGTTG ATTCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG 180  
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC 240  
TGCTGTGGTG CCGGGANGTG AANGTGTTGT GTCACCTGAG CTGGGCCAGC TCTGGAAGT 300  
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA 360  
CGAACCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCCAA AGCCTGAAGT TATGGTGTCTN 420  
TCAGGTAANA ATGTGTTTC AGTGTCCTG GGCNGCTGTG GAAGTTGTA NATGTCCACC 480  
AAGGAATAA GCTGTGGT 498

## (2) INFORMATION FOR SEQ ID NO:160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC 60  
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT 120  
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGTCTGA GGAAGCCATT TGAGTCTGGC 180  
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCA GATGCCTCTC 240  
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACT TGTATAATTC TAACATCCTG 300  
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA 360  
CTTGTAAGAT GAAGCTTGA 380

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTGGCC TTGCCTGTCA    60
CACTGTCCAC TGGCCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT      114
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
ACTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTAT ATATCCTCAT ATATATCAAA    60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT    120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT      177
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC    60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT    120
CATCAGCGGC ATGATGT      137
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA    60
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA    120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAACTCGG AGTGGCAGAC TGACAACTGT    180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG    240
GGTTATGACA AAGACAACCTG CCAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG    300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCACTG AATGGATAAT CTAATGTGCT    360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT    420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT    469
```

## (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG    60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCT    120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT    180
TCCTCTGAGA TGAGT    195
```

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 383 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACASTCACTC ATAGCCTCGC    60
CGAGGTGCGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT    120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACTCG CCAAAGAATT    180
TTTGACAGCC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG    240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC    300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT    360
NGGGGCCCTT TTGGTGAAC TTC    383
```

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```
ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT   60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC   120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC   180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC   240
TGANGTC                                         247
```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```
ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA   60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG   120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGGC   180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAATA CTCCAGCTTG   240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA                                         273
```

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```
ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC   60
AGCTCAGACC AGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA   120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTGG CACAGGTGAG   180
GGCAGCAGAA AGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC   240
CTTGCCATGG GCAAAGGCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC   300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACTGG   360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAGGC TTCTGGGGGC CATCAGCTGC   420
TCGAACACTG.A                                         431
```

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGAGTTCA GAGGTGGAGC   60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT   120
CCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGTGAT   180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT   240
TCAAAGCTAG GGGTCTGGCA GGTGGA                                     266
```

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA   60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCCTGG TGCATCCGCA GTGGGTGCTG   120
TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG   180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA   240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAG   300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC   360
GCGGGGAAC CTTCGCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC   420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC   480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GCGGAGGGG AAGACCAGAA GGACTCCTGC   540
AACGCTGACT CTGGGGGGCC CCTGATCTGC AACGGTACT TGCAGGGCCT TGTGTCTTTC   600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAAATTC   660
ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AAGCCATGAA   720
ATTGACCCCC AAATACATCC TGCAGGAAGG ATTCAGGAAT ATCTGTTCCC AGCCCCCTCT   780
CCCTCAGGCC CAGGAGTCCA GGGCCCCAGC CCCTCCTCCC TCAACCAAG GTTACAGATC   840
CCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTC TCCCTCAGAC   900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC   960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC   1020
CCAACCCNTC ATTCCCAGA CCCAGAGGTC CAGGTCCCAG CCCTCCTGCC CTCAGACCCA   1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTGTGGC ACGTTGACCC   1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCCC TAGATCCAGA AATAAGTTT   1200
AAGAGAAGNG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA               1248
```

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:

105

(A) LENGTH: 159 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
20           25           30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
35           40           45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
50           55           60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65           70           75           80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
85           90           95
Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
100          105          110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
115          120          125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
130          135          140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GGCAGCCCGC ACTCGCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC      60
TCGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC      120
TACACCATCG GGCTGGGCTT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG      180
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCCTTGCT CGCTAACGAC      240

```

