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.
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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, $^{125}$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, \textit{Bordella pertussis} or \textit{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 \textit{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\textsuperscript{TM} 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 $10^4$ 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 μg, and preferably about 100 ng to about 1 μg, 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 μg, 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.
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 $^{90}$Y, $^{123}$I, $^{125}$I, $^{131}$I, $^{186}$Re, $^{188}$Re, $^{211}$At, and $^{212}$Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria 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, sulphydryl 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 1
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+ 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+ 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 μg) 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 μl of H₂O, heat-denatured and mixed with 100 μl (100 μg) 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 μl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μl H₂O to form the driver DNA.

To form the tracer DNA, 10 μg 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 μl H₂O. Tracer DNA was mixed with 15 μl driver DNA and 20 μl 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 °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 μl H₂O, mixed with 8 μl driver DNA and 20 μl of 2 x hybridization buffer, and subjected to a hybridization at 68 °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' (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, pancrease, 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
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:ethanediethiol: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.
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
     Dilllin, 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:
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     (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:

(viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Maki, David J.
     (B) REGISTRATION NUMBER: 31,392
     (C) REFERENCE/DOCKET NUMBER: 210121.427C3

(ix) TELECOMMUNICATION INFORMATION:
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     (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

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

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CTCTGAGGCT CACAGCCTTC TCTAGGCTTC CAGGTGCTTC CAGGACAGAG TGGTTTATG 240
TTCTCAAGCTC ATCCCTCCTC TGAGTGCTG TGCGCTTGCG CCCTCAGCTT CTGCTCAGTG 300
CTCCATGAGA AGCTTCTCAG AAGCTGACCT CTCCACCTCT TCAGCTGCCA TCCACATGTT 360
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(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

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

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GCGCCACCCG CGGTCGGTGC CCAGCTTGG TCCCTTTTAG TGGAGTTTAG TGGCGGCTTT 480
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GGNNTNCSCG TTATCCCGAA ACNCGGGGATA CCNCGA 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

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

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TGCTAGACTG GGTGGCTCTAT TCCATCAGCA GCCATGAACT CCCGACCTGC TGCTCTGAAC 360
GCGGTATAGA AAGTCGCTCC ACCATCTCAA AAGTGGTGCCT CCGGAGGGTC GCCTGGGATAC 420
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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

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

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TCGGCTCTCT CCNCTCATT AATNAGGCGG CTGGGATCTTC CCGGCGGGGGG AAACGGGAGC 780
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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

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

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GATATTGGCT ATTTTACCA GCTCTAAAAT CTAGCGCTCC ATGAGGATC TTGGGATTCGTA 720
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TGTTATTTAG TTTAAAATAA AAATTTAAGG TGTCGGGGG TATTTCAAGA ATNA 824

(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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(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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TGGTTCTGGC GCTGGCTCCTG AAAGGCTAAC TATAGGTTA GCTGTGGCTG 720
TTATATAGCC GGAACTGCGG CATTTTGG GTGGGAGATTA AGTCATGAGG 780
GCACTGAGGA CAGAGGATGTC GAGGTTGGG CTGGCTGCGA CCGGACCTCG 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:

CATTTCCGGG TTGGTCTTCT AACAAAAGCC GAGCGGAGCG TTCTAATGGG GGAATCGCGG 60
CATAGGAGA ACTTTCTCTT GGCGAGGGG TTGGAGAAGC GGGAGGAGGG GCAGCCCAGCTGGCTG 120
CTGAAGCCCA CGCTCCAGGA GTGGTGGACTG TGACCTGAAAC AGCTGGGACA CATCCTGGAG
TACGGAACACG GGTGGGAGGT GTGGTGAGCG GAGTTGCACG AGTGTGAGCC GCTCTGGGAG
TGCGTGCGCC ANGCTCTGANC GCCTCTGACT TGCTGCCCCC ANGTGGGCGCC CACCCCTCAG
ACCCTTGGCTG GTCCACAAAC TGAGCCCTGC TGCCGGAGCTA CAAGGAAACA CCCACGANG
GGATTGTCTT CCTANANTAA GCCTCAGCTTG GCCCTTCGCC CCCCCACCTG GTGCTGCTTG
TCTTTTGAAGT GCGGCGGACT TGCCAGTGGG CCAACCGACTT NGGGAGTGTG 480
CTCCCTTACAA CCAACNNACTT CCCGAAACCC ANTCCACNNCA TGGNAGAGAT 540
CAAGNCGCCTT CCTCCTTNTCT CNTANAACCG GCNNCCNCCNG CGGTGAAACCC CNTCTTTNGT
TCCCTTTCTC TNAAGGCGTTA TNCCCCCTTG GCCCTNCNAN NGCCCTTNCNT NCTTTCTCNNT
660
GTTNAAATGTT TTANNGCNCCNC NCCNNTCCCN CCCCACCNACN NCCGCCACGN AMNNNNANNN
720
NCTGGGGCGT NCNNCGNNGT TGACCCNCCN NCCNTNTANT TGCTNTNGGG NCCCNTGGCC
CTTTCCCTCT NGGGANGCG
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:
ACGCTTTGAA CTTCCACAGGC TGCGAGCTGT TGCGAGGGAGA GCGCGCGGATG CTGCTGTTTG
TAAANGATGAC ACITCCCAAGG TCGTGCTCTGA CAGTGCGGCCA GATGCGATGT GGGTCAGCAT
CAGGAGCAACG GCCACGACGG GCGGCGCGGG AAACCGCACAT GCCTCTCATC TATAGCCCGA
AATCCGCCCCT GCGGGCTCTC CTGGAAGCTG GCCCGANAGG GCTGAGCTTG TGGGACGCC
CAGGCTCTGAG GTGGTGGNGC CAACCGGAGG CCGCNACAGA AAANCGCNCAG GCGCTCNGNh
CACCACCATGC ANGACGGCGG TACATCNGCT CACCCCTCNC GCACGACCGT CACGCGGCTG
TTCTNAGCGG CNHATNNTG CCACTNCTTT NCNGCCCNAC CACANCTCCT TNGAGGCTGG
CTACMTAGCC CGCGANTCNCC NCCGCCGCCT GTGCTCTACTAC CGATGNCNAN CCACAAATTG
CNCCNANTGC ACCNHTTCCG CACNNTTNNC AGNNTTCCNC NNCNGNCTCT TGCTNAAAGT
GTTTGANCCC CGKAAANNC CCCCCAGCGG GGGCGCGNCGG TACCCCAACTN CCCCCTNTAA
GCTGAAANTCC CACNTCNCAAG NCNTNATGG ANNCTNCCNT TTTANNACNC TCTTNAACTT
GGGAAANNCC TTCGCCCNNTN CCCCCNTTAA NCNNCTAGGG CACACNNCAAC TCTCCCTNCC
CACCACCTCG AAATCGCGCCN 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:
CAGTCTTNTAT GGCACGTTGG CGACGCTTCC CTGCTGCTTCG CGGTGCCCACA TGCCCTTCC
ACAGTGCTGGC GTGGTGAGCA GCCCTGGCGC CCCCCGGCGG GTCCTAGTTC TGACACCCGCG
AGATCCGGCC CTACACACGG GCCCTTCTCC ACCACCGCGGA GAGAGGGTGG TCTTCTGCCA
AAATCCCGAGG GACAGCAGGA CTTGGAGAGA GTGAAAGACG CTTAGTGGACG AGCTCTCGCC
CGAGCCCATG CGCAGGCGCT CTCTCGCTCTA ATGACACGTT CGAGCTGGGG CCGAGCTGAG
TGCTCCCGAC CTCACCGCGG CTGGCGCGGG CTTCTGGCTTG GATGTGCTCC TACGCTGGT
TGCTTTGAGT GAACCCCGAN GCGCGGCTGAG TCCCGCGCGG GGGCGAGCTG CTTGACGCTG
CCTCCTGCTT TGACTGCTCC TAAGGGGTCT CACCGCGCGC
420
CCATTGCTAG TGAAGCCGCT TCACGCGGCG CACCGCGCGG TGGGGGCGGC 480
TGCTCCAGCCT AGCGAGGTCC TCAGCTGCTTT
540
(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

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

CCCACCTCCTAC CCAAAATATT GACACACCAAC CAGAAGAGCT AGCAATGGGAT TCCCTTCTAC 60
TGTGTATATG GATAATGGAG TATTTTTAAA TGCAATGATG CTCCTGTGGCT 120
ACCACACGCG CACATCCTCTG TACACAAATGAG TGGGCTGTTG GAGAGCTGAC 180
TGGGCTGCTA GGGGCGCTGCT GGCTGTGCTGG CTGGTGGGCTG GACACATTCTTC 180
ACCTCTTGGTG GCCGTTCTGC TACTCTCTGC TACATTCTTC 300
CTACATATAA CAAGGCGTGC GCTTAAAGGCT CTAAGAGTGG CTAGGTAGTTG 360
GATCCAGGTG GCAAGAAAAAC TGGCACTGACT GGGGCGCTGAG GTGATCAGGC 420
CAATGGGCAC GTGATCCTTC AGTGCAGAAA TCGATGGGCA AATGGGCAAA 480
GAGGGGGGCA AGGGACATGGAG TGGGATCAAG GAGGAGGGCA ACACGATGAC 540
GCCACGATGG TCAAGAAAAAG CCCATGCACTG ACACTGGGAC AGGCGCTGAC 600
CAGCCACACAGA CAGTGGGACAC GTGATCCGAG CACACAGGGA TGCCTTTACA 660
ACCTTTGGGC AAGCTATGAG GAGGAGCTGG GCTGTGAAGT CATTGCTCGG 720
GAGAGCTGAC AGGGAGGAGG AAAGCTTATT AGCAAGACAT GCAGGGGTCA 780

(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

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

CCACCATCCTAC CCAAAATATT GACACACCAAC CAGAAGAGCT AGCAATGGGAT TCCCTTCTAC 60
AGCTGATGGA CAGACACCGT TACATGAGTG CTCCTGTGGCT GGCAATGGTCG 120
TTGGCTGCTA GGGGCGCTGCT GGCTGTGCTGG CTGGTGGGCTG GACACATTCTTC 180
AAGGATGCTGT AATGGGAGTT TCTTAAGATTG GATGGGGTCG GTGATCAGGC 240
AGGAGCTGAC AGGGAGGAGG AAAGCTTATT AGCAAGACAT GCAGGGGTCA 300
GCATGATGG TCAAGAAAAAG CCCATGCACTG ACACTGGGAC AGGCGCTGAC 360
CAGCCACACAGA CAGTGGGACAC GTGATCCGAG CACACAGGGA TGCCTTTACA 420
ACCTTTGGGC AAGCTATGAG GAGGAGCTGG GCTGTGAAGT CATTGCTCGG 480
NCCTGGGCGA AGGGAGGAGG AAAGCTTATT AGCAAGACAT GCAGGGGTCA 540
CCACCATCCTAC CCAAAATATT GACACACCAAC CAGAAGAGCT AGCAATGGGAT TCCCTTCTAC 60
AGCTGATGGA CAGACACCGT TACATGAGTG CTCCTGTGGCT GGCAATGGTCG 120
TTGGCTGCTA GGGGCGCTGCT GGCTGTGCTGG CTGGTGGGCTG GACACATTCTTC 180
AAGGATGCTGT AATGGGAGTT TCTTAAGATTG GATGGGGTCG GTGATCAGGC 240
AGGAGCTGAC AGGGAGGAGG AAAGCTTATT AGCAAGACAT GCAGGGGTCA 300
GCATGATGG TCAAGAAAAAG CCCATGCACTG ACACTGGGAC AGGCGCTGAC 360
CAGCCACACAGA CAGTGGGACAC GTGATCCGAG CACACAGGGA TGCCTTTACA 420
ACCTTTGGGC AAGCTATGAG GAGGAGCTGG GCTGTGAAGT CATTGCTCGG 480
NCCTGGGCGA AGGGAGGAGG AAAGCTTATT AGCAAGACAT GCAGGGGTCA 540
AGCTGATGGA CAGACACCGT TACATGAGTG CTCCTGTGGCT GGCAATGGTCG 600
TTGGCTGCTA GGGGCGCTGCT GGCTGTGCTGG CTGGTGGGCTG GACACATTCTTC 660
ACCTTTGGGC AAGCTATGAG GAGGAGCTGG GCTGTGAAGT CATTGCTCGG 720
AAGGATGCTGT AATGGGAGTT TCTTAAGATTG GATGGGGTCG GTGATCAGGC 789

(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 TCCCTCTGGC TCCGCACTCA GTGGCAACAC CCGGAGCTG TTTTGTCTTT 60
TGTTGGANCTT CACGAGTCNH CTTTTCAGAA ACTCACTGCG AAGANCCCTG AACAGGAGCC 120
ACCATGCAAG GTCTGAGCCT CTTAAGACCC ATGATGATCC CTTCCTATTT GCTCATCTTT 180
CTGTGTGTGT GACGCTGTGT GCGAGGCTGC ATCTGAGGTT CAATCAGATG GGCATCCCTT 240
CTGAGAAGCT GCGGAGCACT CTCCTGTCAG CCGCAGCAAT GCTGGAGACG TCTCTGCAAT 300
CTCATGCAAG CCGGAGGTTG GTCTCTGACT CTAGCTTACC TGGGCTGCTA TGGGCTACTG 360
ACTGAGAGACA AGTGCGCCCT GGGACGTTCC TCTCTACTCC TCTCCTCTAT CTTCATGCTG 420
GAGGTGGGCAA TGCTGCGTGC GCCTTGCCGT ACCAACCAAT GCGTGGACGC TTCTCTGCAAT 480
TCCTGCTATC CCGTGGACTAT AAAAAAGAT TATGGGTCTCC CAGAAAACG TCTCTGCAAT 540
GTGGAACAC CACCATGAAA GGGCTCAAGT GCCTGACCTT CNGCCAAGCA TACGGATTTT 600
GAAGATTTCA GACCTCTAAA GAAAAGATG CTTTCCCCCG ATTTCTGTTG CAATTGACAA 660
ACCTCCCAAA CACAGCCAAAT TGAAAAACTG CACCCCAACCA AANGGCCCTC CCAACCAAA 720
ATTNAGGG 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 CAAGAATGTT CTTGTTGCCA TACACAACAC CATAAGTAAA GGGGCGCGAG 60
TGCTGTGAGA AGGG TGCCACCA GTAAGCCAGC GGAGTGCTCT CTTGTGCTAT 120
GCGAGCTCA CCGAGGCCGC TTTATCGACT GGGAAATTGA TGCGCTGAGA CTCTTGCAAT 180
CCACTCTGAT ATTTTTCAAC CGCAAGCTCTG TCCGAAGCTT CGGCGGATTT GGGGGTCTTG 240
TCACAATCTA GCAAGACTGG TCGAGCCTCC TCCATGNNAN GGGGCTTGGN GGAAAGCTCC 300
TGACCCCAAN ATCTGCCGTT CAAAGGCCCG ACCCTGAGCA CCCCCAGGCG TCTGAAATGA 360
ATCTTTCTCC CGGAAGTATG TTTTCTCTAT TGCCAAANCC ANCCCACTTT ACAAACTCTT 420
GCANATCTGG TGGCGGCGG TGNTAANTCC ATCGGGAAAG AAGACCCCA GGGCGCCGAC 480
CAANATTTCTG TGAGTNGGAA GTNATACCT CNTNTCTTCC TTGTTGGGCA GCACANNTA 540
CTGNNANACT TTANNGCCNTG GTCCNTGTTG GTGGNCCCTT AACCTAATCN CNGNCAAAC 600
GGCGAGACT GAATNNCGNT CTTNNATTT CNGNANNTN CNGNNCTTTG TTGNGGNNTT 660
CNKNTCTCTA CCCGGAGNN NNCGTTCTCC CCCCACACTA GGGCCNANA CNGNNNTTNT 720
CACAACCTNN CCCCAACCCG GSGGTCNNT GGTGNG 780

(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:
(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:

GCCCAAAATTG CAGCTGCACAT ACCACCCAGG GTGACTGATAT TAGTTCGGAAT GTCATACAAA  
AGCTGATGGA AGCAACCTCC TACTTTTTGG TGCTGAGCCTT TTTGCGTGATG GCAGGTTTCA  
GACTGCGTG TGGTACGCTGTA GCATCAGGAC CAGAAATGGG  
AGTAAGGATG ATGCCTCAAATA AGCTGATAGA TTGUTGAAAGC CAGACGCATCT GACACCTTTC  
GCTGAGGT GCTGTTATATT CATAATCTTTTTT CTTGATGAAC  
GCGACTCCAA GCAACCTGAG GAAGTCTGCA GCCATCTGG TGTACAAGCAA GCGACACAAC  
GCCAGGCAG CACACATTG CACTACGAG CCANGAACAC AAAGGCAAGA  
CCGCTGCAGA ATGAAAGAAA GTACCCGGAT GGGACACAGT GGAACACTG  
TGCGCAAAT ATCCCTCAAGA AAGGGTGCC CGCCATGATT CACCACCAAN TGACACCCAG  
CNACAGGCG ATCTGATCAGA AAGGGTGGCC CAGCACTTGG CGCTGCTGCAAG CTGGAATGCA  
AAGGAACGNGC NTNAGCCCCC CAAACANGAA AAGACCCCGC GGCTGCTGAGG CTAATGGTGC  
GCCAAGGGCC CACCTGCCCCG G  

801

(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:

GTCAGACGCCA GCCCATCCCTC TGCCGTCACCA CTGATGGCACA ACACCAGGGA GCTGCTGGTG  
CTTGTGTTGA TGGCTGCCAC TGCCTCCTCC TGGACAGCC TGGACAAGGA GTGACGCTCAG  
AGCAAGGACTG CATGCTTGGC GCTGGATGTT AAATCAGATTG CAGGCAACATTTTGCTCATT  
CTCTTCTGAG ATCTGACAGGC CAGCGCTGCTC CAGTGGCAAGT CAGTGATCTGA  
CTCTTACGAG CTGGTGTCTTG TGGCAGCTTGG AGGCGGCTAAG  
CTGCTGCTGG CAGGCTCTGTG CAGGGCAGCAG ACGGCGAGGCT  
GCTGCTGCTGG TGGCTGCTGCTG TGGCTGCTGCTG TGGCTGCTGCTG  
GCTGCTGCTGG  

60

120
TAAGACGGAG AGCCATGCTG GTCTCTGCC ATATCCCTCC TCATCTCTAT
TGGTCAAAGT GTGCTGCTGG GCTTGCCTCT GTGGATACCC ACAATGCGGT AACCATCCT
GAGTTGTGCG GTANTGGCTG CAATCAANAA AGATTATAGG TTTCCAGGAA AAAATCACC
AACACTGGAA GACNACCACTT AAAAGGCTTG CAATTCTCTGN AGATATACGCG
QAAATTGGA AGANTCNCCT TACTTCCTAA AAAAANNT TGCTCTTCNN CCCNTCTCGT
TGCAATGAA ACNTCCCAAN ACNGCACAATN AAAAATCGCC CUNNCAAAAA GCNTCNCAAA
CUNNCAANNT NNNNNNNNNN

(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

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

CCCGTGTTGG CTGGTGCCCA GGNAGCCCAAG GAGCACTTCTG GCCCATACACA GCCTCAATCA
CAAGGTCCTGC CAGGTGGCCG ACCATTAAGCA GGCAGAATGC ATCAGCGACG ACTGATATG
GGTAGACCTT TACATTGAGA CAATGGAGGA GTGCTGCAGC AAATGATCTC TATATCTCTC
GGATCTCTTG TAAGGAGAGA AGATTCCGGG CCTGCAAGAT GTAAGCACCG ATAGCTCCTG
AAGAAGAAGC CTCCTGACAG CAGCAAGGATG GCCATCCAGC ACTGCCTTGT
CATTGCGCAT TGTCCGAGCT TTTCCCAAAC CAGTCAACCC AGGCGCTCTG AGCACTGCTAT
GGTAGAATGC CAGGCGGCCT GGGCGCTTTGG GGGATCTGAG TAGGAAAGGA AATTCTCTCT
GGTCTGCGCC TGTCTACCTT ACTTCCGACGC TACCTACCTG ACTGAGTGG AGGGTACTTG
GCTCAGGATG TCCAGGACG TGTCCGCGCC CCCCTCTTGA ATGACACCCG CCAANCCAA
GTCGCCGCGTT GCAGATAGG TTTGCTGGTC GGCTCTGGCG GCTGCTGTGC GCNTACTTTG
AANCTCCGGC NGCGCCCTAGG AATCAGCCAC ACCGGAACTN GTGAAATCCA CTNNTCTAT
AACCAGGCCG CACCGNCACT GCCAAGCTTG GTTCTTGGCG GCTGAGTGGC ANACCTGGNA
ACCCCTNNNG TTACCTCGGT CCAAAACGNTT GNTGGTGGCG ANATNCGTNA CTCNGGNCNA
TNNCCANCNC ATANANACCC NG

(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 AGGTNAAGGG GGCGCNAANC TGAGCCNAGG TANCAANANG CAGNCGCGGG
GAGCCCAACCG TCCAGNNGGTT TAGATGGATG CAGAACTGAA CTGATGGTGG CTGCGTCCAG
CNTGACCAAC ACACTGCCAC NCACNACCGA GTGATGAGT GAGAACCTGG GTGACGGTCT
CAGGACCAAA GACAAANNNCT TGCTCCNNT ACCATCGAGN GCAGGCGGGG GCTGGCACCAC
GCNCTGCNTT AGNATGCCTT AAAAGGCCNNC CTTGCTACTT GTGGATGAG ACGNCNNGNA
CATGCCCAAG GTTATACAA CGCGCCAGAG TNAATTCGCC TCTCCCTTTC GCTGCGGCCAN
CGNHTGCTG TANCGAGCA ACCCTGACTA ACCCTGGAA ACCCNNGATCT TCCNCCCTCT
CCACTGAATC CAGAACAAAG ACACTGCAAC CCAATCTCATT GTGCAACTGC TGGTCAAGGT
AAAGTAGTACC CACACNCAAA TCCTGCGACGC CACACNCGCTT CCGCTCCGGC CCGCTCCTGG
GAGGACTAT CAAATNACGC TGTGTCTCGT ACTGCGTCCT GCTCCCGATN ACAAONCCAC
CAGGNNNTCA ACCGGGCCGG GCCCGCCCAAA CCCCCAAACT TNAAATNNTN TTTTANCCCN
CCCGCGCGCC CGCGCCCTTA CNACNTCNGN NNACNGCCNGG AAACCNNGGC TTTTCCGAC
NNAAATCCNC 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 TTTTTTTTT TAAAAACCCC CTCATATNAA TGNAAAATTC CGAATTGTC 60
CAACCCCATC NTCCAAANNN CCHTTCCGCG GNNSGCGTTNC CAACCCCAAN TTANNNTTGG 120
AANNTAATTA AATNTTNTNT TGNGGNNNAA ANCCNAATGTT NANGAAAGTT NAACCANNTA 180
TNNACTTCNA TCNGCGAAAAC CGNCNCGGTTG CGAACATNTT TNNAAAATTTTC ATTCACCGGC 240
AANNTTNTNA NNGAAACCNN AANCNGTTCN TACNGTTTTG GAAGNGNTNA TNNAAANNCCT 300
NNCCAAATCG TTTNTNGGCAC CGCCTGAGAT TTTTTTTCGG CNGAATAAAT CGCTCCTNAGA AAAAAANCTC 360
GGNANCCCCG CGTNTATNAA TCCCCCNCCN CCCCAATTA ACGAATTNC CNGAATTCNG 420
GGNACNCGGC GATTTAACGG GCCNNNTCCCG TNNNTGCGGG CNGNMCNCCG CCCCCNTTGGG 480
GGGCGGCTCAG ATTTNTNCTC CCCCTNNTCC TCCCCCNCNG CCNNGGCAAG AGGTNGGNGT 540
TTNGTNCNCCG GCGCGGCCCG NAGANCTTTN CCGAATCNGT TTTAATCCTT CCGTNGGGCGA 600
AGTGCNNTGG AGGNNTAAN NGCGCGCTTN NCCCCCGNNGGG 720

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:

ATCANCACCAT GACCCCNAAAC NGGCGACCCN TCACCGCGNC NNNCNACCCNG CCGCCNATCA 60
NNGNACNACGN ACTNCNATTC NNNCNACCC GGGCCACNAC NGACNGCNAC 120
NNNANACNTAC ACTGNNGCCG CGANNGGAN NGAGAAANCT NNNACNACNG NNNACNACNGN 180
CCACGCTGCC NHAAANCGG NNNATACNGG NNNATACGAT NGNNANCCNGT CAAAAGATNTN 240
NCCNCCNACG GATTTTCCTN ANCGGATAGT CNTNCCNCNG TANCCNHCCG CCCCCAANCA 300
CGAAGGCNCTT GGGCGCCANNGG NNNCNCCNCG CGCGTCGAGCT CCGNCCNAGT CNGNCNCTA 360
AACCTCNCAG NNNATCGNC TCNTGAGAAG TCATCGCGCGGAATTCACCCA TACTCAACTC 420
AAANAAATGT CATACAAATT AATGACCGCC TGGNTATNNAC ACTNTGACTG GGTCTCTATT 480
TNTGGTTCGT NTNANACNTA CTAAATCTGT CACTCTCTCC TNNACAAAA GTAAGGACTG 540
GCGTGCTCTGT TTTTTTTCGG TTAACTCGG TTNCCNCCCG CAGTATTTAT TTTCCNNTTT 600
AAANATCCTC NTNATTAATTT TGCGTCTCNA AACCNNCGCCCGG CTTTGAAGAG GCCCGGCGT 660
AAAGGTTGTTT TTTGANAATAA TTTTGGTTTT GCTTC 720

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:

TTTTTTTTTT TTATGCTGCA GGTAGAAGCT TACTACAANT G7GAANACGT 60
ACCGTNGGAA TAANCGGACC CCAATTCATG GANNCNCTCT AAAATCANNAC T7GAAGATAN 120
ATCCTGGNA NA CAGAAGNGCT ACCGNNNGCT NHTGGCTAAGG TGGCNCCTCCT CANNNCNNTT 180
CAT AACTCCNG NGCCCGCGCC CACACCTCTGC GCGGCGGCGNG NNGCCGGGCC CGGGTCATTN 240
CNGCNGTACN CACTNCNNCC NCCGNCNCGNG NACCGNCNGCG TGGGCGGNCNG 300
TCTGCTCNCC CTCGAGNAAC NAAAATNGGG CCGCNGCNCCT TTTATCACCCT N7NAAGGCGCA 360
CNGCNGTCTA NNCNGCGCC CCCCCTCNGCN N7NGGGNGGCT G7CNANNNGCT C7GCTTNGTNT 420
NNACCCCGNCN GGGTCNGCTCG GTGTGCTGANT C7AACAGNGAC C7CAGGGATTG C7NGAGGAGG 480
TGCATNGTNCG GCTGCTNCNG NNCACCCCTCG CGACNNACNG AGGCGCTCGCG 540
CGCGCNNGNG CCGCNGCNGC CAAGACCGCG NCTCNCNGNTG N7CGNNNGCCC CC7CACCACCG 600
NACCCCNCCN CGCAGCNANC CTCGCCCTCCG G7CTCGANNC GCAGCGCGCCG GGCCGCGC 660
NCTGACACCN GCNGCNGCNGC G7CNANCNCCG GGCNGCGCGCC GC7GCNGCNGGC 720
CTCNGCNGCNG CGAANCGCCCG T7CAANCGCGGC C7GCGCGCGCC C7G7ACGNCNGC 780
NCCCTNGCGAA G7CTCNGCGCN CT7TCCNNACCC ANGNNNTCCNG C7GAGACACNG N7C7CCNGGC 840
NCCNGCGGCG 849