```

CTCATGCTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACACCATCCG GAGCATCAGC 300
ATTGCTTCGC AGTGCCCTAC CGCGGGGAAC TCTTGCCCTG TTTCTGGCTG GGGTCTGCTG 360
GCGAACCGTG AGCTCACGGG TGTGTGCTG CCCTCTTCAA GGAGGTCTCT TCCCCAGTCG 420
CGGGGGCTGA CCCAGAGCTC TGCCTCCAG GCAGAATGCC TACCGTGCTG CAGTGCCTGA 480
ACGTGTCGGT GGTGTCTGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCACCCCA 540
GCATGTTCTG CGCCGGCGGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG 600
GGCCCTGAT CTGCAACGGG TACTTGCAAG GCCTTGCTG TTTGGAATAA GCCCCGTGTG 660
GCCAAGTTGG CGTGCCAGGT GTCTACACCA ACCTCTGCAA ATTCACTGAG TGGATAGAGA 720
AAACCGTCCA GGCAGTTAA CTCTGGGGAC TGGGAACCCA TGAAATTGAC CCCCATAATAC 780
ATCCTGCGGA AGGAATTGAG GAATATCTGT TCCCAGCCCC TCCTCCCTCA GGGCAGGAG 840
TCCAGGCCCC CAGCCCTTCC TCCCTCAAAC CAAGGGTACA GATCCCCAGC CCCTCCTCCC 900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC CTCTCCCTC AGACCCAGGA GTCCAGCCCC 960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC CCAGCCCTC CTCCCTCAGA CCCAGGGGTT 1020
GAGGCCCCCA ACCCTCCTC CTTCAGAGTC AGAGGTCCAA GCCCCCAACC CCTCGTTCCC 1080
CAGACCCAGA GGTNNAGTCC CCAGCCCTC TTCCNTCAGA CCCAGNGGTC CAATGCCACC 1140
TAGATTTTCC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCCAACCTT ACCAGTTGGT 1200
TTTTCATTTT TNGTCCCTTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAA 1260
AAAAA 1265

```

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

GGTCAGCCGC ACATGTTTC CAGAAGTGAG TGCAGAGCTC CTACACCATC GGGCTGGGCC 60
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG 120
TACGGCACCC AGAGTACAAC AGACCCTTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG 180
AGGAATCCGT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTCCTTCG CAGTGCCTTA 240
CCGCGGGGAA CTCTTGCCCTC GTTCTGGCT GGGGTCTGCT GCGGAACGGT GAGCTCACGG 300
GTGTGTGTCT GCCCTCTTCA AGGAGGTCTC CTGCCCAGTC GCGGGGGCTG ACCCAGAGCT 360
CTGCGTCCCA GGCAGAATGC CTACCGTGCT GCAGTGCGTG AACGTGTCGG TGGTGTCTGA 420
NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACACCCC ANCATGTTCT GCGCCGGCGG 480
AGGGCAAGAC CAGAAGGACT CCGCAACGT GAGAGAGGGG AAAGGGGAGG GCAGGCGACT 540
CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CCGCATGGCG AGATGCAGAG 600
ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AAAGTGAAG AAACAGAGAA 660
ATAAACACAG GAATAAAGAG AAGCAAAGGA AGAGAGAAAC AGAAACAGAC ATGGGGAGGC 720
AGAAACACAC ACACATAGAA ATGCAGTTGA CCTTCCAACA GCATGGGGCC TGAGGGCGGT 780
GACCTCCACC CAATAGAAAA TCCTCTTATA ACTTTTGACT CCCCCAAAAC CTGACTAGAA 840
ATAGCCTACT GTTGACGGGG AGCCTTACCA ATAACATAAA TAGTCGATT ATGCATACGT 900
TTTATGCATT CATGATATAC CTTTGTGGA ATTTTGTGAT ATTTCTAAGC TACACAGTTC 960
GTCTGTGAAT TTTTAAAT TGTGCAACT CTCCTAAAAT TTTCTGATG TGTATTGA 1020
AAAAATCCAA GTATAAGTGG ACTTGTCAT TCAAACAGG GTTGTCAAG GGTCAACTGT 1080
GTACCCAGAG GGAACAGTGG ACACAGATTC ATAGAGGTGA AACACGAAGA GAAACAGGAA 1140
AAATCAAGAC TCTACAAAGA GGCTGGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTTT 1200
GGGAGGCGAG GCAGGCAGAT CACTTGAGGT AAGGAGTTCA AGACAGCCT GGGCAAAATG 1260
GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCCTGT 1320
AATCCCACT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT 1380
GAAGTGAGTT GAGATCACAC CACTATATCT CAGCTGGGGC AACAGAGTAA GACTCTGTCT 1440
CAAAAAAAAA AAAAAAAAAA 1459

```

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```
GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCCTGCTC GGGCGTCCTG      60
GTGCATCCCG AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCCTGC ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCITGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAACCT TTGCCTCGTN TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCCAGCATG TTCGCGCCG GGGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGCCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTC GAAAAGCCCC GTGTGGCCAA CTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCA CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCCCTCCT CCTCAGGCCC AGGAGTCCAG GCCCCCAGCC CCTCCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCCT CTCCTCTCAGA CCCAGGAGTC CAGACCCCCC AGCCCCCTCNT      840
CCNTCAGACC CAGGAGTCCA GCCCCCTCCT CNTCAGACGC AGGAGTCCAG ACCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCCCACCCCC TCNTCCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC      1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNCCTGTGA CACAGTGCCC CCTTGTGGCA      1080
NGTTGACCCA ACCTTACCAG TTGTTTTTTC ATTTTTTGTG CTTTTCOCCT AGATCCAGAA      1140
ATAAAGTNTA AGAGAAGCCG AAAAAAA      1167
```

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1           5           10           15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20           25           30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35           40           45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
50           55           60
```

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
195 200 205

## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC AGCCCTGGCA GCGGGCACTG GTCATGGAAA ACGAATTGTT CTGCTCGGGC 60  
GTCCTGGTGC ATCCGCAGTG GGTGCTGTCA GCGGCACACT GTTCCAGAA CTCCTACACC 120  
ATCGGGCTGG CCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA GATGGTGGAG 180  
GCCAGCCTCT CCGTACGGCA CCCAGAGTAC AACAGACCCT TGCTCGCTAA CGACCTCATG 240  
CTCATCAAGT TGGACGAATC CGTGTCCGAG TCTGACACCA TCCGGAGCAT CAGCATTGCT 300  
TCGCAGTGCC CTACCGCGGG GAACTCTTGC CTCGTTTCTG GCTGGGGTCT GCTGGCGAAC 360  
GATGCTGTGA TTGCCATCCA GTCCAGACT GTGGGAGGCT GGGAGTGTGA GAAGCTTTCC 420  
CAACCCTGGC AGGGTTGTAC CATTTCGGCA ACTTCCAGTG CAAGGACGTC CTGCTGCATC 480  
CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGAA CACTGTGATC AACTAGCCAG 540  
CACCATAGTT CTCGGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT 600  
ACTAACCATG CCGATGTTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA TCTTGTATC 660  
CAGTTATCCT CACTGAATTG AGATTTCCTG CTTCAAGTGC AGCCATTCCC ACATAATTTC 720  
TGACCTACAG AGGTGAGGGA TCATATAGCT CTTCAAGGAT GCTGTACTC CCCTCACAAA 780  
TTCATTTCCT CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCAGGG TGGGTGTGCA 840  
GGTCACAATG ATGAATGTAT GATCGTGTTT CCATTACCCA AAGCCTTTAA ATCCCTCATG 900  
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTAGT GTATGCTGTC CATTATGCA 960  
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTTGGG 1020  
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC 1080

TTAATAAACA GAAGCTGTGA TGTAAAAA AAAAAAAA

1119

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15  
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30  
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu  
 50 55 60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val  
 100 105 110  
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu  
 115 120 125  
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg  
 130 135 140  
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser  
 145 150 155 160  
 Pro Gly Thr Leu

## (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCGTC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60

CCAGCTGCCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT 120  
 GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGGCAAGCG CTTCTGCTGA 180  
 AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA 240  
 AAAAAAAAAA 250

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA 60  
 TCACCCAGAC CCGGCCCTG CCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA 120  
 CTCTGCTACT CGGAACTAT TTTATGTAA TTAATGTATG CTTTCTTGT TATAAATGCC 180  
 TGATTTAAAA AAAAAAAAAA AA 202

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG 60  
 AATGTTTAGG CAGTGCTAGT AATTTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT 120  
 TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA 180  
 GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA 240  
 AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC 300  
 CTACTCTGTT CCTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GCGAAGCCAA 360  
 ATTGATAATA TTCTATGTTT TAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW 420  
 TTTTATTTCC AGGAATATGG KGTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT 480  
 AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC 540  
 CAAAAAAAAA AAAAAAAA 558

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTGTTGA TCCAACCCTG GCTTWTTTTC 60  
 AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG 120  
 CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG 180  
 TTWGCATTC ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA 240  
 CTAAGGTAA ACTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA 300  
 TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT 360  
 NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TACGCATARA 420

AWTGSTGARA AAATTAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAA AAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC | 60  |
| AGTACCACTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCAGTGCT | 120 |
| GGTGCCAGCC TGACCGCCAC TCTCACATTT GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT | 180 |
| GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTCCTCCT ACAAGTGAGA TTTAGATAT  | 240 |
| TGTTAATCCT GCCAGTCTTT CTCTTCAAGC CAGGGTGAT CCTCAGAAAC CTACTCAACA  | 300 |
| CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT | 360 |
| GCCATTTCAA AAAAAAAAAA AAAA                                        | 384 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCGAATGG GACCGCTGGC TTATAAGCGA TCATGTYNYT CCRGTATKAC CTCAACGAGC  | 60  |
| AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG | 120 |
| CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA | 180 |
| AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGGCGCCTGT CCTCTGAGGG TCCCTTAAAC | 240 |
| TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAAC CTTCGGACTG  | 300 |
| TGAGCCCTGA TGCCTTTTG CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCGATTG  | 360 |
| ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCATA AAGGGAACAC ATTTGACTTT  | 420 |
| TTTTTCTCAT ATTTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST | 480 |
| TAAAAAAAAA AAAAAA                                                 | 496 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC | 60  |
| CAAGTATCYT GCGCSGCGTC TTCTACCGTC CTFACCTGCA GATCTTCGGG CAGATTCCCC | 120 |
| AGGAGGACAT GGACGTGSCC CTCATGGAGC ACAGCAACTG YTCGTGGAG CCCGGCTTCT  | 180 |
| GGGCACACCC TCCTGGGGCC CAGGCGGGCA CTGCGTCTC CCAGTATGCC AACTGGCTGG  | 240 |
| TGGTGCTGCT CCTCGTCATC TTCCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA | 300 |
| TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG | 360 |
| GCGCAGCGTT ACCGCTCAT CCGG                                         | 384 |