(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:24:

GCGCACAAGTA TACCTCGCTCG GNACTCGTGC GCCTCGCTNC TCTTTTCTCG CGCAACACGT 60
TCTGACACNG CCGATNGGNG NGATAATCNGN AGGTGGNGAC AGTCAAAACT GANTAAACCA 120
CAGACNNANC AGAANACACNG CCTGCCTCTCN ANAGTTANAC ATGTAAAGCN AGACNNANCG 180
NGCGGAAACTC TAATAGNGGCG TGGCGCGGCGCA ATNTGCGANG GTTATTNTC CAGCGTNGNC 240
CTCNGCNGCC TACNTCTCN AAGTCTCGNGC ACCCNGTCTG GC7CCGCGCGC N7AGCGCGGA 300
TGGGTTNNGG NNTGACCGNG CNCGCCCTCC CCCCNGCTANCC CAGCGCGGNCC G7C7ACGACNG 360
NACNGCNCGCN CCCCCCGCGCG CTGCTCGTNGC CT7GCGNGCNCG 420
ACCGAGTNGG CCCCNGCGCN C7TCNNGGAAA GC7GACNGACG CGGGTTGNNN ANANCGTCTG 480
TGGGNNNGCG TCTGCGCCNG GTTCCCTCNN C7CNNGTCTCA C7ATCTTCCNG TA7GCNTGCT 540
CCNGCNGGNC CTNGACNGCN CGCGGAGGCC NTTCCNTNGC C7CCGNGCGCC C7C7CNGCTTNT 600
CGNGCNGGCC NC7CNNGGCGCN TCTNGTNNGN N7AGCTTNGCC ACAANNGCNG G7GCNGTNGNCC 660
NACNGCNCGCN GT7CNCGNNAC G7GAGGNGNGGC GN7GN7NCNGT N7TTGACGNGTNG NG7GNGTNGTC 720
CGAANANTCG TCNGCNCGCN CTNGTCCNGC CGGCGGNGCNG CT7GCNGTNGC AACTTANCCAC 780
N7CTCNGCGCG NGCGCGNGCNT CGACCGCTCNG CNCGCCNGCNT CT7TGCANGTG TN7TCTCNNGCT 840
T7NACNGNTAC GANTTNGCCNG CNCCTCTNTT CC 872

(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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCA7GCAAGGC T7GATGATCTC T7ATAGNGTC C7CTAAATANC T7GCGCTAAT C7ATGCTNTA 60
NCTGGCTTCC T7GTGCATATG GT77ACNANAC T7ANATATGAA T7CTNATNGA C7AGANGNTA 120
(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: DNA

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCNTNCATTA GTAACAANTG TNNTGCTCAT CCTGTCNGAN CANATTCCCA TNNATGNCN 180
CGATCTCCCN GCNCAANTAH TAAATNGGAA NTTCTNNTNN NCACNNCAT CTATCTGNNCC 240
GCNNCCGAGG TGGAGAGGAT GNATNNTCC TNNNTGACC NACATGTTCA TCTTGGATTN 300
AAANACCCCG CGCGNGCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGGTAGGCT 360
AACCTGCGTG AGANNTTCAC AACNTGTCGA AACAAGCCGC ACCGCNCNCC ANGGNDCNAG 420
GATCCCGAGC AGNHNNACNN ATCCCTCTNC AGGCCCGCCCT TTNGTCCCTT ANAGGNNNC 480
GTGTCCCNANC CNCTCGACCC AGAGGAGGAC ACGCCACGCA AATTTGGCCA CAATGTGNCN 540
GACCCCCCTTA GGGGGGNTNA TGNAAANACC CAGGaAGTTGC GNNNCGAACG AATCCCGCNAC 600
GCCCNCCACT ACCNCTTGTG GACNGTGGAC AATNTCCGGA GNNNGCNGTCC GCCGNCNGTC 660
CCCCCGCTGT NCNNCTGGCG GGCTGAAACNT CNNNNTACNC CNNGCGAGGN NTGGNACNGA 720
ACCCGNGCTNN GCNGCAANNNS ANCNNTCNGA AGNNCGCCNNT GTATACACCC CCGTTCNCNCA 780
NCNACNNGNT GCNNTCCNCAC CCNGGNGNCN AANG 815

(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 TYPES: DNA

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTIAATCT TTTCCCAAGC GGGTG7TANAG GAAGACG9GGC CTTAGACCAT 60
CCCANANAGA NCTTAANACG ACAAGGCTCTT GACCAAGAAG TCTGGCGGAC ATTTCCCTCA 120
GAAAGGAGTTCC GTCTCCCAT CACTCCCTCTC CTCTCAATAC CACTCCAGAG GGGTGAATGC 180
CCATCANGGC TTTGCTGGGGA GGAGGACTAG GAACACACAN ACCACAAGAC ANACACAGCA 240
NTGATGACCA TGGGCGGGCG CGAGGCCTCTT CTTGGACGCA GGGTGGCCAG GNNACAGCTA 300
NTGCTGAGGCG CACTACATTCA AGTATACAGA CAGACGTGAC ACGCTGCGCC 360
TCTTCTACTCC AAGNGACACNG ACGNNACNATG CNGGCTGAGG GACNGGACGCTA 420
ACNNAGCGACG CAGCTCCGCC CCGCATGGCGC TGCGCAGCTC AGAGGGAAGCT 480
CCCTTGGAGG ATTNGGAGGA NACAGAGGAA NCCGCTCTCT CCACGTGTA GAAGAANNAAN 540
GATGGAAPTTT TNCTCTTCCC GCNNTCCNCAC CCGTTCAGTA CAGGCCCTT NNTACTCNCT 600
TCCTCCTNTT NTCCCTGNCC ACCTTTTNNCC CCCNNATTTTC CTTTNAATTGA TGCGANNCNTN 660
GANATTTCAC TNCCGCTCCT CNCTNATCGC NAANACNAAA NACTNTCTNA CCGCNGGCGAT 720
GGGNNCTCCTG NTCACTCCCTCT TTTTTTNCNTT ACCNNCCNTT CTTTGCCTCCT CTNNNGATC 780
TCCAACCNTTG CNTGGCCCNNTT CCCCCCNNTT TCTTTTNCCCT 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

(3) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGATGAT GGCGCTTCCC TCTCTGACTG ATTTGGGAGG ATGCTGAGCC TCTGGGACCA AAGAATCTCT 60
TGTTCTTCTCC CCGAGCCCCA GGAGGAGGTA ATTCAGCGGC CTCATAGCGT GGTGGGAGTA 120
CTGGCAATGC TGGGGGAGCC CCAAAGCGCA AATAAGGCTCC CAGGGGTCAG CAGGGGGCCG 180
CTGGATGAGCA CTTGCCTGCC TCAGCCGCTG GAGCCCTGTC CAGAGCTGGT GGGCTGGGTG 240
TCCGCCCTCA GGAGTTTCTG CTCTTCAGAC GGGCAGAGCG TGGGCGCTGG CCACTGGCCTG 300
TCTGGTTGCTG CCCTGCTGTC GCCCTGCTCC GCTGGGTCCGC CAGCCTGCTC ANGGCGGTTG 360
GACCTGCTGT TCTCTCTTCT ANGGAACTCT GGGTCTGCT GCTCGCTGAT_ ACTNTGANTT 420
TATNNACNAN TGGNGCTGTC TGTCNACATT TAATAGGGCN GACCGGCTAA TGCCCTCCT 480
NCTTTCTTCTG CNTCTNCGNTT CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC 540
CCTTCTTCTG CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC 600
CTTCTTCTG CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC 660
TNCTCTTCTG CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC CNTCTNTTTC 720
CNRNCTNANC NRNCTCNCCAT NRCNNCCCNCC NRCNNCCCNCC NRCNNCCCNCC NRCNNCCCNCC 780
CCCNCCCNCC CNNGGATTCG CTCCTCNNTT 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

(3) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAAGGAGG GGAGGATATT GTAGGGATT GAAGGATAG GGAGGATGGT GGGATGGTG 60
TCCCAACATG AGGGTNGGNT TCTCTTGTGA ANGGAGGTGT NGTNTTNTNN CCNGGTGGGT 120
GAATTNAAAC CCATTGAAGG AGNNAAGGN TTTNAGGAGTT TTTGGCGGCTT TTTAGCTAGT 180
NTNNATCTTG CTTAATGGCA AAATNTNNTT TNCHNGNGAA AAATTTGCTC CATATTGAA 240
ATTNCTCCGG AGTGTGATTT ATNNNGGGCN NCGCCANNTT TCTACAGCCTG CTANAAATCGT 300
ACTAAGNTTT NAAGTTGGAN TNCAATGGAA AACTCTNCAAC AGAGATCTCN TACCAGACTG 360
TNNTNTNTCT TCGGCTCTNT ACCTGCGGGN AGCCCGAAAT CCGNNGNCAAT GTCTCGCCNG 420
NNGGCCNCNC TGAAANNNAN TCNGGGCTNN GANCATAGN GGGGTCTCCT GCAAAGGNN 480
GTTTCTNATGA NAAGCACTCT TNCCCTCATC CAACNCTNG CTTCCCTNCA TTTNGGGCTC 540
NGGGCTNCTCT ACCTNCTNG CHNCTNNTN GNANATTCNG CCGCTNGG GNNANAANCTC 600
GNNATGCGAT GGCNCTNTCT TTTTNCNNCN GNNTTNTACT ATCAATNCTC AGCNNTNCTT 660
TCTCNACGCC CCCCCCTTTT CATCCTCANC GCNNTATGCG GTCTCCCGNN CGAGGGGCG 720
NNGGCCANNC C 731

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(ii) MOLECULE TYPE: cDNA

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

ACTAGTCGAG TGGTGTTGAA TTTCCATGTG TTGGGNNCCN TTTCTATGAAW AHNTTATGAT
CGCCANAC TACCAANCCCT CCAACNNANC TCTATANAG AANAANAGAIT ANNTNTNACNT
ATNNTACNC TCATANNCTT CNNANCCCAAC TCCCTCTTTAA CCCCTACTGT GCCTATNNGCN
TNNCTANTCT TGGGCGCGTN CNAANCCACCN TGTGCGCNNAC CCRNNTNACNT TCTCNACCTC
TCNCCATNTC GCTANANTAA GTGNTCACTCC CTATACCNAC NCAATCGCTA NNTNCTAACC
TCATANTTTT ANNTNTACTA CCACGTACNT NGASCTCTNC AATNACCTCT AATTTGAATC
TACTGACTG CCACGNCCTC ANNNATACCC ANCNCNCACCC NACNNATTCTC CAACCAAATC
NTACAAACCC TATCTACTNGC TTNCCANAC CCNNTCTGCG ATCCCDNACC AACCCCTNAC
CCAATATCAC CNAACCGGAC NCCTACCCCN CACCATCCGG CGAACGCAAN GCCATTTNAC
CCACTGGAAT CACNATNNGA NAAAAAACAN CNAANCTCTC TANNCNNTA CTCCCTAAACA
AAATNCTCTN NAATCTACNT CNAANCCACCN TGAACNNANAC AAAAAACACN CCCCCCTNAC
TANATCCCTT CTTTCGGAAC CACNACCTTC ANNCCCAAC ATTTNGGCGC CCCCCNCCTCN
CCNAATGGAG GNNCCCAACT CNAGAAGAAC NCCNNTGAAM ANCNAGCAGA ANANNNCTCGA
CANATCTTAAT CCCCCATTTN GGGGCNCCCTT NCCNGGGGCC CC

(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:

CGGCCGGCTG CTGTGGGCCA GTGCTCTGGA ATGGCATCAA AAGTGATGGA CTGCCCATTTG
CTAGAGAAGA CCGTCTGCTC TACTGTACCT ATGGAGGCCCT GCCAGACTGAG GCCTCCCCTT
GTCTGCAAGA TTGGAAGCTT GAAGTGGCTTG ATGTTGGCTT ATGAGCTCCT ATCTCATATNA
GCTGGAGAAC CGTGGAGGCG TCCTCGCGCA GCCCTCCCCCT TCTCTCCAGG CTTCCGANGG
ACACACGGGC CTCAGGACAG CCGATATTCC CCAAGNNAGC ATGTTTGGTTC TCCAGGCGGA
CCATGSGGC CTGAANAGCC AGGCTCTCCT TTGACACAT CTCTCCTCGC CTCTCCTGACA
GGCGCGGAGA TCCACTANNT CTANAAACGN GCACACCGCNG GTGGGAGCTC CAGCTTTTGT
TCCTNTTAAT TGCCGCTTG CGTGTAATCT AAGTGACNAC TNGTCAANAC TGTNTGTTCT
GTGAAATTTT GCTNTCTCCT NCNATTCACN NCNACATACN AANCCGAAGA CATAAGATGT
TAAGGCTCGG GCGTGGCGCTA NNGAATNAC CNAATCAAT TAATTTGCTT GCAGTCAGGC
CCGGTCTCCN CGTNGGAAAAG CTGGCNTCCN CCGTCTNNTNT GTAACGGGCAA CCCCCNGGG
AAAAGGCGCT GCTNTTGGTG CNTCTCCCTT CNTCTCTACN CNTCTNGCGC CNTCTNGCGC
CGTGGTGGN NGGTGGCGGC GAAGGGNATTN NNNTCTCCNC NAAAGGGGGNG AGNNNGNTAT
CCCCTGAA

(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 TTTTTTTTGT TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTT 60
CAGTACACAG GGCATTAGA AGAAGAAGAG AGAAGGAGAG AGAACAGGAG CACTGCTGGAC 120
AACAGAGGTC TCTGCCCAGG TCTCTTGCT TCTCTCAGG TGAGGGGCGT GGGAGGGGCT 180
CCCGGCCGCG GGGGCGCGCG GGGGCGCGCG TGGGGCGCGT TGGGGCGCGT 240
GTGGTCGTCGT NCAATGGCGT GCCACANATC CTTCAAGATT TGGACAGGCT GATTCACAGT 300
GGGAGCCTGC TTTCCGCCCA TGGGAATCTC NNATATCCCT TGGGAATTCT CTCTCTGCCTG 360
CNGCANTATG CGTGTTCTCA GAAAAAGGCA GGTGCTTTCA TNGGCTTTG ACTCTGCTACA 420
TATGTTTGCG GCCACCTCTC CCCNTCAANG AAGTAAATTG CCCCCCCCCC CCCCNTCAAG 480
CCGGGCGGCT TAAATGCCCA ACCGGAAACT CANTATTTA TTTATTTTTA GNTTGGGTGT 540
NTATCNGCCN CNTGGAGGAC GCAAGTGTGAA AGGCCAGCGC GTNCCCNTCTT CCCCNTCAANG 600
NTATCNGCCN CNTGGAGGAC GCAAGTGTGAA AGGCCAGCGC GTNCCCNTCTT CCCCNTCAANG 660
AGCCAGGNGC CGGGCCCAAGC CCGNATCCN GCAATGCGTG TCCATGCGTC CCAATGCGTG 720
CCNGNGCNCC CGGGCAGCGC GCAAAGAGG TTGGAGCCCG CGCANNNNNN NGNNTNCCNC 780
CTCCGCCCGC CCCCCGCCNN 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 TTTTTTTTGT TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTNCNGGAG GCAGACGTAA TTGGCAACCT CCNCGACCAC CCNCGACCAC ACCNACGGCTG 120
GGCAGAGAGC TCTGGCAGGG GCAGAGAGC TCTGGCAGGG GCAGAGAGC TCTGGCAGGG 180
CGCTGAGGAG TCAGGATGGT CAGGGTGGGT AGAGGAGGTG GCTGGGCGCC GCCCGCGCGG 240
GCGGGCAAGC TTTGCACTATG AGAAGGCGGG AGAAGGCGGG AGAAGGCGGG AGAAGGCGGG 300
NTATAGGATG AATGGATGCG CCGGCGCGCG CCGGCGCGCG CCGGCGCGCG CCGGCGCGCG 360
GGGCGTCGCG CAGTGGCGGCT TTTAGAATCC ACCCGCGGCG CCGGCGCGCG CCGGCGCGCG 420
NCCNGCAGCA ATCCTATGC CGAGCTGCG TCCCCGCCG GCCGCGCCG GCCGCGCCG GCCGCGCCG 480
GGCCAGGAGC TTTGCGCGCGT TGTCTGCGNG TNCATGCAGT CCGGCGCGCG CCGGCGCGCG 540
NCNGCAGTGC TTTGGCGCGG CAAANNTCT CAGGGGCAGC CAGGGGCAGC CAGGGGCAGC 600
CCCGTGTGCG CCAGAATCCT ATGGGCATGGT TTTGGCGCGG CAGGGGCAGC CAGGGGCAGC 660
TGGNGGCGAG NNTGCNTTCC CCGGCGCGCG CCGGCGCGCG CCGGCGCGCG CCGGCGCGCG 720
NTATATATAT CGATACAACCG GGCCGCCGGC NNNNNNNNNN TANCAAGGNN TANCAAGGNN 780
CCCGCGCCCG 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:

GACAGAACAC GTGGCATGCG GCCCGCACGT TCTATACGAC TATACAGGAC AGCAATGCGG 60
AAATATTAGC TGTTGCGAGA ATANAAACCC ATGCTGATGG ATGCTGATGG ATGCTGATGG 120
GAGATCTTGC TTTGACGAGT ATGAGGCGGA AGAAGGCGGG AGAAGGCGGG AGAAGGCGGG 180
AGAATTTTGC AGATATTTTG CCAAGGAGA CGAAGCGGAG GTGGGCTTCA ATCTTTGACG 240
GCGACAGATGC CTGGTGAGCA CGGCTTGGTA CTTTGGAGA GTTGCTTAT CATGATCAGA 300
WO 98/37093

(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:

GCGCGCCAGG GCATGTCAGA GCAACTCAAG GCGAGTCAGA ACCGTAAAGG CCCCAATCTT 60
ANCAAGTCGG GGGAANACCT GCCTGCACAG GCCATCCAAT CACTCTCTTG CACTCTGCTG 120
CCACCCAGACG GACCAAAGCG CAGCTAACGT TGGCCGCTAG CATACGTAG 180
ATCGGGGCC GCATGACAGC ATCAGCCGAC CCGAAGTCAG ATGATGACAG 240
CAGTCCAAAAT GCTTACTACTT TGATGACAAG GAGCACTCAG CGCAGCTAGC TATGATGACG 300
CAGCTTCTTG GGCCTCAACCT CCTTCTCTCG TGCTCCACAG ACCGGTGAGC TGATNCCAC 360
ACGCTANTGG AGCGCCTGGG CGCGCAGAGT CACACGACAG TGGCTACAGG ATGACGAGT 420
AAAAATCGGG TGTGGCTCAG GAAAGCTCTG AAANAAACTGC TATCTTCNTGG AGGGGGGGG 480
ATNNCTACTG NCTAAGAACG GCCGCCCATC GCCTGGGAGC CTCTAACCTT TGTTNCCACT 540
TTACTGAAGG TNATGCGCG CCGTGGGCT TATCATTGCG ACNCGNNTTN CCGTGTTGTA 600
ATNNNTAAC CTCGCCAAAT TCAGCAGGCA CATNNG 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:

GGGGATCCCT ANATCNAACCT GNATGCAAGT TGGTCTGCTG TGGTCTGCTG GATGAAAATG 60
AACAGGATCC TGCCCTGGA A GTCTGCGCT GCTGTNTTTTA AGTGGTCAAGT TGGGCTCGCA 120
TAGTCGACAG CNTCTGTTGG CAAAAACAAAC GAGGATCTGA GCTTGATATT CACTCTCCTA 180
AATTCACCAG GCCTGTTGCT GCCTGGAATCT GATGACNNNG GCCAGCTGCT TGGTNTNTGA 240
AAANCTCCANC ANGTTCCTCTT TGGTACACTC CCCTCTCAAGG TGGTCTCGCC CTCTATACAA 300
CTCTTNAAAAG AANANNNACCT CNCTTGGCTC GAGGCTGNAT TGGANAAAGC GGCACGCTT 360
GGGAACCTATT CCACAAATGTT AGTATGGCTA TGGCCTCAGC TGGCGGCAA AACTGCGCTT 420
GGCGCAAAATC GCCTGCGACC TGGTCTGCTG GCCAANATCG GACCCGCGCT CCGCTAGTGCG 480
NNAANNGACT CNTCCGGCTT CGCGCCCTNG CCAGGCTGTTG GAGGAANCGG CCGCCCTGCC 540
TTTTCGCGC ACCTGCGNNT NTTATCTACGC CCCTCTCCGA GCTTTNNTAT CTTCTGAGGG 600
AANTCCTGGG CGGCGTTTCA ANTCCTTCG CTTGNNCTCN CCGTGCGTCC TTTGAATTTT 660
NCCNAACTTC TTCTCTCCCCNCCCNCGGG NGTTTNNGNT TTCTATGNNGG CCGCAACTCT 720

(3) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

GGGTCCCTCG TATCCAGATC GATGGGTGCT TGGTCTGCTG TGGTCTGCTG GATGAAAATG 60
AACAGGATCC TGCCCTGGA A GTCTGCGCT GCTGTNTTTTA AGTGGTCAAGT TGGGCTCGCA 120
TAGTCGACAG CNTCTGTTGG CAAAAACAAAC GAGGATCTGA GCTTGATATT CACTCTCCTA 180
AATTCACCAG GCCTGTTGCT GCCTGGAATCT GATGACNNNG GCCAGCTGCT TGGTNTNTGA 240
AAANCTCCANC ANGTTCCTCTT TGGTACACTC CCCTCTCAAGG TGGTCTCGCC CTCTATACAA 300
CTCTTNAAAAG AANANNNACCT CNCTTGGCTC GAGGCTGNAT TGGANAAAGC GGCACGCTT 360
GGGAACCTATT CCACAAATGTT AGTATGGCTA TGGCCTCAGC TGGCGGCAA AACTGCGCTT 420
GGCGCAAAATC GCCTGCGACC TGGTCTGCTG GCCAANATCG GACCCGCGCT CCGCTAGTGCG 480
NNAANNGACT CNTCCGGCTT CGCGCCCTNG CCAGGCTGTTG GAGGAANCGG CCGCCCTGCC 540
TTTTCGCGC ACCTGCGNNT NTTATCTACGC CCCTCTCCGA GCTTTNNTAT CTTCTGAGGG 600
AANTCCTGGG CGGCGTTTCA ANTCCTTCG CTTGNNCTCN CCGTGCGTCC TTTGAATTTT 660
NCCNAACTTC TTCTCTCCCCNCCCNCGGG NGTTTNNGNT TTCTATGNNGG CCGCAACTCT 720
(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:

GCTNTTGCC ANTCCTCGC GGCTCCTNT CNCCCTCCTN GCTCCCTNG GGCC

(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:

GCCGCCCTTT CCTGCCTGGGC CCCCCCTCTCCG TGCCCTGGTG TCATTACG TGAATACNG

(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

(xi) MOLECULE TYPE: cDNA

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

TTTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTAAA CCCCCCTCAT TGAATGAAA 60
CTTCACAAAT CTGTCACACC CCTCCNCACA ATNNCCATTT CCCGGGCGGG GTTCCACACC 120
CAAAATTTTT TTGGGAAATT AATTAATNRT TNAATTNGGG AANANAACCA ATGTAANAGA 180
AATTAATAC ACATTCAACT TAAATNACT TGGAGCCNCC AGNNTCCAA AATTNTTACC 240
CTTAAACCTCC TGCCCAATTG NTAANNGGAA ACCAAATTCN CCTAAAGGCTN TTTGAAGGTT 300
GAGTTAACCC CGCCTTTNACT TTTTNNTTCC CNNGCTNARA NTATTNNTGNT TCCGTGCTT 360
TCTTTTTAAAN CTNTNGTAAAC TCCGNTAAT CAAANNCCTTC AANCCAATTA AACCCAATAA 420
TTTTTAAAGG GGAAATCCCN NNGGAATAANA CCAGGGTTTT TCCCNNTTGGG GCCGCAATNC 480
CCCNCTTCTG GGTGTTGCGN NTAGGTTGNN TTTTNTNANNG NCCCAAANAA NCCCAAANAA 540
AAAAAAGCTCC CAAGNNTTAA ATNNGAANNTC CCCTCTCCCA GGCCTTTGCG GAAAGNGGAGG 600
TTTTGGGGGG CONGGGANNTT CNTCCCCCGCN TTNNCNCCCN CCCCCNGGGT AANNGGTAT 660
NGNNNTTGGTT TTGGGGSNCC CTTNNNGGAC CTGCCGGATN GAAATTAATN CCCCCGGNCG 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 TTTTTCTTTG CTCACATTTA AATTTTATT T GATTTTTTT TAATGCTGCA 60
CAACGAAATA TTAAATCTAT TTGTTCTTCT TATTTCAATT TATTGTTTGG CTTCCGGCTT 120
TTATTTATTT TTTATCGAAA GGGAGGGGAA ACTTTTGTTG CCTTTTTTTCT CTTCTCCTGA 180
GCCCCCCTTTA AAGGTCTCTA ATTTGACACA TCAGAATGAA AAGGCTCGTTT 240
CCCAAAATCA CCCCAGGAAAA NGAGGAAGGT GCGTGTGTTA TCCATCCGCCT TGGTCTGTTA 300
TTAATCGCTT CTGAACATTG NTTCCACTCT TAATTAATTTG TCTNANNGC TTTAATNTAN 360
CTGTTGGGGT CCTCCCCCGCN ACCAACCCCN CGGACAAAAA GCCTCNGCNG TCAAATNTAG 420
TCGCCGGNCC ANNTGCACAACA CGCCTGGGAA NTTTCCTCATT NNNNCTTCNGC CGAGTNAA A 480
TGGGTTGCTT CAATTTTAAA CCACCAACTT ACNTGGCNGN GCCTGATACC TNNAAAANCN 540
CTCTCAANCN ATTTCTNGNC CCCCAGCCTNC GCNTNGCTNC CNCCGGCGCT CCGGAANTN 600
CACCCCCGCA ANNCNNTNCN NAACNAAATC CGGAAATAAT TCCCNNTNCC TCAATTCCCN 660
CNAAGACTNTT CTNCTCNAN CNCAATTTTC TTTTNNTCAAC GAACNGCNGC CNNAATNTGN 720
NNNNOCTCCT CNTCTGCTCNA NAATCNCNAN 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:

GTGCTATTGTT GGTTATTGTT TTGGGACAGA ACACCGCGCT 60
AGACACAAAC CCCCACACGA CAACAGACAC ACACTGGCAG AGGGCGGCGG CTGGGAGGG 120
CACCCCCGCA ACAGCAGGCG CTTTGAGAGA GAGGATGAT 180
TGCTCTTGAA GGGCGGCGCTG TACCTGGCTGA GGGCCACACC GTCAGGGCCC ACCAGGAAC T 240
TCCTCAAGTTC CGAGGCAACN TCCTTCGGAC ACACCGCAGA CGAGTTGATN AGCTTGGGCT 300
CGGTCTAAAC CGGGTGGCCG TCCTCGCTGG GAGCTGGAAG CGCCTGCCCC ACCAGAAGCNA 360
ATAAAGAGGTG CGGCCCCGCA CGGTTTCACT CGGACTTCTC NAANACCCTG ANGTTGGGCT 420
CNAACCCACC ACCANNCCGG ACTTCCCTGA NGGAAATCCCC AAAATCTTCTC GNTCTTGGGCG 480
TTCTNCTGA2 GGGCTAANCTG GTGGCXXCGNX AXXGAANCA AXXCCANCC CXXGGGTXCT 540
AAANCCACCC CXXCTXXCAATX TXXCTXXGXX XXTXXCTXXXX CGACXXGXXT CXXCTXXCAAG 600
GGANXXCAATX TXXCTXXCAATX AXXCTXXCTTXX NXXCCXXCTXX NXNAXXXA AXXCTXXGNX 660
TTXXCCXXCGX NXXCTXXGXX CNXXAXANAN CXXTNXXCAXX XXGTTXXCTG CXXCTXXCCCC 720
TNXXCTXXGXX GNXXCCXXCNX TXXGTXXCTAX X 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 TCACAAAGCA CATGCTTCCAT CCCATAGACT TCTTGA_CAT A GCTTCAATG 60
AGTGAACCCA TCCTTGGATTT ATATACATAT ATGTCTCGAG TATTTTGCGA GCTTCTCCAC 120
TTCTTTAACACT CGTGCTTCCAT ATGAAACTG AAAAAGGAGA TTTGTAAGA AATAAAAAAGT 180
TATAGCTTTGT TTAGCTAGTAGG AGITTTTTGAA GTCTACATCC AATCCAGACA CTTAGTGAG 240
TGTTAAAACTG TGATTTTTAA AAAATATCAT TTGAAATAT TCTTTTCAGAG GTATTTTCCAT 300
TTTACTTTTT TGTTTTTATG TGTTTTATAT ATTAGGGTAG 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 TTATAGCTTG TGCTCTTCCAT TATTTAGGG TGTATCATAA ATACTTTGAT 60
GTTTCAACAAT TCTAATATAAATAATTTTCA 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 GATGTTTCT TAAATAACCA TTCTCTCTCG TGGTCCAACC
TCCAGGTGGG TCTCACAACGT TAATAGAGC TATTGGAGAG GTCTTCAAAGC AAATGAAATG
TCAGATCTGG TACCTAAGTCT AGTTATCAGT AGTTATGTTT CAGAAGACTC AGAAGACCTCA
CTTCCTGGAG GGTCAAGTTAA GAGCAGTTTA TATTCATAT CTACAAAGTT ACCACAGGAT
TGGATAACAG ACAGAGGTTA TCCCTGATAA ACGCAGCTCA AGTACGTGCC CGGGGCCGCG
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:

ACATAAAATAT CAGAGAAAG TAGCTTTTGA AATATTACCG TCCAGGAAGT CTTTTTTTCT
GATTATTGG GTGTGTTTTT GTTTGCTTC CAAAGATTGC GCAGCTTCAG TTTTTATTT
CTTCAGATCT TCCCTGACTC TCCCACAATT TATATAACG AGCTCGTCCA TCCACAGCCT
CCAGAATTTT CTTCTTGTAG TAAATACCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC
TGCTGTGTTT TCTCTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTT AGAAACCTCA
AGACCCCTCT ACATCGGTCT TCCCATTTTA TTAATCTGG GTTCTCTGT CAGGTTCAAA
GAGTCGCTGG CAGAAGTCGG TACAAAGGAG TCCCTCTCGG GTGTTGTCTT TTGTGTTGGC
ACTGGGCGGG CGGCTCTTCG TCTCTTTTTA TATCGAGTTG CTCGAGCAAC GGAAGTGGAC
TGCGGTGTAT CATCGAGATC TCGGCCGCCG AGAAAGTTTT TGGCCGCAAC AAATCTACTG
TGCTACGCTT TATTTCTACG TATATAGTCT CTNNCTTCTT CAGGGTGGGC ATGATGGAAG
GGCTCGGTTT TCTACTCTTTG ACAAGCATCT TGTTGTGGGA CTGGAAAGAG TCACTCTCG
ACCTGGCGTTT CCACATCGGA TGCTGCAAGT TGCTGTAAGAG AGANGGCCCC GCCGGCTCTG
CGCGCGGCCT GAACTCCGTC AAATCCTAGC TGCAAAGGTT CTCCCAGCTAG AGTCTTGA
CNTGAGAAAG TACAAATTTG GCATCCAGCT GTTGGGTGCT CAGGAGTGT AGTGACCACT
CGCCACACCTG CT

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:

ACACACAGACC CTCTCTCCTG CACCAACTCA TGCTCAGTCA GTGAGCGAAG TCGGCTGTCCG
AGCTGAGACAT CAGGGGACGG ATCTGGGACTT GCAGGGATCG CTGGCACTGG AGGAGCTATT
GCCTGCTTTT TGGCTCTGCGT CTGGCTTGGCA AGCGCAAGAT CACCACCGAA GCCTTCAAGT

120

180
(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

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

ACTTTTATT TAAATGTTTA TAAGCCGATG CTATGAGAAT GATAGAAACAT ATGGTGTTGTA 60
ATTTGATAGC AAATTTTCTG AGATTACAGA GTTTTACTAA TTACCAATTA CACAGTTAAA 120
AAGGATGATA TATATTTCTCAGCANATCA AATFCTTAAT GAAGATGCAACGCAAGA 180
TGATATTACAA TCAGAACGCTAGGAAATC ATTTTTATGT GAATGACAACTATTTTTTTA 240
AAAGCTTTCCA AAAANAANAA TTATTGCACT GTANNTTAATT CAACAGATGT TAAATGGTAT 300
CAGGATTTAAAAATTCTTCACCATNCAATGTTAAC CACCCACAAT 360
TTACAAATGC TTAAATGCACN GGAANAGCAG GTGGAAGTAG GGAAGTANTC AAGGATTTTTC 420
TGTTCTGTTA ATTTATGCCTGTCAGCTGAGTGATGGTGAT CTCCTTGGAGCAGCTCAGCAG 480
GGCTTTCTGT ATATCACCAC TCCACAGACG AAAGTGAAGG GATGAAAAAG GACACATGCT 540
GCTTCTTCTT GAGGAACCTT CATCTCAGCTG GCAACACTC AGTCCACAT 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

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

ACAAGGGGGC ATATGAAAGG ATGCGGGGAA GATTTTATAG AAAGAAAAAA AAGGAGGCCC 60
TGAACAGAAAT TTTCCTGACAT AAGCGGGCTT CAAATAATTG TTCTGCGGGA GGGTCAGAAC 120
GCTTCATCTG TTGAAACTTTT AATGGATAGTG GGCAANATTG TTCTGTAAT GACCTGAGGG 180
CATTACAGC GGAGCTCTGAG GAGGAAGGAT AAACGAAAGG GGGCAAAAGC CTAATCCCCC 240
AACATCAAGG AAAGGAAAGT GGCATGCTT CACAGCGCTTTT TTTTCTCAGCTT 300
CCTATAGCTG GTGCGGGTG GACGCGCTTTGGT GAAGCGGCCC CCTCTGTGATG CTCCTGGAGC 360
CTGGCTCTCCGC GGCAGCCTTG GAAGGCGCCC GAAGGGCGG CTCCTGAGGG 420
CCACACTCTG TGGACACAGA TGGCGGCTG ATATGTCTTG ATAGGGTCTG AACCCTCTTT 480
CCTATCCTTC AGTGCTGGTG CTCCTGGGCAA GTGCTGAAAT GACCTGAGGG 540
ACGGCGATGGG AAGCTTTCTG GACTGCGGCT ATTACTCCAG CAGTTCGAAAGAACAATCT 660
TTCCGAGATC CTTAGAGGCAA AGAAAGGCTA GTTAAAGAAGT GGCCTGGACG ACTTGGAGAC 720
AGGGCTGGTT GCATCAATCT TGGCTTTATT AGGAGCTATTG GCAGCTTGGG CAAATATCTT 780
TCATCTCTAT GGGTCATGCT TGGCTTATGG TGCAAATGGGG GATGAATAAAC TAG 840

(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:
CANAATTTGA AATTTTATAA AAAGGCAAATTT TTCTCTTTAA A TCCATAAAAT GATATAATT 60
TTGCAANTAT ANAAATGGT GTATAAATT AATGGTCTTT AATTACAGCT CACAGCAACT 120
TGUT 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:
GCGAGATCT CTATTTTAT GCGAGGTGTT TTGATTTTCT TCCAGCTT 60
GGGGGTTTT TATTTTGGT CTTCACAGCT 120
TTTAGCACC CATATCCCAC 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 AATAAAAAGGA CGTTGGGGT TCCTCTAAAA A CACATGGCTT GATATATGC 60
ATGGTTGGAG GTAGAGGA GTAGGCTA TGTTTTGGA GAGGGT 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
(vi) ORIGINAL SOURCE:
   (A) ORGANISM: Homo sapiens

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

GTCCTAGGGAA TCTTACGGGA CACAGACTTC TGGGTCACGG GGGCGGACAC ACTTGCACGG 60
CGGGAGGGAA AGCGCAGGA GTGACACCGCT CAGGGGAAAA TGACAGAAAAG GAAAATCAAG 120
GGCCTTGGCAAG GTGAGAAAGG GAACATCAAGG CTTCACACCC AGGCCGTCGGG CACTTGCCCA 180
CCCTCCCTTTT GGACACGCA ATGT 204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 491 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

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

ACAAAGATGAA CAGTTAATTCG ATAAACAAAAA TTTGATAGTT TTAAGGTATTA GTATTGTGA 60
GGTATTTTTC TAAAGACTA AAGGATAAAC TCAGTTAAAAA AGTGAAGATA TTGAAAACAC 120
CCATCAGACA GGTGTTTTAAA AACAAACATA TTACAAATTT AGAATCAT ATCTAAAAAA 180
AAAACCTTTT GTAGACATTT CTTTTGTCTCA AAAAGCTGCA CTGAAATATT TTTAAATATT 240
TCAGAACAAC TCTCCTAAAA ATTTTCAANA TGTTAGCTTT CANATGTTGCC CTGAGTCCCA 300
AGTGGCTCCT GATAAATGAA CTCTGCTGAG ACTACCACCC CACCAGAAAG CTTCGCGGCC 360
ATGCAACAGT GTCTTCTTCT TNCTTTTTCT TTTTTTTTT TTACAGGCAAG AGAAACTCTA 420
CAATTATTTT TGGATACAAA AGGGTCTCCCA AATTATATG AAAATAAATA CCAAGTTTAT 480
ATACTCTGCG T 491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 484 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

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

ACATAATTTA GCAGGCGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTAT TATGATCTGA 60
GTTAATAACG TCTGCTGAAAT TGTGTATATT TATGAGACAT TTTCTTTTTG CTTGGATIAAC 120
ACTACACGAC CCTGAAGAAC ACTGGAATAT ATGAGATGAAA GCTCAAGAAC ATTAGCCTCT 180
CAGTCGATAC CGTAGTCAGC AACTAGATTA TTAAGGTATT AAAAGAAGTG TCTGAAATCT 240
GCACTGTATN ANACGCCCTG TGCGAGGATA ANACTCCTTTT GGACAGCAAAG GGAGAANNC 300
AGCTTTGONNT TNCTTTCTTCC TGTATANGAGG AAGGGCTGAA ATGCTTGTTT GCTCTCTCGCT 360
AATGGATGGCG AGCTGCGGTA AACNCGAAA CATACTCAGAA CTCACACTGT CTGTTCNCNG 420
TANCTTGANT CTGGTAGATAC CAGGANCAGG CGGATGGAAAG GGCCCGGccc NGCGATGTTG 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

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

ACTAAACCTC GTGCTTGTGA ACTCCCATACA GAAAACGTTG CCATCCCTGA ACACGGCTGG 60
CCACTGGGTA TACCTCTGAC AACGGAACA ACAAAAAACAC AAATCTCTTG3 CACTGCTAG 120
TCTATGTCCT CTCAAGTGCC TTTTTGTGTG 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

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

ACCTGGCTTG TCCGCCGGTG GTTCCCCGCG CCCCCCACCG TCCCCAGAAG GGACACCTTC 60
GCCCTCCAGT GGGTACCTGA GCCAAAAGGTG 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

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

GGCGGATGTG CGTGGTTTAT ATACAAATAT GTCATTATAT GTAAAGGACT TGAGTATACT 60
TGAGATTITG GTATCGTGG GTGGGGGGGA CGTCCAGGAA ACCAAATACCC CATGGAATAC 120
AAGGGACGAC 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

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

ACTCTGGAGA ACCTGAGCC CTCGCCGCC TCTGAGATGA GGTGATGCAN GCGCTGGCCG  60
GACTGAGAGC TACGCCCTTG CCGTGGGGCC TGCCTCAGAG ATGTGGGCCC GACNTGCAAA  120
TCTGACTGCG CTCAGAGCGA GCAGGGT  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

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

ACAAGGGATAT AGGTTTNAAG TTATTGNTAT TGTTAATAC ATTTGAAATTT CTGTAATCTC  60
TGATTACATA CATTATATCT TATAAAAAAGA TGTTAATATT AATTATATG CCAAATATT  120
ATTACCAAT AGATTACCTT GAAAAATGAGA AGATCATGATA GCACCTGATT TAACTAGTT  180
TTGACTTCTA AGGTTGAG  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

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

ACAACAAATG GGTGTTGAGG AGTCTTATTC AGCACAACATG GTGATGGCTA CTGAAAAGAT  60
CCATTGAAA TTATCTATAA TGATTTAAA TGACAGATTA TCAAAAAACTC ACTCAATTTT  120
CACCGTGGCT AGCTCTTGAA ATGGGAGTG TACTCTAGAG CAATATAGCT ATCTCTGAAA  180
TACGGTCAAT AATGACAAA GCCAGGGCCT ACAGGTCGTT TCCAGACTTT CCAGACCCAG  240
CAGAAGGGAT CTTATTATAT CAGTGTCTAT CCGTCTGTGC TCAAAAATTC TAATGATATT  300
TTTGCGCTTAT ATGGACTCTC TTGGAAGGT  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:

ACCGGGGGTG CCTTCTACAT TCTGACGCGC TCCTTCAACCA ACATCTGGTT CTACTCCGGC 60
GCTGTTGGCT CCTTCCCTCT CATCCCTTCAT CAGCTGGTGTC GCCTCACTCGA CTTTGGCAGC 120
TCTTGGACCC AGCGGCTGGCT GOGCAAGGAGC GAGGAGTAGG ATTTCCCGTG TGTG 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:

ACCCACTTT TCTCTCTGGT AGCAGTCTGG ACTTCTCTACT GCTACATGAT GAGGTTGAAT 60
GGTGTGGCT CTCCAAACAG ATCCCTCCCCT TCTCGGATCT GCTGAACCGG ACACGAGYGC 120
TGACTGACCT AGCCCCCAGG CTCACACTG 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:

CGCTCGACCC CTATAGTGAG TCAGTATTAGA 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:

ACAAAGTCATT TCAAGCAACCT TTGCTCTCTCA AAACATGACCA TCTTTATAT TTAATGCTTC 
CTGTATGAAT AAAAATGGTT ATATCAAGT

60

CTGTATGAAT AAAAATGGTT ATATCAAGT

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 ACCCTGGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG 
60
AATCAGTGCA TCCGAGATG GTCCTTGGA TGTGCGT

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:

ACAAACAAANAA NTCCCTCTCT TTAGCCCACTG ATGAAACCT GGAACCCTCT TTTGATGCGCA 
60
GCATGCGCTC CTAGGCTTGG ACACACGGGC TGGSATGGTG GCTNTCCCAA ACCGAGAACC 
120
CCACCCCTTG TCTACACCAAA NTCTGTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAAGST 
180
TGCTCATAAA NATGAAATCC CAANGGGAGC AGAAGCTGAG CAGGGAAGCT CAAATGAGAA 
240
GGTGTGTGTT CTAGCAAGCC AAAAAAGCTG CAGGGCATTG GCCGCTGAAC TATGAACCCG 
300
TGAGGCTGGA CTACCACCCAN GAGGAATCAT GCTGCGGCGA TGCAGAGGTG CCAAAGCGAG 
360
GGGCGGAGG 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 AGTGGAGGACA CTGGCTGCTG CCTCCTCCCG TGTTGCGCTG 60
AGGACCCAGT TGCCCCGTCACACATACAGC ACCTCCGCTT CACCAATTTG 120
GAACTACAG  TGCCACCTCGG TCCTCCTCCCC AGTCCCGAGT TCCACCTTCA 180
TCCTCCACCTC TAAGGGATAT CAAACTGCTCG CAGCGACAGG GCCCTGAATT 240
TTATATATTG TTTAATAAGG TGCGCTTATG GTCATTTTTT AATAAAGCTT 300
GAAGAGTTAC TGTCTT 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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:67:
ACTACACACA CTCCACTTGTC CCTTGAGAGA CACTTTGCTCC AGGCACTTTAA GGAATGCTGA 60
GGGCGGACCA GCCGACATCTC ATGAGCAAGA TTGCCACGCA GACATAGGCT GTGAGAGTTC 120
CCCTTTAAAA AAGGGGACTG TCCTATAAAA AGGAAGCTCAAG CCACGATTGG TCAAGGCCAGC 180
TGTCCTGAGTG TGAAGATTTCA CTTCCTGAGAG AGTTCTCCCTC TGAAGACCTGA TCTTTAGAGG 240
CTGAGGAGTG CTCCGATGTA GATGGGCTG TCTGGAATCTC AGCAGCTCCTT AGTCGCTTCTG 300
CTCTCCCCAG GGGCCCCGCG TGCCCAACCC TGCCTACAGG GCACCTCCTC ATGCCCGATAC 360
CATAGTTTCT GTGCTAGTGG ACCGTT 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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:68:
ACTTAAACAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTTAAAAA TGAAAATAAA 60
GTTTTTTAAA TAGG 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:

ACTAGTCACG TGGTGGGGAAC TTCATTGTTG TGGGGCCTCT GCCCTCTCT GCCCTTGAGCG 60
TCCAGCTTGG TGCTCTCGTT CAGAGGAGAC CATGGGCAAG CATGAACTA CATGCTCGCTCT 120
CTGGCTGACC ACCTACTGGG TCCGGCCTGCG CTGGAGGCCC AAGAGAGAGG ATAGGATAT 180
CCCCGGGATGC ATCTTAAACG CAGGCTCCTA TGGAGGTGTTG TGTAGCCTGT GCCTCTCATCTT 240
GCGCCATACG GAGCTATAAC AGGCCCA CCTACGACTAC TACAGAGCTC GCCTGCGGCTGT 300
ACTAAGGACCG AGGCAACAGC CCGTGGCGG CTGTTAATAC TCTCTGCCAG CTGAGGTGAGGG 360
CCAGAGCATA TGACACCACTT CCCAGGGCTT CTTGACACCC TGCTGGCTTC CATGACACGC 420
AGAACCTCAG AAGAAAACAGGT TGGCTCCTTGT CGAGATCTAC GAAGTTCTCCT GTGGGAGAACA 480
GAAGGCTCCCT GGGGATGACC ATGAGGCTCA GTAGATTCTAG AGATGCTGG 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:

ATGACCCCTTA ACAAGGGGACC TCTCGGAGCTT CTAATGACC TCCGGCCCTAG CCATGCTGTATG 60
TCATTTCTAC TCCATGACCG TCTCTACTAC AGGCCGACTA AGCAACACAC TAACATATA 120
CAGAATGAGG CCGGAGTAA CAGGAGAAAG CACATACCAA GCCCAAGCACA CACCACCTGTT 180
CAGAAAAAGGC CTCTGATACG GGAATAACTCT ATTTATATCG TCAGAAAGTTT TTTTTCCTGCG 240
AGGAATTTCG CGCTGCTTTT TACCCATCCA GCCGAGGCCCA TACCCCGTACCA CTAGGAGGGC 300
ACGGCCCCAC AAGCAAGATAC CCAGGCGGTA ATCCGCTGAGA GTCCCGCTC CTAAACACCAT 360
CCGTATACCT CGGTCTCCAGA GTATCAATCT CCTGAACCTCA CCAGTACCTA ATAGAAACA 420
ACCAGAAACA AATATATCTAA AGGAGCCTTT ATGCAAATTTT TGGCTCCCT CTTTCTT 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:

AGAGCATAG GTACAGTGGT ATCTCAGCCTT TGCAACACACA TTTTCTCATA ATAGAGTACT 60
AGATATTAT AGAAATATGAA AGAGAAAGAA CACCACTATA ATATAGTGAA GATTGGTTTA 120
TGATTTTTTA GTGATTTTTT TGCAACCTTAT ATATATATTT ATGAAACCTT AAGCATGAT 180
TTATATTTCCA TAACTAAAGG AGGAGTGGTG AAAAAAGAAA TCTCCAGCACA GCTCTCCATT 240
TAAATAAAAAG TGGAGGTCTG TGAAATATAC AGGAGATGG GATTTTAAA AAAGAGGTCG 300
AAATAGGAGT GACGGCCTAATT ATAGTATAA GAATACATT TTTAAACACT GAGTACCTCA 360
AGTACGCTTG CTTGAAAAAT TAGCAAAAT ATACCTTACG GAATCTGCA TAAAGAGATG 420
CTCTGTAAAT TGGGATGANG AGTTCCCTCC CTCAATTGTGT TAGTTTTAAA AAGTACAGGG 480
(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