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT      120
CCAGGAAACT CTCAATCAAG TCACCGTCGA TGAACCTGT GGGCTGTTT TGTCTTCCGC      180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT      240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAG CTCTCTGACA GTGAGGTCAC      300
CAGCCCTATC ATGCCGTTGA MCCTGCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAGT      360
CTCACCAGAG TTCTGCATTA CCAGAGAGCC GTGGCAAAAG ACATTGACAA ACTCGCCACG      420
GTGGAAAAAG AMCAMCTCCT GGARGTGCTN GCCGCTCCTC GTCMGTGGT GGCAGCGCTW      480
TCCTTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC      540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT                                577
```

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```
AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGCTGSGT AGAATYCAIW      60
ACTKGGAAAA GMAACATTA AGCCTGGACA CTGGTATTAA AATTCACAAT ATGCAACACT      120
TTAAACAGTG TGTCAATCTG CTCCCYYNAC TTTGTCATCA CCAGTCTGGG AAKAAGGGTA      180
TGCCCTATTG ACACCTGTTA AAAGGGCGCT AAGCATTTTT GATTCAACAT CTTTTTTTTT      240
GACACAAGTC CGAAAAAAGC AAAAGTAAAC AGTTATYAAT TTGTTAGCCA ATTCACCTTC      300
TTTATGGGAC AGAGCCATYT GATTTAAAAA GCAAATTGCA TAATATTGAG CTTYGGGAGC      360
TGATATTGTA GCGGAAGAGT AGCCTTTCTA CTTCACCAGA CACAACTCCC TTTTATATTG      420
GGATGTTNAC NAAAGTWATG TCTCTWACAG ATGGGATGCT TTTGTGGCAA TTCTGTTCTG      480
AGGATCTCCC AGTTTATTTA CCACTTGAC AAGAAGGCGT TTTCTTCCTC AGGC          534
```

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT      240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTKGACKARG      300
GGGGACAAAG AAAAGCAAAA CTGAMCATAA RAAACAATWA CCTGGTGAGA ARTTGACATA      360
ACAGAAATWR GGTAGTATAT TGAARNACAG CATCATTAAT RMGTWTWKTT WTTCTCCCTT      420
```

GCAAAAAACA TGTACNGACT TCCCGTTGAG TAATGCCAAG TTGTTTTTTT TATNATAAAA 480  
CTTGCCCTTC ATTACATGTT TNAAGTGGT GTGGTGGGCC AAAATATTGA AATGATGGAA 540  
CTGACTGATA AAGCTGTACA AATAAGCAGT GTGCCTAACA AGCAACACAG TAATGTTGAC 600  
ATGCTTAATT CACAAATGCT AATTCATTA TAAATGTTTG CTAAATACA CTTTGAACATA 660  
TTTTCTGTN TTCCAGAGC TGAGATNTTA GATTTTATGT AGTATNAAGT GAAAAANTAC 720  
GAAATAATA ACATTGAAGA AAAANANAAA AAANAAAAAA A 761

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT TTGCGGAIN CTACTATTTT ATTGCAGGAN GTGGGGGTGT ATGCACCGCA 60  
CACCGGGGCT ATNAGAAGCA AGAAGGAAGG AGGGAGGGCA CAGCCCTTG CTGAGCAACA 120  
AAGCCGCCTG CTGCTTCTC TGTCTGTCTC CTGGTGCAGG CACATGGGGA GACCTCCCC 180  
AAGGCAGGGG CCACCACTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG 240  
TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTGACCCAG 300  
GTCATTGTGC CCGCCCAAG CACAGCGTAN ATCTGAAAA GACAGAATGC TTTCTTTTC 360  
AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTNG GCTNGGTCTT GGTACNCTTG 420  
GTTCCGCCCA GCTCCNCGTC CAAAAANTAT TCACCCNCT CCNAATTGCT TGCNGNCCC 480  
CC 482

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT TTTAAAAACA GTTTTTCACA ACAAATTIA TTAGAAGAAT AGTGGTTTG 60  
AAAACCTCTG CATCCAGTGA GAACTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA 120  
AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAG 180  
CGCTTTTGAC ATACAATGCA CAAAAAAGG AGGGGGGGG GACCACATGG ATTAATAATT 240  
TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT 300  
TGAAAAATTT CATGTATGCA ATCCAACCA AGAACTTNAT TGGTGATCAT GANTNCTCTA 360  
CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAA ANCACNCGT ACAAANAANA 420  
TCTGTAATTN ANTTCAACCT CCGTACNGAA AAATNTTNT TATACACTCC C 471

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTT TASTGTCGGM CTGTTACGCC ACCAACTCTA ACAAGTTGCT 60  
GTCTTCCACT CACTGTCTGT AAGCTTTTAA ACCCAGACWG TATCTTCATA AATAGAACAA 120

```

ATTCTTCACC AGTCACATCT TCTAGGACCT TTTTGGATTG AGTTAGTATA AGCTCTTCCA 180
CTTCCTTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTAGAAAGG AATTYAATTG 240
CTCGTTCTCT AACAATGTCC TCTCCTTGAA GTATTGGCT GAACAACCCA CCTAAAGTCC 300
CTTTGTGCAT CCATTTTAAA TATACCTAAT AGGGCATGK TNCAGTAGG TAAATTCTGC 360
AAGAGTCATC TGTCTGCAA AGTTGCCGTTA GTATATCTGC CA 402

```

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT 60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATCCC TGAGTCAGAC 120
ATGCTYTTTT GAYTACCGTG TGCCAAGTGC TGGTGATTCT YAACACACYT CCATCCCGYT 180
CTTTTGTGGA AAAACTGGCA CTTKTCTGGA ACTAGCARGA CATCACTTAC AAATTCACCC 240
ACGAGACACT TGAAGGTGT AACAAAGCGA YTCCTGCATT GCTTTTTGTC CCTCCGGCAC 300
CAGTTGTCAA TACTAACCCG CTGGTTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA 360
TACATCTCCT GACAGTACTG AAGAACTTCT TCTTTGTTT CAAAAGCARG TCTTGGTGCC 420
TGTTGGATCA GGTTCCTATT TCCCGATCYG AATGTTTACA TGGCATATTT WACTTCCAC 480
AAAACATTGC GATTTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATTG GCTGCAAGAG 540
CCTCGATGTA GCGGGCCAGC GCCAAGGCAG GCGCCGTGAG CCCCACCAGC AGCAGAAGCA 600
G 601

```

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

ATACAGCCCA NATCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TCGGGTCACT 60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACCTCYTT 120
CCCAACGCAG GCAGMAGCGG GSCCGGTCAA TGAAGTCCAY TCGTGGCTTG GGKTKGACGG 180
TKAAGTGCA GAGAGGCTG ACCACCTCGC GGTCCACCAG GATGCCCGAC TGTGCGGGAC 240
CTGCAGCGAA ACTCCTCGAT GGTCTGAGC GGGAAGCGAA TGAGGCCAG GGCCTTGCCC 300
AGAACCTTCC GCCTGTTCTC TGGCGTCACC TGCAGCTGCT GCCGTGACA CTCGCGCTCG 360
GACCAGCGGA CAAACGGCRT TGAACAGCCG CACCTCACGG ATGCCAGTG TGTGCGCTC 420
CAGGAMMGC ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCTCCGCGG GTRATGGCGT 480
CTGCAGTGT TTTGTGATG TTCTCCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA 540
CTCGCGCTG CGTGAGCAGC ATGAAGGCGT TGTGCGCTG CAGTCTTCT TCAGGAAGT 600
CACGCAAT 608

```

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
GAACGGCTGG ACCTTGCCCTC GCATTGTGCT TGCTGGCAGG GAATACCTTG GCAAGCAGYT    60
CCAGTCCGAG CAGCCCCAGA CCGCTGCCGC CCGAAGCTAA GCCTGCCTCT GGCCTTCCCC    120
TCCGCCTCAA TGCAGAACCA GTAGTGGGAG CACTGTGTTT AGAGTTAAGA GTGAACACTG    180
TTTGATTTTA CTGGGAATT TCCTCTGTTA TATAGCTTTT CCCAATGCTA ATTCCCAAC    240
AACAACAACA AAATAACATG TTGCCTGTT AAGTTGTATA AAAGTAGGTG ATTCTGTATT    300
TAAAGAAAAA ATTACTGTGA CATATACTGC TTGCAATTC TGTATTTATT GKTNCTSTGG    360
AAATAAATAT AGTTATTAAA GGTGTGCANT CC                                392
```