(x) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
TAATACGACT CAAAGACACCA CATAAATCAA CTACAAAGA ANACTGCTTC AGGCGGTGA
AAATGGAAGG CTTCAGGCAT ATTATCAGA TAAAGAAGCC TAAAAAGGG ACAAAGCTAA
AAACGCCGAG AGTGTCTACG GCTATTGGG TTGGCTGAG GAGCTGTGA 120
AAACAGAGG AGATGGTGCG CCGAGATATT CTCATCGATT ATTACAGATT 240
GACGTCCTCG GTTGAGCCAG CCGTTGGAAG ACCGTTTTCN AATAATGATA GAATAGTACA 300
CACAATGAGAG CTGCAATGCC CCAACCCCGA AAAGAGGACG CACACTAGTC CTCCAANAC 360
GCTTGACGG ACATTTACCG ATGAAAGAAA GATGGCGCTCG TTGTGCCTCCC GTATGGTACG 420
AATTCTCC ATCCAGCGT NAAACCGCTT CTCTTAAAGCA AAGTACGCTG ATGATGCNA 480
AAATACACCC CTCCTTGAAG NACNGGAGA T 511
```
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

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

TTTCTAAGGA GAACACACTG AGGAGAATCT TGAAGAATTG GAATTCAGGC CGAAGGAGAT  60
TTACTCAGCT TACCTCAATG AAATCACTGGA AAGTAAATAG GTAAAAAGCTA GTTCTACT  120
TCCAGCCCC GTTCTCAGAA GCATTTTCTA GTATTATTTA CAGATGTGGT TAACTACTAA  180
CATTTGATGC ATGGAACATG GAGGAAGAAG TATTTCTCCT TCTTACCAAT CTAATCAAGA  240
AAAGAAATAG AGACTCTGTG TCTACAGTGA TGATTGAAT CTAAAAATTG TAACTATTAG  300
GGCTTGTGAT TTATATAACT TTGGGTCAACT ATACTAAATT ATGGTAGTTA TACTCGCTTC  360
CAGTTTGTCT GATATATTTG TTGATATTAA GATTTCTGAC TTTATATTGT AATTAGTTCTC  420
ACTGAAAATG GAATATATGA TTTCTGAGGA CAGCTGATAG ATTTATATTG CACTTCTGAT  480
TCTACATGTT AGAAATGCAA GGAATGCCCC CAAATTGTTT GGGGATACAA GTTCCGGT  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:

CAANACAAAT GTTCTAAAG ATGCAATGA TACACTACTG CTGCACTCAG CAAACACCTC  60
TGCTATTCAT ACUTACCTCC TCTCTCTCCT CAATGATGAT GGGCTATTTT GGCATACTCA  120
CCTGCTGTCT GTGTAAGAAG MGMGTCTCTCT GCCTCAAAGG AGAGAAATCA TAAAGACCG  180
TGTCAGAAGG AGGCGACTGCT TTCTCCTACCT GTATATGTTC GAGAGGCTG GCTCTGAGGA  240
TCCTGTTTGG CTTCTCCTCT GGGTCTTGGC CATTCTATTT CTGATATGGT TACTACCTCA  300
TCATTATGTT ATACAGGGTT TCAACACTGCT GGGAGCACAG AGAACCCTCAG TCTCGAAGAA  360
CAGCATGGGA TCTCCAGGCT GATTCCTACG ACAGAAATCTC TCAGCTTTCTG TCCAGCGCT  420
CTCCAGCCAA CCAAAATAGC CGCTCATTCT GTGACTACAA TCCCTGG  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:

AAAGCTGACAG CATCTGGGCC GAGATGCTTC GCCTCCGTGCC CTAGCTGAGT CGCTGCTAC  60
TCTACTCTTC TGCGCTGAGA GCTATCAAGC GTACCTCCAA GATTCAGGTT TACTCAAGT  120
ATCCGCAAGA GATGGAAGA TCAATTATGCT GAATGCTCTA TGCGCTGAGT CTCTACTG  180
CCACGGACAT AGATTGTTCTA GAGACAATGT TGAAGAAGTG GAGATGACTG  240
ACTTGCTCTT GGCAAGAGG GCTGCTCTCT ATCTCTGTGA CTACATGCAG TACCCGCCCA  300
CTGAAAAAGA TGTGATGCTG TGCCGTGCTA ACCATGGTAC TGGTTCACAG CCAAGATNG  360
(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:

   CTGGAGGTGCC TTGCTGTTCAC AGGCCCTGCAG AGGAAGCAGA ATGCAACCTTC TGAGGGCACT  60
   CCACGCTGCC CGCGCGCGGCG GTGAGAATTC GGAGCAACCT TGCCCCGGCTG TCGATTGCTGC  120
   CAGGAGCTGG CGACCTGGAC TTTTCTGGTCT CTTTCTGGCCC GCCAAGCGCT TCGCTTGGAA  180
   GTTCATATCT GGAGCGCTGAT GTCCTTAACGAG ATAAAGCTCC CATGCTCCAC CCGAAAAAAA  240
   AAAAAAAA  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:

   ACTATGTCGAG TGTGATGGGA TTTCTATTGTT TTGGGCCCAA CACAATGCGCT AACTCTTTCA  60
   TCACCCAGAC CGCGCGCGGC CGCGCGGCTAC CGCTGCTGCT ACAGCATGTA TCGGCCTTAC  120
   TCGCTACCGCGAAAAAGATTTTTATATTATGGTCACT TTCTGTGTTTTATATTGACCT  180
   GATTTAAAAA AAAAAAAAA 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:

   TCTCTTGTGT AGGTTTTTGA GACAACTCTA GACCTAAACT GGTGTCACAGA CTTCTGAAATG  60
   TTAGGGCATG CTCTAATATT TCTCTGAATAT GATTCTGATT TACTTCTCTCT ATCTCTTTAT  120
   CTTCTTCTTT CTGAGAGATTA ATGAAAGTTGA AAATGAGATG CGTAAAGATAC AAAGAGGTAG  180
TGTTGATAGTA TAAGTATCTA AGTGCGAGATG AAGATGTGTTT ATATATATCC ATTCGAAATT 240
AGTCAACGTTA GTAATATCTC AGGGTTAATCT AAATTCTTTT TAATGCTTGT TGAACCCTACT 300
CTGTTCTCTG AGTGAAGAAA ATTATAAAAA GACCTTTGTTT AGTTTGAGAA GCGAAATTGA 360
TAATATTCTTA TGTTCTAAAA GTGGGCCCTAT ACATACAATN TNAAGAAATG TGGAAATTTTA 420
TTGCCAGGAA TATGGGCTTG TTATTTGAAT ANACCGGGG AAGAAAGTTT GTGANTAAAC 480
CNGTTTTGGTG TAATACGCTTA ATATGTCCTG TATNAACAG ACGTGACCTTA 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:
ACAGGGATTG GAGATCTCTAA GGGCCCCAGAG ATGCTTTGAT CCAAACCTCT TATTTTCAGA 60
GGGGAATATG GGGCTTAGGA GTTACAGACG ATCTAGCTGG TGGCTGGGCA CCCCCTGACT 120
CACACACACT CCCGAGTACG TGGGACTACA GGCACAAGCT CACTGAGAGC GGGCCCGTTT 180
GCAATTCAGC TGGCCACTCT CAACCTAAAC ATCTTTCCAT TGTGATGCTCC TTGTGCACCTA 240
AGTTAATACG TTGCCACCTCA AAAAAAGCAA CTATGATAAAT ATCTTAGAGT ACTTTTCATAC 300
CTACTCAAGTC CCTTCTTCACG CCTTACTTTG ATGCTTCTTT AGGTTGTAGT AAGGAACTNCTC 360
TCTGTGCTCT GCTAACAAAACT TCTCCTATCC TCTCATGTTT AATTTGTTAC GCTGAAAAAT 420
GCTGAAAAA TTTAAATGTGT CTGTTTTCTC TTTAAAAAAA AAAAAAAA AAAA 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:
TTTTTTTTTTT TATGGCTNCTCN CTGTGGGNTG ATGTTGTGCTG CGACCTCGGA GGAGCCCGATG 60
TTCTCTCTGA TTCTTTCTTCT CGGGGGATC TGCTGGCTC TGCCGGCGC AATCCCAGCCT 120
CTCATCCCAA TTGTGACTCT TGCTAGGGTT TGGAGGCCCT TCTCTGTTAG CCCGTCAAG 180
ACTGACGTAG CGGGGATGCG TCTGGGGCTG GGGGGTGATG GCGACCGCGC 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:
AGGCGGAGGC AGAAGCTAAA GCCAAAGCCC AGGAAGAGTG GCAGTGGCCG CACTGCTGCC 60
AGTACCGATGA CCAAAATACG GCAGTGGCCG AGGTGGTGCC TTTAGTGGTCG 120
GGCAGAAGCT GACGAGGCTG GGCTCTCTCC TGGGCTTGGT GGAGCTGGTG 180
CCACGACACGT TGGGCTCTGG GCTTTCTCTTA CAAGTGAGAT TTTTAGATTT 240
GTTAATCCCTG CCGTAGCTCT CCCTGAAGGC AGGAGTCGTCG TCTAGAATAAC 300
AGACCTTCTG GCAGAGCTAT CGAATCTATT GGAATGACAC CTTGCGATTA AATCATATTG 360
CCATTCTAAA AAAAAAAA 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:
ACCGAATGG CACGCGCTGC TTAATAACGA TCAGTGCTCT CAGTAGATCC TCAACGAGCA 60
GGCGAGATCG GTCTACAAGG TGAAGAAGAT TGACCGCGAA GGAACAACAG CCTGTCAGAC 120
CCATCTCTGT CGGTCTCTCC CCGATGACAA ATACTCTCAG CACCGAATCA CCAACGAAGA 180
ACGCTTCAAG GTGCTCAGTA CCGAGCAAGG GCAGCCCTGC TGCTAAGGGT CCTAAACTG 240
AGGCTTCTTG TGGCCACTGT TTTCCAAGGAG ATACCTCGGA ACCAAACTCT GGGAGAGTGG 300
AGCCCTCGAT GCTTTTTTTG AGCCATACTC TGGGCTTGGC AGCTCTCGTG GCCGATGAGT 360
TATGCTCTTG TGAGGCAATCT ATGTTGGGAGT CACCGCATAA GCCAAGACAT TGGATTCTTG 420
TTTCCGATAT TTGAATATTG NACCAGAAAT TTTGAGATATG AATGAATGAA AAAAACTCTA 480
AAAAAAAAAA AAA 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:
GCTCGTACCC TATGCTCGGG CCGCAGGGGCC CTGGCTGAGG CACCGAGACG TGACTCTCAG 60
AGATACCTCG CTGCCTCAGC TTGTGCTACG TCTTCGGCCAG GAATTCCGAG 120
GAGGACAGTG AGCTACGCTT AGTGGACGCA AGCAACTGCT GTGAGGCAGC CGCTCTCTGG 180
GCACACCATCT CGGCGCGCCG AGGGCGAGAC TGGCTGCTCCG AGTATGGGCA CGTGCTGGTT 240
GGTCCGTCCCT CCGTTGCTGG CCACACATGC TGCGCTTGGC TGCGCTTTTG 300
CCATGTTGAG TATGATCTCTG GCGAAGAGCC AGGGCGACAG CTATCTCCTAC TGCGAGCGG 360
AGCAGTCCCG CTCACTCTGG 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 CTCACAACCC TTGATGAGGT CTCCTGCAAG TGCCCTCTGC GCCTACCCGC 60
TNCATCCTG TAATGGGTAG TGCCACCA CGCTGCGTAT TGGGCGGAG CTAATATCCA 120
GGGAAACTTC AACATCTGCA CCACTATNAA AACTGTGGGC TGATTCTGTC TCCCGCTCCG 180
TGAGAAGAGA TCTCCAGAAG GAGAGCTGCA TCTTCCCCAC ACTTTGTTAG ACTCTATTGA 240
GTCATGGCTG CATCTGGAGCG AGAGAGTTGT ACCAGCTTGC TGCACGGTGA GCTACACCGC 300
CTATCATGCT NTGGAAGGTG CGGAAGACACA CGGAGCTACT TGTTGGGAGTT GNAATCTCGC 360
CCAGATTTCTG CATTACCAAG NACCCGGTGCC AAAAGANATT GACAATCGCC CCAGGNCAGAA 420
AAAAAACCAC CCCTTGGAAGT GCTNGGCGCT CCTGCTCCNT TGGTGGNNGC GCNINCTTTT 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 TGGAATAAGCT TGTTAAATAT CGATCGAGATN TGGGCTCCTG AGAATTCAAT 60
ACTTGGAAA GGAACTTNNAA CCCTGCCAC CTTATTAAA ATCAAGAATA GCCACACTTT 120
TTAACAAGTG GTCAACTCGC TCCCTTACTT TTGTATCACC AGTCGGGGAA TAAAGGTATG 180
CCCTATTCC ACCTGTAAAA AGGCCGCTAA GCAATTTGCA TTCAACACTT TTTTTTTGTA 240
CACAAGTCGG AAAAAAGCAA AGTAAACAAG CTNTTAATTTT GTTACGCAAT TCACTTTCCTT 300
CATGGAGCAG AGCCATTTGA TTTAAAAAGC AAATGCATAA ATATTGAGCT TGGGAGCTGG 360
ATATNTTACG GGAAGANTAG CTCTTCTACT TCACCAAGCA CAACTCTTTAT CATATTGAGGA 420
TGTTCAACAA AGTTATGCTCT CATACAGAT GGGATGTCTTTT 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:

AGAAACACGAG ATCCTCTAAA ACAACCTCCTC ATACCTTGTG GACCTAAATTT TGTTGTCGGT 60
TGGTGTCGGG CCGCATTATAT ATAGACAGC GCACCTTTTT TACTTTTGGTA AAAGCTTATG 120
CTCTTCTGTG ATCTATATCT GTGAAGATTT TTATGATCGT CCAAATATGC TTGGGACCT 180
TTGTCTCTCTG TGGAAAGATG ACTAGAAGAA ACCAACATNT TATGAGTCAA CTCATTTNGT 240
TTTATTCGAC ATAGAANATN TTTCCAGATN ACAACACTNA CAAACTTCCG CTTGACTAGG 300
GGGACCAAGAA AAAAAACAAAT CTTGACATNA GAACAAATNT CTCGCGTGAGA AATTNCATSA 360
ACAGGAAATTG GGTGTTATAT TGAANANANN CACTTATNA 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:

CGCAGCGGCT GTCTCCCTAC TAGCTGCCGC CTCTGCGGTG CCCCAGCTGCG CGGCCTGCGG 60
GTCCTAGGCG ACCATGGGCCG GGGCCCTGGC CGGCCCTGCTG GACCTGTCATG CCATCTCGGC 120
CGTGCGCGGCT CCGGAGGCAG CCAGAGCCGC CGCCAGCTGG GCAGCGCTGG TTGGTGCGAT 180
GGGAAGGCCCA TGAGGCACCG ATGGAAGAAAG AAGGTTGCTG GCAGTGACTG ACTTTGACCG 240
TGCACAGNTA CAACACAAGGC GCAACCAGGT TTACCAAGCN CGCGTCTCGAG GGTTGGCCAG 300
CCCAANCAAAT TTTCTACTCG GGTTAATAAT TATCTTGGAGA TGGAACCGTGC GGCAACACNG 360
TTCAGGAGG CCAACAGCAT ATGAACACAT GACCTCCAC AGACGGCGCT TTTAAAAAGG 420
GAACACTTCTC CTTTCCTTCC 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:

GAATTTGTTG CACTGGGCCAC TGTGATGGAA CCGATTGGCC AGGATGCTTTG GAATTTATCA 60
GTGAGGCTTG TCTCGCATTG GGTGTTTGGG CATGACTGATG TAAAAGTCGA AAAAAATTGGC 120
AGAGGCTAGT GTGCTGCAATG ACACAGAAGT TTTGCTCCGT TATTTTTGTA CTTGAGTGGT 180
CTCATGCGACA ATGTTNTTCT GATGGCAAGA GTCTATCTCA GGTGGTTAGT CCTTGTGCATC 240
TTNANATNTN AGACTGCTCC CTTNANATTT GGTGTNTGNT CTCTCAAGCTC TAATCTCTGTG 300
TTAAANAAAAT TGAANNNACT TCTCTGCTTN GANNTTNTGA ATATCTTCAA TCTNANANATN 360
AATGTTGCG CCAATGAAA ACGGACCCCG TGGGAAATAT TGGAAAAANG GCCCTCTGNN 420
AATGTTGCG ATTCTACTG NTCAATCAA NAAGGGGAGC 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:
AGGGATGGAA GGTCTTTNT AACTGCACAG GCTTCAAACT CCCCTCTGAC AAGTTGACTG  60
CTTCCACTCA CTTCTCGTAA GCTTNTAAT TCCAGCTGG TCTCTACAA AAATAGGAC 120
TGTCAACTCA TGCAACCTTC TGGACTTCG TTTAGTGGAG TAGTGGACTC GCTGCAACTC 180
TCTTGTTGTT AGACTCAGT CTTGAAACTG TTAAAGTTGA GAAATTGCTTGGCTGGG 240
GGTCTCTAAA CTAATGCTC TCTCTGATTG AATTGCTCA AAACACTGCAA CCACTGCAATC 300
TGTGCACTCC ATTTTAAAAA TACCTAAATG GCTGACCTGT TCTGCGGTTA ATATCTGAC 360
GAGTCATCTG TCTGCAAAAAG TTGGCTTATG ATATCTGACCA 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:
GAGGTCCGAT CCAATAATCT TTTGCTGACG GCAAGACACGA TATNCAGTCG CATGCAAAC  60
GCTTACACCC ACACTGAGAC AGCATGCGCT AGNTATATAA GCTGATCCCG TGAGTCGACG 120
ATGCTCTCTT TCACTTCCCTT CIGGAGTTCTG GGTGATCTCTG AGACACCTGC NCCCGGTCTT 180
TGTGAAAAAA CTGCACTATT CCGGGAGACTA GCAAGACAC GCATTACAAAT TCACCCCCGA 240
GACACTGAA AAGCTGAAACA AGCGACGACT TGGATGCTT TTTGCTCCCT CCGACCCAGT 300
TTCGCATTACT AACCTGGCTG TGGGCTCCCA TCACTTTGCT GATCTGTGAC TCGGATACGC 360
TCTCTGACCA GTACTGAAAG ACTTCTGACT TGTGGTCAAA AGCAACTCTTG GGTGGCTGTTT 420
NGATAGGTT CCCATTTCCC AGTCGGAATG TTGCGATGAC ATATNTTACT TCCACAAAAA 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 NATGCCACCA CGAAGATGCG CTTGTTGACT GAGAACCCTGA TGCGGTCGCT 60
GGTCGCCGCTG TAGCCGCCAGC GACTCCTCC ACTCTGGAAG CGTTGTAGTC TGCACTCCTT 120
CCCAAGCAGG CAGCAGCGGC GGCGCTCAAT GAACCTCACT CTTGGCCTTG GCTGGACGGT 180
TAATTGGAGG AAGAGGCCTGCA CCACCTCCGG GTCCACCAAGG ATGCCCGACT GTGGGGGACC 240
TGGAGCGAAA CTTCTGCAATG TCTGATGAGG GGAAGCGGAT GANCCGACGG GCCCTGCAAC 300
AAACCCCTCC CTTACGTCTC GGCTGCAACT GCAGCTGCTG CGGCTCNACG TGCGGCTCCG 360
ACCACGGGAG AAAAGCGCGT GAACAGCGGC ACCTCAGGGA TGCCCAATGT GTGGGCCCTCC 420
AGGAGCCGCG CCAAGGCTTC CAGGTCATGT TCAGTGAGCT AATGCGCG 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:

GAAGCGCTGG ACCTTGCCCT GCTATTGCTG CTGGCGAGGA ATACCTTGCG AAGCAGCTCC 60
AGTGCGAGCA GCCCAGACCC CTGGCGGCCG GAAGCTAAGC CTGGCTCTTG CCTTCCCCCTC 120
CGCCTGAATG CAGAACACCT TAGGAGGAGCA CTGGTCTTAG AGTTAAGAGT GAACAGCTGN 180
TGATTTTACT TGCGAATTTA CTCTGTTATAGG AATGCTTATG TCTCCTATAAA 240
CAACAAACAA ATACACTGTG TGCTCTTATAG GTGTATAGAC AGTANGTGAT TGCTATNTA 300
AAAGAAATAT TACTCTTACT GCAANTCTAG TATTTATAGG TNCCTCGGAA 360
ATAAATATAT TATTTAA 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:

CCCTTGGAGG GGTATAGGTC CAGTTCCAGG TGGAAGAAAC AGGGCAGGAG AANTGCGTGC 60
CGAGCTGANG CAGGTCTCCG ACAGTGACC CAGAGCCCTG GCTATAGCTG TCTGACCCCT 120
CGAGGCAAAG ACCACCTTCT GGGGACTAGG CTTGGAGGGC AGGACTAGA GGCACCAAGG 180
GAAAGGCCCA TTCCCCGCCG GCTCCAGCGG GAAGAAGAGG AGGGGCTCTG TGGGCCGCCCA 240
AGGGAGAAGG GCCCTGAGNT CTGGGATACG AACCTCCTTG CAGCTGTATC CCCACACAAA 300
TGCAAGCTCA CCAAGGCTCC CTCTCGACTCC CTCTTTACTC CCCTCGAACC NCACCTGGCC 360
ACAACCCGCC AGNACANCCCA CCCGCCATGG GGAAATNCT AAGAGATGAG CNGGCGAAGG 420
TGAACTCCTNG TCCCNAAAGG GGGCAAGATC TCCAAATTAG GGAAMGGAACC CTCTGCTNANA 480
AAAAAANA AA AAAA 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:

```
GGTTACTTGG TTTCATTOCC ACCACTTAGT GGAATGTCATT TAGAACATT TTGTCTGTCG
CCTCTGGAGG CCTGCCGAG AGCGGACTTT GTAATTGGT GGAATAAAC GTCTGATTGTTT
TAGCATTTTT GAGTGGATT GCACACTGG ACCACAAAAT AATAGAAAAA CTATTNNACT
TATTTATTAT CTATGGAATA GTATAAATG AAAATTTTGG TCACTGCTA TTTATCAAGT
ATGATGAAAA GAAATGATA TATAATCTTT TATTATTTN AATTATGATT GCCATTATT
ATGGTTAAGA TTGGAAGATG TTTGCTTTT TATATACATA TATGCTTTTT GTAATCTTGCA
TTTATTATTAT TTATATTAAT AATATCAACAA ATCTCTATTT TAAGAAAAGG GTANGTTATA
TTTANTICAN TAATTTCTTT CCTTGTTTAC GCTAAATTTG AAAAAATGCC AT
```

(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:

```
CTGAAAGCATTT TCTTGAACCT TTYCTACTTT TTTYCTTTGT TGYCTCTGAT ACCTGGTAGT AGTTGACAAT
GGTGCTGAAAT CTCAAATATT TATGTTAATT CTCTACTTTT TACTTTCTCC CCCAAGCTTT
TTTCTTACTCT GAATTTSTAC ACACCACTTG TATGTTAGCT GCTTTCTTT TCTTTTTTCT
ACCTCTCTAC GTAGATGATG AAAGACCTT CCAGTTCTCT GNGCCAANATG TCTTGATNT
AGCTCGATAC ATACATGGAG AGTTCTTATA ACTAACTCCT CAGTGGACT NAACCAAATAAT
TTGGTTAGTC TCAATTCCTTA CCACACTGAG GAAGCCTCCC AAAATCCTAT ATTTCTTACT
GCAGGTATCT TCCGACAGAA ACNCGAAGG CATTGCTTCA TGAAAGTN ACATCTGCCT
TACAAAGCT ATCTCTTCTCA NANGTCTGNT AAGGAACAAT TTAATCTTCT AGCTTT
```

(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 ATGCTGAATAT GATCTTGAGT ATAAAGAATGC ATATGTCACT AAGATGGATA
```

60
(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:

```
AAATAATGCT GCAAATCTAA TGGTCTTATG CAAAATGGAAC CCAAATGGAAC ACAAAGCTTA 120
CAATCCGAGA TCAAACATCA CAAAGGCTCA TCGTTGTGAG ATTTAGTGAA ATGAGACTTA 180
GATGCTGCTCC CTTGAGATAT GATGTTTTCT CATACTTGAG CCAAATTCCTG TTAGTCAATG 240
CAGGCTACTAT GTAATCTGTT ATGGATATAG TGAAGCTAGT AAAATTTAAA NATAACACTT 300
GTGAATTATNA AATTAATCACA AAACTTTACT TATACCTGCT ATCACGAGCT AGAAACACTAT 360
NNNNTTTTNTA NACGGAATG TAATGCAGTT GTGGAATTTGA GAAATGATC TGAAGCTGAGG 420
TTCCATCTAA TTTTCTCCCN GACNACTANT TNCTTTTTTA GGGNCTATTC TGANCCATC 479
```

(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:

```
AGTGACTTGT CCTCCCAACAA AACCCTTTGA TCAAAGTGTG GGCACTGACA ATCCAGACCTA 60
TGCTAGTCCC TGGTAACTATT GGCAGACGGT GAGGGACCCA AAAAGGGCA 120
TCCACTCCAG CGGAGTTCAG CGGCCACCAAG GGAGCTTGAGA TCTCTTGGA 180
AGTGTTCTAG TGGGTATCTC TGGGAAAGAG GAAATCCAGA TGGGAAAGAGG 240
TGGAAATTCT CTGCAATGAG AGGAGGCAGT GGGGTAGTAC CTTCCCTCCCTT 300
TTACCACTTG AACACGGAGTT AGAAAAAGCC TGGGTAGTAC CTTCCCTCCCTT 360
TTAGAAATTT ATGGATTTAG TGGGAGCTTG AGGAGGCAGT GGGGTAGTAC 420
TTGGGAAATG TGGGTAGTAC CTGCAATGAG AGGAGGCAGT GGGGTAGTAC 480
```

(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 GCTGAGGGCC GTCGAGCAAGA GATTCTGCCA GAGATGTGTGC 60
CGACTGCAAC CAGGGGGAAG GCAAGATTCG CAGGTCGACG GCGGGGGCCT GCAGTCTTGC 120
AAAGCTGAGC TGCATCGCCA GAGGTTGCTG CAGCTTCCAC GACCTTGAAG CCGTCCCCGA 180
CAGCCGGGAC AGAGGCGGAG GAAAGCGGAG GGCCTGCGGA GGCCTCGGGG AAGGGCGGCC 240
CGAGGATACG GCAGGGGCGG GTCGCCCCGC 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:

TTTTTTTTTT TTTTGGAAATC TACTTGGGAGC ACAGGGAGTGC ACAGCAACAGT TTATTTGGCA 60
GCTAGCAAGG TAAACAGGTAA GGGCATGTTT ACATTTGTCG GTCACTTCGC TTTTGGGGTG 120
TTGATTGCTT TGCTCTTATG GGCGGGGGGT GGGGTGGGGG AAGCAGACCA AATAGACCGG 180
AGGGGGAGCA CCCCCCAGTT AGAACCTGTT TACAAAGGTT GGGCCAGGGT ACCTGGGCTG 240
TGACCTGCTA TTTTGTGAC ACAAATCGTT TAGAAGTCAAG GATATTTTCA AGAGAGCGGA 300
CTTTGCTGGA GGGAGATTAG GTTTTCTGCG CAAATCCAC AAAAAACTCC AAAAGAATTG 360
GATGATCACT AGGAATACGG AGGCATATTTC TCAATCGCGT GCACCA 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:

TTTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTTTT 60
GCCATTAAT TCAAGAAGTGT CTACACAATTCT AACCCACACAA TACCTTTGTTT 120
TCCTGACTA AATATATACAA ATAGCCCAAA GCCCTTACCC ATATACCCAA AAAATCAAAA 180
ATAATACCT CTACGCAAAC CTGTTACATA ATATAAAAAAA ATATATACCC CGTGTTTTTT 240
CACAATGAAA CTATTTTACG CTACACGCAA TTTTTAGGAA CTAATTAACAA AAAAATACCT 300
CAGACACAGT TAAAGGGGAA AGAAATATCT TTCTACACCC CATTAAAAAA ATACATATCT 360
AAATTCGAGG AAAAATACAA CTACACAGCG GACCTTACAT TTACTACACT TTGTATTTTT 420
TTTAAACCAA TGTTGTCGGG CAAACACACAA GAAATCCCCC CTCGGCTATG 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

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

TTTTTTTTTT TTTTTTTTT TTTTTTTTT CCCCCCTCTTT ATAAAAACA AGTTACCATTT TTTTTTTACT 60
TACACACTTT TATTTTATTTA TTGTATTTAG ATATTTCAAAA GGCACCTTTTT AAAATCAAC 120
TAAATGCAAA CTGCCTTTAGA TACATTAATTC TTAGGAATTA AGTAAAATTAC TCCTTTAAAA 180
GAAAATCTTC TCTAGCTCTTT TTGACTGTAAT ATTTTTGACT TTGTAAACAC ATCGAAATTT 240
ATTGTTCTGG TTGTTTTAAA TACCTATATT TTCCTTTTTTT TCTCTATTTCT 300
GGCTTCCTTAG CTCTCATTCC TAGCTTTCTAT CTACTTATTAG TAATGCTTCT TTCTCTAAA 360
AGGGAAACAA GGAAGAGAAA TGCGACACAA AAAAAAATTT TTATATATATATTTCTCTATG 420
ACGTTAATTTA AATAGCTATTT TGTTGAACCA GCTCAAAAAG AGCTTTAGAT CTTTTTTATG 480
CCATTTCATT CACTAAAGCA TATCAAAATG CGAAGATGCA AAAGTTTTGT GAACATTAT 540
TCAAAAGCTAATTTAATAATTTT TTTCCAATTAC TCTATTTTCT 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

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

TTTTTTTTTT TTTTTTTTT TTTTTTTTT ATAAAAACA AGTTACCATTT TTTTTTTACT 60
CAGCTCTTAG ATAGGCGATA AGAATAACTT ATCTTTCCAT CTTTTAAAAA ACACTTCAAAC 120
CTCTTTGCTT ATACATATT TTAAAGTTAACA CTAATGAGCT ACCTGTCTAT TCTCTCCTGA 180
AGGAATCTCG TCTACATCTTC TACATATAT ATGTTATATCA AGTACTACCT TCAAGTATTG 240
GAGGTTTTTT TCTCTATATT AACAATATAT TTGCGCTGTA ATTTGTATAG TACCTTTATT 300
TCATCAGCAG ATGAAATAATG AGGTCTCTTTT TGCTAAAAGG AGAGAAAAACATA ATAGCT 360
CAACACTCT CAAATTTGTGTT GAAGGATATAT CAAATTATAT TAGTTGGCTAG GAACTAATAC 420
AAATCTGACAT TACGAGACCA ATAAAATATC CAAAAGTATCCCC GTAAATAATCC AAAATAATT 480
AAAGGAAACAT TTTPATCCTTG GATAAATTA GCTAATCCAT TTCAAGACCA TTATATAGAA 540
TGAAATTACA TGTATATTGT CTACGCCCCAC CAAATAGG 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:

TTTTTTTTTT TTTTTTCTAGT ATAATACGAGA CAATATTTAT TTTTATATTT AAAAAATCATAT 60
GAAAAGTGCC TTACATTTAA TAAAAGTTTT TTTTCTCAAG TGATCAGAGG AATTGAATAT 120
GCTTGTGACA CCAATATTTAA TTTGAGGAAA ATACACCAAA ATACATTAAG TAAATATTTT 180
AAGATCTAG AGCTGTGTAAG TGAAGAAGATA AATTTGAGCC TCAAGAATCTC TGAGATATCA 240
AAATTCACAT ATAGGCAAATA AATATATATG GACCTTCGTC TTTTAAATGT TGATGAATAT 300
GCGGTGTACAC TGGTTAAACCA ACAATTCTCG AAGATACAT TACTTATGGA TAGATTCTCTTA 360
TGACTTCTGC TAAATCATGGA ATATGAGTGT ACAAGTTTCTT CATTTCTCACA TCCTTATTAG 420
GCGGAGAAT TGGGAAGAAA AGAAAAAGGAT TACGCTATCT GTCTTTTCCTA TGGAAAGATT 480
AGATATGTCT CTTTGGCCAA TATATAAAAA ATAATAATGT TTAATCTATG 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:

TTTTTTTTTT TTTTTTCTAGT AAGTTTCTAT TTTTATATTT ATTAAGATCT TGCTCATTTTC 60
ATTATTTAGC TTCGCAACTT CACCAGAAAA ATTAAGAAA CTTTTTGAGA AACGTGACCA 120
TTTAAATATG TAAAGCTGCCA TTTATGTTAG ATATTTCTTC CCAAGAGTGG AGTGTCTCCCT 180
TTCCTCCACCA ACAATGAGAC AGCAGAATTA GTTTAATTTT ATATGATGAT ATACACTGCT 240
GCAAGGGCTA ATCTCTTTGC CAGTCCCATG TAGTATTTTG ATATATGTGG GATGTCTTAG 300
AATGCACTCA AATCTGACAT CACAGGAAGC ATGAAGATAG GTAAGGCTCTT CGTGAAAGCT 360
AGACTGTTGC TTGTCTGCCAA ATATGTCTCG ACCTATTCCTG GGTGGCAAGA ACCTTCTCGA 420
CCGCTTCTGC AAGGCTCTCG CGACATTTGT GGCCTCTTGG ACTCTCCTCCA 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:

CGCCATGGCCA CTGCAGGGCA TCTGGGTCTAT GGAAGCTGTC CCAGCTGGCC CGGCGCCCGTT 60
CTGCTGCTAGC GTCTGGAGCT ACCTCGGAGG CCGTGGAGTA CCGTGGAGCC GGCCCCGGCTC 120
CCCTCTGGAC ATGGAGCCGCT TGGGCGGCGG CAAAGCTCGT CTAGYGGGTC ATCCGGAAGCA 180
GCGCCCGGCGA GCGGCCTGGTC TCCTGAGGCTG TGCGAGAAGG TGCGATAGCC TGCGGAGGCC 240
CTTCGGCCCG GGGGTCGGG CGAAGCTCCG GCTGGGCGGCA GAGATTGCGC AGCGAGAAA 300
TCAAGAGGCTT ATATTTCGCA GGTGAGGTGG ATTGGGCCAG TCAGAAGACT TCTGGGCGTT 360
AGCTGCGCAG CAGATACAACT ATTGGGCTCT GTCAAGGTTG CTCTCAAATAA TGGGCAAGAG 420
TGCTTTGGAA CGGTTACTGC CCGTGGACTT CTGCTCTGGT GGGCGCTCTT 480
GTGCTCACTG GCCATTAAAA TGCGCTTTTT TGCGCCGACA CGCAGGCGCA AGGGTGAGGT 540
CATTGATGCA AATATGGTG AACGAACAGC ATATTTAAGT TCTTTTCTGT GAAAAACTCA
GAAATCGAGT CTGTTGGAAG CACCTCGAGG AGCAGAACGT TTGGATGTGGT GACCCATTCT
CTATAGCAGT TACAGGACAG CAGATGGGGA ATTCATGGCT GTGGAAGAAGA TAGAACCCCC
GTCTTCAGCT CTCCTGATCCA AAGGACTGCG ACTAAAATGCT GATGAACTTC CCAAATCGAT
GAGCATGATG GATGGGCGAC AAAAAAGAAGA TAGTGGTGC AATAATATGTT CAAAGAGAAC
GAGAAGCAGG AGTGGTCGCAA TCCTGTTGACG GACTGATGCC TCTGTTGACTCC TGGGGTCGAC
TTTTGAGGAG GTTGGTCATC AGATGACATA CAAGGACAGG GCTCCCTGTTA TGCCAGATGA
GGACCAGAG GTGAGGCACCC GCCTGCGACC TCCTGCTGTA AACACCCCGC CCATCCTTCTC
TTTTAAGGAG GATGCTCCTCA GAGGAAGACT CACTGAGGAAT ATACTGAAGG ATTTGAGATT
CAGCGGCGA GAGATAGTATC AGCTTAAACTC AGATAAAATC ATTTAGAGTTA ATAAAGTGAA
AGCTGACTTC TAACCTCAGG GCCCGACGCT CAAGTGAAAT TGAATACTTG ATTTACAGTG
TAGAGTAAACA CATACATGTT TATGCATGGA AACATTGGG AACAGATATTA CAGTCTCCTA
CCACCTCTAA CAAAGAAAGA ATTACAGACT CTGATTCTAC ATGTGATTAT GAAATATTAA
AAAGGTTATCT ATTGGCGCTT TTGATTTATA AAACCTTGGG TACTTAATCT AAATATGATG
AGTATATCCTG CCTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAGATTCC TGGACTTAT
TTTGAGATGG GTTCTACGGA AAAAGCAATG ATATATATCT GAAACACATG ATATACATTT
ATTTCCTTCA CTGATGACAA ACTGAGAAGA ATGAGAATAT GCCAACAAT TCTGAGTTAT
AAAGGCAGCT TGGAAACAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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

(xii) 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 4 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 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 Ser Gly Asn Pro Tyr
130 135 140
Ala Pro Leu Asn Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145 150 155 160
Ala Leu Gly Ile Met Ala Leu Phe Asp Arg Thr 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 Glu 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  Thr  Tyr  Arg
210          215          220
Thr  Ala  Asp  Gly  Glu  Phe  Met  Ala  Val  Gly  Ala  Ile  Glu  Pro  Glu  Phe  Pro
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  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  Ser  Glu
305          310          315          320
Gln  Asp  Val  Ser  Pro  Arg  Pro  Ala  Leu  Leu  Asn  Thr  Pro  Ala
325          330          335
Ile  Pro  Ser  Phe  Lys  Arg  Asp  Pro  Phe  Ile  Gly  His  Thr  Glu  His
340          345          350
Ile  Leu  Glu  Glu  Phe  Gly  Phe  Ser  Arg  Glu  Glu  Ile  Tyr  Glu  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:

GGCACAGAGGC TGCCCGCAGGG CCTGACGGGA GGGCGGGCAG GCCCTCCGCGC CGGGCGCCCC 60
GGCCCTGCCC ATGCCCTACT GAGCCAGAAC CGTCGCTCTT ACCTCGCCCA GACGCTGAAAAC 120
CAGTGACGCT TAGTGCGCTCT CAGCCTGCGG TGGCTGGCAG GTGCAAGGCC 180
GCTTGTGACC ACCTGCGCCG CAGCTGCTCT TCACCGAGCT TCGACGCTTT TCAGGCGGGG 240
CTGCTTACA CTTCTAGCTT CAACAAACAG GTCGGCGCCA AGAGCTGCTAT GTGACAGGAG 300
ATGAGAGAAG AGCGTCTCCCT CTCCCTTCCT CCCTCGCCGCT GCTGAGCTCTG 360
GCTGACGAGG AGGGCTCCTT GTAGCAGAGG AGACGCTGAC TCCCGAGAGG TCCCGGCGGC 420
GTCCGCTTAC CGACCTTACT CGCAAGATCT GGGCGGATGG CGAGGCGAAG GAGACGTGAC 480
GCCCTCATTG AGGAGCAGAA CTCGCTGCTG GCCCGCGGCTG TCGCTCTGCG CCGGAGGCTG 540
GCCGAGGGAG GACCTGCGCT CTTACAGTAT CAGCAGTGGC TCGTGTGGCT CTGCTCTGCT 600
ATCTCTGCTC TCGGGCTCTA CTTACCTGCT GTCAAGCTCT GTACGACGTCAT GTACGAGATC 660
ACATGGCGCA AAGTACAGGG CAGAGCGAGT CTTACTAGGA AGGCGAGCG GACCCGCTGC 720
ATCGCCGAAT TCCACCTTG CGCCGGCGCTG GGCGCGGGCT TTATCTGCTAT CTCCCGGCTG 780
CGCCTCTGAC TGGCAGAATT GTGCAAGCGA CGCGGCGGCG CCAGGCGGCC GCGCGAATGC 840
CTGGAGCAGT TCCGCTCTTA GCTCTCCTAA AGAGGCGGGA GAGGCTGCT ATGCGGCTAA 900
TCTCCGTCAT AGGAGCTATG TCTGCTGTCA CGCCTACGAG AAGGACGCGA AGGCACGCTC 960
GACGCTGCTG AGGCGAGCGT CGACAAAGTG TACCGCGCAG TGAACCGGCT GACGACGACT 1020
GGCCGGTGCG AGAACGCCCT GAAGGCTGCTG AGGGCTGCGG TCGAGCACCT TGGCCGGGTC 1080
CTGCGCGAGG TCGCGGCGGC CTGGACGCCG TTGCTCGGGC TCGCGGCGCC TGGCGGGCCA 1140
CCCGCAACTG ATGGCTGTCC CAGAAGCTGC GCCGCTCAGG CGAGCTCTCAG GAGGACGCC 1200
CCACAGGGAG TTTCTGCTCT AGAGTAAGCA TCGACGCTGCG CTCGGCGCCC GACCTCGGTG 1260
GCCCTCTCT TCAAGTGCGAC CCGCGCTCGC CTTGCGCCAC TTGCGAGAAC ACCCTGGAGA 1320
GTGTCGACCT TACAAACAC ACCACTGCGCG GCCCGCTCCCA GAGCAGGCGG GACCCGCGGA 1380
GGATCAAGGC CTGGATCCCG GGGCGTTCAT CATGCTGGAGG CTGCAAGGCTC CTTGGGCTAA  1440
CAGGGACCCAC ACAGCTCTCCA CCACCTCACAG ATTCCTCACA CTTGGGAAAT AAAGCCCTTT  1500
CAGAGGAAAA AAAAAAAAA AAA  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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GGGAACGCGG CTGTCAGGGCG TGGTGCTCGGG TGAACAGCCGC GGCGCTGGCG CAGGATCTGA  60
GTGATGAGAC GTCTGCCCAAG TGAGTGCTCC CAGAGCGAGA GGTGGTGAGG AGTGGGCTGAG  120
AAGCCTCAGT GCGCCCAAGA GGGGCTGAGCA AATCAGGCGG TGGTGCTTCT CTGAGCAGTT  180
GGCGGCGAGA AGGACGACAG GGGCCGCTGT GGAGGAGCAG ACGACTTTGG  240
GAGTGCTCGA AAGGCGCCCC GAGGCGCACC AACTGATTGC AGAGGCACGT  300
GTTTGCGCGC CTGCTGCGGG AAGGAGACCA CAGGGCTTTC CTTGCTACAC GTCAACCTGT  360
TGCTGCTGGAG GTGTTTGGCG CGAGCGCAT CACCTATGGTC CGCGCCTCCT GTGCTGAGAT  420
GGGAGTACAG GAGAATGCCTA TGAGATGCCT GGCTGGACTC GTGCTGCGAG TGGCCTGCTG  480
CTGAGTGCTCG CTGCTGCTGC ATGGACTGGA TGGAGCTGCA CGTGGGACCT  540
GCCCTCCTGC TGGGCTGCTG CTTGGGCTTC CTTGGCCTGC CTCCTCCGTC TCGGCTCAGT  600
GGCTGGCCGA ATGGCTGTGG CAGTGCTGCTC AGCTGCTGCTG TCGGCTCAGT  660
CTTCTCTGCTG CTTGCGGCTG CGCTGGGCTG CAGCTGGGCTG CAGCTGGGCTG  720
GCCCTCAGG ATGGCTGGCG AGGGCCCGAG CAAGCTGGGT CTGCAGGCGGT  780
CATGCTGACT CTGCTGCGCC CTCCCTGCTG CGCCATGAGT GGGACAGCAT  840
TGCTTCTGCTC GGCGCCAAGA GAGTGGCTGG TTTGGGCTCC TGGGCTCCTC  900
CCTGGCTGCTC GGCGGCAAGA CAGCTGGTAC CTGGCTGCTG TGGGCTCCTC  960
GGGCTGGGCTG CAGCTGGGCTG CGCTGGGCTG CAGCTGGGCTG 1020
CCGCCTGCTC TGCTGCGGCTG GGCTGGGCTG GCTTCTGCTG TGGGCTCCTC  1080
CATGCTGCTC TGCTGCGGCTG GGCTGGGCTG TGGGCTCCTC TGGGCTCCTC  1140
GACCTTACAG CTGCTGCTCG CAGGATCTGC CGCTGGGCTG CAGGATCTGC 1200
AGCTCGGCGG ATGGCTGGCG CGCTGGGCTGCT ATGGCTGGCG TGGGCTCCTC 1260
GGGGCTGTTC CTGCTGCTGCT CAGCTGGGCTG GTGCTGCTG CAGCTGGGCTG 1320
GCAGCTGAG ATGGCTGGGC CAGCTGGCCTC GGGGCTGCTG TGGGCTCCTC 1380
CGCTGGGCTG ATGGCTGGGC CAGCTGGGCTG TGGGCTCCTC 1440
GTTCTCACTC AGGCTGCGGCT ATGAGCTCTG GCTCCTCCTG CACCCGCGGA 1500
GAACGCGGCT TGGCTCGGCA AATCCGGCGA GGAGCGCTGA GTGCTGACAC 1560
CCCTGATGTC CAGCTCGCTG CAGCCGGCGG CTCCTCCCTA GTGAGGCTGG 1620
TGCTGCTGCTC GAAGCTGCGG CTGCTGCTCG CAGAGAGGAG CAGAGAGGAG 1680
TGCTGCTGCTC GTGCTGCTGCT GCTGCTGCTG CAGCTGCTGCT CAGCTGCTGCT 1740
GGGCGCTCAG CTGGGCTGCTG CGCTGCTGCTG CAGCTGCTGCTG 1800
ATCCGCTGCTC GTGCTGCTGCT CAGCTGCTGCT CAGCTGCTGCTG 1860
TGCTGCTGCTC ATGAGGCTGG GTGCTGCTGCT GCTGCTGCTG 1920
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 1980
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2040
TGCTGCTGCTC GTGCTGCTGCT CAGCTGCTGCTG 2100
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2160
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2220
ATCCGCTGCTC GTGCTGCTGCT CAGCTGCTGCTG 2280
TGCTGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2340
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2400
TGCTGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2460
GGGCGCTGCTC ATGAGGCTGG GTGCTGCTGCT CAGCTGCTGCTG 2520
GATCCACCC CCCTCTTACT TTTATACAGG TGTTGCGTGT TGCTTCCCTC GTTGGCCATCA 2580
CAGAGGAGCA GGGATTAAAA TATTTAATT AATTTATTTA CAAAGTAGAAA GGGAATCCTAT 2640
TGCTAGTTCT TCTGCGTTTT AAGGGTGGTA GAGGGGTTTT CCCCCAAAT 2700
GATTCCCTGA GAAATGCGGT CATGGGCGTG ACTGAGCCCA GAACTCTCTT CTTGCTGGGT 2760
CTGGGCCCCC AAAAGGCCTA ACCAGGAGCC TGGGAGAATT TACCTATCCC AAATTTAAT 2820
TCAAACTGTT GGTAAACGAG TGATAGGCTG TGAAGGGAGG TAGAGGTTGG GCTTCAGGAT 2880
CTCAAGCGGT TCCTAAGACC CCCCCCTCTT CTTGGGCAGC CTTGTTCTCC CCCCCATCCA 2940
CTCCCCTCTTA CCCTAAGCCC AACCTGCTCC ACCCTGAAAA TACCCGCTCC 3000
CCCCAACTTTT CCGTACCCAC AACTTCTAAA ACAGACCCAC AAAAAATAA 3060
GCAGAAGCAAG CGCCCTTCTCC TACGGCCTTTA CAAATCTTGG CAAAATATGCT 3120
ATATCTCTGC TTGGGGGCTT AACACAGAAA AACTGAGGAG ACCCGCCCCG TTGAGCTACT 3180
GAGGTCTTAT TCTCAGAGGC GGGTTTAAAT GCGCTTCCTA AATAGTCTCT CTTTATTTT 3240
TAGGGGATTT AAGTTCTATT CTTAGATTGA GACAGCTTGCA TAAATTTATT TATGGAACAA 3300
AAATTTAAAG CTCCCTTCAG TTTTTAAAA AAAAAAAA AAAAAAAA AAAAAAAA 3360
AAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 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:

AGCCAGGCCT CCCTCTGCTT G GCCCACTCAG TGCCCAACACC CGGAAGCTTG TTTGTCCTTT 60
GGGAAGCCCT ACTCAGACTC TCTTTCTGAAA TCTCAGCTCC AGAGCCCTGA AGGAAGCCA 120
CCATGCAAGTG TCTTAACCTC AGGATTAGCA TCTGTATGCTT CTGTATGCTC TCTGAACCCT 180
TGTGCTGTCG GCACAGGGGA TCTGGGGGTC AATGACAGGG GCATCTTCTC 240
TGGAAGCACT TGGGCGTCC TCTCTCAAGT TCTCCATACG TCTCCCTATG 300
TCATGCGGAC CGGGGATGG CGTGGTGGAG GTGCTTTGCCT TCTGCTGCCTAT 360
CTGAGGGCCG TGTTGCTTCC CTGAGGCAATG TCTCATCACTT CTTCCCTGAT 420
AGGGTCTGCC TCTGCTTGTG GCCCTGAGTG ACACACCAAT CTACTCATGAT 480
TGCTGACCTG CCGCTTCCAA AACAAAGATT GTTGTCCCTA GGAAGAAGTG ACTCACTGGT 540
GGAAACCCAC CATGAGAAGG CTCAAGAGCT TGGCCTTGATG CACACTGAGC TCTGCTGAG 600
ACTCCCAACC AACACTGACG TTCTCCCAAT TTCCTGCAAT GAAAGCCTGACA 660
CCAAACAGGA CAAATGAAAAC TGGACACAGG AAAAAAGCCTA CGAAACAAAA GTAGAGGTTT 720
GCTCTGCTCTCA GTCTGGTATG GACATCCGGA CAACTGCAGT GCACCTGCTG TGGGTAGCGG 780
CTGGAAGTAA CAGCGGGCGG CTTGCTGCAG TCGTTGGTCT CAGAGATCTG 840
TACAAATGACT CCACCTCCGC TCCTGCGCACT AAGCGGCAAGC CAGGAAGAGG 900
ACCCTGGCCA TGCGGGAAGG GCACAGGATC TACAAAATCT ACCGGGCCTA 960
GAATGACGCCG GCCTTTTGCTC CCTCAAGCTG CGGGGTAGAT AGGAGCACGT CACCTTGAGG 1020
ATGCCGACTG TTCTCTCCAT TGCTGGGAGT AGGTGGGTTA GCACCTCCGA AGCCCTAAGA 1080
GTAGCCGATTC TTCTGTCGCA CTCTCCACTT CTATTAACCC TCTGATAGCC CCCCCATGCG 1140
TAATGTTGTA CTCGGGGCGC TACTGGGGGA TGGAGAACAG GACCTTTTAT TGGCGGCGAT 1200
AAGGTGAAATC AGGAGAGCCT CGTGGTGATG GTGAGGAGG CACTCCTAAA TGCGTAACCC 1260
TGTTAACATTG TTTAAAAAAA AAAAAAAA 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 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 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 Arg Gln
180 185 190
Leu Cys Arg 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 Glu 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
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 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 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 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 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
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 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 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 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:

GCTCTTTCTC TCCCCTCCCT TGAATTTTAT TTCTTCAACT TGCAATTTGC AAGGATTACA 60
CATTTCACGT TGATGTATAT TGGTGTGCAA AAAAAAAA GTCCTCTTGT TTTAAAATTAC 120
TGTGTTTTGT AATCTCTTCT TCTTTTCCCC CATTGGAACCT AGCTCATTAC CCATCCTGCA 180
ACTGTTAGAA AAACATCTGA AGAGCTAGTC TATCAGCACC TGACAGGTGA ATGGATATGTT 240
TCTCGAACC ATTTCCACCA GACACCTCTG TTTATCCCTG TTTAATAAAAT TAGTTTTGGGT 300
TCTCTACATG CATACAAAAAC CCTGCTCCAA TCTGTACACAT AAAAAAATGTG 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 ACCATTTCT ATATATGAC AAAATTTAAA TCTACCCGTA TTCTAATATT 60
GAGAAATGAG ATNNAACAGCA ATNTATATAA GTCTACTTAC AGAAGATCAA GTGACCTCAA 120
AGACCTTACT ATTTCCATAT TTTAAGACAC AGATTTATAC CTAATTATAT AACCTGCTTC 180
ATACGTTAAA CAAAGGATAA TGTGACAGG AGAGAGGATG TGTGACAGA AAATCTATGT 240
TCAATCTNGA ACTATCTTAC TCAAGCAT ATCTATTCTT 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 CTTCACTGCA TTCTCTGAAG TCTTCTGCTCA ACATANAGGA ACAGGGACCA 60
TATTTATCTT CCCTCTGAA ACAATGC GAAATACACAA AATGATGAA AACAATTGCAA 120
AAATAAGCCAA AATATATGAA ACAACAGTGC TCAGAATATT GAAATCAGT TAATGAAGGA 180
TACTGATCCC TGATCAGCTT CCAATTCGAG TATGGGAAA ACAGATGAGG TCACCTCCTG 240
GACTGCCCCCA GCTTACTGCG TTAGAGAGTT TCTTATCTTG CATTCACAG ACAGGAGAAT 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 NTGAAATCTCT GACGTGGGGA TCTCTGATTC CCGCAATACT TGAGTGGAAA 60
AANCTCAGG 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:

ACTCCGTTGG GTGTCAACAG CACGTGGGCA TGAACATNC GAAATGGGAC CCAAAACCACA 60
GAAAATGGGG TGAAATGGGC CAACCTTCTA TNAACCTGA TGGCAANNT TGCCACCAAC 120
AGTAAGTGGG CCCCTCTAAT AAAAAAATAA TGAAGGTTT TCTCCTAANC GGAATTAANT 180
AATGGACTCA AGAANACTCCC AGGCGCTCAGC 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:

ACTCGTGCA NATACAGGGGC CCCCCAGAGT CACCGTTGCA GGAATCTCTTC TGGTCTTGGC  60  
CTCCGACGGC GCAAGGACAT CTCGGGTGCT  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:

TGTTANCGTGTA ANAGCAGAGA NAGGCTGTGC AAAATGGA GAAACTCTGAA GTCATTTTGA  60  
GAAATAAGATT TGGCTAAAAGA TTGGGCGGCTA AAAACATGGT ATTGGAGAGC ATTTCTGAAG 120  
ATATNCGAGT AAATTANGGA ATGAAATCTAT GGTCTTTTGT GGAATCTCCTT TAGATNGGCC 180  
AGCATANACT TCATGCGGG ATANACAGCTA CCGCTGTGA 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:

TAGGGTGTGA TCAACTGTA AGGACAAAAA TTGAGACTCA ACGGGCTTAA CCAATAAAAGG  60  
CATTTGTTAG ATCTAGGAC AGGAATCGG ATGGTGGGCG ATCTTCAGTG CTGCATGAGT 120  
CACCCACCCG GCAGAGTCAT CTGGCCACAA GGTCTCTGTT GACAGTGGG 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:

TGTAGCGTGGA AGACNACGAG ATGGTGTGTC CTGTGCTATC CAGGAACACA TTIATTATCA
TTATCAANTT TTGTGT

(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:

ACCTTTCCCG AGGCGCAAATG TCTGTGTGTC TAATGTGGCCGG GCTGCAAGAC AGCTGCAATT
CAATGCGCTG GCTCATATGG AGGGGAGGAC ACTCTAAAAT AGCCAAATTAT ATTTCTTGAG
TTAAGATTGG T

(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:

ACCTTATCTA CTGCTCTATGA AATAGAGGT GGAAGATGC CTTACCAACT ATACCACTGG
CTTGAAAAAG AATGGTAAAC CTCTTCAAGG ACTCTGTGACT TTGTACAGGA TGCTGAAAGA
CTACGTCTCG CATTTGCGAC AAATGAAAGA TAAATGGGAG TTGCGATGATG
TTGCTTCACC AAACAAAGT GAAACAAGTG AGAAGAAAAT TCTAGGAAAA AAGACAGTG
CTCTTGAAGT ATCACTGACT TTTGAGAAATG TTTCTTATGT ACTGCTACTC TCACTGATTC
CATGGTGGGG GTCTTGCTAC TTAAAGAATG GAAATGGATTT TGCTTTTGCA AGAATCTAC
CAGGAACACAT CAGAACACCAC ATTTTTCAAG CCTCTGTCAAG AGCCAAACTC AGTGCCCTTC
CTCTTGTCTT GT

(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:
ACACAACCTG AATAAGAAAA TAGAAACTGA GCTGAAGATT  CTAATTCACT TTCTAACCAT  60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT 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:

ACACGAAAC CACAAACAAG ATGGGAACAT CAAATCCA CTG 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:

ACCTCATAG TAATGTGTTT GGTGTTCAT TTGTGCCCAA TGTGCCTCCTA TGCTGCCCT ATACAGTCTC  60
ACCTGAGATA ACAAGAAGGAA AATGGAAGAG CAGCCAGATT TCTCCTGTGC TCTCTGCTCA  120
TCTCTCAAGT AGCCTAGGTT ACCCGATTG GCCGACCATG ATAGGCAATA AACAAGTTC  180
CCAAAGGCTT TGGGACCTTT CTTGATGTGT TTAGAATAGG TTTCCTTTTT TCTAGGCTTT  240
TCTGCACCAA AGCGTGACCT AGTCCTGGTC TGGCTCACTG GACTGGGCTC CCCAGGGCTT  300
AGCCTGCCTT CTTTTCCATG 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 GTGGATATTT TTTAATATCA CTTTGTTATC AGCTCTGACTT TTTAGCATACT  60
TGGAAAAACA ACAAATATTT TTTNCTGAAC CATGATACG TACAAACCAC AATCTTCATC  120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCCTCACG TTGCACATG
GATAAAGAAA GT

(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:

CCCTTTTTTA TGAAATGATG AGACTGTATG TTGGAAANAT TANCCACAC ACCTTTGACA 60
TATAATGACG CAAACAAAAAG GTGCTTTTGA GTCTATGTTG TCAGTTTTATG 120
CTTTCCATGG TTTTTTTTGG ACCTTGGCC TAAATCCTGTG ATCCTCTCATG TTAATGTAAC 180
TTCTGTATTG CATTTTTGTG ATGCCCTGTTA GATGTAACCT GCTANGAGCC TAACTTTTATA 240
CTATTTAAA AGCTTTAATTT TTTTGTTCTCAT TAAAATGGCA ATTTATGTGC AGCAGCTTTAT 300
TGACGAGGGA ATCCAGCTGTG GTTGGTTGTTG AAAAGCTCTTT GCTAATCTTTA AAAAGTTATG 360
GG

(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:

CTTTTGGAAA GATGCTGCTG ACGCTGCCGG ACAATCTTGT TTAATGGAGT TTTCCATGCA 60
GTANGACTGG TATGGTGCCA GTGTCGCCAA TAAAAACATT TGAAAGCTTC CAAATGGAGA 120
CTTTGCCAG GTTCCTCGTG CTGCTCGCAAG TCTGAACGAC AGCTCTTTTT AGGAGCCATC 180
TTCTGAACA ATGAAAGGCC GTTGGAAAAAT CTGATGTGAT TTGGTTTTAT ATCCCAACTAA 240
CTTCCATCTG TTATACCTGG AGAAGAGCCCA GACTCCCAAN GACNGTGCAG GATTGTGGGC 300
ATANAAAGGAT TGCGTGAGGC TGCGGTGTTGTG GT