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
CCSTTKGAGG GGTKAGGKYC CAGTTYCCGA GTGGAAGAAA CAGGCCAGGA GAAGTGCCTG    60
CCGAGCTGAG GCAGATGTTT CCACAGTGAC CCCCAGAGCC STGGGSTATA GTYTCTGACC    120
CCTCNCAAGG AAAGACCACS TTCTGGGGAC ATGGGCTGGA GGGCAGGACC TAGAGGCACC    180
AAGGGAAGGC CCCATTCCGG GSGTGTTCCT CGAGGAGGAA GGAAGGGGC TCTGTGTGCC    240
CCCCASGAGG AAGAGGCCCT GAGTCCTGGG ATCAGACACC CCTTCACGTG TATCCCCACA    300
CAATGCAAG CTCACCAAGG TCCCCTCTCA GTCCCCTTCC STACACCCCTG AMCGGCCACT    360
GSCSCACACC CACCCAGAGC ACGCCACCCG CCATGGGGAR TGTGCTCAAG GARTCGCNGG    420
GCARCGTGA CATCTNGTCC CAGAAGGGGG CAGAATCTCC AATAGANGGA CTGARCMSTT    480
GCTNANAAAA AAAAAAANA AA                                502
```

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
GGTTACTTGG TTTCATTGCC ACCACTAGT GGATGTCATT TAGAACCAAT TTGCTGCTC    60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTT    120
WAGCTGTTTK GAGTTGATTS GCACCACTGC ACCCACAAC TCAATATGAA AACYAWTTGA    180
ACTWATTTAT TATCTTGTA AAAGTATAAC AATGAAAATT TTGTTCATAC TGTATTKATC    240
AAGTATGATG AAAAGCAAWA GATATATATT CTTTATTAT GTTAAATTAT GATTGCCATT    300
ATTAATCGGC AAAATGTGGA GTGTATGTT TTTTCACAGT AATATATGCC TTTTGTAAC    360
TCACTTGTTT ATTTTATTGT AAATGARTTA CAAAATCTT AATTTAAGAR AATGGTATGT    420
WATATTTATT TCATTAATTT CTTTCCTKGT TTACGTAAAT TTTGAAAAGA WTGCATGATT    480
TCTTGACAGA AATCGATCTT GATGCTGTGG AAGTAGTTTG ACCCACATCC CTATGAGTTT    540
TTCTTAGAAT GTATAAAGT TGTAGCCCAT CNAACTTCAA AGAAAAAAT GACCACATAC    600
TTTGCAATCA GGCTGAAATG TGGCATGCTN TTCTAATTCC AACTTTATAA ACTAGCAAN    660
AAGTG                                665
```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```
TTTTNTTTTT TTTTNTTTCG AGGAAGGATT CCATTATTG TGGATGCATT TTCACAATAT 60
ATGTTTATTG GAGCGATCCA TTATCAGTGA AAAGTATCAA GTGTTTATAA NATTTTTAGG 120
AAGGCAGATT CACAGACAT GCTNGTCNGC TTGCAGTTT ACCTCGTANA GATNACAGAG 180
AATTATAGTC NAACCAAGTAA ACNAGGAATT TACTTTTCAA AAGATTAAAT CCAAACTGAA 240
CAAAATTCTA CCCTGAAACT TACTCCATCC AAATATTGGA ATAANAGTCA GCAGTGATAC 300
ATTCTCTTCT GAACCTTAGA TTTTCTAGAA AAATATGTAA TAGTGATCAG GAAGAGCTCT 360
TGTTCAAAAG TACAACNAAG CAATGTTCCC TTACCATAGG CCTTAATTCA AACTTTGATC 420
CATTCTACTC CCATCACGGG AGTCAATGCT ACCTGGGACA CTTGTATTTT GTTCATNCTG 480
ANCNTGGCTT AA 492
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```
TTTNTTTTGN ATTTCANTCT GTANNAANTA TTTTCATTAT GTTTATTANA AAAATATNAA 60
TGNTCCACN ACAATCATN TTACNTNAGT AAGAGGCCAN CTACATTGTA CAACATACAC 120
TGAGTATATT TTGAAAAGGA CAAGTTTAAA GTANACNCAT ATTGCCGANC ATANCACTT 180
TATACATGGC TTGATTGATA TTAGCCACAG CANAACTGA GTGAGTTACC AGAAAANAAT 240
NATATATGTC AATCNGATT AAGATACAAA ACAGATCCTA TGGTACATAN CATCNTGTAG 300
GAGTTGTGGC TTTATGTTTA CTGAAAGTCA ATGCAGTTCC TGTACAAAGA GATGGCCGTA 360
AGCATTCTAG TACCTCTACT CCATGGTTAA GAATCGTACA CTTATGTTTA CATATGTNCA 420
GGGAAGAAT TGTGTTAAGT NAANTTATGG AGAGGTCCAN GAGAAAAAAT TGATNCAA 478
```

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```
AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCAGTGACA ATCAGACCTA 60
TGCTAGTTCC TGTCATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA 120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA 180
AGTGATTCAG TTTCTCTTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA 240
TGAAGCCNAC TCTGAACACG CTGGTTATCT NAGATGAGAA NCAGAGAAAT AAAGTCNAGA 300
AAATTACCT GGANGAAAAG AGGCTTTNGG CTGGGGACCA TCCCATTGAA CCTTCTCTTA 360
ANGGACTTTA AGAANAACCT ACCACATGTM TGTNGTATCC TGTGCCNGG CCGTTTANTG 420
AACNTGACN NCACCCTTNT GGAATANANT CTTGACNGCN TCCTGAACCT GCTCCTCTGC 480
GA 482
```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60  |
| CGACTGCGAC | GACGGCGGCG | GCGACAGTCG | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGTCGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCCGGT | GAANGCGGGA | GGCCTCGGGG | AGCCCCCTCG | GAAGGGCGGG | 240 |
| CCGAGAGATA | CGCAGGTGCA | GGTGCCCGCC |            |            |            | 270 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTGGGAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTTGCA | 60  |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTTTC | GTCAACTTCC | TTTGTCTGGG | 120 |
| TTGATTGGTT | TGCTTTTATG | GGGGCGGGGT | GGGGTAGGGG | AAANCGAAGC | ANAANTAACA | 180 |
| TGGAGTGGGT | GCACCCTCCC | TGTAGAACCT | GGTTACNAAA | GCTTGGGGCA | GTTTACCTGG | 240 |
| TCTGTGACCG | TCATTTTCTT | GACATCAATG | TTATTAGAAG | TCAGGATATC | TTTTAGAGAG | 300 |
| TCCACTGTNT | CTGGAGGGAG | ATTAGGTTT  | CTTGCCAANA | TCCAANCAAA | ATCCACNTGA | 360 |
| AAAAGTTGGA | TGATNCANGT | ACNGAATACC | GANGGCATAN | TTCTCATANT | CGGTGGCCA  | 419 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTNTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT  | 60  |
| TGGCACTTAA | TCCATTTTAA | TTTCAAAATG | TCTACAAANT | TTNAATNCNC | CATTATACNG  | 120 |
| GTNATTTTNC | AAAATCTAAA | NNTTATTCAA | ATNTNAGCCA | AANTCCTTAC | NCAAAATNNAA | 180 |
| TACNCNCAAA | AATCAAAAAT | ATACNTNTCT | TTCAGCAAAC | TTNGTTACAT | AAATTAAAAA  | 240 |
| AATATATACG | GCTGGTGT   | TCAAAGTACA | ATTATCTTAA | CACTGCAAAC | ATNTTTNNAA  | 300 |
| GGAACTAAAA | TAAAAA     | CACTNCCGCA | AAGGTAAAG  | GGAACAACAA | ATTCNTTTTA  | 360 |
| CAACANCNNC | NATTATAAAA | ATCATATCTC | AAATCTTAGG | GGAATATATA | CTTCACACNG  | 420 |
| GGATCTTAAC | TTTACTNCA  | CTTTGTTTAT | TTTTTTANAA | CCATTGTNTT | GGGCCCAACA  | 480 |
| CAATGGNAAT | NCCNCCNCNC | TGGACTAGT  |            |            |             | 509 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

TTTTTTTTTT TTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT    60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC    120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAAATC TGCCTAAAGT    180
GAAATCTCTT TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC    240
ATTTTCTTG TCTTTAAAT TATCTAATCT TTCCATTTT TCCCTATTCC AAGTCAATTT    300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCTTAAA    360
AGGGAACA GGAAGAGANA ATGGCACACA AAACAAACAT TTTATATTCA TATTCTTACC    420
TACGTTAATA AAATAGCATT TTGTGAAGCC AGCTCAAAAG AAGGCTTAGA TCCTTTTATG    480
TCCATTTTAG TCACTAAACG ATATCNAAAG TGCCAGAATG CAAAAGGTTT GTGAACATTT    540
ATTCAAAAGC TAATATAAGA TATTCACAT ACTCATCTTT CTG                                583

```

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

TTTTTTTNT TTTTTTTTT TTTTNTCTC TTCTTTTTT TTGANAATGA GGATCGAGTT    60
TTTCACTCTC TAGATAGGGC ATGAAGAAAA CTCATCTTTC CAGCTTTAAA ATAACAATCA    120
AATCTCTTAT GCTATATCAT ATTTTAAGTT AAACATATGA GTCCTGGCT TATCTTCTCC    180
TGAAGGAAAT CTGTTTCATTC TTCTCATTTA TATAGTTATA TCAAGTACTA CTTTGCATAT    240
TGAGAGGTTT TTCTTCTCTA TTTACACATA TATTTCCATG TGAATTTGTA TCAAACTTTT    300
ATTTTCATGC AAACATAGAAA ATAATGNTT CTTTTCATA AGAGAAGAGA ACAATATNAG    360
CATTACAAAA CTGCTCAAAT TGTGTGTTAA GNTTATCCAT TATAATTAGT TNGGCAGGAG    420
CTAATACAAA TCACATTTTAC NGACNAGCAA TAATAAACT GAAGTACCAG TTAATATGCC    480
AAAATAATTA AAGGAACATT TTTAGCCTGG GTATAATTAG CTAATTCATC TTACAAGCAT    540
TTATTNAGAA TGAATTCACA TGTTATTATT CCNTAGCCCA ACACAATGG                                589

```

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```

TTTTTNTTTT TTTTTCAGT AATAATCAGA ACAATATTTA TTTTATATT TAAAATTCAT    60
AGAAAAGTGC CTTACATTTA ATAAAAGTTT GTTCTCAAAA GTGATCAGAG GAATTAGATA    120
TNGTCTTGAA CACCAATATT AATTGAGGA AAATACACCA AAATACATTA AGTAAATTAT    180
TTAAGATCAT AGAGCTTGTA AGTGAAGA TAAATTTGA CCTCAGAAAC TCTGAGCATT    240
AAAAATCCAC TATTAGCAAA TAAATTACTA TGGACTTCTT GCTTTAATTI TGTGATGAAT    300
ATGGGGTGTC ACTGGTAAAC CAACACATTC TGAAGGATAC ATTACTTAGT GATAGATTCT    360
TATGTACTTT GCTANATNAC GTGGATATGA GTTGACAAGT TTCTCTTTCI TCAATCTTTT    420
AAGGGCNGA NGAAATGAGG AAGAAAAGAA AAGGATTACG CATACTGTTT TTTCTATNGG    480
AAGGATTAGA TATGTTTCCT TTGCCAATAT TAAAAAATA ATAATGTTA CTACTAGTGA    540
AACCC

```

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
TTTTTTTTT TTTTGTAGC AAGTTTCTNA TTTTATTAT AATTAAAGTC TTGGTCATT 60
CAITTTATTAG CTCTGCAACT TACATATTTA AATTAAAGAA ACGTTNTTAG ACAACTGTNA 120
CAATTTATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT 180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTTA ATTTTATTAG TAGATNATAC 240
ACTGCTGCAA ACGCTAATTC TCTTCTCCAT CCCCATGTNG ATATTGTGTA TATGTGTGAG 300
TTGGTNAGAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT 360
TCGGTGAAAA TAGACTGTGT CTGTCTGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG 420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATTT GTGGONTCTN TTGCACCTGT 480
TTCAAAA
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```
TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTTCTTT CCTTTAAAAA 60
TACATAGCAT TAAATCCCAA ATCTTATTTA AAGACCTGAC AGCTTGAGAA GGTCACTACT 120
GCATTTATAG GACCTTCTGG TGGTCTGCT GTTACNTTGG AANTCTGACA ATCCTTGANA 180
ATCTTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTTCA CAGAGGAANA ACACAGCGCA 240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG 300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA
```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 524 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
AGGGCGTGGT GCGGAGGCGG TTAAGTGTTC GTCTCAGTAA CAATAAATAC AAAAAGACTG 60
GTTGTGTTCG GGGCCCATCC AACCACGAAG TTGATTCTTC TTGTGTGCAG AGTGACTGAT 120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC 180
TCCCGCGTGA TTCACATTTA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAATAACT 240
TTTGGCAGAA TACTTNTTGA AACTTGCGA TGATACTAA GATCCAAGAT ATTTCCCAAA 300
GTAAATAGAA GTGGGTCATA ATATTAATTA CCTGTTTACA TCAGCTTCCA TTTACAAGTC 360
ATGAGCCCGC AACTGACAT CAACTAAGC CCACTTAGAC TCCTCACCAC CAGTCTGTCC 420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTTCTA CCAGTCAATC ATCTATCCAA 480
AAACCATTAC CTGATCCACT TCCGGTAATG CACCACCTTG GTGA
```

(2) INFORMATION FOR SEQ ID NO:209:

120

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCAGT GTCAGCATTG TTGCTCCTTG      60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA      120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA                               159
```