(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 TTTGGTATAT ATAAACAACG TCTGAGAAGCAGG CTACACCCAT TCTGTGTTCC 60
AGTTGCAATG AGAATGTGAT TTCAGCAAT GCTGAAAGGA AACTACACGAT GACACAGAAT 120
CTCAAGATCC CAAAGAAGGG CTCCTGGAGA AAATGGTAA CGGACCTTTG TATCTCTGCTT 180
TATGACTAAT TAAATGGAA ATGACAGAAG AGGCTCTATT ATCAACAAGG AGAAGGATGT 240
GGAATCTCTT AAAAGAAACT TTAGTAGAGA AAATAGGAAT GCTGAAATCT AGGGAAAGCTT 300
GTAACATCT ACAATGGTCG 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:

ACAAGCCCTC ACAAGTTTAA CTAAATGGG ATTAATCTTT CTGTAATTCT CTGCAATT 60
CTGGTTTTTC TTTCCAGTCT GTCCTGCCTG TGACAATTG TGAAAACAGT CTATTGTCTGTA 120
CTATTAAAA AAAATCAACAA ATCTCTTCTCT TTAGCTATG TTTAATTCAA ACTATTCTCTG 180
CTATTCTCTG TTTGTTAAAG AAATATATT TTTCAAAATA TGTTATATTG TTTGATGGGT 240
CCCAAGAAC 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:

GTTTANAAAA CTTGGTTTAC TCCATAGGG AAAGAATGTG AAACCCGGTTA TTTAAAAACA 60
TGATCTCTGT AGCCTAAACT TGGTTTTTCAA ATGTTATTTT TACTGTTAT TTTCCCTTGG 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:
ACTTANAAAC ATGGCTAGCA CATCGAAATC CCTCTAAAGAA CATCAGTATA ATCCTATACC 60
ATANCAAGTG TGACGTCTTT AAGGCTGCCA AAGGACGCTG CTGGCACTAT ACTGTGGTGC 120
AAACCTGTATA CTTTGCTTCT AAGTGAAGAA TAGTATACAG TNCTATGAGA TGTTACTCCA 180
GGTGGGCCGC CAACCTCTCCGC AGGCCCCTTCT CTGGCCAGN CCGTGGAGGC AACTTGGCCT 240
CAGTCTGACG CCTGCCGCGG GCCCCTGACT CTGGAATGGG CTGAAACAAAC GCTCTGCTGAG 300
TTCCCGAGGA TGCGAAGCCT GCTGCTCAAC TCTGCGGCGG TCAACTCTAGT 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:
TGTACCCTGTA AGACGACAGA AGTGGCATGG CAGGGACAAG GCAAGCAGCCA GSCAAGGCTT 60
GCTGGTGTGG TATCAGAATA NTCTCTGTGA GAAAGATAA TGAGATGAGG TGAGCAGCTT 120
GCAAGACTGT GTCTCCCTCC ANAAGCAGGC ACAGAAGCAG CCTGCCGAGC TGGCGCTGGA 180
CCTGCGCGCC AGGGACAGGC CACAGGTGGA CCTCTCTTCCT TTCTGGGTGA CAACNNCCAG 240
AAAACCTGAC AGGCCAGCG TCGGTGTGNTA TGCGTANGTG GACATAAAACA CACCAGGCTC 300
TCCCGAGGAC CGGCGCAAG GCCATCCCCA CACAGGCGA GCCAAGCCCA TCGCGTGTGAG 360
GCTGCAGANG GATGAAAGCG CCAAGNTGTC TGCTGTGTG 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:
ACTGCGTGGT TNGGGGCTGGA TGCTCGCTGTG ANAAGCTGAG GTGACTTTCA ATGGGCTGCT 60
GGAGGGAAGTG TGTCGAACGTA GGGATGATGA NGTTCTGCCC GTGATTAAATG AGCTCGAGGA 120
TTGGCCTGCT CCACTGCGGCG TCAGCTCGCAT TGCGCGCTGTC CCTG 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:

ACTCAGGCGA ATGSCCACTT CAAACACGGAT CAGAGGCTCT ACTGAAAACAG TATGGGCTCC
60
TTAATCTTTCTT CAGTAAGAAT CAGGAGCTTG AAATGGAACAG TTAACAGGCCC AATGGCCCAA
120
TGTCTGGGCGA TTTCCTCATCT TTTCACAGATC GAAAGGCTTT GAAAATATCAT ACATCCATGT
180
TCATGGTTTTT CCAAGCAGCACC AAAAGGTGCG TTGGGCGGCA GGGCCTGGGG CATANAGGCT
240
CANGGCTCAG GAAAGCCTCAAG GTTCCATATCA GTGTGCGCAC TGTACATCTCC CCAATNTAA
300
AAAAACTGAT GGCCTTTTTT TTTTTTTTGT TAAAATTC
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:

GSSGAATCTTG GTTTTTGCGAC TCTGCTTTGC CTTATAGCGAG GSCTCACTTTG ACGAGGACAA
60
GSSAAGGGCTT CCGATGAAAG AGCTGATATTCA CAGGCGACCT AGCAGGCGAA GTGAAGGAGA
120
ATTCAAACAG ACGTTGTCAT TCTGGTGTGG AGCTGCTGCG GCTCCAGGGG TATCAGCGGC
180
ATTGGCTTTA C2AGGCTCTG ACCGGACTTT GCCTCCCTTGT GTGCTGATTT TCAAGGAGATG
240
CCCTATTTTT CTCTCAGCGC CCAAGCGGCC CCGACTTCTTC TGGAAGTGTG TTTTAAATAT
300
GTGACGCTAGC TGGGCGCGCC TGGCGCATGC GTCTCCCTGCC TTTGCTACCA CTGGCGAGCT
360
GCCGTCACTG TGTCTAAAGGT 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:

ACCAAAANCTT CTTTCTGGTG TGTNGAATT TACTATAGGG GATTNGCTTN TCTTAAANAT
60
ACTTTTCTGT TAACANCTTT TGTTAAGTG CAGGCTSCAC TTTGCTCCAT ANAATTATGT
120
TTTTCTACCT ATCAACTGTTA TGTTTGTGC TCTTANAGCA TTGGTGAAT CACattaTTT
180
ATAATTACGA TAARGGAAAG
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 ATATGTGCTCA AAAAAACACAT AGAAAAATAA AGTTTGTTGG 60
GGGTGCTGAC TAACTTCAA GTCAAGACT TTTATGTGAC AGATGGAGAC AGGGTTTGGT 120
ATGCTATYAG AGAAACCAA TTAATTTTTT AAACAAGATA GAAACAGCT TCTGGTTTGA 180
AATGTGTCTG AGAAACATCC AATTCACCTG TCAAGTCTGG ATAAAATAGTG TCTCAAGATG 240
TTTTTCTACC AGCTGCAAGA TGGGTCAAGG ACTTATTCTCA ATGGGAAAAA AGCAAGAGTG 300
ATTCCACAAC CAAGAATTT TAAACAAGAGA CACCT 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:

ACCAAGTTAA TATGGCCACA TATATCTTTT CCAATTGCGG GCTAAACAGA COTGGATTAT 60
GGTTGTGTTA CGAACACCC AGCTTAATAT CAAGAGAAA ATGAGCCCTT CATGAGATAT 120
CTGATGCGAG AAGACACTAG TTTGGACAAA TCTTATTTTA TTTCAAGATGC AGTCCTGAC 180
CACCTGCTCC AGAACACTGC AAAATATAAA GAAATATCAA TCAATTCAGG AAGATTGCTC 240
TTCACAACTC ATAGCCCAATG ATGCCCAGCT TGGCTATATCT CTCTCCGACA TAAACCCACA 300
TCAACACTCCT AAGGAGCACC AAAAACTTCA GCAACAGCTC CTAATCGGTG AGCTGTTTGA 360
AGCTTACGGT CTGAGCACTA TTGCTACTAT TTTTCCAGCT CTGAAATAGCT CTAGGCAATCT 420
CAGCANGGTT TGGAGGCAA AGCTCAACCT TGCGCTATT 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:

ACATTTCTCTT CCACCAAGTC AGGAGCTCTGA GTCTGCTGAG GAGTTCTATT CACCTGAGGG 60
AAATCCCAAC AGTCTTCTCTG AAAAAAGTAT AGTCTCAACA ACCCCACCTA TCCTCCTGAG 120
ACCATCCGAC TCTCCTGITT 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 CAAATACAA TAACACTTTT AAGGTATAT TGCCATCTTT GTCATTTTCT 60
ATCTATACCA CTCCTCTTTC TGGAAAACAA AATCTACTAC AATACCTTAA TACCAATTTG 120
AGGCAATTAA TCCATATTGG TTTTCAATAA GAAAACAAAG ATUT 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:

ACGTGAGCCA TCCAACCCTT TAATGTAAAT GCGAACATCA CAGACGCAAAT TCCTAAACAA 60
ACTTGAGCTT ATTTATACCC AATATTCCCA TTCAATACCA TCCCTCTTCT CTCGAGCTAT 120
GCGCGGAGCT TACCCATGTT CGCGCAGAC GTCCGCAATAG TACCAATTTG ATAAACCTCA 180
GTAGGGTATG CACCTACGTT GACAGGCTTA ATCAAAGGAG GAATGGAAC ATAGGGCCAG 240
TAGTAAATAT TGGTTCATGCT GAAACAGCCA CAAAAGACCTT ACCGGCGTGG 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:

ACTGGCAGTCA AATTGAAAGT GTGCTCTGAC TTTCTACANC TTCTCCCTTG GCTCCATGAC 60
ACTGGCTCAG AGTGAATCAT TGCTCCTGTT GGTGAGGAGA GCTGCTTGGC CACAGCCTCT 120
CCAGTCAAGG CCTGGAGATT GTTCCCTTTCC CACATTCTAG CACAAATATG CTGGCCACTT 180
CCTGAAACAGG GAGGGTGGGGA GAGAACCACGA TGGAACAAGC TGCCACTTTC TAAAGTGACC 240
AGACTTTCCC CTTGCGGCGCT CACACCTACT GATGACCCCTT TGCGCTTGCA GAGATGAATG 300
TAGGGGTAGG CTGTTGACT CTAAGGT 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 TTGAGATAAA AGCATTGANA GACCTCTCCT TAACCTTGACA CAATGGAAAGG 60
ACTGGAAACAC ATACCCCCACAT CTTGGTTCTG AGGGATAATT TTCTGATAAA GCCCTTGCTGT 120
ATTGCAAGC ACATATGTTA TATATTATTC AGTTCCATGT 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:

ACAACACCTT TATCCTCATCG AATTTTAAC CCAAAACTAC TCACCTGGCC TTTCCTATCT 60
ATGGGATATA TTATTTGAGT CCTCCTTCCA TCAACATAT ATGAAATAAA CACCCACAC 120
GCCTCCTAC CTGTGCTCAAT AACACATTC CCACTCATTC CTGCCCTGGA AGCACTGCGG 180
GTGCTCTCAG TGCCCATCG TCCAGCCTTG CACCTTGAGC CCTGGAGCTC CATGTGCCAC 240
NCCANCCACC CTACACCCGG CCATCTCCTC ATACACGTAC CTCTTGGCTC TCTAACCACA 300
TAGATTATNT CCAAAATCTG TCAATTAAGT TACATATAAC ACTCTACCAG ACATGTCCAG 360
CACCAGCTGG AAGCCTCTCC CACCAAAACAC ACACACACAC ACACNACAC ACACACATAT 420
CCAGGCGACAG GCTACCTCAT CTCACAAATC 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:

ACATTGTTAT TATAATATCA AGAAATAAAC TTAGCAATGAG AGCATTTAAG AGGGAAAGAC 60
TAACCTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAAG GGGGCGGTCCT 120
(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

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

ACCTTGATTT CATCTGCTCT CTGATGAAAA CCAACATATGC TAACTTTGCT AAAACATGGG 60
CATTTAAATG TGGTCAGTGT TGGGACTTTG TAACACTTTGG CATCTTTGCG 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

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

AGCGCGCAG GTCATATTGA AAGATCCAGA TACCTATGAT TACCTGATGC TGTGGATAAC 60
AGAAAATGCTTGGACACCA ACAGTAGTATG GACCTTAACAG AAAAAACCAT 120
GGATAACACC CGGAAAACC CATCCTCCAG CAGGCACACGT TGGTCCCCAC TGTCTACGAG 180
GTGCACTCCGG 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

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

ACACGACCTTT CACATTGAA AAGGAGAAAA TTCCATAATG TAGGAGAAAA ATAAAAACGACGATGCTTGGACACCA ACTGCTTTAT GTGACAGGAA TATAGACCAAC 60
CTTCCCCCTTT TCATCTAGTG GTGAAAACCT GATGCTTTAT GTGACAGGAA ATAGACCAAC 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 CTGSCCGTGG TGTCATGCCC TCCAAACATG AAAGTGTCAG  
CTTCTGCTCT TATOTTCTCA TCTGACAATC CT TTACCATT TTATATCTCG CTCTAGCAGA  
120
GCCACATGAT AAGCTCAGAA GTCTTGAGCT TGAGGAGGAGA TTGAGACACG TCTCCAACAC  
CCCTGGCTAT TCAAGGOTCAG CCCTCCTCT CGATGACGCG ATCTGTGGAAG TGCGGCAACA  
180
GTCTGCAAGGC CCTGTGGAAG GCCTGGCACC ACGGAGTNAG GAATT  
240
GTCTGCAAGGC CCTGTGGAAG GCCTGGCACC 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:

ACCDGAGGCT TGCTGGGCGCA GGCTTCCATG ACACCCTTCG TGAAGAAACCA TATATACACC  
60
ACCCCAATT TTTCTCTTTA TACCTTCTAC TGAAGGCGTC AGCTCTTGGA CTCTGAAAGAC  
120
CCTAGCCGAG TPCAGAGACT AAGGCCACGT GGCGCTGATT TGGAATAGTG CTCTGCGTCTG  
180
ATGGCAGAGG GAGTTGAAGAG GGTCTGAGCT CCTGCCCCTGG TGAACGAGA CTTGATTTTG  
240
AGTTTCCACA ATTTCTGGCG CCACCCTGCA TTGCCTCTCT GAAATAAAAT CGGGAGAAATG  
300
GTCAGGCCTTG TCTCATCCAT ATGGATCTTCC OGG  
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:

ACTGGGAAATA ATAAAAACCA CATCAGAGT TGTOTCAGAA GATCATCAGG GATGGGATGG  
60
GAAAGTGGCT TGAGAACTCTG AAAGTGCCCTA ACACATGATC GATGAATTTTT GTTTATATAAT  
120
TTAGTACAGC GTCTACAGAA ACTCTCTCTG CTGCACCTCC TGCCGCCCGG CCCACACCCC  
180
ATCACGCTC ACTGCTCTGT TCACTCAGGG CCCAGATGTA GTGGGCTGATT CTTGCTGGCT  
240
GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAAACC TCTANGTOTA AGGCATGCTG
GCCCTGGT

(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:

ACCTGCTCTG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA AGAGTGCCTA 60
TTATATGTTA CATAGAGAAC TGTTAGACAT TTAGTGGAG ATTTCTCTCA CAGGAAGTG 120
GAATAGAGAA TTGGTTTGGG CCCCACATATT CTCTCTATTC CTCTCTGCTT CATTCTATGT 180
CTAAATATAT TTCACATCAA TAAGGTTCAG ATAAATAGGA AATCGACCAA ATACCAATAT 240
AAAAACGAGAT GTCTATCTCTT AAAGATTTCCA AATAGAAAAAC AAATACACAG 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:

ACAAAGTTTAA ATAGTGTCTT CACTGTGCCAT GCTCGAGAAT GTGGAATTCA CCAACCTTTCT 60
GAAGAGCAA ACAAACTGCTG TCACTGAATC TCTATCTTGG GTCTGCGGTA 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:

ACCCACTCGT GCTCGAAACA CCACATCTTA ATACGATGAT TTTTTCTCTCG TGGAAAAATG 60
AANCCAGGAA GCTGCCCTCA GCACGCTCCTT CCCTCCAGAG AAAAAAGAGAT TTGAAGATG 120
GCCTGGGTAAC TCCACATCTA ATTTCTTCCC CAAACTCTC TGAGCTCTCC CTTAATATT 180
CTGGTGGTTC TIAACAAAGC AGCCTCAGTC TTGGTGGAGCA TTTGGGATCC CAGTGAGGTA
NATGTTTGGTA GCCTGCTATA CTTAGCCCTT CCAACCACAA AAGCGAGTGG CAGAGTGGTG
CCAGACCATGT TTCCCGATGC CACCTGAGCA GATCTCAGCT GGAGGCTCTC GGAGACCTGGA
NACAAGCGG GCCTTGCTCG AGCCGCGGACT CTGGAGGNGGA CATGAGGGCC TCTGGCCTCTG
TGTTCTTCTT CGATGCCTCCT GT

(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:

ACTTCAGGCT AACGTTGTTG TTTCGCTGQA GCCGTAACCTG ATGGGTCAGC TGTTAGGTTCT
TCAACAAGAG ACTAGGTGTT CGAGCAGGGGT AGGGAGAGCT GCTGGTCCCG TGCCACTCGG
GCTGCTGGTG AGCTAGTGTG ATCCCTGACT AGCGCCCAAG GTGGTGAGAGC TGCCANAAAA
GTGGTACGTT CGAAGTTGAAC TCCGGCCGCGTT TGGTAGGTTG TGGTGCCTTT CAACAGGGGC
TGGTGGTGTT CGCGGGAGTG AAGGGTTTC TGGACCTTTG CCAGCCACGC TCTGGAAAGT
ANTANNTCTT TCCTGACGAGC CAGGCTGTGG GAGAGGTGCA NGGGTCAATG CTTGGTGTA
CGAACCAGTG CAGCGTGGGG TGGGGTGTAN A TCTCCACAAA AGGCTGAAGT TATGGTGTCN
TCAGGTAANAA ATGGGTTTTC AGTGGCCTGG GCCGCTGGTG GAAGAGGTGA NATMGTCACC2
AAGGGAAATAA CCGTGCTGTT

(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:

ACCTGCACTCC AGCTTCCTCTTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACACAGAAA
AGGAGAGACAA TACTTCCAGG AGACAGACAC ACCAGAGACAA AACAACAAAT TCCCATGCGT
GGAGGTGAGGC ATAGAGAGAA CTGAAAAATG TGGGTGCAGT GGAAGGCA ATGGTGGTCC
CAGTACACCT CTTACACGCC ATCTGTTGTA AGAGATGGCC CATGCCACCA GTAGGCTCTC
CCAGGCTTAC CTTCCATCTCA CACACTTGAA TCTCCCTCCC TGATATAATTG TACACCTCG
GGAGAAAATG GCAGCTGGAAC CCGACTGTTT CACACAGGTA GAGGCCTGAT TCTAACGAAA
TGGTACAGAT GGAGCCTCGGA

(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 CCCCCTGAGC AGGCGGTGGT GTTCAAGGT GATATTGAGC TGGCCTGTC A 60
CACTGCGCCAC TGGCCCCCTA TCACCTGTTG GCTTAATCCC TCGAAAGGC 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:

ACTTTCTGAA TCAGATCAAA TGATATCTAG TG1AGTTTTA ATATCCCTAT ATATATCAA 60
GT1TTATAC TCTGATAATT TTGGAAACCA GGT1ACCAAGA ATACCCAGTC ATACAGCTTT 120
TGGTGATATA TAACTTAGCA ATAAACCCAGT 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 GACAGGGGTC AGAGACTCTA CGACAAAAAC GG1AAATTCT ATCCCGTGAC 60
CANAGGGGC AGCTAAGGCT ACTCCTACAT CCTGGCGTGG GTGACCTTGG CCTGCACCTT 120
CATCAGGGGC 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:

CTATACAA TGAATGCTCT CCGGACAGC GGTGGAATCT TTGCCACTTT CGTGACTTCA
TGGAATCAGT CATGCTATTT CATATCTAAT GGGAGGCTTC CAGGAGATCC CCAAGAAGAA
TGATGATGAT CCAAAGGAAA CAAACACCCA ATAAACTCAG ACGGCCAGAC TCGAACACTG
GAGACATGCA CCGCTGACAG AAGCAGAATT TCAGTGGTCC CCGCTTGTTC TACACCTGCT
GGATATGCA AAGAACACTG CCGAAGAATCC TTAAGAGGAG AGAAGACTGCA GTATATCGTG
GTGGAAGAAC ACCACACAAA AAGAGCCTGT CCTGTCAGTG AATGGATAAT CTTAATCTGC
TCAGTGGGC AGCAGCCCTCC AGGCGAGGCC CTCATTCCTCC TTCGACCTCTC AATAGCTAAAT
GATCTGAGT CCATGCCTAT CAGTTAAAAG ATTTTGGAGC AAGACCTTT

(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 CACCTTGCTT CAGTTTCATA AAGCTGTGCG
ATCGGCTGTC ATCGTACTTT CCTGCGCTAG AGTAAAAATT ATTCTTAGG CCGGCTGGCC
TGGGCGCGC CCGCCCGTAG TTCGCTGGCC AGTCGTCCTTG GCAACAGGCG TGCCGAGACT
TCCTGAGA TGAGT

(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:

ACATCTTATG AGTGAGCCAC ATACAGGGGGC CATCAGGCCTC ACAGTCACTC ATAGCTTCGC
CGAGTTGGGA GGCCACACCA CGGCGTAGG TGGGGCTAAT CTGGGCGTTC CGGCCACACT
TTGAGAAAGG GTAAGGCTGC ACACACTG CCACAAAGCC TTGAACACTG CCAAGGATTT
TTTGGAGAGG AGCCGTACCA AGGGCGCGGT GTTGGACCTT GCACCTCTGT CTTGGCGGTG
GTAGCCCAAC TCGCTTANGG TCCCGGGAAA GCTGGGTGCTC ACNTCACTTA CAACTTGGGC
GANAGATCTTA TAAAGAGGCT CGNAGATAAA CTTCACGAAA CTTCGTGCTG AGCTGCTAGT
NGGCGCTTT TGGTGGAAGT TTC

(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 ACCTTGCGCC TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT 60
TGAGACGAA AACTGAGGCAA GAAGTGCGCC TGGGCTGAA GTCAGAGCCA AGCGCCTGAC 120
TATANCTATA CACAGGACCA CACTCTAGGC CAAAGCCATG GTGTGSGGCAAG ATCCAGAGAC 180
TCAATCTGAG TCCAAAGGGG TGCTGCGAAC CACAGGCTACG ACTGCTAGTC AGCAAGACAG 240
TGATGCT 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:

ACCTTCAAGT TTCTAGAAAG TGGAAAGGATG TANATCATCC TGAAAAGGGG TTATCTGAA 60
AAATCCCTGAN CCTTGTTCTTT CAAACTAGTC TTATCTGAGA GTGTCATGTT TCCAAAGG 120
GCTGACACCT GGCTCCTGAT TTCTACCTAG CCGTGAAGAG CCGCTTCCAG ACGGTGCGGC 180
AAATCCCAAC TCTCTGGGCA CAGCCTTCCC AGCCCTTCTGC CCCCAGAAAA CTCCAGCTTG 240
AGCTCCAGAT AAACACTATGG GCTGCCCTGGA 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:

ACAGCTTGGC CTCCCCAAA CTCCACAGTC TCAGTGCGAA AAGATCATCT TCCAGCAAGTC 60
AGCTCAGACC AGGGCTCAAG GATUGCATG CAACAGTTCG TGTTTCAAGA AGACGTTCTA 120
CTACTGCTAA ATGACCCCCC ATACCTCCCTC AAGGCTGAGT GATAGTTTGG CACAGGTTGAG 180
GGCAGCAGCA AGGGGTGGTA TACTGAGGA CACCATCTCT TCTGTATTAC CCCAAGCTCAG 240
CTCGCAATTG GCAAGGCCCT CTACCCAAAA AAACATGCGA TCACCTGGGT GCACCGCCTC 300
ACGCACATCA CTGGACACGG GAGTGGAAAA AGAAGTGGCA ACTCTCATAC ATCCAACTGG 360
AAAGTGAATTT GATACGTAT CCTTAATATCC TCCAAAGAGG TCCTCGGGGCG CATCAAGCTGC 420
TGCAACACTGG A 431

(2) INFORMATION FOR SEQ ID NO:170:
(ii) MOLECULE TYPE: cDNA

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

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTTTTA TGCTGTGCAA GCCTGCTGAA AGGGAGTTCA GAAGTGGAAC
60
TCAGAGACCT CTGCAGCAT TTTGCAACAG CTCTCTCAGAG CAGAGGGGAC AAGCTCAACT
120
CCCCCCTAGA AGAGCCCAAG ATTTGGCTCC TGCGAAGGCG AGTGGGAGGT GGCATTTGAT
180
GTTACCTTGT CACCTGAAAG AANGGGCAAG AGAGAANGGA GACAANATG ANATTGGCCT
240
TCAGAGCTAG GGCTCTGGCA 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:

GCGAGCCAAA TCATAAAACGG GGGAGGACTGC AGCCCGCATT GCAAGCCCTG GCGGCGGCA
60
CTGGTCAGTG AAAACGAGTT GTCTCGCTCG CGGCTCTCGG TCACCCCGCA GTGGTGCTG
120
TCAGGGCAAC ACTGTCCAAG CAAGTGGAGG CAGAGCTCGC CAAGAGCTCG CCGCTGGGCC
180
CAGATCTGTG GGAGCTCTGA CACCATCCTG AGCAGTAGCC TGAGGCAGCG CTCTCCGTA
240
GGCAGGAGCT CTTGCTCTGTT TCGTCTGCTGG GCTCTGCTGG CGAAGCAGCG AGTGGCTAC
300
GTGCCTGACG TGCTGACGCTG TGGGAGAGG TCTGGAAGAT GCTGCACTAA GCTGATCTAC
360
GGCTGGTACC CCACCGAGCT GTGGCAGCCC GCAGGAGGCC AAGACCAAGA GGACTCTCGC
420
AACGCTGACT CTGGGGGCCC CCTGATCTGC ACAAGGTACT TGACGGGGCT TTGTCTTCTC
480
GGAAAAAGCCA GCCTGCGGCCA AGTGGGCGTG CGAGGTGCTC ACGACAACTT CGGACAAATC
540
ACTGAGTGGAA TAGGGAACAC GTTCCAGGCG AATTTTCTGT GGGGACTGGG ACACTAGA
600
ATTTGACCCCA AAATACACAC TGCCGAGGA ATTCAAAGAT ATCTGTCTCC AGCCCGTCTCT
660
CCTCGAGGCA CGAGGCCCAG GCACCGGCCC CACCTGCCCT TCACAAACAG GTACAGATC
720
CCAGGGGCCC CCTGGGCTCAG AGCCAGGATT CGACCGGGCC CAGCCTCTCC TCTTCTGAGC
780
CCAGAAGGCC CACCTCTCCT ACCAGGTCAG CACAGGCTCG ACCGGGGCTC CCGGGTCTC
840
CTCAACGCCC GGCTGGTGGT CCCCCAGCCC TCCCTCTGCT TCCGTCTAGA AAGTGGCGTG
900
CCGAGAAGCG GAGGCCCTCT CCGAGGGGTA CGCAGGCCCC CAGGCCCCCT TCTTCTGACA
960
CTCAACGCCC GGCTGGTGGT CCCCCAGCCC TCCCTCTGCT TCCGTCTAGA AAGTGGCGTG
1020
CCGAGAAGCG GAGGCCCTCT CCGAGGGGTA CGCAGGCCCC CAGGCCCCCT TCTTCTGACA
1080
GGACGTCCG GCACCGGATT GCTTCGCTCT AGACAGAGAG GTCCAAGGC CCGGGGCTTCT
1140
AAGTGGGATT CTGCTGGTTTT CTTTTTNGT CTTGCTCTGG TAGACCGAGA AATGAAGTTT
1200
AAGTGGGATT CTGCTGGTTTT CTTTTTNGT CTTGCTCTGG TAGACCGAGA AATGAAGTTT
1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(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 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 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 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:

GSCAGGCGCG ACTCGCGAGG CTTGGGATGCG GCAGCTGAGA TGGAAAAAGA ATGTGTCGCTG 60
TCGGGGGCTC TGGCGCGATCC GCAGGAGGCG GTGGCGCGCG CGACCTGTTT CCGAGACTCC 120
TAGCAGCATG GCGTGCGGCT GCAGCTGTTT GCAGCCGCAG ACCGAGCCAGG GAGCCAGTTG 180
GTTGGGGCCA GCCCTCGCGT ACSCGACCGA GAGTACAACA GACCCTGCTG CGCTAAGCGAC 240
CTCATGCTCA TCAAGTTGAG CGAAATCGCTG TCCGAGTCTG ACACCACCTCG GACGATCACGC 300
ATTGCTTGCAC AGTCGCCCCAG CACGGGGAAG TCTTGGCTCTG TTCTGGCCTG GGGCTCCTCTG 360
GCGAACGCTCT AGCTCATGAG TTGGTGTCTCT CCGCCCTTCAA GAGGAGTGCTC TGGCCAGTCTG 420
CAGGGGCTCGA CACGCAGCTCT GCCGCTCAGAG GCAATGCTCC TACGGGTCTG CAGTGGGCTCGA 480
AGCTGCTGCA GGGTGTCTGAG GAGGCTGCAC TCTAGCTCCA CTACCCGGCTC TATCCACCACCCA 540
GCATGCTCTCT CCCGCGGGGTA GCGGAAGACG AGAGGAGACG CTGCAAGCTCT GACCTCTGGG 600
GGCCCTGAGAT CTGAAACGCTG TACCTGGCTG GCGCCCTTCT CTTGCGAAAC GGGGCTGTCG 660
GCAGGATAAGTT CTGCGCCAGT GTCTACACCA ACTCTCTGGAA ATTACCTGAA TGAGTAGAGA 720
AAACCGTTCCA GGCGTTTAAA CTTCTGGGAA ATGGCCACCA TGAAATTTGG CCCCCTAACAA 780
ATCGCTGCAG GAAGATTTGGA GAAATGTGCT CCGACGCTCC TGGCCAGCAG GGGCAGGAGG 840
TCAGCCGCAG CAGGCGCTCC TCTCGCAACG GAAGGGTACG GAGCCTCCGG CCCCCCCCTCC 900
TCGACGCACC GAGCGCACTC CGGCGCTTCT CACTCTCCTC AGACCCAGAG GTGCCGACC 960
TCCTCCTCTA CACCGCGAGA TGGCAGACGC CTGCCCTCTC CTTCTGTAGA CCCCCGCGTT 1020
GAGCGGCGCA ACCCTCGCTC CTACCCGAGC AGAGGAGCGA GCCCGCCGGC CCCCCGCTCC 1080
CAGACCCGCAG GSTTGNAGGTC CAGCCCGCTC CTGCCCTCTG CCCCAGGCTGC GACATCGACC 1140
TAGATTTTCT CCAGAACAGC TCAGCAGCCTG TGAGGACTG ACCAACTGCT ACCAGTTGCT 1200
TTTCTATTTT CWG7CCCTTT CCCCCAAGATC CGAAAAAATG TTATTAGAGA CGACCGAAAA 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:

GOTGACCGCC ACACCTCTTTC CAGAAAGCTG TCCAGAGCTC TACAGACACT CGGCTGCGCC 60
TGCAAGAGCT CTAGGACCGC CAGGAAGCGC GGAGCCAGAT GTGGAGGGCC AGGGCTCTCC 120
TCAGGCGACG AGAATTACAG AGACTGCTCTG CGGCTAACAG CTGTGATCGG ATCCAGAGG 180
AGCAAGGCTG TCTTCTGGCG GTTGGTCGCT GGGCGACCGT GACACCTGCG 300
GTTGGTGGCT GCTTCCCTCTA AGAGGGGTCTC TCAGCCCTCG CCGGGCTGCTG 360
CTGCGCTCAG CGCGACGGGT CAGACGCTGC TGGCTGTCG GACGCTGTCG 420
NGAGCTGCTC ANTAACTGCT ATGACCCGCT GCATCAAGGG GCCCGCGCAG 480
AGGGCGAGAC CAAGAGGAGT CCTGACAGCT GAGAAGGGAG AAGGGGAGAA CGAGCCGAC 540
CAGGGGAGAG GGAGACGAGG ACAACAGACG CCGCATGGGC AGATGCAGAG 600
ATGAGAAGAC ACACAGCGAG ACAGTGAGAA CTAGAGAGAG AAAGTACAGG AAAACAGAAA 660
ATAAACACCG GAATAAGAGG AGAAAGAAGG AAGAGAAGAA AGAAACAGAC ATGAGGAGAGC 720
AGAACACAC ACACATTAGA ATGCGTGGGA CTTCTACAGCA GAATGGGCAGC TGGAGGGGT 780
GAACCTGCCA CAAATTAAAG TCTTCTTATA ACTTTGTCAC CTTTCAAAAC CTGCAAGAAA 840
ATACACCTTC CAGACGCGCG ATACATATAAA TGTGCAATTT ATGACATGCTA 900
TTTAGCATG CAGATATAC ATTCGGTGGA ATTGTCTGAT ATTTCTTGA TACACAGTTTC 960
GTGGTGAAAT TTTTTAAAAT TGTTGCAACT CTTCAAAATA TTCTCTGAAG TTGTTATTTG 1020
AAAAACAAAC GTATCATGCGAT ATGACAGTGA ATGGACAGGG GGGTGACATG 1080
GTACCCAGAG GGGAAAGTCG ACACAGATTC ATAGAGTGGA AACAGGAGAA GAAAGGAGAA 1140
AAATCAAGAC TCTACAAAGA GGCTGCAGTG CTGAGCGCTA GCTGCAGGAT CGGAGGACTT 1200
GGAGGCGAAG CAGCGAGATG CACTGAGCTT AAAGGATCCA ACAGCAGCCT CGGCAAAAGT 1260
TGGAATGCTC TGTGCTCAGA AAAAAACAAA AGTTTGATGAG ATATCGTGAGG GGGCCGCTGT 1320
AATACCCAGT AACGCTGAGG CTGGAGCGDG AGAGATCTTT GAGATCGGGA CGAGAGATTG 1380
GAACTGAGTT GAAGATGAGC TCACTGACGC CACTATACCT CAGCTGGGAC AAGAGSTGAA GACTCTGTCT 1440
AAAAAAA AAAA 1459
(1) 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:

```
GCGCAGCCT CGCAGCGCGC ACTGGTTCATG GAAAGAAGAT TGTTCTGCTC GGGGCTCCTG  60
GTCACATCCCG ACTGGTTCCT GTCAACCAGCA CACTGTTTC AGAAACCTCTA CACCATCGGG  120
CTGGCCCTGTC ACCAGGAATCA GGCGGACCAA GAACCAGGAA GCAGAAGTGGT GAGGGCCAGC  180
GGCCGAGCGA GTAAACAAGA CTCTTCTCAG CTAAAGACCT CATGCTCTAC  240
AAATTTAGCA AGTCCGTGTA CGAGCTCTGAC ACCATCGGCA GCATCGCATG TGCTTCCGAG  300
TGCCCTATCG CCGGGAAATCT TGCTCTGCTG TCTGCTGCTG GTCTCTGCTG GACGCGCAAG  360
ATGAGTACGG TCTGGCACTTG CTTGAGGCTG TCAGAGCTGTG CGAGGAGGCTG CTGAGTGAAG  420
CTCTATCTGAC CGGCTGTACAA CCCCCAGATAA TTCTCCGCGG GCGGAGGCGCA AGAAGCTAAG  480
GAGCCTCTCAG ACAGGAGCTCG TGGGGGCCCC CGTACATGCA ACAGGTCACT GTAGGGCCCTT  540
GTCGGCTGCTG GAAAAACCCC GTGTTGGGCAA CTGGCTCTGCA CAGTAGTCTA CAAAACCTCC  600
TGCAAATCTCGTGAAGGTGGAT AGAGAAAAAC GTCTCAAGGCA GTTAAATTGCT CGAAGTGAGA  660
ACCATGAAAA TTTACCCAAA AATACCATCTT GCGGAANGAA TTCAGGAATA TCTGTCTCCC  720
GCCGCTCTCC CTCGATGCC CCAGGGCTAC AGAGCTCGG GCCCGGACCC CCTCTGCTCC CAAACCAAG  780
GTACGGAGTCC CGACGGCTCT CTTCTCAGAC CCCCCAGGAC CGAGACCACC ACCCGCTCNT  840
CCNTCAAGCC ACCAGGCTCA CCCCTCTCCTC CNTAGAGCC AGAGTGCTCA AAAAACTGGG  900
CCNTCAAGCC TGAGCCGCAC GGGGGAAAGG CCCAGGCACC TCGCTCCCTA GAGTGCCAGG  960
TCAGACCCCG GGTTGCAAGCC CCCACCGGTT CTCCGGACAG CCAGACGTNC AGTCGGCCAG C 1020
TCAGACCCCG CGTGCCAATG CCACCTGAAG TTCCCTGTAA CACAGTCGCC CCTGGAGGGA 1080
NGTTGACCCG ACCTTACAGG TTGGTTTTTC ATTTTTGTGC CTTTCCTCCAG AGATCCAGAA 1140
ATAAAAATGA AGAAGAGGCA AAAAAA
```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 205 amino acids
   (B) TYPE: protein
   (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
```
(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:

GCGCCTCGCC AGCGCTGCGA GGCAGACACTG GTCATGGAAA AGCAATTGTG CTGCTCGG GC  
GTCCTGTCGC ATCAGGATGT GTCTGTGACA GCCGCACACT GTTTCCAGAA CTCTTACACG  
ATCGGGTGCT GCCTGCAGCC TCTTGTGCAG TCTGACACCA CTGCAGGCTC TCACTCTTG  
TGGACGTCC CTACGGGCGA AACTCTCTGC TCGCTTTGCT GCTTGCAGAC  
GATGCCGTGA TCTGCCAGCA GTCCAGAGCT GTGAGGCTTG GAAAGCTTGA GAGCTTTCC  
CAACCCCTGCC AGCGGGTTCG CACTTTCGCA ATCTCCAGTG CAAAGAGCTC TCGCTGACG  
CTCACTGGGT GCTCAGTACT GCTCAGTCGA TACCGGGCA AACTTGATAT  
CACCAGTATT GCTCGGGC AGCACTATTG CATTACTTG CTGACTTGCC  
ACTAACCATG CGACTTATTTA GCTGAAATTTA GCCGCTCTTG GCTCCACACA TCTTGGTATC  
CAGTTTATCC CACTTGGAATG AAGATTTCCTG CTTCACTTG CAGCATTCC ACATAATTTC  
TGACAATCAT AAAGGAGGAA ATCTACGACT CGCTCATCTG CCGCCAACAA  
TTATATATATG TGGATCTGTC CACTTGCGG CTTTCAGGAG CTTCCACGGG TGCTTGTCGA  
GACTATATG AGAACATATGG TCTCTGTGCT CATTACCA AAGCTTTATA ATCCCTAGTC  
CTGACATACAG AGAGGGCGAAG TCTACAGTTC TACCCTGATT GTATGCTGTC CATTACATCA  
ACAACCTGCA GACTTTCACCA AGCTTGAATC TCCGCTGTCG CCGCTTGGGC  
GAGGTGAGGG AGAGGGGCAA TGGCTCAAATG GAGATCTGTCG AGTGGTAGACA CATTAGTGC  
108
**(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
Val  Leu  Ser  Ala  Ala  His  Cys  Phe  Gln  Asn  Ser  Tyr  Thr  Ile  Gly  Leu
  1  5     10   15
  20  25   30
Gly  Leu  His  Ser  Leu  Glu  Ala  Asp  Gln  Glu  Pro  Gly  Ser  Gln  Met  Val
  35  40   45
  50
Glu  Ala  Ser  Leu  Ser  Val  Arg  His  Pro  Glu  Tyr  Asn  Arg  Pro  Leu  Leu
  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  Asl  Gln  Cys  Pro  Thr  Ala  Gly
  85  90
Asn  Ser  Cys  Leu  Val  Ser  Gly  Trp  Gly  Leu  Leu  Ala  Asn  Asp  Ala  Val
  95
 100  105
Ile  Ala  Ile  Glu  Ser  Xaa  Thr  Val  Gly  Gly  Trp  Glu  Cys  Glu  Lys  Leu
 110
 115  120  125
Ser  Gln  Pro  Trp  Gln  Gly  Cys  Thr  Ile  Ser  Ala  Thr  Ser  Ala  Arg
 130  135
 140
Thr  Ser  Cys  Cys  Ile  Leu  Thr  Gly  Cys  Ser  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:**