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```
ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC      60
ACTGAATTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA      120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGCGAGG CGGGAGAGAT      180
TTGCAGGGTG NAAATGGGAN GGCTGTTTGT TTANATGAAC AGGGACATAG GAGGTAGGCA      240
CCAGGATGCT AAATCA                               256
```

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```
ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG      60
ACTGGAACAC ATACCCACAT CTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT      120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA      180
GGGGGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA      240
AAAAAAGGAG CAAATGAGAA GCCT                               264
```

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA 60
GGATTTAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG 120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG 180
TTNAATTTCAT TTCCCATTTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAATAATTTA 240
CCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTGGGCCACA 300
TTTTTTTTTC CTTTATTCTT TTGTCAGA 328
```

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
ACTTATGAGC AGAGCGACAT ATCCNACTGT AGACTGAATA AAAGTGAATT CTCTCCAGTT 60
TAAAGCATTG CTCACCTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT 120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT 180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT 240
TCTCATCGGT 250
```

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG 60
GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG 120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT 180
TGAATTTTCA TCCCATTTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTTAC 240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT 300
TTTTTTTTC TTTATTCTCT TGTCAGAGAT GCGATTATC CATATGCTAN AAACCAACAG 360
AGTGACTTTT ACAAATTTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT 420
ACTTTGCTCT CCCTAATATA CCTC 444
```

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAAGTGAATT CTCTCCAGTT 60
TAAAGCATTG CTCACCTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT 120
```

CATTATGCCA AAGGANATAT ACATTTCAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT 180  
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT 240  
TCTCATCGGT AAGCAGAGGC TGTAAGGCAAC ATGGACCATA GCGAANAAAA AACCTAGTAA 300  
TCCAAGCTGT TTTCTACT GTACCAGGT TTCCAACCA GGTGGAAATC TCCTATACTT 360  
GGTGCC 366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAC AGAACTCCAC TGCANGAGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC 60  
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTNC ATTTTTTTAT 120  
TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTCCC TINGGCTGGA AAATTTAAAA 180  
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT 240  
AATTCCTCCT TCCCTCCTT 260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTCAGGAA NAGGAACGCA TATAATTGTA 60  
TCTTGCCTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGAATGTAG 120  
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT 180  
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCTA 240  
ATATCCTTCA TGCTTGTAAG GT 262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA 60  
CCCCTATCAA CTCCTTTTGT TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC 120  
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGT TGCTAGGAAA 180  
ANAAATCAGC AGACACAGGT GTAAA 205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTGG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA 60  
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA 114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTCTTTTA 60  
AAATAAGCAT TTAGTGCTCA GTCCTACTG AGT 93

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCTT TCATCTTGA TTCCATGAGG 60  
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC 120  
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT 167

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC 60  
GTTCTTCACC TGTCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA 120  
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGG CATAATCCAA 180  
TTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAATCTTT 240  
TAGGTGAGCA TGATTAGAGA GCTTGAGGT TGCTTTTACA TATATCTGGC ATATTTGAGT 300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

(2) INFORMATION FOR SEQ ID NO:223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAACAAACA AACAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG GGA          | 60  |
| CTGATAT TGGTAATTAT GGTCAATTTA ATWRTT TKT GGGGCATTTC CTTACAT       | 120 |
| TGT CTTGACAAGA TTAATGTC TGTGCCAAA TTTTGTATTT TATTGGAGA CTTCTT     | 180 |
| TATCA AAAGTAATGC TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC      | 240 |
| TGTTTGGAG TGTGCTATTC TAAAGATT TGAATTCCTG GAATGACAAT TATATTTTAA    | 300 |
| CTTTGGTGGG GGAAANAGTT ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT | 360 |
| CTTTTATGCG ACTTGTTTGG ACCATTAAGC TATATGTTTA AAA                   | 383 |

(2) INFORMATION FOR SEQ ID NO:224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCCCTGAAGG CTCTTGTTA GAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA   | 60  |
| AAAAGTTTGT GACATGTAG TAGGGAGTGT GTACCCCTTA CTCCCATCA AAAAAAAAT    | 120 |
| GGATACATGG TTAAGGATA RAAGGGCAAT ATTTATCAT ATGTTCTAAA AGAGAAGSAA   | 180 |
| GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC | 240 |
| AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT | 300 |
| TTTARACTCM GCATTGTGAC                                             | 320 |

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

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- 128 -

24. A method of inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administrating to the patient an effective amount of the vaccine of claim 22.

26. Use of a polypeptide according to claim 1 in the manufacture of a medicament for inhibiting the development of prostate cancer in a patient.

27. Use of a DNA molecule according to claim 2 in the manufacture of a medicament for inhibiting the development of prostate cancer in a patient.