```
CTGGAGTGGCT TGGTGTTTC AAGCCCCGTG AGGAAGCAGA ATGCACCTTC TGAGGGACCT
```
(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:

ACTAGTGCGAG TGGGGTGGAA TTCCATTTGG TGAGGGCCCA CACAATCGGC ACCCTTAAACA 60
TCACCCAGGC CCCGCCGCGC CCGTGGCCCA AGCCTGGCTG TAACGACAGT ATGATGACTTA 120
CTCTCTCTAT CCGAAACTAT TTATATGATA TTAATGATAG CTTCTTCTTGTT TATAATGCCC 180
TGATTAAA AAAAAAATA 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:

TCCYTTTTKT NAGGTTTTKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACCTCYNGG 60
AATGTTTAGG CAGTGCTAGT AATTTCTCGC TAATGATCTT GTATTACTT TCTTNTACTCT 120
TATTTCTCTCT TTCTCTCTGAA GATTTAATGAA GTTGAANAAAT GAGGTGGATA AATACAAAAA 180
GATAGGTGAG TAGTTAATGTC ATCTAAAGGC AGATGAAAGT GTTTATAATT TACATCTTCA 240
AAATTTTATG AATTTAATAAT TACCTAGGCT TAACTAACCT ATGCTTTGAAAC 300
CTATCTCAGTT CTCTCTGTAG AAAAAAATT AAAAAAATT AAAAAAATT AAAAAAATT 360
ATGATGAAATA TTCTATATTC TAAAGCTGAG GAATATACAA AATTTAAGG AATATGGAAG 420
TTTATATCCCG AGGATATTGK TGTCTTTTAT ATGAAATATT CACCGATGAT AATGCTGACT 480
AAAAATTTT GTGTTTGAAT TGYATATACAA AAGACAITAT AAATGCTTATAC 540
CAAAAAATAAAAA 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 GROGATGCTA AGGSCCCCRGA RWYGGTTTGGA TCCAACCCTG GCTTWTTTTC 60
AGAGGGGGAG AAAGGCTICTA GAAATTTAGG KGACATTTAGY TGCTGCTGGG GACACCCCTG 120
CSTCCACACAG AATCCCGAGT AGCTGGCACT AGCCGACAC AGCTACTGAA GACGGCCCTG 180
TTWGGAAATTC AGCCTTGGCA CTCAGCTAGA AACATCTCCTC ATGATGACTT TCTTTAGCTG 240
CTAAGGTAA AACTTCCGAC CCGARAAAAG CAACTCTGAT AATCTTTAAG ATGACTCTTT 300
TAATGCTCCTA AGGCTCTTTC CACCGCTCCT ATGGAGCCCTG CYTGAGGTTT GATAGGAANT 360
NTTCCTTTGAC TTTCTTAAATA AARTCTCTAT YCATCTCTATG TTAATATTGG TACGCACTARA 420
(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:

AGGCAGGACC AGAAAGCTAA GCAAAAGCCC AGAAGAGCTG GCAGTGCCAC CACTGCGGCC
AGTACCCAGTA CCAATCACAG TGCCAGTGGC AGTGCACCCCA CAGTGCGGTT CTTCAGTTCT
GGTCCGAGCC TGACCACCAAC TCCACACATGG CAGCTTGCCG TGAGCTCTGG
GCCGCCACCA GTGGCCGCCTG TGCTGCCCCGT GCTTTCCTCT AGAAGTGACA TTATAGATAT
TGTTAACCTG GCCAGCTTCT CTTCACCAGC GAGGTGTGAT CTCATCAAGA CTAATCAACA
CAGCACTCTCA GAGCGGCGACT AATGATCAGT GTAAGTGAGC ACTGCTGATT ARAATCTATTT
GCCATTCGAA AAAAAAAAAAAA AAAA

(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:

ACCCAAATGG GACCGCTGCG TTATAAGCGA TCATGTYYNT CCCGTATKAC CTCAACCGAG
AGGAGATCG AGTCTTATCG CGAAGAATAT TGGCACCAGA GGGACAACAG ACCTGCTGAG
CCCATCTGCG TGCGTCCTCC CAGATGACA AATACCTCTG ACAACGATAC ACCATCAAGA
AAGCTCTGTG CTGGCTCCTG ACCACCCACG GCGCCCTTCT CGCTTCGGG
TGAGTCTCTG TTGCAGATGG TGGCGAGCTG TACCCAGATC TCTGCTGATG GTGGCGATGG
ATTACCGCTG TGATGGCGAGA CAGCCCCAGA AAGGAAACAC ATTTGACTTT
TTTTTTCAT AATTTAAATT ACTACMGAGW TATTWMAWW WAAATGAWTT GAAACTST
TAAAAAAA AAAAA

(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 TATGCGCGKG CCCACCGGAG GGCCTCTGAG GCCGGCAGGAC AGTGGACTTT
CAATGATCCTT GGCGCGCTGC CTTCACCGTGC CTCCATGGCA GATGCTGCGG CAGATTCCCC
AGGAGGCATG GAGCGCGGCC CTCATGGGAC ACGACACTG YTCCGCTGGAG CGGCGCTTCT
GGCGCACCC TCTGGCGGCC CAGCGCGGCA CTGGCGCTTG CGCAATGCCC AACCTGGCTG
TGCGCGCTCT CCTCGCTAG TCCCGCTGCG TGGCGAAATC CTCCTGCTGC AACTGCGCTA
YTGGCAATGT CGATAGCAAC TCGGCGAAAG TACGCGGCAAG CAGCGATCTC TACTGGGAG
GCGCAGCUTT ACGCCCTCAT CGCG
(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:
GAGTTAAGCT CTCACAACCC TGGATGGAGT CGTCTGAGST GGCCTCCGAC TTCTAAGCCG  60
TNCATCGTAT ATACTGTAAG TTTGACCACCA CTCTGCTGCA CTGTTGGGCG GCNTAATATT  120
CCAGAAGAAC CTCAAATCAAG TGACCGTCGA TGAAACCTGT GGGCTGTTTC TTGCTTCGGC  180
TGCTTGAGGA AGGATCTCCC AAGGAAAGTG CTCGATCTTC CCCGACTCTG TGTGAACCTG  240
ATGGCTGAGA TGTTCTATGG CAGCCGAGAG GTCTTACCGC CTCTCCGACA TGAGACCGAC  300
CAGCCCTCTG ATGCGTGGGA CGCGCCGGAA GAGGCGGGAG CCTGAGGAAG GGAAGAAC  360
CTCCAGCGAG TGCTGGATCA CGAAGAGGCC GCGGCGAAAG CATTTTAAAG ACTGCACCCG  420
GTGGAAGAAC AGCCCGTCGG CGCGGAAGCG GTCCAAAATGG GCAAGCTGCTW  480
TCTTTTTGAC ACACAACAAAC GTAAAAGCGA TTTTGACGCC CCAGAAATTT GTCACTACCC  540
AAGATNTCGC ACAGCTCACTA TCCAGTTGGG ATTAAT  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:
AAGATCTTCG TCCTGAATGG TGTGTAATAT CGATCCGTAN TTGTCTGCTG AGAATYCATW  60
ACTKGGAAAA SMACAATTAAG GGCGGAGACA GTGTATTAAG AATTCCACAT AGTCAACACT  120
TTAAAACAGTG TGCCATCTCG CTCCCYNNAA TTTGTCTCAC CGATCTCGAC AAAAAAGCTA  180
TGCTCAACCTG ACACCTGTIA AAGGCGGCTG AGCTTTTTGGATCAATGC ATTTTTTTTTT  240
GACACCAGGC CGAAAAGAAC AAGCTTAAAC AGTTATYYAAAT TTGTGCAGCA ATTTACCTTC  300
TTCTATGGGAG AGAGCCATTG GTATTAAAAA GCAGAATGCA TAAATTGAGG CTGgyggggc  360
TGATATTGGTC GCGAGGAAGT AGCCCTTCCTA TCCTCCAGAC CAAAACCTCC TTTCCATATT  420
GGATATNNAA NAAAGTGTWAG TCTCTWACAG ATGGGATGCT TTTGGGCAAC TTCTGTTCTCG  480
AAGATCTTCG TGTTTTTTATG CACCTGTCAAC AAGGAGCGTC TTTCTTCTCC ATGGC  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:
AGAAACCGAT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGGTTGCGTG  60
TGGTTTGGCG CCGATATTAT ATACGACGGC ACATCTTTTT TACTTGGTGA AAGGCTTATTG  120
CCTCTTGGGT ATCTATACCT GAAAGGT TTAATGATCGG ATCAATGGCT TGGGCGACCT  180
TTGCTTGATG TTGGAAATGCT ACTGAGAAG ACACCTNTNT TATGACTCAA TTTCTCTNTG  240
TTTATGGGAC ATGAAAGGAA TTTCCCAACN ACAACACTNA CAACACTTCC CTGCGAKARG  300
GGGCGGAAA AAAAAACCTTG AGCAGCCTAA AAAACATGAA CCCTGTGCAG AAGCTCAATA  360
ACAGAAATWR GGTATATAT TGAARNACAG CATCATTAAA RGTTTWTGTKT WTTCTCCCTT  420
GCAAAAAACA TGTTACGACT TCCGCTTGAG TAAATGCAAG TTTTCTTTTT TATNATAAAA 480
CTTGGGCTTC ATTACATGT TNNAAATGCT GTGGTGGGCC AAAAAATGTA AATGATGGCA 540
CTGACTGATA AGAAGTACA AATAGCAAGT TGCGCTAACA AGCAACACAG TAAATTTGAG 600
ATGCTTGAAT CAGAATGCTG AATTTCATTATA TAAATGTTTG CTTAAATACG CTTTCAACTA 660
TTTTCTCTGT TTCTCCAGAGC TGAGATNTTA QATTPPTATGT AGTATNAllA GAAATAATAC 720
GAAAATAATA 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 TTTGCGATAN TCTACTATTTAT ATGGCAGGAN GTGGGGGTGTG ATGCACCGCA 60
CAGGCGGCTT ATANGAAAGCA AGAAAGAAGAG AGGGAGGGCA CAGGCCCTTG ACGAGCAACA 120
AGGGCGGCTT CGGTCCTGCTC TTGCTCTTGAG CAGGGGGGCA CACCATGGGGA GACCTCCCC 180
AAGGGCAAGG CCACAGGCTC AGGGTGGGGA ATAGCGGGGGA TGAGGTGTGT GCTTGAAGAA 240
TGATAGCGGCA CGGCGCACCAGC TGAGCCGCTGAG CAGACGTNGA TTTGCGACCC 300
GTGCATTGTGC CCTGCCCGAG CAGGGCCTGN AATCGGAAAAG GACAGGAATGC TTTCTTTTT 360
AAATTTGCGT GNTGCAAGGA AAGGAGANNTT TCCAAATNTNG GCTGNCCTTG GGGGNCTTT 420
GTTGGGCGCA GCCCGCCGGT CAAAAANTNT TCCACCCNCTT CCNAAATGT TGGCGNCC 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 TTTAAAGACAG TGTCTTCCACA CAAAGATTAA TTAGAAGAAT AGTGTTTGG 60
AAAACCTCGG CATCCAGTGA GAACCATATT ACACCAACTG AGACTNGGAA ATGNNCTCCA 120
AAGTGCTGTG CAATAATGAC AATGGAGACAT TCGAATCTCA CACATGCGAC AAAGACCAAG 180
CGCTTTGGAC ATACAGTGA CAAGGAAAAAGG AAGGGCGGGG ACAGCAGTGA AATTTAATT 240
TAAGTGACTCA TCACATATAT TTAGAAGACAG TCGTGGTCTCA GNGNAAAAC ATGAGCTGNT 300
TGAAAATTTT CATGTAGTCG ACAGCAAAAG AAGAAGANNTT CGAGTGTGAG GATTNCTCTA 360
CTACATCNAC CTGAGCATGT GCCAAAGAAC AATAAGTTNA AAACAACNGGT ACAAANAA 420
TCTGATATTN ANTCCACCT CCGTACNGAA AAATNTTTNT TATACACTCC C 471

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGGAGTA AGGTCTGTTC TASTGTGCGG CTTGTCAGCC ACCAATCCTA ACAAAGTGCT 60
GTTGTTTACT CACTGCTGT GAGGTTTTTA ACCCAGACCG TATCTTCAATA AATGAAACAA 120
ATTCTTCACG AGTCACACCT TCTAGGACCT TTTGGATTC AGTATTAGATA AGCTCTTCCA
CTTCTTTTGT TAAGACCTCA TGCGTTAAG TCTAAAGTTT TGATGAAAGG AATTYAATTG
CTCTTTCTCT AACAAAGTGC CTCTCTTCTGG GTATTGATCT GAAGAACCCCA CCAAAGTGC
CTCTTGTGAT CAATTGGATG TTAACTCTTT ATGAGCATTG TTAGACCTGT TAAATCTGCA
AACAGTGCATC TGTCGGAGAA GTGTGCGTAA ATATAATCA CA

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCCTCGAG TCAATAATCT TTTGCTGAGG GCAGCAGACA TATNCAGCGC CATAGGNAACT
GCCTCACCCC ACATGGGAGG AGCATCCGGT AGNTATATAG GCATCTCACC TTGCTCGAGAC
ATGCTCCCC GATTACCTGG TGCCCTGAGT YACACACAT CATCTTCTAT CATCTTCA
CCTTTTGTGGA AAAACTCGCA CTTTCTCAGA ACTACAGGAA CATACATGTAC TAAATCAACC
ACCGAGACAG TGGGAAGGTA ACAAAGAGGAA YTCCTTCCAT TTGCTTCTTG CCTCCGCGAC
CAGTTGCTG TACTACCCGG CTTGCTTGATC TCCCATGACG TCTGACTGCT AAGTCTCGGA
TACAGTAGTCG AAAAGCTTTC TCTTTTGATT GAAAGACGC TTCTTGGTGAC
TGCTGACGCAG TCTTCACCG GAAATCCCTG GCCCAGCCAG CCGCCCGTGG GCGCCACGAG
AAAAATGGTG TCGAGGAGG CAAGAGGACT CCGCTTCTGA GGAGCAGCAT

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGGCGCA NATCCCGACG CGAAGATGCG CTGCCGACAG TGAAACGCTG TAGCCGCTACG
GGTTCCGGCTG TAGCCCGACG CAGGCTCCAC CGGCTGGAAG CGGCTGGAAG TCGAGCTCCTT
CCCGAGCCAG GCAAGAGCGG GGCCGGTGGA CGGAGAAGCGA TGGCTGGTGAG GGGTGAGCCG
TAAATGTGAC GAAAGAGGCT ACCACCTCGG GGCAGCAAGC GATGCCCCAC ATGGGTGAGAC
CTGGAGGACA ACGTCCGGAG GGTGCTGACG TTGGGTGGGC TGGGCGTTGG CGGAGCCAG
AGGAGCCTCC GCTTCTTCTC TGCGTCGACG TCGAGCTGCT GGCCTGCGAC CTCGGCTCCG
AGACGCCAG AAAAGGCTCGT GAAGACCGCA CAGCTACAGG ATGGCAGCTG TGGGTGAGCTC
CAGAGATGGC ACGGGCTGGA CAGGAGGCTG TGGGGTGGG CCGCCCGG CGGAGGAGCG
CTGGGAGCTGGTTGCGCTG TTTGGCGAGG TTTCCGCGACC AGCGGCTGCG CAGCTGCGCTG TATCAAGCG

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGCGCTGG ACCTTTCCTC GCATGTCGCT TGCTGGCCAG GAATACTTGG GCAAGCAGTT  60
CCAGTCGGAG CGAGCCTGAAG CCCTCTCCTCC CCCAGCTAA GCCCTCCCTC GCTGTGGGAG  120
TCCGGCTCCAC TGCAAGAACG GTAATGGGAG CAGCTGTATT GGATTTGGGA GTGACACTTG  180
TTGACTTTTAA CTGCTGGATT TCCTCCCTTA TATAGCTTTT CCCAATGCTA ATTTCCCAAC  240
AACAAAGCAAC AAATAACAGTT TATCTGTATT ACAATGACGT ATTCTGCTATG  300
TAAAGAAACAT ATTAATGTTA CATATAATTC TGCAAATTCC TGATATTTATT GCTNTCTSTGG  360
AAATAAATAT AGTAAATAAA GGTGGCTGACT 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 GTGTKAGGGXY CAGTYTGCGA GGGSGAGAAA GAGGCGAGGG GAAAGGCCGTG  60
CCGAGTCTAG GCAGATGGTC CCACCAGTGAC CCCGAGAAGGC STGGGGTATA GTYCTTGAGC  120
CCCTCAAGAG AAAGAAACAC TGGTCAGGGA ATGGAATGAG GGAGCGACCC TAGAGCAGCC  180
AAAGGAGGAGG CCCATCGTGG CAAGCGCTTG CAAGGAGGAA GGAAAGGGGC TCTGGTGCTC  240
CCCCGAGAGG AAAGAGGCCC GTGGCTCGG GAGCAGACCC CCCTCAAGGG TACTCCGCAC  300
CAGATCTGAG CCTACAGAGG TCCGCCCTCA CCCCCCGACTT STACACCCTT ACAAGCGGACT  360
GCSCGACACG CACCCAGAGG AGGCCGCCCC GGTGGGGGAG TGCTCTCAAG GARTCGCNGG  420
GCAAGTTGCA CATTCTCTGCC CAGAAGGGGG GAAATCTTCC AATAGAGGGGA CGARCMSTT  480
GCTNNNNAAAA AAAAAAAAA AA  502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTATCTTGG TTTTCAATGG ACCACATTGAT GGAATTCATT TTAGACATT GGATCTCTCC  60
CCTCTGGAAG CTTCTGGCAG AGCCTGGATG GTTTTGGGA GAGATTAATAGG GGAATATTTT  120
WAGCTGTGTK GAGTGGATGS GACCACTGCG ACCCAACATG TCAATATGAA AACYAWATGG  180
ACTWATTTAT TTAATTGTGG AAATGATATAC AATGAAATATG TGTGCACTAC TGTATKACT  240
AAGTATGAGG AAAGCAGAAG GTAAGATATT TTTTATAATT GTAAAAATT GATGACATTG  300
ATTAATGGGC AAAAAATGGGA GTGTAATGTT TGTTTCCAGT AATATGACCC TTTGTGAACI  360
TCGCTGCTGT ATTATTTTGA AAATGATATCAAAATTCTTT AAATTAAGAR AATGATAGTTT  420
WATATTATTT TCTAATATT CTTTCTCCTGT TTTGCUTAAT TTTGAAAGAA WYGCAATTG  480
TCTTGACAGA ATATGCATATG ATGTTGGTGG AAGYAGATGG ACCACACATCC CTATGAGTTT  540
TTCTTAGAAT GTTAAAGGTT GTAGCCCTAT CNAACATCAAA AGAAAGGAAT GACACATAC  600
TTGCAACTCA GCCTGAAATT TGCCATGTCT TTTCAATTTCC AACCTTTATAA ACTAGCAAAAN  660
AAGTTG  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:

TTTTTTTTTT TTGTTTTTTG CAGAAGAGTT CCTATTTTATT TGGATGGATTT TTTTCAAATAT 60
ATGTTTATTG GAGCGTCTCA TTTACAGTGA AAGAGATCAG AAGTTTTATG CATTTTTAGG 120
AAGGCAAGTT CCTGAGCCAT GTGGAGTTTT ACCTCGGTAGA GATACCGAG 180
AAATATATGC NAACAGGAAT ACAAGGATAT TACTATTTCC AAGATATTAA CCAACTGCAA 240
CAGATGATCT CCCTGAAGCT TACTTCAATCC AAATATGCGA ATANAGTCAA CATGGTATAC 300
ATCCTCTCTG GATATTTGA TTTTTAGAA AAATATTGAA TAGTGACAG GAGAGCACT 360
TGCTACAGGA TACACNAAGC CAATGCTTTCC TTACCATAGG CTTTAATCCA AACTTTGATC 420
CATTATCATC GCACGAGGGA AGTCAAGTCT AGCCTGGGAC ACGTATTTTT GTCTACATGTG 480
AMCNTGGCTT AA

(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:

TTTNTTTTTG ATTTCACTCT GTANNAANTA TTTTCAATAT GTTTATTANA AAAATATNAA 60
TGTNTCCACN ACAAATATN TTTNATNATAA CAGAGGCACN CACACCGAT ATACACAC 120
TGAGTATATT TTGAAAGGGA CAGTTTTGAA GTANAACNAT ATGAGCGCNC ATANACNAT 180
TATATCAGGC TTGATTTGATA TTGACCAAGA ATAAACCTGA GTGAGTTAC AAGAAANAAAT 240
NATATATATGC AATCGATATT AAGATACCAA ACGACATCTAC ATGCATATG CATCNTGATG 300
GGTNGGTGC CTNTATCGCTG ATGACGCTCC ATGACCAAAAG ATGAGGCCNTA 360
AGCATTCTAG TACCTCTACT CCATGGTTAA GAAATCGTACA TTTATGTTTA CATATGATCA 420
GGGTAAGATG TTGGTTAAGGT NAATTATAGG AGAGGCTCAG CAGAAAATTT TGAATNCAA 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:

AGIGACCTTTG CCTCCCAAAAC AACCCTCTGA TCAAGTTTTG GGCACGTACA ATCGACCTA 60
TGCAAGCTCC TGCAATCTAT TGCTCCTACTA ATGAGACTCG GAGGGGACCA AAAAGGGGCA 120
TCAACTCCAG CGTGGATTAT TGGAGGCTTG AAATACCTAT CCTAATGCTG CATGTGTGCA 180
AGTGATCGAT TTTATCTTCAC GGAATGAGCA CTGCTCTCCAG AATATCCCTG TTGACCTT 240
TGAAGCCNAC TGCTAAGCAG CGTGGATTAT NAGATAGAA ACAGAGAAAT AAGATCNTA 300
AAATATACCT CTGNGAAAG AGCGTTTGNG CTGCGGCAAC TTCCCATTGAA CTTCTCTACT 360
ANGAGCTTTA AGAANAAACT ACCACAGTTN TGIGNTATACG TGIGCGCGGG CCGTTAATTG 420
AAGCTGACG NCAACCTTTGT GAAATANANT TCTGACGCGN TCTGACACCTT GCTCTGTGC 480
GA

(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:

CGCCGCGACA TGCAACTCCA GCTGGGGCGG TGCGGACCAG GATTCTGCAA GCAGTGGTC 60
CGACTGCGAC GACGGCGGCC GCGACAGTCG AGGATGCGAC GCAGGGCGGGT GGCTTCTGCG 120
AAGCTGGGAC TGACGCGGCAC GAGGTGGTGT CACGACCCGAC GACCTGACGG CGTGCGGGGGA 180
CAGCCGCGACAGAGGCGGG GAAGCCGGAG GGCTCGCGGG AGCCCGCTGG GAAGGCGCGCC 240
CCAGAGAGATA CGGAGGGCAA GTGGCCGCGC CCAGAGAGATA CGGAGGGCAA GTGGCCGCGC 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 TTTTTGATAC TACTGGGAGC ACAGCACGTC ACAGCAACAG TTATTTGCA 60
GCTACGAGGG TAAAAGGGTAA GGCTAGTGGT ACAGTGTCCG GTCAACTCCG TTGTGTGCTG 120
TTGATTGGTGT TGCTTTTATA GGCGCGGCGT GCAGTGGGGG AACACGCAAG ANAATTAACA 180
TGGAGGGGCT GCACCTCTCG TGTAGACTGG GCTGACGAGC GCTGGGGCTA GCTGACTGCTGG 240
TCTGAGGCGG TGAATTTTCT TGTACCAAGG TTAATAGGGCT TTAATAGGCG CTGGCAGATG 300
TTCAGGAGGAA ATATAGGTTT GGAAGGAAAG TCAACATCTAA AATGGAAAG GAGGCGCGGCA 360
AAAAGGTGGA TGATNCGACG CGAGAATTAT CGGGCATAT TTACCATTAT CCTGCGGGCA 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:

TTNNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TGGCAGTAAA TCGATTAAA TTTCAAAATG TCTAACAANT TTNAAATNCC CATTATACNG 120
GNTATTITNCAAAAATCTAAA NTATTCTAAA ATNTNAGCCA ANTCCCTTAC NCAATNNAAA 180
TACNCCNCAA AATCAAAAT ATACNNTFCT TTCAAGCAAAC TTNNTTACAT AAATTAANNA 240
AATAATAGCG GCTGKTGTGTT TCAAGATGAA ATATACCTAA CACCGAAAC ATNTTNNAAA 300
GGAACTAAAA CATACNCGGA AAGTTTAAAG GGAACAAACG ATTCNTTTIA 360
CAACANCNCC NATTATAAAA ATCATATCCT AAACTTTAAG GGAATAATATA CTTCAACNG 420
GGATTTAACAT TTTTACTNCQA CTGTTGTTAT TTTTTTANAA CATTGTNTT GGGCGCAACA 480
CAATGNAATN NCCNOTNCNC 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 TTTTTTTTTA CCCCTCCTCT ATAAAAACA AGTTACCAT ATATTTTACT 60
TACACATTT TATTTATATA TAGGTATAG ATATCACAAG GGCAGCTTTT AAAATCAAC 120
TAAAAGGAAA CTGCTCTAGA TACATAAAT TTTAGTAAT TGGTAAAATC GGCTAAGGT 180
GAAACCTTCT TTGGACTTAA ATTTTTTGAC CTGGAACACT ATCCAAATTC 240
ATTTTTTCTG TCTTTTAAAAT TATCTAAATCT TCCCTTTTCT TCCCTACCTC AAGCTACATT 300
GCTCTCCAG CGCTATTTTCT TACGTTCTAT TCTACATATG TAACTGGCTT TTCTCTAAA 360
AGGGAGAAAC GAAGAGAGA ATGACACACA AAAACACCAT TTTATATTTA TATTTCTACC 420
TACGTATATA AAATACATTT TGTTGAACGC AGCTCAAAAG AGGCTTAGA TCTTTTATTG 480
TCCATTTTAG TTCCTCAAGG ATATAAAGG TGGCGAGATT CAAAAGTTTT GTGAACATTT 540
ATTCAAGAC GAAATTTGAT GAAATCATT CTCCATCTTT CTG 583

(ii) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:204

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTTT TTGAAAAATGA GGAACGAGTT 60
TTCTCACCTC TACATTACGT ATGGAGAAGA AGCTCACTTTG CAGCTTTAAA ATACACACTA 120
AAATCTCTAT GCTATATCAT ATTTTAAAGT AAACATTTGA GTCATCAGCT TATTTTCTCC 180
TGAAGGAATA CTGTCCATTT TTTCTCACTA TATAGTTTAA TCAAGTCTA CTTCCGAT 240
TTGAGAGGTT CTGGAAACGA TTATACATATA TATCTCAACG GAAAATGCAA TCAAAACCTT 300
ATTATCATGC AAACATAGAAA ATATAAGTTT TTCTGCAATA AGAGAAGAGA ACAATATNAG 360
CATACACAA CTGCTCAAAAG GTGTGTTATT TATAATTCAT TATAATAGG TNGCAGGAGQ 420
CTTAATTCAA TCACATTACT NGAAGAGGCAA TAAATACACT GAGTACCAAT TAAATATCC 480
AAAAATTTA AAGAAACATT TTTGAACCTCG GTTAATATAG CTTAATCATT TTCAAGACAT 540
TTATTAGAA GAAATTTGAT GAAATCATT CTCCATCTTT CTG 589

(ii) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 545 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO:205

TTTTTTTTTT TTTTTTGCATG AATAACAGAA CAAATATTCA TTTTATTTA TAAAATTCACT 60
AGAAAAAGTGC CTTACATTAA ATAAAAATTT GTCTCTCCTTAA TGATGACAGG GAATGAGTA 120
TNGTCTGGAA CAACTATATT AATTGAGAGA AAATACACCA AAAATACATT AGTAAATTAT 180
TTGAAGACAT AGAAGCTGTA AGTGAAGAAA TAAAATTTGA CTTCAAGAAC TCTGAGACATT 240
AAAAATCCAA TTTACAAATCA TGCTTTCCCT GCTTTTTTTT TGTGTGAAGAT 300
AGGAGGGTGTC AGCTGGAAC CAACACATCT TGGAGATAC ATACCCTATT GATAATTTTC 360
TTAGTACATT CTTAATACGT GTGGACATGA TGGACAGATT TTCTCTTCTAT TCACATTCCT 420
AAAGGGGCNGA NGAAAGTGAAG AAAAAGACA AAGGATTACG CAACTCTGTC TTCTATNGG 480
AAGGATTAGA TATGTTTCTT TGGCAATAAT TAAAATATA ATAAATTTCA CTTACTAGTGA 540
AAACCC 545

(ii) 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:

TTTTTTTTTT TTTTTTTGTC AACCGGAGCTT TTTTTTTATT ATTAAAGTCT GGTTGCTCAATT 60
CATTTATAG CTCGGAGAAT CTCGTTATTT AATTAAGGAA ATGTTTATAG ACACTGTNA 120
CAATTTATAA ATGATTTAGC TCATTATTAG CTGATATATAT TTCTCTAGAAG AGTCATTTGAT 180
CCCTCTCCAC ACCAATATATT GAGAGGAAAC CAGTTTATTG ATTTTTATAG TAGTTTATAC 240
ACTGCTCAAC ACCGATATCT GTGTCCTGCA ATACGTCTCTG TTACGTCTCTG TAGGCTGACT 300
TTAGTCTCTT TTAGCTTTAA AGAGCTTTAA CAAAGCAAGC CAAGCTAACG CAGGATGACTAG 360
TCGGTTGACTA TAAGCTTCTTA CTGCTGATTTT AATAAAGTTT CACTTACATG CAGTGTCACAG 420
AAATCTTCCCA ACCGCTTCACT CAAAGCCGCA TGCCACATTT GTGCGTCTCT TTGACATTTG 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:

TGAATTTGCT AAAAAACGCT ATTTTTGAAA CTGAGGACGT CTTATTTCCTT CTGTTTTAAAA 60
TACTATGAC CATTTACCAAA CTGCCATTAT AAGACCTGAC AGCTTGAAGA AGCTGCTTACT 120
GCTTATTTAG GGCAAGCTGCT GTGATTTTCTT TTGTTATGTA AAATACGCTA ATGGTTCTGA 180
ATCGTCTGAA CTGAGGAGGA TAAACGCTAT GAACTTTCTC CAAGGAGGAA ACAGAGGCCA 240
GCAATGCGAG CAGCTGCAGT TCCAGGCTTG GCTGCTGAGA GCTGCTATCG TGGGACATCG 300
AAAAGAGGCG ACCTGAGGCC CTGGGGAGCC CA 332

(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:

AGGGCGAGGTG GCGGAGGGCG TTAATGTGTGG TTGCTGAATA AAATAAAATAC AAAAAAGACTG 60
GGTTTGTGCC GCAGATCCTC AAGCAGAGGTT TGATTCTCTT CTGTTGAGCAG AGTGAAGATAT 120
TTTAAAGGAC ATGAGGCTTG TCAAAATCGT ACAATGTTAC AGTGAGAAGG GCACACTCAG 180
TCCCGGTGGG TCCACATAGT GCAAAACACAT ATGAGGCTTG AGGCCACACTG TGAAAATCTG 240
TTTCAGGAGA ATCAATTGCTG AATCGAGAAATC AGTCAAGATG ATTTTTTTTAT 300
GTAATTTAAA GTGAGGATCA TTATACATTG CTGAGTACCA GCAGCTTTGCT TTTACGAGTC 360
ATGAGGCGAG ACACTGACAT CAAAGCTGGC CGCTTTAGGC TCGCTGACTT GAGTCTGGCT 420
TGCTCAAGCA GAGAGGCTGT TCACTTGGAC CAAAGCTGCA CCAGCTGACT ATCTATCTCA 480
AAACCAATTG CTTGATACAT TCGTGTAGAC CACGACCTGG CTGAGATAGCT 524

(2) INFORMATION FOR SEQ ID NO:209:
(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:

GGTGGAGGAA ATCCAGAGTT GCCATGGAGA AAATCCAGT GTCAGCATTG TTGCTCCTTG 60
TGCCCCTTCT CTACACTCTCG GCCAGAGATA CCACATGCAA ACCTGGGAGG AAAAGGAGCA 120
CAAAGGACTC TCGACCCCAA CTGCCCCAGA CCTCTCCA 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:

ACTCCCTGCG AGACAAAGGC AGAGGAGAGA GCTCTGTAGG TTCTGTGTTG TTGAACCTGCC 60
ACTGAAATTTC TTTCCACTTG GACTATCACA TGCCATAGA GGACTAATG GAAAAACGTA 120
TGGGGAGATT TTAAGCCATT TATGCTGATTAGTTAGGAGA CTGGGGCAGG GGAGAGAATG 180
TTTGAGGCTT GAAATGGAAG GCTGGGGTTTG TTANATGACG AGGGAGACAG GAGTAGAGCA 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:

ACATTGGTTTT TTGAGATAAA AGACATTGAGA GAGCTCTCCT TAACGTCGACA CAATGGAAGG 60
ACCTGGAACAC ATACCCACACT CTTGTTCTCG AGGGATAATT TTCTGATAAA GCTCTGCTCT 120
ATATTCAAGC ACATACTGTTA TATATATTTC ATGTCCAGTT TTAAGAGGAGA 180
GGGGAGAATAC ATCTGAAAG AGAGCTAGAAG GAATATCTCAA ATGGGGAAAA CAGA AAAAAAAGGA 240
CAAAAGGAGC AAATGGAAGA GCCCT 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 CCAAAGCTGA ATATTGCGCT TCATTATGCC CCANATTCTT GTGGTCGAAA  60
GAGTATTAGG TGCTCAGAC GTGCGGACCT GAGTGGAGGC CTGAGGCTGC AGGCCCGCAG  120
GTTATATACAC TGGCAAAGTG AAGACAACAG GTGATGAGTAT CTCCTGGGCGA  180
TTTAAATCCG TTCCCAATTG ACCTGGGATG TTATAGGAGC CCAGAGAGATG TACAAATTTA  240
CCCCCCACGCT TCCTTATCTCT GAGGAAAGGG GCAGGCTGTCG TAGCTATAAG CGTGGCCACA  300
TTTTTTTTCTTTTATGCTC TTATCGAGA  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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACCTATGGAC AGACGCACAT ATCCAACTGA AAACATGAAAT CTCTCCAGTT  60
TAAAGCGCCG TTCCCTGGAAG AGATAGAAGG GATAACCGAG AGGAAAAGTA AGCCAGGCT  120
CATTGAGCCA AAGGAGATAT GCATCTTACG TCTCAGAACT CTTCTCCAT ATCCAGAGT  180
TTTAAATGCTT GTAAGTATCC GCTGATAANC CATGTTAANA ACAAAATATC TCTCTNACCT  240
TCTCATGCCT  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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAAATC CATTGCCTGA TATTTGCGCTT CATATTCCC AGATTTCTTG ATTGTCAAG  60
GATTAAATGT TGGTCCAGCT TGGGACATCC ATGTTGGACCC TAAGGATGCG AGCCCGCAG  120
TTTATATAG TGGCAAGAT ATTCAAGGCG GCAAACAGAT GTATTGAATT GCCCGCGAGT  180
TGATTTTCTC TCCCGGATGC GTGGAGGATTCT ATTGATCACG CAANAGAGATT AAAATTTAC  240
CCCCGAGTCT CTGTTACCTCT GCTGAGGAGGC CAGTGTTGCTG AGCTATAAGC TTGCCCACAT  300
TTTTTTTTCTTTTATGCTC TTATCGAGA GCGATCCATG CATATGCTANT AAACAAACAG  360
AGTGCATTGT ACAAAATCCG TATAGAAATT GTGAAATATA CCTTACCCTAT AGTGGCACATT  420
ACTTTTGTGCTT CCTCATATA 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

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACCTATGGAC AGACGCACAT ATCCAACTGA AAACATGAAAT CTCTCCAGTT  60
TAAAGCGCCG TTCCCTGGAAG AGATAGAAGG GATAACCGAG AGGAAAAGTA AGCCAGGCT  120
CATTTGCCA AAAGANATAT AGATTTCAAT TCTTCAAACCT TCTTCTCTCAT TCCAAGAGTT  180
TTCAATATTG GCAGGAAGCT GGCTGATACG CATAGTTGAGA AAGAAATATC TCTTCCGACC  240
TCTCTACGCT AGACGGAGGC TGAGGCCAAC ATGGACCATA GGGAANAAA AACTTAGAAT  300
TCCAAGCTGT TTTCTTACAT GAAAACGAGGTT TCTCAACCAA GGTGGAATACT TCTTATACCT  360
GAGGCC  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:

CTGTTATARAC AGAACAATCAC TCCAGAGAGG AGGCGCGGGG CAGAAGAATCT TCCAGTCTTTC  60
CAAGAAGAGGC GCGTAAAGGG GGGCTCTCAAC CTTGCTNNTAA GGGCINTTMC ATTTITTTAT  120
TAAATAAAAAG TNAAAGGCGG CTTCTTCTCA CTTTTTTCCC TNGGCTGAGA AAATTTAAAA  180
ATCAAAAAAT TCCCTNAAGATT NTCAAGCTAT CATATAATCT NTATCTTGAA AAGCAAGAT  240
AATTCTCTCTT TCCCTCTCTT  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:

ACCTACGCTG GTAAGTTTAA AATGTTTATA ATTTACGGAA NAGGAACGCA TATAATTGAA  60
TCTTGCTCTA AATTTTCTAT TTTAATAAGG AATAGCCAA TTGGGCTGAG GGGAAACGTAG  120
GGCAATCTAC AGTGGGACCA AAATGCGAAT AAATGGCGAA GGAACAGACT GAAAATTTTT  180
ATGAAATATC TGATAGATTA TATGTCTCTCA GAGTAGATTT ATAAATTAGCC ACTTACCCCTA  240
ATATCCTCA TGCTTTGATGA 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 TCGTGCGCAA CCCCTTGAGCA  60
CCCCATCAAC CTCCCCCTTG TAGTAAACCTT GGAACCTTGG AAATGACAGGG CCGAAGACTC  120
AGGCTCCGCC AGTCTCTGTT ACCCTTTGTTT TTGTTTAAAGG AGTCAAGGTTG TCTTAAAGAA  180
ANAAAATGAC AGACAAAGGT GTAA  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:
TACTGTTTTG TCTCAGTAAC AATAAATACA AAAAGACTG3 TTGTGTCCCG GCCCCCATCCA 60
ACCAGGAAGT TGATTTCTCT TGTTGTGCAAG GTGACTGATT TTAAGGGACA 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:
ACTAGCGCAC ACAAAAAGGCA GGGTGGCTGT GATGCTTTAC TGCTCTTTTA ATTCTTTTA 60
AAATAAGCAT TTAGTGCTCA GCTCCTACTG 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 GGTGGCGCAA AATAATTGGCT GATATCCCT CTATCTTGGA TTCCATGAGG 60
TCTTTGGGCC AGCGGCGTGC CTACTCTTAG TAAAGCTCTG CTGATGAGGA GCCAGAATGC 120
CCCCACTAC CTTCCTGAC 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 GGGAGGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGCACCCCC 60
GTTCTTCACC TGCCGCCCAA TTCTTAAAAAG GCCATACTGC ATAAAGTCAA CAACAGAPAA 120
ATGTTCCTCG AATTAAGGGA TGATGAAA AAAAAAATAT TAAATTTTTG CATATTTGTG 180
TTCTCTTTTT TTATATTCTGA GAAGATTTT CTGTGACCT ATTAGATGCC GGGAATCTTT 240
TAGGGAGCGA TGATTAGGAGA GCTGTTAGGT TGCTTTTACA TATATCGGG ATATTTGACT 300
CTGATCAA AACAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

(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:
AAAACAAAAA ACAAAAAAAA ACAATCTTTC ATTCCAGAAA ATTATCTTAG GGACTGATAT 60
TGGTAATTAT GGGCAATTTA ATWRRRTTTK GGGGCATTTT CTTACATTG CTTGACAAA 120
TTAAAAATGTC TGGGCCAAA TTTTGATTTT TATTGAGAGA CTTCTTATCA AAAGTAATGC 180
TGCCAAAGGA AGTCTAAAGG ATTATGATTG TCCCTAATAC CTTTTGCGAG TTTGCTATTG 240
TAAAGATTCT GATTTCTCG GAAGACAAT TATATTATTA CTTTGCGGGA GGAAANAGGT 300
ATAAGGACCAC AGTCTCCACT TCTGATACCT GTAAAATAAT CTTTTACTGC ACTTGTCTTG 360
ACCATTAAAGC TATAAGTTTA 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:
CCCCGAAAGC TTCTTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA 60
AAAAGTTTTG GACATTTGAG TAGGGATGT GTACCCCTTTA CTCCCCATCA AAAAAAAAAT 120
GGATACATGG TAAAAGGATA RRAGGCAAT ATTTTATCAT ATGTGTCTAA AGAGAAGGAA 180
GGAAAAAATAC CACTTATCTT AAATGGAAAG CCCAAGGGTT GCTTTAATAC TGAAAGGACAC 240
AAATGGGCCC GTGCCATCCCT CTTCGATAGT GCATGACTTG GACACGGTAA CTGGTGCAAT 300
TTTARACTCM GCATGGGAC 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.


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.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.